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Abstracts

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Ontogenetic responses of physiological fitness in *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in response to repeated cold exposure

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Categories

• Physiological Ecology

Abstract

In this era of global climate change, intrinsic rapid and evolutionary responses of invasive agricultural pests to thermal variability is of concern given the potential implications on their biogeography and dire consequences on human food security. For insects, chill coma recovery time (CCRT) and critical thermal minima (CT min), the point at which neuromuscular coordination is lost following cold exposure, remain good indices for cold tolerance. Using laboratory reared *Spodoptera frugiperda* (Lepidoptera: Noctuidae), we explored cold tolerance repeated exposure across life stages of this invasive insect pest. Specifically, we measured their CT min and CCRT across four consecutive assays, each 24 h apart. In addition, we assessed body water content (BWC) and body lipid content (BLC) of the life stages. Our results showed that CT min improved with repeated exposure in 5 th instar larvae, virgin males, and females while CCRT improved in 4 th, 5 th and 6 th instar larvae following repeated cold exposure. In addition, the results revealed evidence of cold hardening in this invasive insect pest. However, there was no correlation between cold tolerance and BWC as well as BLC. Our results show capacity for cold hardening and population persistence of S. *frugiperda* under cooler environments. This suggests potential of FAW to withstand considerable harsh winter environments typical of its recently invaded geographic range in sub-Saharan Africa. Keywords: climate change, fall armyworm, plasticity-trade off, thermal tolerance.

Integrative taxonomy and biogeography of ants in the genus *Anoplolepis* (Hymenoptera; Formicidae) in Southern Africa

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Taxonomy has played an important role in biodiversity assessments. It provides an understanding of biodiversity components, data that are essential for making decisions on conservation and sustainable use and is also a foundation for phylogenetic studies. Although this field of study has played an important role in identifying and describing biodiversity, the issue of cryptic species has posed many taxonomic challenges. In most taxonomic groups, species with high intraspecific variation are often misidentified when other methods do not support morphological, e.g., genetic data. The genus *Anoplolepis* is one of several polymorphic groups of ants. Despite its economic and ecological importance, and being widely distributed in the Afrotropical region, this genus is understudied. This study aimed to: 1) resolve taxonomic challenges of the ant genus *Anoplolepis* in southern Africa, using morphological taxonomy and molecular data; 2) to understand and update the geographical distribution of species within *Anoplolepis*; 3) verify the existing distributional records for the invasive species, *Anoplolepis gracilipes* in South Africa; 4) to assess the overall changes in ant assemblages of ants collected between harbours and provinces and test the effectiveness of the pitfall trapping and baiting method in sampling ants. Material from various institutions and organisations and newly collected material were used. A total of 16 species were identified, of which 11 species were determined using morphological features and DNA barcoding analysis, with the five remaining species identified using only morphological features. Overall, the distribution of *Anoplolepis* species shows that it is widely distributed across Southern Africa. The invasive species *A. gracilipes* was not detected across all the sampled harbours, nor from any of the material used for this study. However, early detection and eradication of this species should be prioritized as this species is highly invasive elsewhere in the world.

An investigation on edge effect and ground-living arthropod predators in a walnut agroecosystem in the Free State province

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Categories

• Agroecology

Abstract

Since 2000, walnuts (*Juglans regia*, *L*.) have been cultivated in the Aliwal North region. Various pest species including armoured scales, codling moths, aphids and mites have become established on the walnut trees. This study aimed to reveal the predatory arthropod assemblages in the walnut orchard and natural grasslands that may act as natural enemies of walnut pests. *Epigeic* predatory macroinvertebrates were sampled with pitfall traps to determine their abundance and diversity. A total of 2533 individuals representing 33 arthropod families and 105 species were sampled. Ants *(n = 2019, 21 spp*.), spiders *(n = 287, 41 spp.),* and beetles *(n = 134, 28 spp.),* were the most diverse and abundant groups of organisms. Well-known bio-control agents uncommonly sampled using pitfalls, like *Coccinellidae* and *Chrysopidae* were sampled at low abundances. A two-way ANOVA found that the spatial scale had a significant effect on the α-diversity and abundance of organisms between the grassland and orchard interior, and between the edge and the grassland ($p<0.05$), but no significant difference was observed between the orchard edge and interior $(p>0.05)$.The nMDS and cluster analysis showed distinct assemblages for each land use type, though some overlap was observed based on seasonal data. Edge health can be improved through the implementation of habitat manipulation. We found that seasonality had a major effect on not only the presence, but also the abundance of many species ($p<0.05$). Future studies are required to determine the possibility of using any of these predators as biological control agents of pests found on walnuts.

Mountains shape responses at multiple levels of ecological organisation in orthopterans

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

South Africa is a megadiverse country. Here natural communities are unevenly distributed across, and within, seven distinct biomes. In such heterogenous landscapes, understanding behavioural and distributional responses is essential for planning and implementing efficient biodiversity conservation measures. The southern Kalahari, forming part of the Savanna biome, is an arid region of particularly high diversity and endemism. Orthopterans in this system, go through shifts in behaviour, density, distribution and diversity that relate to spatial and temporal environmental changes at multiple scales. We conducted two studies of orthopterans in the Tswalu Kalahari Reserve, focusing first on ecoacoustic variation, and second on how biodiversity patterns change, across distinct vegetation types and topological features. Sampling methods employed varied in accordance with the taxa being sampled, including non-invasive acoustic sampling of calling male Tettigoniidae, and traditional methods such as sweep netting and active searches to sample Acrididae species. In both studies, various ecological drivers of diversity and behaviour were identified, yet interestingly both behavioural (single species) and diversity (community level) responses were impacted primarily by topology of the landscape, with distinct differences occurring across the transition zone between the mountainous and plains regions of the landscape. Mountains and hills thus play a key role in maintaining spatial diversity of both single species populations, and whole communities across the southern Kalahari landscape, and should be targeted as priority areas for conservation beyond the boundaries of protected areas.

DNA profiles of forensic related *Calliphoridae* from greater Johannesburg.

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

Studies on the population genetics of flies can give valuable insight into the population structures of species. Genetic studies have aided in identification of mutations that have led to adaptations within the fly populations. Population studies are useful in determining if the greater population consists of isolated pockets of different sub-populations or smaller fragments of a single larger population as well as identifying locality uniqueness of a sub-population. In forensic entomology molecular studies have been vital in aiding with the correct identification of species and thus the correct application of said species in post-mortem interval estimations. The most commonly used regions of DNA are the cytochrome c oxidase subunits I and II, ND5 regions and ITS regions. *Calliphoridae* were collected over a one-year period using modified RedTop Fly Traps. Collections were done from three distinctly different areas of the city of Johannesburg to allow for representation from the following areas: industrial; urban and rural; the three defining regions of the city. The dominant species collected were *Calliphora vicina*, *Chrysomya marginalis*, *Ch. megacephala*, *Ch. albiceps*, *Ch. chloropyga*, *Ch. putoria*, *Lucilia sericata* and *L. cuprina*. DNA was extracted from all species using the Collins salt precipitation method with overnight precipitation. The COI and ND5 regions of each species were targeted via conventional PCR. After optimization, each species was amplified and sequenced (Sanger). Profiles of each species will be presented. The samples were grouped according to location and analysed to show unique features for each region for each species. Unique heterozygotes for some species will be presented. The potential will be discussed for possible application of these findings to forensic entomology research as it highlights the unique molecular characteristics of the sub population of the *Calliphoridae* occurring in greater Johannesburg.

Intra- and Inter-species variation of *Amblyomma* ticks from southern Africa

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Categories

• Systematics and Taxonomy

Abstract

Amblyomma ticks, known for their bright ornate appearance and aggressive hunting behaviour, are vectors of a vast diversity of pathogens. In southern Africa, 17 *Amblyomma* species are currently documented. Of these species, *A*. *hebraeum* and *A*. *variegatum* have been well studied due to their wide geographical range and their status as competent vectors of pathogens that are of veterinary and medical importance. Studies on other *Amblyomma* species in southern Africa have been neglected, including ongoing debates on the validity of certain species such as *A*. *pomposum*. This indicates the need to revise the intra- and inter-species variation in the genus *Amblyomma*, building on the work of Jane B. Walker from 1987 in which she highlights the dispute about the discrepancy between *A*. *pomposum* and *A*. *variegatum*. This study, therefore, investigated the inter-species and intra-species variation of *Amblyomma* ticks collected in southern Africa, focusing on resolving the dispute about *A*. *pomposum* and *A*. *variegatum* as distinct species. Four tick species were collected from Angola, Mozambique, South Africa, Zambia, and Zimbabwe and were identified morphologically using identification keys. Gene amplification was done targeting the *12S, 16S, COI, CytB* and *ITS2* genes, and MrBayes analyses was performed. Phylogenetic analyses revealed little intraspecies variation amongst ticks of the same species from different countries, clustering together without marked geographic structuring. Inter-species variations were clear amongst the species, forming distinct clusters. With this information we can conclude with a great deal of confidence that *A*. *pomposum* and *A*. *variegatum* are separate species, with *A*. *variegatum* diverging from the putatively ancestral *A*. *pomposum* lineage. We propose mating and hybrid viability studies between the two species to confirm this finding. Furthermore, this study emphasises the need to use multiple markers when assessing species diversity.

Postharvest treatments for quarantine insect pests on citrus: the case of fruit flies and mealybug

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Categories

- Agricultural Entomology

Abstract

On citrus produced in South Africa, effective pre- and post-harvest treatments are required to mitigate the risk of quarantine insect pests for export fruit. For two quarantine insect groups with different modes of infestation: internal - fruit flies (*Diptera*: *Tephritidae*) and external - mealybug (*Hemiptera*: *Pseudococcidae*), research is focused on the development of long duration physical and short duration chemical post-harvest treatments, respectively. For fruit flies, mild cold treatments (above 3°C) are being developed. For mealybug, fumigation treatments using two chemicals: ethyl formate and sulphur dioxide are being developed. In each pest group, multiple species are targeted. On fruit flies, trials were first conducted to determine the coldest tolerant species and continued to determine effective durations for treatments on this species, at 3.5°C and 5°C. For mealybugs, the species that is dominant in citrus orchards - *Planococcus citri (Risso)* was selected for tests to determine the most effective dose of each fumigant. Trials on cold treatments for fruit flies showed that *Ceratitis capitata* (Wiedemann) is the coldest tolerant species on citrus and that treatment durations of 24 days at 3.5°C and 27 days at 5°C effected complete fly mortality. Preliminary trials on the treatment of ethyl *formate* on *P. citri* showed that doses of 60 – 120 ppm, under ambient conditions, for four hours, effected over 90% mortality of eggs. When fumigation with ethyl formate was immediately followed by cold treatment at 5°C for three consecutive weeks, complete egg mortality was recorded. Preliminary trials on the treatment of sulphur dioxide on *P. citri* showed that doses of 530-580 ppm, under ambient conditions, for 24 hours effected almost complete mortality of *P. citri* eggs. The physiological mechanisms underlying cold treatment and fumigant toxicity for the target insects would need to be elucidated to optimize control.

Metal exposure on larvae alters the gut microbiota of laboratory-reared and first filial generation of the major malaria vector *Anopheles arabiensis* Patton (Diptera: Culicidae).

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

Anopheles arabiensis is a major malaria vector in South Africa. It is an adaptable vector and is difficult to control by conventional vector control methods. The gut microbiota is a key determinant of the life history of mosquitoes and plays a role in development, insecticide resistance and immunity. As such, it represents a potential target for vector control interventions. The larval environment is a key determinant of the composition of the adult gut microbiota. Although *An. arabiensis* typically breeds in clean water, the species is adapting to breeding in polluted water. Heavy metals are a common pollutant in mosquito breeding sites, often originating from fertilisers. This adaption of the mosquitoes to breeding in polluted waters could alter the gut microbiota and as such alter the life history of the mosquito. In this study, the effect of larval metal exposure on the gut microbiota of the major malaria vector, *An*. *arabiensis*, in metal pollutants copper and cadmium was characterised using 16S rRNA gene sequencing. This was tested in insecticide resistant and susceptible laboratory strains as well as in the first filial generation. Metal pollution had different effects on the diversity of the gut microbiota within each mosquito strain as well as between the strains for each metal treatment. Additionally, the gut microbiota of metal treated, and untreated strains had changes in the differential abundance profiles. These alterations in the gut suggests that metal pollutants affect the gut microbiota and therefore suggests that the adaptation to polluted breeding sites affects the life history of *An. arabiensis*. These findings have implications for the use of gut bacteria as a vector control intervention in South Africa.

Can changes in agricultural production practices sustain insect biodiversity in agricultural systems to ensure future food security?

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Categories

• Agroecology

Abstract

An additional threat to sustainable food production, besides climate change, is declining biodiversity, especially in insects. To mitigate this threat, we need to understand the drivers of biodiversity decline. Insect biodiversity decline can be mainly attributed to the intensification of agriculture with the main drivers being habitat loss and use of agro-chemicals. We must view changes to more sustainable practices in agricultural management critically to determine whether these changes will sustain insect biodiversity.

Dung beetle assemblages were used as indicators and monitored in different systems, a system not disturbed by agriculture, a conservation agricultural system and a conventional agricultural system. Both the abundance and the diversity in dung beetle assemblages differed between the different systems, with the system undisturbed by agricultural activities having the highest diversity and abundance.

To reach the goal of sustaining biodiversity farmers will have to find a trade-off between economic gain and protecting biodiversity. They will have to decide how much land they can spare for natural areas and still make a profit. Farmers will also need incentives to consider this. We will have to concentrate more on the restoration of habitats in agricultural lands and find interventions to limit the expansion of land use for agricultural development.

Striking gold: progress and future prospects following two decades of taxonomic research on Afrotropical dark sac spiders (Araneae: Trachelidae)

Charles Haddad

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Categories

• Systematics and Taxonomy

Abstract

Dark sac spiders (Araneae: Trachelidae) are a cosmopolitan group found on all the continents except Antarctica. As presently constituted, it is a moderately-sized family, with 265 species in 20 genera (of ~53 000 species described globally). Historically, Trachelinae was considered part of the Clubionidae and then Corinnidae, and was only elevated to family level in 2014. At the start of the century, there were only five genera and 19 species recorded from the Afrotropical Region (124 species globally), but a concerted taxonomic effort subsequently has resulted in the description of nine new genera and 60 new species from the region. However, this is only the proverbial tip of the iceberg. A largely unpublished revision of *Trachelas* L. Koch, 1872 included descriptions of approximately 70 new species from the continental Afrotropical Region alone, while new species are continually being discovered in already revised genera, e.g. *Thysanina* Simon, 1910, with six described species and more than 15 new species, and *Afroceto* Lyle & Haddad, 2010, currently with 16 species and an additional five new species discovered. At least seven new genera have been recognized from southern Africa alone. Furthermore, the Madagascan fauna has not been subjected to any modern revisions, but preliminary assessments of museum material from the island show similar richness. The Trachelidae is therefore a taxonomic goldmine and has proven to be a very rewarding group for species discovery. The taxonomic effort on the Afrotropical fauna has also stimulated research elsewhere, with revisions of the Asian and South American faunas now also gaining momentum. This has facilitated focused research on the phylogenetic relationships of the group in a global context through international collaborative efforts, using both morphological and molecular approaches. Collectively, ongoing taxonomic research will likely result in the Afrotropical species richness more than doubling current levels once complete.

Traditional knowledge, classic taxonomy and genetic information show limited overlap for documenting the biodiversity of edible grasshoppers in South Africa

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

The diversity of edible grasshoppers in South Africa is poorly documented due to inconsistent reporting of vernacular species names and scientific species, and limited availability of reference DNA sequences for African Orthoptera. We worked with communities in Limpopo for the collection and identification of *ethnospecies*, resulting in 176 specimens and 34 *ethospecies* in four languages. We used alpha taxonomy and DNA barcode analyses to infer phylogenetic groups that likely represent distinct species and performed sequence queries on BOLD Systems and NCBI. Acrididae dominated the dataset with nine subfamilies and 17 genera represented (*n = 167; 96%),* and *Pyrgomorphidae* were only represented by the genus *Zonocerus* (*n = 8; 4%).* Genetic groups likely were determined by phylogenetic analysis and maximum intragroup pairwise distances. Phylogenetic analysis and pairwise distances showed 36 genetic groups likely to represent distinct species. Database queries yielded high sequence similarity/identity matches (>*95*%) for only *59*% of the sequences on BOLD and 37% on NCBI. Comparison of the results obtained from *ethnospecies* identification, alpha taxonomy and genetic analyses showed limited overlap. Furthermore, the representation of African Orthoptera in public repositories was strikingly low, and further contributed to the low resolution of the dataset to species level; nevertheless, a large proportion of the specimens were identified to genus level. It is also worth noting that DNA barcoding of Orthoptera is challenging due to high level of polymorphism in the PCR primer annealing regions, which results in a high rate of failed amplifications and hampers Sanger sequencing. Despite the difficulties, the overall diversity of edible grasshoppers utilized in South Africa seems to be higher than previously reported and this study may inform future efforts for documenting the diversity of edible insects traditionally utilized by communities in Africa and other world regions.

Building blocks to local entomopathogenic nematode commercialisation in South Africa: Proof of concept of the mass production of *Steinernema yirgalemense* in bioreactors

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Stellenbosch University, Stellenbosch, South Africa

Categories

• Invertebrate Pathology

Abstract

The demand for entomopathogenic nematode (EPN) based biopesticide products is increasing as chemical pesticides are phased out. EPNs are environmentally safe alternatives to chemicals and have a plethora of attributes with a successful in-field track record, supporting their commercial development. EPNs ability to be produced in large scale bioreactors using artificial means of mass production, is key to their commercial success. However, mass producing EPNs using *in vitro* liquid culture technology in commercial bioreactors is a difficult science, incorporating multiple scientific disciplines, and is more complex than standard microorganism mass production. This is mainly due to the multicellularity of the EPN, and its symbiotic relationship with a specific bacterium. Furthermore, each new EPN species being mass produced has vastly different culture requirements, further complicating the process. At Stellenbosch University, the difficult task of mass producing local EPN isolates was undertaken and a standard protocol for the *in vitro* liquid mass production of multiple local occurring species that can achieve high infective juvenile yields, is now possible. The proof of concept for mass production in bench-top bioreactors has been demonstrated and encourages further development of this technology in pilot and industrial sized bioreactors.

What do we know about the Charismatic Mantodea of South Africa?

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North-West University, Potchefstroom, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Despite human fascination with the Mantodea or praying/preying mantids over millennia, very little is known about of their diversity, biology and ecology, especially in South Africa. Praying mantids are not only important because of the ecosystem services they provide, but also because they have a "mystical" status and are regarded as a kind of oracle in some cultures. Due to the cultural value of the Mantodea, these insects could be used as a flagship or gateway species to advance peoples' awareness of insects and increase their appreciation which can ultimately increase conservation efforts. The literature regarding South African Mantodea is very limited and the most recent species list was compiled 20 years ago. In this study, we updated the checklist of the Mantodea of South Africa, using approximately 4000 historic museum records as well as data from citizen science platforms such as iNaturalist. The updated checklist reports 164 species, 68 genera, eight superfamilies, 15 families and 22 subfamilies of Mantodea to occur in South Africa. The distribution and biology of *Galepsus lenticularis* (Tarachodidae) (Grass-like mantis), *Popa spurca* (Mantidae) (African twig mantis), *Sphodromantis gastrica* (Mantidae) (African mantis) and *Harpagomantis tricolor* (Galinthiadidae) (False flower mantis) were also described during this study. This study provides a glimpse into a group of insects that has basically never been studied in South Africa and is a benchmark of the knowledge about South African mantid fauna.

Biological control of the polyphagous shot hole borer, *Euwallacea fornicatus*: challenges and opportunities

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Categories

• Invasive Insects

Abstract

The polyphagous shot hole borer, *Euwallacea fornicatus*, is a highly polyphagous invasive ambrosia beetle that poses a threat to urban and natural forests, and agriculture, in South Africa, First reported in the country in 2018, *E. fornicatus* has already caused considerable tree mortality across the country. Outside of removing infested tree hosts there are currently limited control options available for this pest. Biological control holds promising potential to manage this invasive beetle, but various challenges need to be addressed before this can be implemented as a feasible management tool. Initial trials investigating commercially available entomopathogenic fungi (*EPFs*) were highly effective against *E. fornicatus* in lab bioassays. However, infestation assays using castor bean (*Ricinus communis*) had little effect on beetle boring or mortality. Results from these trials found that current application methods of EPFs limit their use against *E. fornicatus* and further work to develop improved application methods is needed to determine whether augmentative biocontrol using EPFs is a viable option. The behavioural response of *E. fornicatus* to the volatiles of *EPFs*, as well as their symbiotic fungi, are also being investigated for the development of repellents or attractants. One of the most exciting opportunities is to introduce classical biological control agents from the native range of *E. fornicatus*, with initial exploration trips in Vietnam underway. In addition, the possibility for native natural enemies of ambrosia beetles in South Africa to parasitize or prey on *E. fornicatus*, and be utilized in a conservation biological control approach, is being investigated. We report on completed and ongoing research to develop biological control for *E. fornicatus*.

Atherimorpha latipennis: the first record of brachyptery in the Rhagionidae

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Categories

• Systematics and Taxonomy

Abstract

The genus *Atherimorpha* White 1915 is a Gondwana relic with 51 species recognised as valid. Globally, the genus has received sporadic taxonomic attention, with most revisions only addressing regional faunas, though acknowledging the link between Australia, Africa and South America. Of the twelve Afrotropical species, both sexes are known in only four species, and the female is unknown for seven species. Many species are known from mountainous habitats and emerge as adults for a limited time. Brachypterous Diptera present a collecting challenge, as the usual techniques employed often rely on passive movement by the target individuals (e.g. Malaise traps) or active searching for flying adults. We describe the female of *Atherimorpha latipennis* Stuckenberg 1956, reporting *brachyptery* in *Rhagionidae* for the first time.

Scratching the surface: investigating the role of surface texture in the camouflage of toad hoppers (*Batrachotetrix*)

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Categories

• Biological Interactions

Abstract

Surface texture affects how objects are perceived, particularly through its interaction with light. It has been hypothesised that camouflage can extend to the mimicry of luminance patterns, potentially utilising surface texture. This study investigates the potential texture mimicry of surrounding rocks by *Batrachotetrix* (toad hoppers), a genus which has been noted for its striking camouflage. Grasshopper and rock samples were selected to cover a broad range of geologies, from a collection gathered across locations in the Northern and Western Cape. Structure from Motion photogrammetry was used to construct three-dimensional models of all samples, which were used to quantify multiple surface texture parameters across multiple spatial scales (topography, waviness, and roughness). Linear mixed effects models revealed that the surface texture parameters of both rocks and grasshoppers vary significantly across geologies. For one functionally important parameter, the pattern of variation for grasshoppers and rocks was similar across geologies, as expected under a camouflage hypothesis. However, significant differences between grasshoppers and rocks were observed for almost all parameters at all scales, which indicates that grasshoppers were not closely mimicking rocks. Broad patterns of match and local adaptation were explored using linear regressions, which indicated a match only for one parameter at the roughness scale for paired samples. The results of this study provide some evidence of texture match by *Batrachotetrix* and highlight the importance of texture scale separation in an ecological context.

Admixture of two genetically distinct lineages of the invasive gall wasp, *Leptocybe invasa* (Hymenoptera: Eulophidae), in South Africa

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Categories

- Invasive Insects

Abstract

The gall wasp, *Leptocybe invasa*, is native to Australia, but is invasive in all parts of the world where *Eucalyptus* is grown. Two genetically distinct lineages (possibly distinct species) are recognized amongst the native and invasive lineages. Lineage A has been reported globally, while Lineage B in known from a more limited distribution in Asia and Africa. Both lineages occur in South Africa, where we studied the genetic diversity and admixture between these two lineages using mitochondrial and nuclear markers. Specimens were collected from six regions in South Africa over a period of six years. Thirteen simple sequence repeat (microsatellite) markers were developed from collections from 13 countries to distinguish between the two lineages. Clustering methods and approximate Bayesian computation were used to characterise the structure and level of admixture in these populations. The results confirmed the occurrence of admixture in all regions in South Africa and that it increased over time. For the earliest collections in 2016 admixed populations were present in 57 sites in KwaZulu-Natal and Mpumalanga, while collections from the final year of this study (2022) revealed admixed populations in 104 sites in the Eastern Cape, Limpopo, KwaZulu-Natal and Mpumalanga. Research is ongoing to investigate the effect of admixture on the host preference of *L. invasa* and the impact on biological control agents, through the establishment of isolated cultures of lineage A, B and A-B admixed populations.

Can we measure the impact of climate change on biodiversity with little historical information about the distributions of taxa?

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Biodiversity (alpha, beta and gamma diversity) is the variability among living organisms in all ecosystems. Mostly, biodiversity has been quantified using alpha diversity while beta diversity lags. Beta diversity provides a link between diversity at local (alpha) and regional (gamma) scales. It therefore allows for identifying processes that structure community assemblages and reveals how communities respond to the influence of climate change, environmental gradients and anthropogenic activities by quantifying biodiversity loss. Understanding how selected arthropod assemblages will change with climate is therefore important in understanding likely future changes in diversity and the processes associated with this change. It is also important to gain a unique insight into long-term ecological processes like community turnover and adaptation by examining elevation gradients. A case of the Udzungwa mountains; an invaluable ant's baseline data was documented along the Udzungwa mountains in Tanzania. A standardized survey using pitfall sampling was conducted across five elevational transects, which were at different distances from each other. The results show that beta diversity was influenced by distance. Dispersal limitations did not play a significant role in structuring ant composition between sites and did not explain variation in the two-beta diversity components; species turnover and richness differences, suggesting that historical processes or biotic interactions structure ant communities with distance. Across elevations, species turnover increased with elevation while richness differences decreased with elevation. The latter elucidates the role of species replacement in structuring ant communities along an elevational gradient and that of temperature acting as an environmental filter in structuring ant compositions. Therefore, what inferences can be made from beta diversity findings that can be used to monitor the effects of climate change in the future across other African tropical mountains?

Species delimitation and diversity of *Mariobezziinae* (Diptera: Bombyliidae) in South Africa

Cassandra Barker, Allan Ellis

Stellenbosch University, Stellenbosch, South Africa

Categories

• Systematics and Taxonomy

Abstract

The *genera Corsomyza* (Wiedeman 1820) and *Callynthrophora* (Schiner 1867, Diptera: Bombyliidae) are prominent pollinators of annual blooming daisies in the Greater Cape Floristic Region (*GCFR*). *Callynthrophora* is a South African endemic genus found exclusively in the Western and Northern Cape. *Corsomyza* has a wide distribution from southern Namibia to the Eastern Cape, South Africa, and a few historical records of this genus in Zimbabwe. Both *Callynthrophora* and *Corsomyza* have been observed to pollinate a variety of *Asteraceae* and *Aizoaceae* genera indicating that these genera are more generalist in flower visitation behaviour. Currently, there are 27 described species of *Corsomyza* and three described species of *Callynthrophora* but the taxonomy of these two genera have not been investigated at a molecular level. This study aimed to assess the species boundaries of these two genera, using DNA barcodes and species delimitation models. The results of the molecular species delimitation of a large, spatially dense sample from the *GCFR* have shown that there are three species of *Callynthrophora* and 13 species of *Corsomyza*. However, the results of ordination analyses of the morphological characteristics show that there are four species of *Callynthrophora* and 16 species of *Corsomyza*. Determining the species boundaries will be beneficial in the assessment of the taxonomy of these genera and will have larger implications in revising the taxonomy of either genus.

Ant biodiversity response to land-use and associated ecological disturbances and stress

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Understanding how faunal communities respond to ecological disturbance remains a contentious issue in community ecology. Although natural phenomena cause some disturbances, recently, anthropogenic disturbances are commonly encountered and are a major cause of the ecological disturbance. Among animals, insects are the highly abundant and now widely studied group. In the terrestrial ecosystem, ants (Formicidae: Hymenoptera) have the highest terrestrial biomass, play various ecosystem services, and respond to a disturbance at a local scale. Here I aim to present various recent studies documenting patterns of ant diversity and assemblage structure and their response to ongoing major ecological disturbances and stress in selected, highly impacted and vulnerable study sites in Limpopo and KwaZulu-Natal provinces. In particular, (1) I will describe the response of ants to various ecological disturbances and stress in major land uses of KwaZulu-Natal and Limpopo provinces. (2) Investigate how the pattern of ant species richness, abundance, and assemblage structure respond to ongoing major ecological disturbances and stress in the provinces. (3) how local (competition, habitat structure and small-scale disturbance (specifically grazing and fire) and regional (alien invasive plants, timber plantations, bush encroachment and reforestation) drive ant diversity and assemblage composition across the major land uses in the two provinces.

High temperature, habitat structure and dominant ants drive diversity and assemblages of ants in Limpopo province. Across KwaZulu-Natal, grasslands have the highest diversity, while natural forest has unique ant assemblage. Dominant ants in the genus, *Pheidole*, *Anoplolepis* and *Crematogaster* seem to control assemblages in highly disturbed systems including sugar-cane plantations and bush encroached systems. Despite recent efforts in the two provinces, most ant species are undescribed; those described, their diversity and distribution are not known. There is an urgent need to describe more species and study their distribution pattern, sensitivity, and response to variation, habitat change and transformation.

Interplay between pond size and matrix extent drives dragonfly diversity patterns in a fragmented landscape

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Landscape fragmentation impacts freshwater habitats and their quality, affecting aquatic insect assemblages. Adjacent terrestrial areas are important secondary habitats where many aquatic insects mature, feed, find mates, and move to locate aquatic breeding habitats. Using dragonflies as model organisms, we investigate 1) how pond size/terrestrial patch size interaction affects overall *odonate* diversity patterns versus habitat quality variables, and 2) determine whether *anisopterans* and zygopterans respond differently to landscape fragmentation. In an exotic tree plantation-fragmented landscape of sub-tropical southern Africa, we used a factorial design with 27 small and large ponds within small and large patches of the surrounding matrix. We compared the importance of pond and patch size interplay relative to habitat quality variables in driving lentic *odonate* diversity patterns and biological trait representation in this transformed landscape. Species richness was similar among ponds. However, *odonate* abundance was highest in large ponds regardless of terrestrial patch size. Zygopteran functional richness and diversity was driven by pond size, implying that zygopterans are sensitive to landscape fragmentation. In contrast, *anisopterans* were more resilient and more likely to select suitable habitats based on water chemistry and vegetation characteristics. The various pond categories were occupied by compositionally dissimilar *odonate* assemblages, and occupancy was strongly associated with mobility traits. Ponds in small terrestrial patches have equal conservation value compared to those in large patches. A pondscape with many pond sizes is important for representing regional *odonate* diversity. The results presented here emphasize that pond conservation needs to be considered in the wider terrestrial context, which host a range of important secondary habitats. These adjacent terrestrial habitats also connect nearby aquatic habitats, which enable insects to move across the landscape in response to natural and artificial stressors.

Collembola diversity in Agroecosystems in South Africa.

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Categories

• Agroecology

Abstract

Soil biodiversity is vital for soil ecosystem functioning and services. Collembola are widely used as indicators of soil health in agricultural systems, especially in Europe. However, knowledge of Collembola in agricultural systems are lacking in Africa. We show, using examples from several different agricultural practices in South Africa, how an interdisciplinary approach can be used to study Collembola in an undersampled country. We sampled various agroecosystems such as orchards, cash crops (maize, canola and wheat) and pasture crops (annual medics) under different agricultural management practices, such as mulch, no-tillage and cover crops, to explore the Collembola diversity. Sampling methods included pitfall traps, Tullgren-Berlese extractions and litterbags, depending on the soil conditions. Overall, Collembola diversity was high, ranging from a minimum of nine to 57 morphospecies, and 7,498 to 22,186 individuals. Although introduced species were abundant and widespread, a surprising number of indigenous species were found. As expected, forms of disturbance such as tillage reduced Collembola species richness. These impacts are discussed, as well as the importance of ongoing monitoring and taxonomic study of this group. We conclude that Collembola are useful indicators of ecosystem health and natural predator abundance.

Characterisation of the tissue-specific microbiota of *Anopheles funestus* Giles (Diptera: Culicidae)

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

Anopheles funestus is a major malaria vector in Africa. The emergence and persistence of insecticide resistance in *An. funestus* has prompted novel vector control strategies such as *paratransgenesis* (a form of bacterial biocontrol) and genetic modifications that would inhibit *Plasmodium* infection and therefore, the transmission of malaria. However, the key to *paratransgenesis* and genetic interventions is the understanding of the immune response of mosquitoes. The immune system of mosquitoes in turn is largely attributed to the microbiota it harbours. Yet, to the best of our knowledge, the diversity, abundance and composition of the core microbiome in *An. funestus* tissues have never been evaluated. Thus, the study aimed to investigate the overall bacterial landscape in three different tissues (salivary glands, ovaries and midguts) in three laboratory strains of *An. funestus* by sequencing the V3-V4 hypervariable region of bacterial 16S rRNA genes. These three tissues represent potential target tissues for *paratransgenesis*. When looking at α diversity, both the species richness and relative abundance indices revealed that the salivary glands harboured a statistically larger number of bacterial species. In contrast, no statistical differences were found between the species richness and relative abundance of bacterial species between the midguts and ovaries. Similarly, when looking at β diversity, the composition of the microbiome was more similar between the midgut and ovaries while the composition of the microbiome in the salivary glands was markedly different than the other tissues. There were however common bacteria across all three tissues of interest: a total of 38 bacterial families were shared between all the tissues which encompassed 49 genera and 60 species. The present study uncovered the core microbiome across three tissues of *An. funestus* and revealed potential targets that could be used in the future for *paratransgenesis* and genetic interventions for malaria transmission.

Determining the presence and abundance of oriental fruit flies is more complex than counting numbers in traps

Christopher Weldon

University of Pretoria, Pretoria, South Africa

Categories

• Invasive Insects

Abstract

The presence and risk of infestation by fruit flies, including oriental fruit flies, *Bactrocera dorsalis*, is mostly determined using trapping. Threshold levels have been established for this pest but trapping levels depend not only on insect abundance but also environmental conditions and the responsiveness of flies to the attractant, methyl eugenol (ME). We have been evaluating the environmental variables affecting the response by *B. dorsalis* males to ME, with a focus on the effects of temperature on lure formulation loss, activity, and trap captures. Weekly weight loss by commercially available ME dispensers in yellow bucket traps over six periods of one month was measured in a lemon orchard and related to mean weekly environmental conditions. In the laboratory, we went on to record undisturbed behaviour (inactivity, grooming, walking, flight) and tethered flight of *B. dorsalis* between 12 and 36˚C. We then ran field cage studies to determine the proportion of a known number of flies caught in ME-baited traps under varying field temperatures. The ME dispensers used in traps lost more weight at temperatures above 20˚C. This temperature also represents a threshold for optimal walking and flight performance of *B. dorsalis*. In field cages, sexually mature male *B. dorsalis* were less likely to be caught in ME-baited traps when temperatures were cool, with no trap captures expected below *21.2±1.8˚C*. The implication of our findings is that *B. dorsalis* males are less likely to move towards and be caught in ME-baited traps when temperatures are cool but well above those that cause mortality. This necessitates those thresholds of ME-based trap captures that trigger management actions, including quarantine, need to be adjusted according to prevailing environmental conditions.

Predicting the possible establishment and spread of the Asian citrus psyllid *Diaphorina citri* Kuwayama in Southern Africa using species distribution modelling

Clarke van Steenderen[1], Evans Mauda[2], Wayne Kirkman[3], Katelyn Faulkner[4], Guy Sutton[1]

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Categories

- Invasive Insects

Abstract

Citrus greening [Huanglongbing (HLB)] is currently considered the most damaging disease to the southern African citrus industry. HLB is caused by phloem-inhabiting bacteria [*Candidatus Liberibacter* spp., particularly *Ca*. *Liberibacter* asiaticus (CLas)], which are vectored by the Asian citrus psyllid (ACP), *Diaphorina citri* Kuwayama (*Hemiptera: Psyllidae*). *Diaphorina citri* has been introduced from its native range in Asia to many other regions of the world (including the Americas and parts of Africa), where it has had devastating impacts. The citrus industry in Florida, for example, has reported a 74% decrease in citrus production since 2005. *Diaphorina citri* has not yet been recorded in South Africa, but there are increasing concerns over its possible spread into the country from neighbouring African countries. We developed a series of species distribution models to predict (1) which regions of the country are most suitable for *D. citri* establishment, (2) possible invasion routes and barriers to spread, and (3) how suitability and invasion routes for *D. citri* might change in the future based on climate change scenarios. Our preliminary results suggest that large regions of the Limpopo-and Mpumalanga provinces, the South African east coast, and coastal regions of the Western Cape are particularly favourable for *D. citri* establishment. The outputs of these models will inform monitoring and surveillance activities and develop an integrated management plan to respond to the potential invasion of *D. citri* in South Africa.

Multi-omic analysis of genetic and phenotypic variation in mass reared Black Soldier Flies (*Hermetia illucens*)

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Stellenbosch University, Stellenbosch, South Africa

Categories

• Insects as Feed and Food

Abstract

A renewable, sustainable and environmentally friendly system for animal protein production is becoming increasingly important in light of a growing human population, adverse effects of climate change and diminishing natural resources. Black Soldier Fly (BSF) farming has been proposed as an alternative livestock production system that may meet the challenges for future food security, with low resource requirements, higher feed conversion ratios and similar nutritional value as conventional animal protein. BSF also has the added advantage that its larvae can act as efficient bioremedial agents, converting organic waste into useable biomass, creating a circular agricultural economy. Despite the industrial scale of BSF mass rearing, little is known about the drivers of genetic and phenotypic variation under these production conditions. This study, therefore used a muti-omic approach to assess the interplay between organismal genetics, functional genomics, the microbiome and feed-substrate on phenotypic development in BSF larvae. The population genomic assessment revealed that genetic drift is the major evolutionary force shaping genomic diversity, even in the presence of direct artificial selection for production traits. Additionally, few loci were significantly associated with these production traits, further illustrating the influence of stochastic evolutionary processes during the mass rearing period. The effects of selection on gene expression were also weak and differential transcriptomic profiles highlighted functional trade-offs between growth metabolism and immune function. Metagenomic analysis found significant associations been bacterial taxa and protein-fat ratios in BSF, and that both feed-substrate and the interaction between feed- and host genetics played a significant role in the composition of larval gut microbiomes. The findings highlight the multidimensional and complex nature of BSF production and its impact on phenotypic development, with applications for future genetic management and improvement strategies for enhanced production.

Does the source matter for SIT? Negligible effects of irradiator source, X-ray vs. gamma, for sterilization and sterile male mating competitiveness in the mosquito *Aedes aegypti*.

Daniel Hahn

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Categories

• Physiological Ecology

Abstract

Sterile insect technique (SIT) has proven to be very effective as a key component in area-wide integrative pest management for multiple agricultural pests, and in recent years interest has been growing in applying SIT to mosquito vectors of importance to human health. SIT may be particularly useful for peridomestic disease vectors like *Aedes aegypti* that live in close proximity to humans, occupy cryptic larval breeding sites with adults that rest in places difficult to reach with sprays, and that have some populations showing resistance to common chemicals used in mosquito control. For SIT, males are typically sterilized by exposing them to gamma radiation. However, these irradiators typically use Co-60 or Cs-137; high activity sources that are vulnerable to theft or misuse and thus require substantial security and monitoring. In support of the National Nuclear Security Administration (NNSA) Office of Radiological Security (ORS) mission to reduce the risk of these sources by encouraging use of non-radioisotopic technologies, Sandia National Laboratories has funded a study to compare the efficacy of gamma versus X-ray-based irradiation for SIT. Specifically, this study seeks to compare an established Cs-137 gamma irradiator used for an operational *Ae. aegypti* SIT pilot program with a new X-ray irradiator for sterilizing male pupae and adults while maintaining male performance after irradiation. We show negligible differences in efficacy of sterilization or post-irradiation male performance between the X-ray and gamma sources. Furthermore, when male mosquitoes were irradiated in either normal oxygen-rich air or severe hypoxia, the hypoxic treatment had a similar radioprotective effect when males were sterilized with X-rays as had previously been observed with gamma-ray irradiation, further showing equivalence of biological effects of radiation across sources. Our results show that insect SIT programs can successfully transition from gamma to X-ray sources and suggests that new programs can begin their programs using X-ray irradiation sources to avoid regulatory and cost hurdles associated with installation of new gamma-radiation sources, overall showing that X-ray irradiators provide a viable alternative technology to radioactive gamma sources for insect pest control.

Citrus leprosis disease and its *Brevipalpus* vectors in South Africa

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Categories

• Agricultural Entomology

Abstract

Citrus leprosis (CL) is a serious non-systemic disease of citrus, endemic to Central and South America, characterised by necrotic lesions with chlorotic halos on twigs, leaves and fruit. It is caused by a number of cytoplasmic- (CL-C) and nuclear-replicating (CL-N) viruses. CL is vectored by species of the flat mite genus *Brevipalpus* (*Trombidiformes: Tenuipalpidae*), with different species vectoring different viruses within the complex. In South Africa, CL-N was detected in 2018 in the Sundays River Valley region of the Eastern Cape. The causative virus was orchid fleck virus (OFV), a CL nuclear-replicating virus. Flat mites from this site were identified as *B. californicus s.l.* and tested positive for OFV. It is assumed that OFV entered South Africa through infected orchid pot plants and was then transmitted to citrus by viruliferous *B. californicus s.l.* mites. Six species of *Brevipalpus* are known to occur in South Africa. However, two of these have been revised as large species complexes, bringing the number of possible *Brevipalpus* species in South Africa to 17, many with unknown CL-vector status. We have examined South African *Brevipalpus* specimens housed in the National Collection of Acari (NCA). We discovered that numerous different *Brevipalpus* species were present in the collection, but never published. Reidentification of specimens using new taxonomic literature revealed 10 confirmed species and five tentative ones. On citrus, CL-vector species *B. yothersi* (vector of CL-C) and *B. californicus s.l.* (vector of CL-N) were identified, with differential distribution within South Africa. *B. californicus s.l.* is more common in the southern citrus areas, including the Sundays River Valley where CL-N is present, thus presenting a high risk for CL-N spread in these areas. *B. yothersi*, on the other hand, is more common in the northern citrus production areas, so the chance of CL-N spread in those areas is lower.

Integrative taxonomy unravels the identity of the grapevine bud, erineum and leaf curl mite, *Colomerus vitis* (Trombidiformes: Eriophyidae)

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Categories

• Agricultural Entomology

Abstract

Colomerus vitis (Trombidiformes: Eriophyidae) is a worldwide pest of grapevine known by the symptoms it causes: bud, *erineum* or leaf curl mite. It has been suggested that these symptoms are caused by three distinct strains or cryptic species. In our study we integrated genetic, morphological and biological data to investigate this mystery. Our analyses of COI sequences from grapevine *Colomerus* mites revealed five phylogenetic groups (G1 to G5) worldwide, with enough separation to be considered distinct species. From South Africa, we collected symptomatic grapevine samples and developed a novel method to identify the mite groups present. We found that groups G1, G2 and G3 are present in South Africa and frequently co-occur in the same sample. All groups were found in bud and erinea samples, with G3 more often associated with buds and G1 with *erinea*, but not exclusively so. We used cryo-SEM to investigate the morphology of mites from buds and *erinea* from a single site. This technique enabled us to view detailed features on these tiny mites. We observed variation in the *prodorsal* shield pattern and number of *empodial* rays that could be significantly, but not exclusively, associated with plant niche. The results show that *C. vitis* should be viewed as a complex of co-occurring species not associated to a particular plant symptom. We tentatively propose two possible ecological scenarios. 1: Different genetic groups are responsible, separately, for bud and *erinea* symptoms (possibly G1 and G3, respectively); but are not restricted to the damaged plant tissue and may often be found as inquiline species in other niches. Other groups may cause the same symptoms or may merely co-occur (G2, G4 and G5). 2: There is no causal association between any genetic group and grapevine symptom, and symptomology is instead related to some other aspect of biology or physiology.

The more you introduce the more you get – but only if you're stressed

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Categories

- Physiological Ecology

Abstract

Successful establishment of an introduced population is a complex interaction between environment, life history traits and introduction dynamics. Given a non-lethal environment, the most consistent predictor of successful establishment is the number of individuals introduced. This is termed propagule pressure and comprises the size, number and frequency of introductions. We tested these factors in a mesocosm experiment using *Drosophila melanogaster* (Diptera: Drosophilidae) to examine the interactions between propagule size, propagule number and environmental suitability. Adult flies were introduced to standardised non-lethal environments differing only in temperature – one ideal, one extreme hot and one extreme cold. Propagule pressure varied from two to 16 founders in different founding population sizes and over different numbers of introduction events. We found that, as expected, temperature played the biggest role in founding success, eclipsing the role of other factors. Surprisingly, at ideal temperature both founding population size and number of introduction events were of negligible importance. At extreme temperatures larger founding population size significantly increased the likelihood of successful establishment, with this effect considerably stronger at the cold than at the hot extreme. Similarly, changing the number of introduction events for the same overall founding population size (i.e., whether individuals were introduced all at once or in increments) significantly influenced the probability of successful establishment at the thermal extremes, but with differing effect at the cold and hot extremes. Adding flies incrementally at the cold extreme increased their establishment success but decreased it at the hot extreme. These differing effects implies that different physiological mechanisms are at play in extreme hot and cold environments. Understanding the interactions between populations and environment, especially in non-ideal scenarios, enables us to better predict what can be done to prevent (or conversely, to facilitate) introductions of species.

What insects do *Vespula germanica* prey on in South Africa?

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Categories

- Invasive Insects

Abstract

Invasive Alien Species can potentially spread rapidly, cause a broad range of significant changes to recipient ecosystems, out-compete, prey on or hybridise with native species. *Vespula germanica* Fabricius, 1793 is an invasive alien social wasp distributed worldwide though native to Europe, Asia and North Africa. It is a scavenger and a ferocious predator that preys on indigenous insects important for several ecosystem services. However, its predatory impacts are currently unquantified where it occurs in South Africa, specifically in the Western Cape Province where it occurs. To investigate what insects *V. germanica* prey on, returning foragers and the prey items caught by them were collected by vacuum sampling from their nest entrance. Fourteen nests were sampled across localities found within the species' distribution and the number of prey items sampled per nest ranged from 13 to 135 on average 68 prey items per nest. Morphological traits and DNA barcoding were used to identify all prey items including those chewed beyond recognition. The morphology-based identifications were very challenging however the integration of DNA barcoding was advantageous. Sequences queried on BOLD revealed a variety of insects with some of the morphological identifications matching the BOLD results, especially insects of the orders Hymenoptera and Diptera. Results showed that 10% of the prey items were honeybees but the majority (56%) of the prey items were flies. Only 3% were unknown food items suspected to have been scavenged. The remaining 31% are unknown prey species belonging to a range of insect orders still to be determined by genetic analysis.

Study of the entomofauna and major pests of wheat and maize in the western highlands zone of Cameroon and monitoring of pest infestation

Djomaha Edwige, Nenba Christian

University of Dschang, Dschang, Cameroon

Categories

• Agricultural Entomology

Abstract

Maize is the main cereal crop in Cameroon. The CORONA VIRUS crisis has created a wheat flour deficit since the end of 2020 and the government has decided to promote wheat cultivation in areas where trials have confirmed wheat cultivation. This is the case in the department of Menoua, locality of Fongo Tongo where it has been practised by a group of producers for 20 years ago. Climate change has caused the extinction and emergence of pests over the past decade, this study was undertaken to determine the entomofauna of the two cereals and to identify the main pests. The trial took place in Bansoa from September 2022 to the end of January 2023. The randomized complete block design with two maize varieties (ATP and KASSAI) and one wheat variety was used. Data collection started 21 days after sowing until flowering. Insects were collected with a sweep net and observed with the naked eye on 30 plants per treatment. The insect's identification keys were utilized. The results revealed that 4185 insects including 3465 specimens for maize corn and 720 specimens for wheat were inventoried. Also, 32 families were identified on maize with a majority of Otitidae (12.1%) and 20 families for wheat with more Syrphidae (30.1%), split in 5 orders. As for the pests, *Spodoptera frugiperda* (FAW) was the main pest of maize with 93.3% of incidence on KASSAI and 83.3% on ATP at vegetative stage. For wheat, the main pest was *Helicoverpa spp.* observed at flowering stage with 56.7% of incidence. This study reveals that wheat and maize do not have common pests and also that the pests are attacking at different phenological stages. Producers are advised to practice monitoring by regularly inspecting their wheat plots to avoid peaks of *Helicoverpa spp.* infestation.

Keywords: Wheat, maize, entomofauna, pests, incidence, Cameroon

Effect of diet and semiochemical exposure on oriental fruit fly respiration at different temperatures

Dylan Dacre[1], Christopher Weldon[1], Frances Duncan[2]

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Categories

• Invasive Insects

Abstract

The oriental fruit fly, *Bactrocera dorsalis* (Hendel) (Diptera: Tephritidae), is an invasive horticultural pest that has rapidly spread across Africa. The sterile insect technique (SIT) is a valuable addition to management of *B. dorsalis*. However, sterile males released into the field may perform poorly due to laboratory adaptation, handling and irradiation. Pre-release treatment of sterile males with a protein supplemented diet and exposure to semiochemicals can boost sterile male reproductive development and mating performance. In this study we used respirometry to evaluate the effects of diet and semiochemical exposure on the resting metabolic rate of male *B. dorsalis*. We used flow-through respirometry to measure the resting metabolic rate of male flies based on their CO_2 emissions. In this system, 14-day-old adult males of known body weight were placed individually in chambers through which dry, CO_2-free air was passed before being directed to a CO_2 gas analyser. The CO_2 emitted by each fly when at rest was divided by its body weight to calculate a mass-specific estimate of metabolic rate. From emergence, males were fed with either continuous access to sugar only or sugar and hydrolysed yeast. Males were exposed to either methyl eugenol (ME) or eugenol (EU) at a 1.25% concentration for four-days prior to experimentation or not exposed to any semiochmicals (control). Resting metabolic rate was recorded at temperatures held at 15, 20, 25 and 30˚C. Results showed that resting metabolic rate of sugar-fed males was significantly lower than that of males fed sugar and hydrolysed yeast. Semiochemical exposure was shown to significantly reduce resting metabolic rate. Depletion of lipid reserves may provide a potential mechanistic basis for poor survival in males exposed to semicochemicals, due to an upregulated rate of living that drives improved mating performance.

Semiochemical lures for improved citrus psyllid monitoring with yellow sticky traps

Dylan Pullock[1], Aruna Manrakhan[2,3], Kerstin Kruger[1,4], Christopher Weldon[1]

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Categories

• Agricultural Entomology

Abstract

South Africa was the 2nd largest exporter of citrus in the world during the 2020/2021 season, making it a lucrative horticultural industry for the country. However, the potential spread of Huanglongbing (HLB; Asian citrus greening) and its suspected causal agent (*Candidatus* Liberibacter asiaticus) into the southern African region poses a new threat to South African citriculture. Various odour-based semiochemicals identified for *Trioza erytreae* (Del Guerico 1918) (Hemiptera: Triozidae; African citrus psyllid), a native vector of HLB, were used in conjunction with yellow sticky traps to determine if chemical lures improved trap performance. Semi-field trials were run in field cages on the Future Africa campus of the University of Pretoria. In these trials, two-week-old *T. erytreae* males (n=10) and females (n=10) were introduced to cages containing potted lemon plants in which two yellow sticky traps were hung. One trap included a polyethylene bulb with a treatment. The other trap had an empty bulb attached to it to act as a blank (control). The treatment was either one of eight chemicals (acetic acid, limonene, sabinene, ocimene, myrcene, ethyl butyrate, methyl salicylate and p-cymene) of high purity, each dissolved in hexane, or the pure solvent or a commercial lure (ACP *Pherolure*). Nine replicates of each treatment were completed. Preliminary results show that *ACP Pherolure*, ethyl butyrate, myrcene, ocimene and sabinene baited traps captured more psyllids than unbaited traps. Limonene and hexane appear to have a repellent effect on both female and male psyllids. Currently, only ocimene and ethyl butyrate appear to be effective for both sexes. Of the pure semiochemicals tested, ocimene and ethyl butyrate show promise as lures for use in the field. Various new blends of the effective chemicals tested might also be developed to improve psyllid detection using baited sticky traps.

Interactions between *Lantana camara* and pollinating insects in an urban nature reserve in South Africa.

Eileen Engelbrecht, Christian Pirk

University of Pretoria, Pretoria, South Africa

Categories

• Biological Interactions

Abstract

Invasive species are considered a major biological threat. The presence of potential pollinators in an invaded environment often dictates the success of an invasive plant species. *Lantana camara* is one of South Africa's worst invasive plants. This study explores the diversity of flower-visitors on Lantana camara in an urban nature reserve in South Africa (the Faerie Glen Nature Reserve in Pretoria), with a specific focus on honey bee (*Apis mellifera scutellata*) visitors. Insect observations were conducted in four seasons (early summer, late summer, spring, and winter, from Nov 2021 to Jun 2022). We show that lantana has a diverse pollinator population spanning 31 families from five insect orders, making lantana a pollinator-generalist plant. The most abundant pollinating insects on lantana were thrips (63% of all observed arthropods). After thrips, honey bees were the second most abundant pollinators in all seasons, apart from spring (4% of all observed arthropods). The number of honey bees observed on lantana varied between seasons, with significantly higher numbers observed in late and early summer. Season was the only significant explainer of variation in honey bee numbers on lantana inflorescences. We were further interested to see how important pollinators are to the pollination success of lantana. Using exclusion experiments designed to exclude pollinators based on size, we investigated the importance of different pollinators on the viable fruit set of lantana. These experiments resulted in no significant differences between the different pollinator exclusion treatments. This study provides insights into the interaction of native pollinators with *Lantana camara* and to what extent lantana relies on these interactions for successful fruit production. Many native pollinators utilize the resources provided by lantana, which likely contributes to its success in South Africa, however, honey bees are not at the forefront of this success.

Characterization of *Anopheles arabiensis* breeding habitats in Jozini, KwaZulu-Natal province

Elelwani Marubini

National Institute for communicable Diseases, Johannesburg, South Africa

Categories

• Physiological Ecology

Abstract

Introduction: The SA government is now implementing winter *larviciding* as a supplementary vector control tool. In order to have an effective *larviciding* there is need to understand larval habitat ecology and their distribution. This study aimed to determine *An. arabiensis* breeding habitats and characterize physicochemical properties of water that promotes development of their larvae.

Methods: A physical search of all potential anopheles breeding habitats was carried out. At each positive habitat, *Anophelines* larvae were collected and the physicochemical characteristics of water namely; pH, conductivity, TDS and salinity were measured using a Consort C5020 meter. Collected larvae were reared to adults, thereafter, morphology and molecular identification were done on the emerged adults.

Results: A total of 38 potential water habitats were survey. Of these water bodies 84% *(n=32*) were positive for *Anopheles* larvae while, 16% (*n=6)* were negative. A total of 434 and 164 *Anopheline* larvae were collected from different water bodies in January and April. Of these, 238 belonged to *An. gambiae* complex. Of the 238 *An. gambiae* complex, 59% (*n=147*) were collected in January and 35% (n=88) were collected in April. Molecular identification of *An. gambiae* complex showed that predominance of species was different between two occurrences of the collection time point. *Anopheles merus p*redominated 56% *(n=83)* in January, while *An. arabiensis* predominated the collections 82% (*n=90*) in April. Physicochemical properties of water showed significant difference in all parameters between the different breeding sites except conductivity (*X2 = 8.5, df = 4, p =0.07*). The habitats surveyed indicated that breeding sites associated with An. arabiensis larvae are temporary water bodies characterised by neutral pH, low salinity and TDS.

Conclusion: *Larviciding* that is targeted to *An. arabiensis* should not only focus on operational aspects but should be include temporary water bodies with neutral pH, moderate salinity and Low TDS.

Lethal, sublethal and behavioural effects of insecticides used in the management of *Bathycoelia distincta* (Pentatomidae) in macadamia orchards in South Africa

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Categories

• Agricultural Entomology

Abstract

Bathycoelia distincta is a key pest of macadamia in South Africa. Knowledge regarding the toxicity and sublethal effects of insecticides on *B. distincta* is important for effective management in the field. In this study, the toxicity of four commercial insecticide formulations and their behavioural effects (i.e., distance walked, angular velocity) were assessed after a short exposure of 10 min. The insecticides tested included one organophosphate (*acephate*), and three pyrethroids (*lambda-cyhalothrin, beta-cyfluthrin and tau-fluvalinate*). The sublethal effects of lambda-cyhalothrin on parent *B. distincta* (F0) (i.e., longevity, fecundity) and offspring generations (F1) (i.e., hatching rate, mortality, developmental duration, sex ratio) were also measured. In contact bioassays, acephate was more toxic to *B. distincta* than lambda-cyhalothrin, *beta-cyfluthrin* and *tau-fluvalinate*. After short insecticide exposure, behavioural changes were only observed in bugs exposed to pyrethroids, resulting in an increased distance walked and decreased angular velocity. The sublethal effects of lambda-cyhalothrin were assessed by treating *B. distincta* adults with sublethal concentrations LC10 and LC30. On the F0 generation, LC30 significantly inhibited the fecundity whereas the LC10 and LC30 accelerated the development of the F1 generation. It is important to consider changes in mobility and effects that sublethal concentrations of insecticide could have on the development and reproduction of the targeted pest. These results suggest that pyrethroids could enhance the dispersal of *B. distincta* and stimulate the growth of the offspring population, which may cause the resurgence of this pest. These results provide a reference point and further experiments should be expanded in the greenhouse and field to confirm these results and understand the mechanism of action of pyrethroids on *B. distincta*.

Investigations into the ecology and management of the polyphagous shot hole borer beetle in South Africa.

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Categories

• Invasive Insects

Abstract

The polyphagous shot hole borer (PSHB) beetle (*Euwallacea fornicatus*) (Coleoptera: Curculionidae: Scolytinae) and its primary fungal symbiont, *Fusarium euwallaceae*, is a pest-disease complex that has killed a wide range of tree species in multiple invaded regions including the United States, Israel and South Africa. As with any newly discovered invasive pest, monitoring programs help reveal the drivers behind species population dynamics in invaded regions, which leads to evaluating potential impacts and informing management strategies. This study included a two-year monitoring program in an agricultural setting of the Western Cape, South Africa. Baited traps were used to determine activity patterns in comparison with temperature, as well as infestation dynamics over time in comparison with important climatic and biological factors. Preliminary results suggest that activity is strongly temperature dependent, with numbers peaking in late summer. Further, factors such as the abundance of hosts increase infestation numbers and rates. This is especially relevant in agricultural areas where crops are often surrounded by reproductive hosts either deliberately planted as windbreaks or growing naturally. We also experimented with two prominent management strategies for invasive forest pests, tree-removal, and therapeutic chemical treatment. Preliminary results suggest that proper tree removal can decrease local propagule pressure, especially if conducted in colder months. Further, some therapeutic chemical treatments reduced fungal growth, number of new PSHB attacks, and beetle colony success, but control was never completely successful. These results suggest that a combination of physical and chemical control options may help to reduce propagule pressure but would likely not prevent infestations for long periods.

The effect of rearing substrate energy source on *Hermetia illucens* larvae nutritional composition

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Categories

• Insects as Feed and Food

Abstract

Food insecurity and climate change are global issues. However, the devastating effects thereof are even more evident on the African continent where millions of people live in poverty. Therefore it is more important than ever to develop affordable and nutritious food products that can be produced sustainably. This is where edible insects show promise. The black soldier fly (*Hermetia illucens*) is a species that can be produced on a mass scale for this purpose. This is due to a number of favourable characteristics. The larvae can be successfully reared on a variety of substrates, pre-consumer food waste. They can then ameliorate this waste into high quality proteins and lipids that can be harvested and incorporated into food and feed products. Therefore production is based on the idea of a circular economy. Research has shown that the larval composition is highly influenced by the rearing substrate. This opens up the possibility to modify the larval composition to better suit their intended use. However, there is still a lack of clarity as to how specific substrate ingredients can affect the larval composition. The aim of this study was to determine the effect of substrate energy source on the larval composition and production of black soldier fly larvae intended for human consumption. Five larval diets were formulated and differed in main energy source. These included sunflower oil, fish oil, sucrose, fructose and corn starch. All the diets were formulated to be isonitrogenous, isoenergetic and to meet the larval nutritional requirements. These energy sources were chosen as they represent the most common energy sources found in pre-consumer food waste. The larvae were harvested at 12 days of age and analysed for proximate composition in order to determine the effect of the rearing substrate. This included dry matter, protein, fat, ash and chitin content.

Field trials to evaluate the potential of a local entomopathogenic fungus (*Metarhizium pinghaense*) and nematode (*Steinernema yirgalamense*) for control of *Margarodes prieskaensis* females

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Categories

• Agricultural Entomology

Abstract

Margarodes prieskaensis (Jakubski), an indigenous subterranean scale insect, feeds on grapevine roots in the Northern Cape, Limpopo and Northwest, resulting in poor growth and eventual death of grapevines. Larvae are protected by waxy cysts. Wingless adult females appear at the soil surface in winter to mate with winged males.

The efficacy of *M. pinghaense* and *S. yirgalamense*, singly and in combination, for control of *M. prieskaensis* females was evaluated against an untreated control in field trials in table grape vineyards in the Northern Cape (Site 1) and Limpopo (Site 2). Treatments were replicated five times in a randomized block design. *Metarhizium pinghaense* conidia and *S. yirgalamense* infective juveniles formulated in diatomaceous earth were suspended in 5 L water plus 0.05% v/v Tween 20 and applied singly and in combination as soil drenches with a watering can to 1 m2 plots where margarodes females were visible at the soil surface. After 48 h females and treated soil were placed in polypropylene bags. After another 5 days, females were collected by sieving and taken to the laboratory to assess mortality and infection by EPF and EPN.

Mortality due to *M. pinghaense* infection averaged 24.61% at Site 1 and 28.98% at Site 2. Infection by *S. yirgalamense* averaged 0.36% and 6.32%, respectively. The combined treatment yielded very low to no infection for both. High mortality in the untreated control was likely because females were damaged during sieving. In a follow-up trial, where females were hand-collected, mortality in the controls averaged 4.6% and 17.2% compared to 38.5% and 62.7% due to *M. pinghaense* infection at Site 1 and 2, respectively.

We conclude that *S. yirgalamense* is not a good candidate for biocontrol of margarodes females, but that *M. pinghaense* shows promise, although formulation of the conidia should be improved to counter adverse environmental conditions.

Chrysomya chloropyga larval meal as a dietary source of iron and protein for broiler chickens and its effect on production parameters

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Categories

• Insects as Feed and Food

Abstract

The state of the global environmental and political climate has highlighted the importance of sustainable food and feed production systems. It has never been more important to identify alternative ingredients in production animals' feed. Insects can provide high quality proteins, fats and minerals such as iron that can be incorporated into animal feed. *Chrysomya chloropyga* is one such species and its larvae have the ability to ameliorate high risk waste such as abattoir waste into nutrients. The aim of this study was to determine the effect of *C. chloropyga* (CC) larval meal on broiler chicken production parameters when included in the diet as source of iron and protein. The larvae were grown of pig abattoir waste until their final larval instar. After self-harvesting, the larvae were blanched, dried and processed into a larval meal. Five soya-maize based isonitrogenous, and isoenergetic broiler treatment diets were formulates and fed to Cobb 500 broiler chickens during their grower and finisher phases, from 14 until 35 days of age. The first two diets contained either $FeSO_4$ or iron lactate as an iron source. For the remaining diets CC larval meal was included at three different inclusion levels: low (CCL) (grower – 11%, finisher 6.5%), medium (CCM) (grower – 13%, finisher – 9.8%) and high (CCH) (grower – 15%, finisher – 13%). The bird weights and feed intakes were measured weekly; and live weight, feed intake, average daily gain (AGD) and feed conversion ratios (FCR) were calculated from these measurements. Significant differences were seen in live weight, feed intake and FCR. The CCM treatment produced heavier live weights and all the CC treatments showed improved FCR. The results indicated that *C. chloropyga* larval meal can successfully be used as a iron and protein source in broiler feeds to replace less sustainable sources.

A survey of fruit fly hosts in the Eastern Cape thicket

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Categories

• Agricultural Entomology

Abstract

Three fruit fly species (Diptera: Tephritidae): *Ceratitis capitata* (Wiedemann), *Ceratitis rosa* (Karsch) and *Bactrocera dorsalis* (Hendel) affect citrus in South Africa. These fruit fly species are quarantine pests and are not tolerated in fresh citrus produce exports from South Africa. All three species are polyphagous, capable of using species from different plant families. A study was conducted over two years (2021-2023) to determine alternate fruit fly hosts in the citrus production area in Sundays River Valley (SRV), Eastern Cape Province. Traps were set up on three farms, distributed across the SRV. In each farm, traps were placed in selected citrus orchards and in the thicket surrounding the orchards to monitor the presence of fruit fly species. Traps were monitored monthly and wild fruit were collected from thicket species as they became available. Fruit collected were incubated in aerated plastic containers in the laboratory to rear infesting fruit flies. Adult specimens collected in traps and reared from fruit were identified using available keys. *Ceratitis capitata* was the dominant species in and around citrus orchards with catches highest in the citrus orchards and in the thicket during the citrus fruiting season (between February and September). Ten thicket species, across 26 samples, were collected. *Lycium ferocissimum*, *Azima tetracantha*, and *Capparis sepiaria* were found to host *C. capitata*, with infestation rates ranging from 33.8 flies/kg fruit to 114.1 flies/kg fruit. Twenty-seven individuals of *Neoceratitis lycii* (Coquillett) was also reared from *Lycium ferocissimum* samples. From these results, fruit fly management can now be focused on the dominant fruit fly pest and its alternate host fruit. Control measures can be timed according to the fruiting times of the cultivated fruit and the alternate hosts. Biological and cultural control techniques could be used to manage fruit fly pests in the natural vegetation surrounding citrus orchards.

Soil fauna contribution to litter decomposition in agroecosystems: effects of management and environmental factors

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Litter decomposition is an important ecosystem process for the maintenance of soil health and long-term sustainability of agricultural landscapes. Soil macro-and mesofauna facilitate decomposition and nutrient cycling ensuring nutrient availability for microbes and plants. Yet, information on how agricultural land-use intensity and environmental conditions influence the contribution of fauna to the process of litter decomposition remains poorly understood. To address this knowledge gap, a litter decomposition study was conducted in agricultural fields under conservation, conventional, and integrated agricultural management, with undisturbed natural grasslands as reference sites. Within each site, four pairs of litterbags of two mesh sizes containing fresh leaves of perennial *Lolium perenne* were used to allow (coarse mesh) and exclude (fine mesh) macro-and mesofauna from reaching the litter. The litterbags were collected at monthly intervals for a period of four months and analysed for fauna diversity and decomposition rates. The highest decomposition estimates were recorded within the integrated and conservation farming sites, and this was attributed to favourable habitat condition which supported a balance of diverse functional fauna communities found in these land-use treatments. Litter mass loss increased in the presence of soil fauna within the coarse mesh litterbags compared to fine mesh where fauna was absent. Litter mass loss was not significantly associated with arthropod diversity or abundance but was strongly linked to arthropod species richness. The contributions of fauna to decomposition were affected by temperature, soil moisture and land-use intensity. These results highlight that less intensive agricultural management maintains functional biodiversity structures which drive the process of litter decomposition and therefore nutrient cycling.

Augmentation of *Aphytis melinus* for the control of red scale in citrus.

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Categories

• Agroecology

Abstract

Aphytis lingnanensis was reared and tested in South Africa in the early 2000s for augmentation against red scale on citrus and was found to be ineffective. *Aphytis melinus* is now available and it is important that the efficacy of augmentation thereof on red scale is determined locally. Field trials, quality assessments and molecular identification on *A. melinus* from two insectaries were done. For field trials, wasps were released during three seasons in three orchards in each of the Eastern and Western Cape, while three comparable orchards were studied as untreated control orchards. Wasps were released over a five- to 10-week period. Red scale infestation was monitored and a sample of 20 infested fruit from each orchard was collected randomly every 4 weeks. *Aphytis* species responsible for parasitism were identified and percentage parasitism recorded. Results of this study of field trials suggest that the augmentation of *A. melinus* did not significantly increase the level of parasitism above that of the untreated control. Five repetitions with six replicates of longevity and flight tests were performed. Wasps from two insectaries were kept at 23°C and 65% RH with honey. Flight tests were performed in tubes of 16 by 30 cm, with a light above a clear sticky ceiling. On average in five replicates, 65%, 33% and 17% *A. melinus* wasps were alive on day one, five and 10 respectively. The overall sex ratio was 1.58 for females to males but 1.05, 2.19 and 2.66 for non-flyers non-crawlers, crawlers and flyers respectively. In flight tests, only 42% of wasps could initiate flight in 24 hours while 52% remained on the tube floor and 6% attempted to crawl upwards. COI genes were sequenced and compared against Genbank sequences using BLAST. Molecular identifications did not confirm morphological identifications for all species, indicating unexpected genetic complexity.

“It’s not what it looks like”: A case of misidentification

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Categories

• Systematics and Taxonomy

Abstract

Psylloids or plant jumping-lice are phloem-feeding insects with about 4000 described species. *Psylloids* are generally host specific and some species are of economic concern. In the Afrotropical region, the indigenous *Trioza erytreae* Del Guercio (Hemiptera: Triozidae) is an important vector of the citrus greening disease. Recently, the exotic *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae), which can also vector the citrus greening disease, became established in parts of East and West Africa. In order to properly manage these disease vectors, their correct identity is crucial. The taxonomy of *psylloids* in the Afrotropical region has been largely ignored with no available updated taxonomic keys. There are approximately 27 described species of *Diaphorina* and approximately 71 triozid species in the Afrotropical region. The aim of the study was to collect and correctly identify *psylloid* specimens in citrus environments using morphological and molecular characteristics. *Psylloid* specimens were collected using yellow sticky traps and sweep nets in and near citrus orchards. Sixteen triozids and 18 *Diaphorina* spp. collected were identified using published and unpublished morphological dichotomous keys. DNA barcodes were generated for each specimen. Specimens of *T. erytreae* from different populations in South Africa resembled morphological similarity but different nucleotide sequence variations in the cytochrome c oxidase subunit 1 mitochondrial gene. The *Trioza erytreae* populations in South Africa could be broadly grouped into 5 clusters. Morphological identifications revealed subtle differences between *D. citri* and some indigenous *Diaphorina* species collected, but molecular techniques used could clearly differentiate them.

The role of diet in establishing pheromonal dominance hierarchies in *Apis mellifera scutellata* workers

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Categories

• Agricultural Entomology

Abstract

In honey bee colonies, the queen is reproductively dominant and produces pheromonal signals that suppress reproduction in workers. In her absence, workers compete to gain pheromonal and reproductive dominance over nest mates. Reproductive status and age-related changes modulate pheromone production in queenless workers and pheromone status (being worker-like or queen-like) influences diet - dominant workers consume less pollen than subordinates as they are fed protein jelly which positively correlates with their ovarian activation. The effect of diet on reproductive physiology or fertility and the subsequent effect on pheromone synthesis has been well established in *Apis mellifera.* However, whether diet is a causative factor in the emergence of pheromonal differences in honey bee workers in the absence of the queen (not mediated through its effect on fertility) is not known. To investigate whether diet affects pheromone production, *A.m. scutellata* workers were fed carbohydrate-only or protein-rich diets for 25 days. The mandibular and tergal gland secretions were analyzed using gas chromatography and the ovarian activation statuses evaluated. A clear link between diet and pheromone profiles were observed with workers fed a protein-rich diet producing mandibular gland chemical profiles more typical of queens. The effect of diet on tergal gland chemical profiles was less distinct, but a shift from fatty acid to n-alkane components were seen in the older workers irrespective of diet, most likely due to ontogeny. Though mandibular gland profiles were queen-like with high proportions of 9-HDA, the levels of 9-ODA remained in the range of non-reproductive workers and their ovaries were not fully activated. Suggesting that diet can prime queenless workers to become false queens but doesn't trigger the transformation into false queens. Understanding the role of diet in establishing pheromonal dominance hierarchies in social insects like honey bees, expands our understanding of the proximate drivers shaping eusociality.

Evaluating biologicals for the control of false codling moth (*Thaumatotibia leucotreta*) in a small-scale field trial

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Stellenbosch University, Stellenbosch, South Africa

Categories

• Invertebrate Pathology

Abstract

False codling moth (FCM), *Thaumatotibia leucotreta*, is a priority pest of citrus, and an important pest of stone fruit and table grapes in South Africa. Its phytosanitary status demands reliable control strategies in a global market that is increasingly sensitive to traditional agrochemicals. Laboratory studies evaluating South African isolates of entomopathogenic nematodes (EPNs) and entomopathogenic fungi (EPF) demonstrate high control potential against FCM. Final instar larvae, pre-pupae, pupae and the emerging moth of FCM are soil-bound, creating unique opportunities for its control using soil-targeted applications. In this study, *in vitro* liquid cultured, cellulose-formulated *Steinernema yirgalemense*, and biphasic-produced, Tween-formulated spores of *Metarhizium brunneum*, were evaluated against late instar FCM larvae in a small-scale field trial in an apricot orchard located close to Ceres, Western Cape province. Dosages of 20 IJs/cm^2 for EPNs, 10^6 spores/cm^2 for EPF, and 5 IJs/cm^2 for EPNs and 10^6 spores/cm^2 for EPF in combination, with water as control, were applied to caged FCM larvae buried underneath the canopy of orchard trees. A completely randomised design was used, with eight application plots of 1 m^2 for each treatment. Mortality was assessed after seven days, and nematode infection was confirmed through dissection (EPNs) or sporulation (EPF). A follow-up study evaluated the effect of temperature on EPN pathogenicity in laboratory trials. This study is part of a larger collaborative effort which aims to commercialise locally isolated biological control agents for use in integrated pest management strategies in South Africa.

Assessment of the spread, host range and drivers of the polyphagous shot hole borer (PSHB) in indigenous South African forests

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Categories

- Invasive Insects

Abstract

The polyphagous shot hole borer or PSHB (*Euwallacea fornicatus*) is an invasive ambrosia beetle native to Southeast Asia. It was discovered in South Africa in 2017 and has since spread into eight of the nine provinces of the country. It has been recorded attacking more than 144 tree species, including 67 indigenous trees. The impact this beetle and its symbiotic fungus (*Fusarium euwallaceae*) will have on indigenous forest health is unknown but given its diverse host range and ability to spread rapidly it could have major ecological impacts. The aim of this project was to gain insight into the spread, host range and drivers of PSHB attack in indigenous forest ecosystems in the Western Cape and Kwa-Zulu Natal provinces. Permanent monitoring plots were used to assess the impact of this beetle over a five-year period. The PSHB has spread into natural forests where it is attacking many native tree species. Certain species are more susceptible to attack by PSHB with many being found to be reproductive hosts of the beetle. The number of infested trees increased consistently over the 5-year monitoring period, with a higher increase in forests in Kwa-Zulu Natal. In the Western Cape 17 attacked tree species were found while in Kwa-Zulu Natal over 20 species were attacked. The PSHB beetle is spreading at a rapid rate and poses a major risk to forest health throughout Africa.

Predicting the effects of temperature extremes on invasive insects requires a multi-life stage perspective

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University of Stellenbosch, Stellenbosch, South Africa

Categories

• Invasive Insects

Abstract

Invasive insects have negative effects on native species and these impacts can increase if invasive species differentially tolerate temperature extremes associated with climate change. While temperature tolerance has been examined in many invasive insects, there is limited understanding of how temperature affects survival across life-stages. For example, the temperature tolerances of mobile stages such as larvae and adults are likely to differ from those of immobile stages (eggs and pupae) as these stages have limited thermoregulation capacities, but these responses are also dependent on the thermal exposure experienced by different life stages in the field.

This study aimed to assess the temperature tolerance of different life-stages of *Harmonia axyridis* f. *succinea* (Pallas) (Coleoptera: Coccinellidae), an invasive beetle that has quickly established across South Africa, with expected impacts on native ladybird communities. We used a combination of lethal temperature assays, field surveys of beetle abundance and microclimate monitoring in semi-urban areas around Stellenbosch, to examine how life stage-specific microclimates mediate the realized survival of the local population.

We found that most beetle life stages occur throughout the year with notable peak abundances in winter when aphids are plentiful. Thermal assays indicated that eggs are less tolerant to extreme temperatures than larval and adult stages. These results go counter to the expectation that non-mobile stages should have increased thermal tolerance breadth to withstand temperature variability and extremes. By combining life-stage specific microsite use, microsite temperatures and acute tolerance limits, we show that eggs remain the most vulnerable stage to thermal stress. Our findings reinforce that consideration of ontogeny and field microclimate data are essential for understanding and managing the response of invasive insects to climate change.

Keywords: Harlequin ladybird; thermal stress indices; activity restriction; ULT50; LLT50; climate warming.

The effects of urbanisation on bee and wasp communities in Cape Town, South Africa

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Bees and wasps provide essential ecosystem services by pollinating urban plants and foods. However, there are massive global declines in many insect groups, and little is known about the impacts of urbanisation on pollinators in rapidly urbanising areas of Africa. Within the Durbanville area of Cape Town, we investigated the effects of urbanisation and availability of floral resources on bee and wasp (pollinator) diversity, community composition, and nesting guild distribution across an urban-rural/natural gradient. Using pan traps, specimens were collected from 18 sites in austral spring 2019 and 2020. A total of 433 bee and 45 wasp specimens, comprising of 45 bee and 27 wasp morphospecies respectively were collected. Bees from the family Halictidae (particularly *Seladonia* and *Patellapis* species) were the most abundant. Except for *Apis mellifera*, all other bee species were solitary, and most (86.7%) collect pollen from flowers. Four different nesting guilds were identified, with the most common being ground-nesters (68.9%). Floral resources, rather than the degree of urbanisation, had a strong effect on pollinator diversity and community composition. This study supports the development of several cost-effective and achievable conservation initiatives, such as adopting no-mow periods during austral spring and developing small-scale bee-friendly floral-rich patches, which can be undertaken by existing municipal structures and private landowners alike. Suggested future studies include investigating the ways pollinator diversity and community composition is influenced by 1) individual floral species and characteristics, 2) the size, shape, and location of habitat/floral patches, and 3) the effects of urban warming.

Generalised pollination of *Nerine laticoma* in the Kalahari

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Categories

• Biological Interactions

Abstract

Generalised pollination systems with both diurnal and nocturnal visitors have been documented in many angiosperm species. These species often contribute in differing proportions to pollen transfer and to seed set. The flowers of *Nerine* species are usually pink to white, with no nectar tube or spur making nectar accessible to a variety of visitors. The anther and stigma however are often displaced from the nectar allowing only a subset of visitors to act as pollinators. In some species of *Nerine* this has been interpreted as specialized for pollination by long-tongued flies or butterflies. In this study, we investigated the pollination of *Nerine laticoma* in the Kalahari region of southern Africa, where large stands of hundreds of flowers can be found. We aimed to (1) describe its pollination biology and breeding system and (2) examine the contribution of diurnal and nocturnal flower visitors to female fitness. A large variety of species were found to act as pollinators for this species, namely butterflies, carpenter bees and nocturnal moths. The diversity and abundance of visitors differed significantly between the two years this study was conducted. Night visitation rates however tended to be higher during both years. *Nerine laticoma* appears to be a generalist species which is not uncommon in arid regions due to the reliance on rain for flowering in these areas.

Labile proboscis length evolution in a lineage of flower-visiting flies (Nemestrinidae)

Genevieve Theron[1,2], Allan Ellis[3], Bruce Anderson[3], Anton Pauw[3], Steven Johnson[2], Timotheus van der Niet[2]

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Categories

• Systematics and Taxonomy

Abstract

Modification of mouthparts into a proboscis allows for the acquisition of nectar from floral tubes. Proboscides evolved independently in most orders of flower-visiting insects and through coevolution, with flowers, they can even greatly exceed body length. However, extremely exaggerated traits likely incur developmental and functional costs. These costs may constrain, and under some ecological conditions even reverse, evolutionary transitions to longer proboscides in lineages. Using species-level phylogenetic comparative methods we reconstructed the evolution of proboscis length in a clade of long proboscid nemestrinid flies from southern Africa that includes the genera *Moegistorhynchus*, *Prosoeca* and *Stenobasipteron*. Using a pruned phylogenetic tree, we found a positive interspecific allometric relationship between body size and proboscis length after correcting for phylogenetic relationship, but there was no clear phylogenetic signal in either of these traits. A similar positive intraspecific relationship between proboscis length and body size is evident across morphospecies with long proboscides. Using continuous character state reconstruction, we inferred that the ancestor had a proboscis longer than the median of the current ingroup. Discrete stochastic character state mapping showed that there were transitions between all proboscis length categories (short, long and very long) and that transitions away from short proboscides were most common. An analysis of structured rate permutations on phylogenies did not detect any association between proboscis length and the rate of diversification. Our results indicate that absolute proboscis length is a highly labile trait that may reflect adaptations to the local environment for optimal foraging on flowers.

Experience and lessons learnt on the application of SIT against the primary vector *Anopheles arabiensis* in South Africa

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

South Africa has begun initiatives to eliminate malaria transmission within its borders. Some malaria-affected districts meet the World Health Organization (WHO) criteria for pre-elimination, requiring control initiatives to be shifted towards elimination. Although effective, current malaria control activities, particularly vector control intervention using indoor residual spraying (IRS), are insufficient to eliminate malaria. Against this background, additional vector control interventions are needed to supplement existing strategies. The use of the sterile insect technique (SIT) was proposed and is now at an advanced stage of development.

SIT is being implemented in three sequential phases. Phase I was the pre-feasibility Phase which aimed to provide scientific arguments and baseline information for using the SIT as a complementary malaria vector control strategy. This phase included identifying a pilot release site and intensive baseline entomological surveillance at the release and control sites that yielded critical information concerning the population dynamics of the targeted *Anopheles arabiensis* population. Phase II involved refining Phase I findings and developing a genetic sexing strain, irradiation/sterilization studies, community engagement including knowledge, attitude and practices (KAP) survey, developing the capacity to mass rear mosquitoes and assessing the technical feasibility of the technology. The project is now in Phase III. This Phase aims to demonstrate the operational applicability of SIT through field pilot trials in northern KZN, South Africa. The purpose of this presentation is to discuss the experience and knowledge gained in developing the SIT as a malaria vector control tool in South Africa, focusing on the challenges and status of the project. Insight into the ongoing pilot sterile male releases will be discussed.

Development of CRISPR/Cas9 gene editing tools to control major insect pests of agriculture and forestry

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Categories

- Invasive Insects

Abstract

The agricultural and forestry sectors are crucial to the development of the African economy. These sectors are critical for the future of food security and sustainability globally. Agricultural and forestry sectors are seriously threatened by the dramatic increase in pest pressure in recent decades through globalization and climate change. Current methods of pest control such as biological control, planting of tolerant material and the application of chemicals are either struggling to cope with increasing pest pressures or have serious negative side-effects on the environment. A new and potentially powerful, environmentally friendly approach is emerging through gene-based, targeted pest management. These developments are particularly driven by the discovery of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) that has revolutionized gene editing for various organisms, including insect pests. Exciting breakthroughs have been made in this field in recent years to use gene editing to target pest of agriculture and forestry. The focus of our work has been to develop gene editing platforms for major insect pests of forestry and agriculture in Africa, but that also has global relevance; these include the Pine woodwasp, *Sirex noctilio*, and the Eucalyptus snout beetle, *Gonipterus* sp. 2., as well as the Maize Stalk Borer, *Busseola fusca*, and the Fall Armyworm, *Spodoptera frugiperda*. Significant progress has been made towards the development on the various elements of the gene editing systems for these insect pests to the point where *in vivo* testing can commence.

‘ThermalSampleR’: An R package and Shiny GUI to perform sample size calculations for thermal physiology studies

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Categories

• Physiological Ecology

Abstract

Thermal physiology studies have become increasingly popular in recent years to understand species distributions, responses to different environmental conditions, predict possible invasions and forecast the effects of climate change. Recently, several studies have shown that results and inferences obtained from thermal studies can be affected by methodological decisions (e.g. pre-experimental acclimation periods, temperature ramping rates and ramping intervals). Duffy et al. (2021) demonstrated that the number of individuals tested during the experiment (sample size) can significantly bias the results obtained and any inferences drawn. Determining the sample size requirements for a study is an essential component of study design, with consequences for the logistics, ethics and rigor of the study. However, calculating sample size requirements is not an easy task. In this talk, we present ‘*ThermalSampleR’*, an R package and R Shiny Graphical User Interface that allows users to easily assess sample sizes required to obtain reliable and accurate thermal physiology parameters (e.*g. Critical thermal limits [CTmin, CTmax*]). We demonstrate the package functionality using a simple worked example to obtain an accurate estimate of the (1) CTmin for a single population, and (2) the difference in *CTmin* between two populations.

Interactions between pest species, crops and control options contribute to resistance evolution by *Phthorimaea* spp.

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Categories

• Agricultural Entomology

Abstract

Insecticide resistance is only one of the possible reasons for the variable results obtained with chemical control of pests under field conditions. Potato tuber moth (PTM), *Phthorimaea operculella* (Gelechiidae), is an important pest of potato and *Phthorimaea absoluta* (Gelechiidae) an important pest of tomato in the world. However, both these pests occur on both these crops. The potato and tomato industries in South Africa are heavily reliant on insecticides for pest control. Control failure of PTM has been reported by several farmers in South Africa. The susceptibility of PTM, sampled from four localities in the main potato producing areas in the country was assessed for *azinphos*-methyl (*organophospate*), *lambda-cyhalothrin* (*pyrethroid*), *lufenuron* (*benzoylureus*) and *indoxacarb* (*oxadiazine*). Results indicated that control failure with *azinphos*-methyl, lambda-cyhalothrin and lufenuron can be expected, but that indoxacarb should provide effective control. To mitigate control failures, spray programs were adapted to include active ingredients such as the *diamides*, *chlorantraniliprole* and *flubendiamide*, *pyridalyl dichloropropene*-derivative as well as the *spinosyns, spinosad and spinetoram.* These active ingredients are, however, also intensively applied on tomato for control of P. absoluta. The polyphagy of *P. operculella* and *P. absoluta* on *solanceous* crops and application of the same insecticides on potato and tomato for control of these pests increases the risk for insecticide resistance evolution by both pests. Integrated pest management strategies that consider both pest species, both crops and different control options on a matrix basis is important for sustainable *Phthorimaea* spp. management on solanaceous crops in South Africa.

Testing reproductive compatibility of an introduced and native population of the parasitoid *Anaphes nitens*, for the purpose of improving biocontrol of the *Eucalyptus* Snout Beetle in South Africa

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Categories

• Biological Interactions

Abstract

The Eucalyptus Snout Beetle *Gonipterus* sp. n. 2 is a destructive invasive pest of *Eucalyptus* plantations in South Africa, originating from Australia. Soon after its discovery, the egg parasitoid *Anaphes nitens* was imported into South Africa from its native range in South Australia for biological control. The parasitoid was generally effective in suppressing this pest, but recent beetle outbreaks suggest a breakdown of biocontrol. Several hypotheses have been proposed as an explanation, one of which is a lack of genetic variation in the parasitoid due to a bottleneck at introduction. In addition, the original introduction of the parasitoid was from an area climatically different to where infestations of *Gonipterus* sp. n. 2 occur in South Africa. A new population of the parasitoid was thus imported from Queensland, Australia, an area which is better climatically matched to the current *Eucalyptus* growing areas in South Africa. This study assessed the reproductive compatibility between the South African *A. nitens* population and the newly imported Australian population. Reciprocal crosses were performed, and fecundity, sex ratio and development time were compared to control crosses. No significant differences were found in the number of replicates producing offspring, or for total, male, or female offspring. Furthermore, no significant differences in sex ratio or development time were observed. This indicates there was no negative effect of crossing on parasitoid fitness, as is sometimes observed when distantly related populations are crossed. No signs of endosymbionts interfering with reproduction were observed as most crosses produced offspring, and sex ratios were similar between crosses. In conclusion, no negative effects of crossing these populations were found, but also no improved fitness was observed under the current experimental conditions. This study opens up possibilities for a field release where establishment of the new population and a potential fitness advantage will be further assessed.

The short-term impact of *Gonipterus* sp. n. 2 damage on *Eucalyptus* tree growth

Harris Keetse[1], Benice Sivparsad[2], Ilaria Germishuizen[2], Brett Hurley[1]

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Categories

- Invasive Insects

Abstract

The Eucalyptus snout beetle, *Gonipterus* sp. n. 2 (Coleoptera: Curculionidae) is a serious defoliator of *Eucalyptus* in South Africa that threatens the productivity of *Eucalyptus* plantations. Although defoliation resulting from adult and larvae feeding has been reported to cause substantial reductions in tree growth, reliable quantitative estimates of the impact of feeding of *Gonipterus* sp. n. 2 on the growth of *Eucalyptus* spp. are lacking. The objective of this study was to quantify short-term impacts of *Gonipterus* sp. n. 2 feeding on the growth of *Eucalyptus dunnii*, one of the main commercial eucalypt species in South Africa. An insect exclusion trial laid out in a randomised complete block design was established at Hodgsons and Sutton plantations in the KwaZulu-Natal Midlands. At each site there were three treated (chemical exclusion) and three untreated plots. Tree growth parameters, namely height and diameter at breast height (DBH), were measured when trees were ~2 years old and used to calculate wood volume. Damage by *Gonipterus* sp. n. 2 was assessed and number of egg capsules and larvae of *Gonipterus* sp. n. 2 were counted every six weeks starting from when the trees were ~1 year old. In Sutton, a site with one initial damage event, there was no significant difference in tree growth between treated and untreated plots. Whilst in Hodgsons, a site with three damage events, there was a significant reduction in height and volume in the untreated plots. Tree damage was fairly well correlated to reduction in volume and density of egg capsules and larvae of *Gonipterus* sp. n. 2 were highly correlated to the damage on the trees. This study highlights the potential loss of volume from defoliation of *Gonipterus* sp. n. 2, but also indicates that the impact of defoliation is determined by the frequency of damage events.

Mechanisms underpinning phenotypic plasticity of desiccation resistance in *Ceratitis* species

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Categories

- Physiological Ecology

Abstract

Closely related fruit fly species vary in geographic distributions with each species encountering a specific set of environmental conditions. This suggests that each species has underlying physiological traits that differ from others. We explored desiccation mechanisms in *Ceratitis* to determine if basal and/or plastic desiccation responses differ between broadly distributed (*Ceratitis capitata*) and narrowly distributed species (*Ceratitis cosyra, Ceratitis podocarpi* and *Ceratitis rosa*). The four species were acclimated with three temperature and humidity pre-treatments after which survival and different water loss traits were measured under dry conditions. Survival of *C. capitata* improved by 43% following both temperature and desiccation pre-treatments, while survival in the other species increased by 4-30% only after a desiccation pre-treatment. *Ceratitis capitata* showed more plasticity in several water loss traits, and small changes in activity, cuticular water loss and excretion after pre-treatments contributed to low water loss. Secondly, the role of metabolic water gain in desiccation physiology was studied by enriching body stores through larval diets with ^{13}C labelled stable isotopes (*^{13}C-glucose, ^{13}C-leucine and ^{13}C-palmitic* acid) in a desiccation resistant (*Ceratitis capitata*) and desiccation sensitive species (*Ceratitis rosa*). Differential mobilisation of *^{13}C-labelled* body fuels during desiccation stress indicates that *C. capitata* was able to increase lipid oxidation both during and after desiccation while *C. rosa* mobilised lipids only after a desiccation event. Therefore, *Ceratitis* species rely on unique combinations of desiccation resistance strategies, and the species with the most flexible responses to stressful, fluctuating environmental conditions (*C. capitata*) derives the largest benefit.

Pesticide residue analysis reveals public health threat in African vegetable markets

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Categories

• Agricultural Entomology

Abstract

Overuse of pesticides in horticulture raises public health risks. The injudicious use of hard pesticides has been exacerbated by increased pest pressure triggered by increasing global temperatures. However, the magnitude of public health risks remains unknown in most vegetable markets in developing countries. We used cabbage as a model crop to assess the magnitude of risk and how farmer responses to diamondback moth *Plutella xylostella* L. (Lepidoptera: Plutellidae) pest pressure translate into public health pesticide risks. Cabbage is staple in Africa, providing nutrition and livelihoods. However, production is hampered by the diamondback moth. Farmers respond to the pest pressure by using hard pesticides, applied prophylactically and in cocktails. Using the quick-easy-cheap-effective-rugged and safe (*QuEChERS*) multi-residue analysis method, gas chromatography mass spectrometry (*GC-MS*) and liquid chromatography-tandem mass spectrometry (*LC-MS/MS*), we investigated the occurrence and magnitude of pesticide residues at three vegetable market levels (farmgates, vendors and supermarkets) in Botswana. We detected pesticide residues in 74.1% of the samples of which 33.4% had multiple compounds. Farmgates recorded the highest pesticide residues ($p< 0.05$). We multi-detected 10 low-highly hazardous pesticides [World Health Organisation (*WHO*) classes 1B & 2], including organophosphates, pyrethroids, neonicotinoids, and carbamates. Fifty percent of the detected pesticides from farms and supermarkets had residue levels exceeding the Codex Maximum Residue Limit (*MRL*) thresholds. However, estimated daily per capita consumption was lower than the WHO Average Daily Intake (*ADI*) and Acute Reference Doses (*ARfDs*). These results indicate presence of multiple and excessive pesticide residues in routinely consumed vegetables on African markets and may contribute to a chronic or cataclysmic public health hazard. Urgent attention is needed to enforce effective regulatory policies against pesticide misuse and invest in non-chemical pest management alternatives. Meanwhile, continuous monitoring of pesticide residues is recommended to determine market occurrence of pesticide residues on other widely consumed horticultural produce and seasonal effects.

Plant-Pollinator Networks Vary across Green Spaces in Western Cape Urban Areas

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Stellenbosch University, Stellenbosch, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Recently, urban areas have been touted as a refuge for insect pollinators, especially bees. This may be because green spaces embedded in urban areas can influence pollination services through the provision of nesting sites and resources which may result in increased niche diversity, enhanced biodiversity and consequently pollination. However, this may not give an accurate picture of the pollination function going on in urban areas. Plant-pollinator networks can provide a description of the interaction between plants and pollinators on a community level and help us understand their influences better. Hence, to assess the effectiveness of cities as refuges for insect pollinators and their ecosystem functions, there is a need to study the plant-pollinator networks in such cities. The study was conducted in eight 25 m2 sites each in the urban zone (home gardens), agricultural area (biodiversity friendly vineyards) and nature reserve in Stellenbosch/Somerset West city areas of the Western Cape. At each site, a meandering walk of 15 minutes was done, and during this time, insect pollinators visiting the stamen of flowering plants and the flowering plants visited were recorded and identified. Species collected were identified using known identification keys and were compared with insect pollinator collections at the institution. The insect-flower interaction network was constructed for each study site and the network indices generated were compared between the green spaces using GLM (Poisson error distribution). Results showed that the networks and taxa composition varied between the green spaces. This shows that every green space is important for insect pollinators and should be managed sustainably to increase habitat complementarity between the green spaces in urban areas.

Illegal sand mining alters species composition of ants, beetles and spiders in a grassland: a case study in Eastern Cape, South Africa

Inam Yekwayo, Asabonga Mngeni

Walter Sisulu University, Mthatha, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

In the Eastern Cape, natural landscapes that are adjacent to rivers and the sea are threatened by illegal sand mining, which occurs without prior assessment of biodiversity. Sand mining activities lead to the reduction of vegetation cover and plant species richness. Generally, species richness of arthropods correlates positively with plant species richness. Thus, it is important to test the effect of sand mining on arthropods diversity. In this study we compared species richness, abundance and composition of ants, beetles and spiders between sand-mined areas and the surrounding undisturbed grassland. Arthropods were collected using pitfall traps in eight sites in sand-mined areas and eight sites in unmined grassland. The sand-mined and unmined areas supported similar species richness and abundance of arthropods. However, species composition of arthropods between the two areas was significantly different. Additionally, both the sand-mined and unmined areas had 11 indicator species each, and there were no shared indicator species. We used the “disturbance-tolerant species hypothesis” and the “competitive displacement hypothesis” to explain these results. High species richness and abundance in sand-mined areas may have been due to disturbance-tolerant species that colonized the area. As such, disturbance-tolerant species may have displaced specialist species, which are sensitive to disturbance. Given that our study showed that illegal sand mining change species composition of arthropods, sand mining should occur in designated areas to reduce the impact of mining on arthropods and enhance conservation.

Host-foraging strategies of five local entomopathogenic nematode species in South Africa

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Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

Categories

• Biological Interactions

Abstract

Entomopathogenic nematodes (EPNs) are obligate parasites of soil-dwelling insects and are used as biological control agents for many insect pests. These nematodes have a free-living third growth stage called infective juveniles (IJs), which are responsible for foraging and infecting suitable insect hosts. Infective juveniles exhibit three host-foraging strategies: cruising, ambushing and intermediate foraging strategies. Understanding the host-foraging strategies can help improve the potential of EPNs as biological control agents. This has been achieved for a few commonly used, commercialized EPN species, but research is lacking for the local and newly identified EPN species/isolates. The current study investigated the host-foraging strategies of five local South African EPN species, including *Heterorhabditis noenieputensis*, *H. safricana*, *Steinernema fabii, S. jeffreyense* and *S. yirgalemense*, by assessing their dispersal behaviour. Of the five EPN species, *H. noenieputensis*, *H. safricana*, *S. jeffreyense* and *S. yirgalemense* showed a positive response to the presence of the wax moth larvae, whereas *S. fabii* showed a negative response. The four EPN species that showed a positive response to the presence of the host also provided 100% mortality of wax moth larvae that were buried in sand at a depth of 10cm, whereas *S. fabii* provided the lowest mortality of 34%. The average distance travelled by all five EPN species decreased on the rough textured substrate compared with the smooth textured substrate. The observed dispersal behaviour suggested that *H. noenieputensis*, *H. safricana*, *S. jeffreyense* and *S. yirgalemense* use a cruiser foraging strategy whereas *S. fabii* uses an ambusher foraging strategy.

An update on the current state of South African pseudoscorpion taxonomy.

Jan Andries Neethling

National Museum, Bloemfontein, South Africa

Categories

• Systematics and Taxonomy

Abstract

Despite recent taxonomic revisions and phylogenetic analysis, detailed morphological and ecological data is still lacking for the vast majority of pseudoscorpions, including the poorly known South African fauna. South Africa currently has 162 known species in 17 families, with over 70% of these species' endemic to the country. Early research on the South African *Pseudoscorpiones* fauna primarily consisted of taxonomic descriptions and, apart from a few local contributions, most of the research was conducted by foreign scientists. When they retired, taxonomic descriptions of new species ceased. Later research includes the publication of a species checklist and contributions to karyotype studies and phylogenetic analyses. The need for detailed revisions of our indigenous fauna was recognized, and in 2017 the first article was published, revising the South African Geogarypidae. The second article, on the revision of the South African Gymnobisiidae, has been submitted for publication in 2023. Future short-term research will first focus on revisions of previously described species, the description of any new species and reducing the gaps in the largely unsampled areas in the interior of the country. Long-term research will focus on gaining detailed biological and ecological data. Here a brief report is presented on the progress of the project thus far, and what still needs to be achieved.

Design and development of an irradiation surface for bulk irradiation of an African malaria vector: Steps towards the development of SIT

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

The South African Mosquito SIT Programme is now in the piloting phase. Several key aspects including bulk irradiation require optimization during field sterile male releases. Current irradiation protocols were primarily designed for small-scale irradiation to determine baseline dose-response curves using a Gamma cell irradiator. It was necessary to develop and optimize tailor-made large-scale methods to ensure consistent and correct dosages delivered to each sterile male *An. arabiensis* on a large scale. This work describes the designing, building, and testing of an irradiation surface for use during bulk male *An. arabiensis* irradiation.

We developed a 3D printed surface capable of holding four modified 50ml Falcon tubes tailor-made to fit into a one-liter canister of a RAD-Source 2400 Q4 X-Ray emitter. Each Falcon tube can hold 5000 adults giving a capacity of 20, 000 per canister. The X-ray device features 6 carousel canisters giving a total capacity of 120, 000 males per run. To map the absorbed dose by each mosquito, Fricke dosimeters were placed into each tube containing 20, 000 mosquitoes and irradiated at 80Gy based on a predetermined reference dose of 19.44 Gy/min. Subsequently, efficacy of the irradiation setup was monitored by assessing the physiological and reproductive parameters of the irradiated males.

Uniform simultaneous bulk irradiation for up to 120,000 adults per irradiation cycle has been developed and successfully tested. Dose mapping showed that each mosquito received approximately 79±3.4SD Gy. The survival rate and flying ability of irradiated males were not affected with respect to controls. Finally, sufficient sterility was induced with no hatchlings observed from eggs laid by females mated by these males.

The brown locust in relation to Karoo ecosystem characteristics and processes - knowns, unknowns and relevance to rangeland management

Joh Henschel[1,2], Frances Duncan[3], Justin du Toit[4], Suzanne Milton[1,5], Helga van der Merwe[1]

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Categories

• Agricultural Entomology

Abstract

Populations of polyphenic brown locusts *Locustana pardalina* (Walk.) alternate between resident solitaria grasshoppers in the Karoo via a transiens phase to nomadic gregaria locusts that periodically swarm across and beyond the Karoo. Concerns about crop damage led to this species being declared a pest in 1911 to be controlled with insecticides. Despite over 225 years of records of brown locust outbreak events and a considerable body of research during the early to mid-20th century, research impetus waned while outbreak events, as well as efforts and financial and ecological costs of chemical control, have steadily escalated. This review highlights J.C. Faure, C.J.B. Smit, and A. Lea's particularly insightful field observations between the 1920s and 1960s, which have yet to be followed up with further research. We revivify knowledge of brown locust solitaria ecology, including their diet, mainly consisting of the short grass, *Enneapogon desvauxii*, the cumulative build-up of egg banks with quiescent embryos, and how five to seven successive generations build up densities until crowding brings about incipient outbreaks of *gregaria* locusts, which can aggregate into large swarms that depart to remote locations. Surprisingly, no quantitative records exist of the potential negative impacts at large scales of brown locusts on rangeland grazing or crop yields, nor has the significance of accelerated nutrient cycling and turnover of Karoo vegetation by locusts been studied. Although the quality of rangeland management affects the dynamics of outbreak centres, this recognition has not been followed up with experiments and detailed observations to make definite recommendations on farming practices. We suggest several avenues of research that build up on the existing knowledge with modern techniques and fill the most important knowledge gaps to improve managing brown locust populations sustainably.

You are what you eat: How the dung beetle gut microbiome differs between five distinct feeding strategies.

Johann de Beer[1], Kazeem Alayande[2], Christian Pirk[1], Rasheed Adeleke[2], Catherine Sole[1]

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Categories

• Biological Interactions

Abstract

Gut microbes contribute significantly to the successful functioning of most insect groups, by bolstering various metabolic and biochemical processes. However, until recently, the microbial diversity within the gastrointestinal tracts of most animals, as well as the variables influencing them, were widely ignored. There are at least five different dietary specialisations present in South African dung beetles, namely; *coprophagy, necrophagy*, *detritophagy, fungivory* and *carnivory*. Due to their large diet breath, this study aimed to compare the differences in gut bacterial communities between seven dung beetle species found within five different genera, each with a distinct dietary specialisation. The guts of each individual were dissected, bacterial DNA was extracted and finally, the 16s rRNA hypervariable region V4-V5 was sequenced utilising the Illumina *NovaSeq* platform. The three most common phyla observed within our samples were Firmicutes, Proteobacteria and Bacteroidetes. Our findings show that diet has a significant impact on the gut bacterial composition of various dung beetle species. Additionally, the five different dietary specialisations grouped separately from one another on both NMDS and PCoA plots. The millipede-feeding species, *Sceliages brittoni* and *S. hippias*, both possess the most distinct and least diverse gut microbiome when compared to all other dietary specialisations in this study. Furthermore, a common bacterial symbiont associated with leaf-cutter ants, *Entomoplasmatales*, occupies between 15%-30% (relative abundance) of their gut microbiome. It is possible that the defensive secretions (*hydrogen cyanide*) produced by millipedes affect which bacterial taxa are able to inhabit the guts of *Sceliages* species. Characterisation of the gut microbiome is the first step towards addressing more complex questions about the function of dung beetle gut microbes. Ultimately, this research provides insight into the impact of diet on the gut microbial makeup of dung beetles.

The search for an effective artificial diet for the Cape fly, *Ceratitis quilicii* (Diptera: Tephritidae)

John-Henry Daneel, Aruna Manrakhan

Citrus Research International, Mbombela, South Africa

Categories

• Agricultural Entomology

Abstract

Fruit fly pests are of phytosanitary concern to markets importing fruit from South Africa. In order to determine best risk mitigation measures for these pests, research has to be conducted in controlled conditions with laboratory reared individuals. Depending on the research requirements, laboratory cultures need to be maintained in high numbers, thus requiring high performance larval diets. In laboratory cultures, larval stages of many fruit fly species are reared on an artificial media. *Ceratitis quilicii*, Cape fly, is a newly described fruit fly species which was previously considered the same species as its congener complex species member, *Ceratitis rosa*, Natal fly. The latter has been successfully reared on an artificial larval medium consisting of Brewer's yeast and dehydrated carrot powder. A study was carried out to determine the larval and pupal performances of the Cape fly on the larval diet of the Natal fly and on modified versions of the Natal fly diet. Modifications of the diet included: (1) the replacement of Brewer's yeast with enzymatic yeast hydrolysate, (2) the addition of paprika to the diet, and (3) the addition of multivitamin and multimineral supplements to the diet. The effects of egg density (50 eggs/100g, 100 eggs/100g, 500 eggs/100g, 800 eggs/100g and 1500 eggs/100g) on the best performing larval medium were subsequently determined. The replacement of Brewer's Yeast by enzymatic yeast hydrolysate, with addition of either paprika or a commercially available multivitamin and multimineral product, further increased larval survival and pupal survival. Larval and pupal survival were higher at a density of 500 eggs/100g of larval medium. Based on the results of this study, an effective larval medium was developed for the Cape fly. This is an important development as it will allow for more research, including development of phytosanitary treatments on this new fruit fly species.

Fall armyworm in Africa: its economic, ecological and socio-political impacts.

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North-West University, Potchefstroom, South Africa

Categories

• Invasive Insects

Abstract

The invasion and establishment of Spodoptera *frugiperda* in tropical and sub-tropical areas of Africa impacts significantly on food security and agro-ecology. The impact of this species is also evident at the socio-economic level, leading to declarations of national 'disasters', influencing regulatory and political decisions. An initial estimate of crop losses in 12 African countries was between US$ 2.4–6.2 billion, and in Ghana and Zambia, the annual loss estimates for 2017 were US$177 million US$159 million respectively. Farmer's perceptions of losses in different African countries range between 11 and 54% but actual on-farm assessments recorded much lower losses, showing that yield losses may be overestimated. To mitigate these impacts, several governments subsidized the use of synthetic insecticides, resulting in their large-scale use on maize in many countries where *S*. *frugiperda* occurs While insecticides were rarely applied by small holder farmers on maize in the past, it is now increasingly being done in areas where this pest prevails. Due to its high invasive potential, fall armyworm also has ecological impacts since it now occurs in mixed populations with other lepidopteran pests where inter-species competition may lead to changes in species complexes. The indirect impacts of this new pest in Africa included the establishment of new and progressive initiatives regarding pest management, training of farmers and general awareness of invasive species and IPM. It is also likely that the devastating damage caused by fall armyworm may influence perceptions regarding genetically modified Bt maize, and that it may affect future decision making regarding this technology.

Larval environment and insecticide resistance in *Anopheles* spp. in the Ehlanzeni district, Mpumalanga.

Kayla Noeth[1,2], Maria Kaiser[1,2], Givemore Munhenga[1,2], Shune Oliver[1,2]

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

In South Africa, malaria, transmitted by *Anopheles* spp., remains a consistent public health threat. While significant efforts have been made to control malaria, local transmission of the disease still occurs. This low-level persistent malaria transmission, often occurring outdoors, is known as residual malaria, and is driven in part by a poor understanding of vector bionomics. The larval environment is a key driver of mosquito fitness. The aquatic environment in which immatures develop can also alter the adult gut microbiota. Mosquito gut microbial composition is a critical determinant of life history traits and can modulate vector competence and insecticide resistance. The development of non-insecticidal driven insecticide resistant *Anopheles* populations may be of particular importance in Mpumalanga, due to the sizeable agricultural, mining and coal industries which produce large amounts of agrochemical, heavy metal, and plastic pollution. This study aimed to characterise the chemical and bacterial composition of *Anopheles* larval habitats in Mpumalanga. In addition, this work examined the effects of larval habitats on gut microbiota of the wild *An. gambiae* complex from the region. Water samples and larvae were collected from ten sentinel sites in the Ehlanzeni District over a one-year period. The chemical composition of the water samples was characterised using calorimetric standardised water quality tests. The bacterial composition of the water samples, as well as in the midguts of the larvae, were identified using matrix-assisted laser desorption/ionisation – time of flight (*MALDI-TOF*) mass spectrometry (MS). The insecticide resistance profile of adults emerging from polluted sites at Vlakbult and Block A was examined. A common microbe found in both the water samples and the larval midguts was the pathogen *Klebsiella oxytoca. K. oxytoca* is capable of degrading organochlorides such as *endosulfan* and DDT. These findings suggest adaptation of the local *An. gambiae s.l* population to breeding in polluted water.

Potential impacts of the emerging invader *Cylindropuntia pallida* (Rose) F.M. Knuth on the arthropods and nematodes in South Africa

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Cylindropuntia pallida (Rose) F.M. Knuth, is an emerging alien cactus species in South Africa. It is native to Mexico and associated with horticulture trade in South Africa. The ecological impacts of *C. pallida* are not well known and thus a limitation in effective management of the species. For example, ground-dwelling insects and free-living nematodes are sensitive to habitat disturbance and can thus be used as indicators to monitor potential impacts. Therefore, we aimed to determine impacts of *C. pallida* on ground-dwelling insects and free-living soil nematodes. We set up the pitfall traps in areas invaded and uninvaded by *C. pallida* at Edenburg (Free State), Karoospruit (Free State), Colesberg (Free State), Richmond (Northern Cape) and Cookhouse (Eastern Cape). Soil samples for nematodes evaluation were also collected. A soil food web analysis based on the c-p indices of the nematodes was conducted to determine the soil quality. Preliminary results suggested that a total of 2371 insects from 9 orders and 38 families were collected. The order Hymenoptera (32.43%) was the most abundant taxon with the family Formicidae being the most dominant among the sites. Invaded areas had higher abundances of Formicidae except in Colesberg. We recorded highest insect abundances in Richmond (633) and lowest in Cookhouse (121). Soil food web analysis suggested that the soils in sites invaded by *C. pallida* were degraded, nitrogen depleted, with a high carbon to nitrogen ratio and a conducive (i.e., unbalanced) food web, whereas the uninvaded areas displayed mature, fertile soil with a moderate carbon to nitrogen ratio. We suggest that presence of *C. pallida* may have a negative impact on the below-ground environment and thus its management must be intensified.

Evaluation of potential repellents for false codling moth, *Thaumatotibia leucotreta* (Meyrick) (Lepidoptera: Tortricidae)

Khalipha Dambuza[1], Candice Coombes[1], Martin Hill[1], Sean Moore[1,2]

[1]Centre for Biological Control, Makhanda, South Africa. [2]Citrus Research International, Gqeberha, South Africa

Categories

- Agricultural Entomology

Abstract

There has been extensive research on the use of semiochemicals as repellents in insect pest management, particularly in push-pull strategies. Much of this research has focused on pests of medical and veterinary importance and has been limited in agricultural pests. This means that there is opportunity for further investigation of repellents to control pests of agricultural importance. No study has previously been conducted on repellents for false codling moth (FCM), *Thaumatotibia leucotreta* (Meyrick) (Lepidoptera: Tortricidae), a key phytosanitary pest in citrus orchards. Consequently, this study assessed FCM oviposition repellence in plants, essential oils, and some commercial FCM pesticides. Choice and no-choice repellence trials were conducted in complete darkness in a controlled environment room. Oranges treated with solutions/suspensions of potential repellents were placed into a cage with gravid FCM females, and oviposition was recorded. Of the 33 compounds tested, eight significantly repelled FCM oviposition compared to the untreated control in the initial repellence trials i.e. two essential oils (lavender and peppermint), two plant crude extracts (garlic and marigold), one fruit (Mango), and three chemicals (*spinetoram, chlorantraniliprole, and emamectin benzoate*). All identified repellents were further evaluated for their ovicidal properties in dose-response bioassays, where all botanicals were identified to have dual action (both repellent and ovicidal properties), as they significantly reduced FCM oviposition and egg hatch. *Emamectin* benzoate was the only chemical insecticide that did not show ovicidal activity when egg hatch was compared to oviposition. Larval penetration was less than egg hatch for all tested repellents, and oviposition was affected by concentration. The efficacy of these repellents can be further tested in semi-field trials, and they may have potential for dispensing in an orchard or for spraying onto trees. Moreover, they can be implemented in push-pull strategies where they can be used in conjunction with FCM attractants.

Pest status of the melon fly, *Zeugodacus cucurbitae* (Diptera: Tephritidae) in Mozambique

Laura Canhanga[1], Yuna Macamo[1], Beatriz Daniel[1], Mirene Mussumbe[1], Domingos Cugala[1], Antonia Vaz[2], Luis Bota[3], Marc De Meyer[4], Massimiliano Virgilio[4]

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Categories

- Invasive Insects

Abstract

The melon fruit fly, *Zeugodacus cucurbitae* is among the most important pests of cucurbit worldwide. Of Asian origin, it was first detected in Mozambique in 2013 in *Mocimboa* da Praia districts in the Northern Province of Cabo Delgado. Since 2013, no information about the spread of the pest was available. Therefore, the present study was conducted to assess *Z. cucurbitae's* distribution in the country. From November 2019 to December 2022, *cuelure* baited traps was placed along the country, at high and mid risk areas (orchards, villages, town markets, sites along the highways and at borders with neighbouring countries). Traps was inspected once per month in the south and centre of country, while for other sampling points where the pest was detected in high densities, sampling was suspended after 2 months. Captures were expressed as flies per trap per day (FTD). Were captured a total of 3456 adults of Z. *cucurbitae*, in several sampling sites in the Northern (Cabo Delgado, Niassa and Nampula province) and Central (Tete, Sofala, Manica and Zambezia provinces) regions. The highest densities were recorded in Mocimboa da Praia (23.58) in Cabo Delgado, Condezi (13,74) in Tete and in Mentagula (14,16) in Niassa province, considered therefore as infested areas. Zambezia (Mocuba), Sofala (Chemba) and Manica (Vanduzi, Barue, Guro, Manica and Messica) are considered as areas of low pest prevalence in which the FTD varied from 0.08 to 0.34. There has been no detection of *Z. cucurbitae* in the southern provinces of Inhambane, Gaza and Maputo. Results clearly shows the spreading and establishment of *Z. cucurbitae* into areas where it was not detected before. Serious restrictions on the access to export markets are expected and appropriated measures has to be implemented to mitigate its economic impact in the country and minimize its spread into unaffected areas.

The bug and the beetle: Are *Vedalia* beetles losing the battle in controlling Australian bug in mandarin orchards in South Africa?

Leani Serfontein, Phindile Rikhotso, Evans Mauda, Aruna Manrakhan

Citrus Research International, Nelspruit, South Africa

Categories

• Agricultural Entomology

Abstract

Icerya purchasi Maskell (Australian bug) is a polyphagous and cosmopolitan pest of plants that includes citrus, feeding on phloem. Dense populations of Australian bug cause plant stress leading to defoliation, fruit drop and a decrease in plant vitality. Australian bug excretes honeydew which supports the growth of sooty mould, disfiguring the plant. *Novius cardinalis* (Mulsant) (Vedalia beetle) is a natural enemy of the Australian bug that is generally successful in controlling their populations. The Vedalia beetle is however susceptible to a number of insecticides used to control Australian bug and other insect pests in citrus orchards. Populations of Australian bug and Vedalia beetle were monitored on a monthly basis over two years (May 2021 – May 2023) in four mandarin orchards on four different farms in Mpumalanga Province, South Africa. Spray programmes for the selected orchards were obtained and correlated with Australian bug and Vedalia populations. High populations of Australian bug (>60% trees infested) were recorded between May and July 2021. After July 2021, there was a rapid decline in both Australian bug and Vedalia beetle populations. This decline was attributed to the use of chemical insecticides targeting spring pests. Populations of Australian bug returned the following year (2022) but remained low. Vedalia beetle was only recorded on two of the farms in 2022 as compared to all four farms in the first year of the study. It was evident from the study that insecticidal spray programmes caused a disruption in the biological control of Australian bug in mandarin orchards. Research is ongoing to quantify the effects of specific insecticides on the Vedalia beetle. Augmentation of Vedalia beetles at specific times of the year when there are less sprays in the orchards is also under investigation.

Do pinch points and barriers affect functional connectivity for butterflies across networks of conservation corridors?

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Stellenbosch University, Stellenbosch, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Insects are among the most biodiverse organisms on the planet and are important regulators of ecosystem functioning. To carry out these ecological functions, insects need complex landscapes that are well connected to move effectively between good quality habitat patches. However, the increasing demand for land and its resources for anthropogenic use has altered many natural ecosystems, and the biodiversity dependent on it. The loss and fragmentation of habitats have resulted in smaller more isolated habitat patches surrounded by non-habitat matrix. Connectivity represents an important factor in determining species persistence, as highly connected areas can promote species dispersal. Commercial forestry plantations in South Africa have adopted the use of ecological networks to enhance connectivity and facilitate species movement. Ecological networks focus on retaining patches of remnant grassland habitats that are connected by corridors of similar habitats. However, these corridors are not often configured in the same way, with varying shapes, sizes, and landscape features. In some instances, corridors might include pinch points (bottlenecks) or barriers that might hinder patch connectivity. Therefore, it is important to identify dispersal barriers and linkages that connect critical habitats together. The aim of the study is to identify what constitutes as a pinch point and/or landscape barrier for butterflies within remnant grassland corridors and how it affects their behaviour. Corridors were ranked in terms of their structure and quality to determine the size of the pinch point. There were differential responses in species richness, abundance and behaviour of butterflies observed and we were able to assess generalist and specialist butterflies' ability to move and exploit the resources in these grassland corridors when exposed to changes in corridor configuration (pinch points). Corridors with large sized pinch points restrict butterfly movement. The substantial decrease in suitable habitat for both generalist and specialist butterflies, ultimately, reduces functional connectivity.

Native-range studies on insect herbivores associated with African Lovegrass (*Eragrostis curvula*) in South Africa: Prospects for biological control in Australia

Liam Yell[1], Guy Sutton[1], Clarke van Steenderen[1], Kim Canavan[1], Andrew McConnachie[2], Pippa Muskett[1], Iain Paterson[1]

[1]Center for Biological Control, Department of Zoology and Entomology, Rhodes University, Makhanda, South Africa. [2]Weeds Biosecurity, Biosecurity & Food Safety | Department of Primary Industries, Orange, Australia

Categories

• Weed Biological Control

Abstract

Eragrostis curvula (Schrad.) Nees. (African Lovegrass) is a native African grass species that was intentionally introduced for pasture in Australia. It has since escaped cultivation and has become widespread and highly invasive. *Eragrostis curvula* has been recorded in every state and territory in Australia where it has altered fire regimes, disrupted nutrient cycles and can reduce livestock carrying capacity by up to 50%. In this study we identified and screened herbivorous insects as potential biological control agents for *E. curvula* in Australia. Native-range surveys were conducted on *E. curvula* at twenty-two sites across South Africa to identify herbivorous natural enemies associated with it. Twenty-nine non-target grass species were surveyed simultaneously to determine the field-host range of the natural enemies associated with the target weed. Four insects were consistently found on *E. curvula*, two of which were herbivorous, as well as a *parasitoid* and a detritivore. The two herbivorous insects were identified as undescribed phytophagous wasps in the genus *Tetramesa* (Hymenoptera: Eurytomidae). Both *Tetramesa* species were found on native congeners under field conditions in South Africa. Based on the phylogenetic proximity of the congeners that the wasps were found on, compared to the target weed, three non-target Australian native *Eragrostis* species, namely: *E. parviflora (R. Br.) Trin., E. leptocarpa Benth. fl., and E. trachycarpa Benth*., are at risk of being attacked by the two *Tetramesa* species. However, further quarantine-based host-range assessments on Australian native *Eragrostis* species are required. The two *Tetramesa* species recorded on *E. curvula* during this project are new species to science, and are currently being formally described by an expert taxonomist. These will be the first native *Tetramesa* species to be described from South Africa.

Assessment of outdoor biting patterns of Anopheles mosquitoes sampled from animal shelters in Umkhanyakude and Zululand Districts: implications to current malaria elimination strategies

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

Residual malaria remains a concern in South Africa even as the country moves towards eliminating malaria within its borders. Thus, it is imperative to study anopheles mosquito behaviour especially with increasing evidence of opportunistic outdoor feeding behaviour of *Anopheles gambiae* complex vector mosquitoes. This aims to ultimately understand the outdoor biting host-seeking behaviour of malaria vectors and enable information-based programmatic decision making consistent with biting behaviour of exophilic vectors. To this end anopheles' mosquitoes were sampled from animal shelters during the 2022/23 malaria season in uMkhanyakude and Zululand districts. The samples were collected from animal shelters at different time intervals from 19:00 up to midnight. All Anopheline samples were identified morphologically using the microscope and vector species-specific using PCR. The laboratory results confirmed the presence of both primary (*An. arabiensis*) and secondary (*An. merus*, *An. vaneedeni*, *A rivulorum*, *An. parensis*) malaria vectors. *Anopheles arabiensis* showed a peak biting time between 21:00 and 22: 00 in Zululand and Umkhanyakude districts. Furthermore, this time interval coincides with the increase in abundance and diversity of Anopheles mosquito found. In conclusion, the malaria vector biting peak times were consistent across the districts. Insights into the biting behaviour of malaria vectors are discussed with implications to the current malaria elimination strategies.

Responses of a grassland ant community to long-term nitrogen fertilization

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[1]University of KwaZulu-Natal, Pietermaritzburg, South Africa. [2]Charles Darwin University, Darwin, Northern Territory, Australia

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Land-use intensification is one of the main drivers of species diversity loss. Grasslands harbour a high species diversity but are threatened by increasing grassland management practices, including nutrient addition. However, the effects of nutrient addition on faunal assemblages are not well understood. The aim of this study was to determine the effect of nitrogen addition on ant communities. Standardized pitfalls were used to sample ants in a long-term (>60 years) grassland fertilizer trial at Ukulinga Research farm, Pietermaritzburg. We sampled 15 plots, each 9 m x 2.7 m in size and with 1 m walkways between them. The treatments comprised of control and two forms of N, limestone ammonium nitrate (LAN, 28%N) and ammonium sulphate (AS, 21%N), each separately applied annually at two levels (high and low): LAN (0.21 and 63.2 g m-2), and AS (33.6 and 100.8 g m-2). Each of the five treatments had three replicates. A total of 35 ant species from 18 genera were recorded, with Tetramorium (8 species) being the richest genus. LAN (low) treatments were dissimilar to other fertilizer treatments in assemblage composition, but all the other fertilizer treatments had similar assemblages. The limited difference among treatments with regards to species richness and assemblage composition, suggests that ant communities are highly resistant to recurring fertilization. This study showed that in our grassland system, low levels of N fertilization are a suitable fertilizer to increase habitat heterogeneity, thereby increasing resource availability and reducing competitive exclusion between ants.

Pollination and insects communities along a macadamia gradient.

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University of Hohenheim, Stuttgart, Germany. University of Venda, Thohoyandou, South Africa

Categories

• Agricultural Entomology

Abstract

Natural vegetation in agricultural landscapes play an important role in supporting the diversity of pollinators and conserving the richness and abundance of species. However, species richness and structural diversity are severely impacted as natural vegetations are cleared and altered for agricultural purposes, leading to a decrease in biodiversity. Alien invasive plants frequently invade on natural vegetation, where their impact can either be positive or negative. The surrounding landscapes of macadamia orchards affect the pollination of macadamia. Landscape modification such as agricultural expansion results in the decline of bee pollination to macadamia. This study aims to assess the impacts of edge plants on pollinators and nutset of macadamia. Temporal observations of pollinators were done before, during and after the flowering seasons of macadamia. This was done through 30 minutes transect walks at the edge of natural and alien invasive flowering plants and edge flowering macadamia. The importance of native and exotic plants in supporting macadamia pollinators inside and outside flowering season are evaluated. The exotic plants will not support macadamia inside its flowering season. Another aim of the study is to assess the functional and taxonomic diversity of ants, beetles, and spiders by using pitfall traps to collect data. The traps were left open in the field for 5 days each month filled with Propylene Glycol. Propylene Glycol helps keep the insects inside the traps and it neither attract nor repel insects. Four different land types were sampled to assess how much biodiversity is lost in the expense of agricultural land expansion. Natural vegetation will be associated with species diversity than other land types.

Effect of long-term mammal herbivory on arthropod assemblages and composition at Kruger National Park, South Africa

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[3]International Center of Insect Physiology and Ecology (ICIPE), Nairobi, Kenya

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Protected savannas are essential reserves for biological diversity, including endangered arthropod species, however, extreme grazing by mammals has cascading impacts on the communities and disrupts the functioning of these ecosystems globally. The current study assessed the abundance, species richness and composition of arthropods at the long-term grazing exclosures of Kruger National Park, South Africa. Pitfalls and active searches were used to sample arthropods at the ungrazed, moderately, and heavily grazed exclosures. We found that Hymenoptera, Coleoptera, Araneae and Diptera were amongst the most abundant groups of arthropods sampled. The abundance of multi-taxon and Hymenoptera alone was significantly high at the ungrazed compared to moderately and heavily exclosures. In contrast, Coleoptera had high numbers of morphospecies compared to Hymenoptera, Araneae and Diptera. Species richness for multi-taxon, Diptera and Hymenoptera was high at the heavily grazed compared to moderately grazed and ungrazed exclosures. Up to 22.2 %, 41.2 %, and 44.4 % of the species were unique to the ungrazed, moderately, and heavily grazed exclosures, respectively. A high proportion of morphospecies shared between exclosures were Coleoptera (41.0 %) and Hymenoptera (38.5 %) compared to Diptera and Araneae with less than 5% recorded across exclosures. Thus, morphospecies within the least abundant groups, namely Diptera and Araneae, were represented by singletons were unique to exclosures compared to the most abundant groups (e.g., Coleoptera and Hymenoptera) of arthropods. We conclude that long-term mammal grazing enhances species richness and composition of niche, sparse and unique arthropods in the protected savannas. Therefore, grazing should be encouraged and managed to maintain the integrity of the protected savannas.

A comparison of false codling moth infestation in organic versus conventional citrus orchards.

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Categories

- Agroecology

Abstract

Citrus packhouses in South Africa report lower infestation by false codling moth (FCM), *Thaumatotibia leucotreta* (Meyr) (Lepidoptera: Tortricidae), in fruit from organically farmed orchards than conventionally farmed orchards. Field surveys and laboratory studies were conducted to determine if, and why FCM infestation was lower on organic citrus farms. Yellow delta pheromone traps recorded significantly higher wild FCM catches in conventionally farmed Palmer Navel and Newhall Navel orchards compared to matching orchards on neighbouring organic farms. Pitfall trapping recorded significantly higher insect generalist predator abundance and species richness on organic farms. Soil sample baiting revealed no significant difference in abundance of entomopathogenic fungi (EPF) and entomopathogenic nematodes (EPN) between organic and conventional soils. However, there were differences in the dominant species. In fruit nutrient analyses, conventional fruit were found to have significantly higher concentrations of magnesium, boron and nitrogen, but significantly lower concentrations of copper and thinner peels. FCM significantly preferred to oviposit on conventional fruit when choice and no-choice oviposition trials were carried out. Farm management surveys showed that spray regimes on both organic and conventional citrus farms can vary widely in terms of their compatibility with integrated pest management (IPM), based on CRI's rating system. Poor farm IPM ratings were positively correlated with wild FCM catches. Results of this study demonstrate the importance of natural enemy conservation as part of an IPM strategy and show how fruit nutrient composition could potentially impact FCM ecology in citrus orchards.

Biological control against *Tecoma stans* L. Bignoniaceae in South Africa

Lulama Madire

Agricultural Research Council- Plant Health and Protection, Pretoria, South Africa

Categories

• Weed Biological Control

Abstract

Tecoma stans (L.) Juss ex Kunth var. stans (Bignoniaceae) also known as yellow bells are an invasive tree or a shrub from Central America and it continues to extend its range in all South African provinces and neighbouring countries. Tecoma stans has been a target for biological control since 2003. The biological control programme using insects on T. stans was started by screening agents in quarantine in 2005. Two leaf-feeding agents, *Mada pollutta Mulsant* (Coleoptera: Coccinellidae) and *Pseudonapomyza sp*. Hendel (Diptera: Agromyzidae), were subsequently released in South Africa at the end of 2013 and 2014, respectively. Currently, Mada polluta has become established in three provinces, Eastern Cape, KwaZulu-Natal and Mpumalanga and the population has become abundant. The *Pseudonapomyza sp*. release sites that were at Eastern Cape, KwaZulu-Natal, Limpopo and Mpumalanga have been destroyed and currently there is no recovery of this agent in the field. A root -feeding flea beetle, *Heikertingerella sp.* Csiki (Chrysomelidae: Galerucinae) was released in South Africa for the first time in 2023 at Eastern Cape. Post release studies of *M. polluta* has been conducted in three provinces by sampling 80cm branches of *T. stans* yearly during February month. The aim of the study was to assess dispersal rate, plant damage, immature recovery and fruit production. The initial results suggests that *M. polluta* is putting a significant pressure on *T. stans* populations especially at Eastern Cape where establishment was noticed in 2018. According to field observations, plant damage caused by *M. polluta* affects both seedlings and mature trees. The restoration of natural vegetation such as grass and other invasive weeds are replacing *T. stans* populations in the field.

Keywords: established, leaf- feeding agents, plant damage, root-feeding flea beetle, post release studies, release

Diversity and virulence of *Beauveria* species associated with *Gonipterus* sp. 2 in South African *Eucalyptus* plantations.

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Categories

• Invasive Insects

Abstract

The *Eucalyptus* snout beetle (ESB), *Gonipterus* sp. n. 2 is an economic pest of *Eucalyptus* plantations in South Africa. The pest is controlled by the egg parasitoid, *Anaphes nitens*. However, sporadic outbreaks of ESB are observed across the forestry landscape. Entomopathogenic fungi (EPFs) can be used in synergy with classical biological control to manage this pest but is not well studied within South Africa. Our study aimed to determine the diversity and virulence of *Beauveria* species associated with ESB in South African forestry. Field collected beetles from *Eucalyptus* plantations were placed in moisture chambers until fungal growth was observed. The fungi were isolated and purified on Malt Extract Agar (MEA). DNA was extracted and the *RPB1*, *TEF* and ITS gene regions were sequenced to determine their phylogenetic identification. To determine their efficacy against *Gonipterus* sp. n. 2. adults, nine field-collected *Beauveria* strains (three of each species) and one commercial *B. bassiana* strain were selected for ongoing virulence trials. Adult beetles were exposed to the spore solutions for 24 hours. Mortality and fungal growth were recorded daily for 14 days at 25°C and a relative humidity (RH) of 75%. Of the 128 isolates sequenced, 32% belonged to *Beauveria* spp., 48% were opportunistic entomopathogens (such as *Fusarium* species) and 20% belonged to other fungal genera. Two species within the *B. bassiana* species complex, *B. namnaoensis* and *B. neobassiana*, were identified, as well as *B. pseudobassiana*. The results for the ongoing virulence trials with *Gonipterus* sp. n. 2 will also be discussed once completed. In conclusion, the study detected cryptic species diversity of *Beauveria* associated with ESB in South Africa and identified natural *Beauveria* strains with potential to be developed as biopesticides for the use in ESB biological control programmes in South African plantations.

Ant communities are changing in response to increasing temperatures

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Climate change is having an impact on ecosystems around the world. Long-term studies along elevation gradients are valuable for quantifying the extent to which these ecosystems are changing. Elevation gradient studies for a range of different organisms have revealed range shifts, predominantly upward, in response to warming temperatures. Most elevation studies have recorded the occurrence of species on elevation gradients at two points in time, typically 20 to 30 years apart. This approach allows range shifts and range size changes of the species of interest to be detected, but it relies on near-continuous sampling from the lowest to highest elevation, and on reliable historical samples. An alternative approach is to sample entire communities at specific points, spaced further apart on the gradient, but at a higher temporal frequency. This enables subtle changes in community structure to be detected in a shorter period of time. The Community Temperature Index (CTI) provides a measure of the temperature tolerance of the community by combining a measure of the temperature tolerance of each species comprising the community. An increase in the CTI indicates that the community is comprised of more warm-adapted species or that the abundance of warm-adapted species in the community has increased. Ants are highly abundant ground-dwelling organisms that have considerable influence on community structure through predation and perform a range of different ecological functions, including seed dispersal. Our study aims to study changes in ant communities over time. We sampled ant communities annually for 15 years on an elevation gradient in the Maloti-Drakensberg Mountains (900 m to 3000 m a.m.s.l.). We have found a significant increase in the CTI of the ant communities at the lower end of the elevation gradient over time. This corresponds with significant warming of soil temperatures during the winter months at these sites.

Bioecology of lepidopteran pests of *Macadamia integrifolia* in South African production areas

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Categories

- Agricultural Entomology

Abstract

Larvae of the Lepidoptera nut borer complex cause economic damage to macadamia in South Africa. The Lepidoptera species that constitute the nut borer complex in South Africa are *Thaumatotibia leucotreta* (FCM), *Thaumatotibia batrachopa* (MNB), *Cryptophlebia peltastica* (LM) and *Ectomyelois ceratoniae* (CM). Mixed populations of these species are often reported in macadamia orchards in South Africa. Previous surveys of the nut borer complex in Limpopo and Mpumalanga showed that the species complex may change within and between seasons. In this study moth activity and larval infestation was recorded at two scales, firstly at a fine scale over a 25-week period, sampled weekly, in two orchards in the Barberton area of South Africa and secondly a coarse scale in which data was sampled once during a survey conducted over the 5 macadamia growing regions. All the species of the borer complex were collected for both surveys. Pheromone trap data showed that FCM were captured in higher numbers and greater frequency than all other moths. NoCM moths were captured in pheromone traps. Increased moth flight numbers were recorded 12-16 weeks after commencement of flowering. Larval numbers varied during the season and was dominated by FCM (67 %), followed by MNB (19 %), CM (10 %) and LM (4 %). The surveyed regions differed in their species complexity and moth abundance. Monitoring data such as this can be used in decision making of various pest management practices, however this study highlights the apparent discrepancy between pheromone trap catches and larval infestation. Casting doubt on whether current monitoring practices provide an accurate indication of the larval community composition and the time of infestation. Reinforcing the need to supplement moth monitoring with ongoing larval ID throughout the season to help verify the population pressure of the moth complex.

The population genetics of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in South Africa

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Forestry and Agricultural Biotechnology Institute, Pretoria, South Africa

Categories

- Invasive Insects

Abstract

The Fall Armyworm, *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae) is a polyphagous pest, with a preference for maize, which is native to North and South America. *Spodoptera frugiperda* became invasive to Africa in 2016, and has since spread to several sub-Saharan African countries, including South Africa. This pest poses a significant threat to agriculture in the region. The aim of this study was to assess the genetic diversity, structure and gene flow of *S. frugiperda* populations in South Africa. To fulfil this objective, ten microsatellite markers were developed using *S. frugiperda* genome data. These data were used along with sequence data of the cytochrome oxidase 1 (COI) gene from individuals sampled from the Limpopo, Mpumalanga and Kwa-Zulu Natal provinces of South Africa. Eight haplotypes were identified from 91 COI sequences. Four unique haplotypes were identified in Limpopo, followed by Kwa-Zulu Natal (3 unique haplotypes) and Mpumalanga (1 unique haplotype). Limpopo populations presented the highest degree of genetic diversity, with a haplotype diversity (Hd) of 0.494. This confirms that Limpopo serves as a source population from which sub-populations migrate into the surrounding provinces. Low genetic differentiation was observed among populations with an overall F_{ST} of 0.0416. Analysis of microsatellite data is ongoing. These results will provide further insight into the spread of genetic traits such resistance to Bt-modified maize or insecticides across the region and could support monitoring and management of such pest traits in the region.

Landscape connectivity of the fruit fly pest, *Ceratitis quilicii* (Diptera: Tephritidae) in Southern Africa

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Categories

• Agroecology

Abstract

Tephritidae species are important agricultural pests and responsible for direct and indirect damage to commercially produced fruit in Southern Africa. Many of them are pests of quarantine importance and their risk in commercial fruit should be mitigated to enable safe trade. Fruit fly management strategies include monitoring, containment, suppression and potential eradication. The spatial scale at which control methods should be applied can be determined by measuring dispersal pathways and identifying management units of this insect pest. *Ceratitis quilicii* De Meyer et al. is a newly described fruit fly pest species which is present in Southern Africa and polyphagous in nature, thus potentially posing a risk to cultivated fruit crops. In South Africa it is widely distributed in the southern, eastern and western parts of the country. However, information regarding this species' dispersal pathways between areas is lacking. Here, we explored the dispersal pathways of *C. quilicii* across Southern Africa to construct potential management units based on friction maps. Landscape friction modulates how species can move naturally in the environment. Friction information will allow us to (1) identify landscape and environmental features that constrain genetic connectivity, (2) predict how future landscape changes might influence genetic connectivity, and (3) explain the ecological processes that influence spatial genetic structure. *Ceratitis quilicii* were trapped widely over South Africa and the southern part of Mozambique between 2020 and 2021. Whole genome sequencing was performed on trapped individuals and population genetic analysis employed to investigate gene flow between 31 trapping sites. Through a combination of population genetic data and environmental factors we generated friction maps to identify and predict the most likely dispersal pathways of *C. quilicii*. Dispersal pathways are a key factor in identifying management units and management strategies for pest species in Southern Africa.

Assessing the efficacy of a point release system for the deployment of sterile moths in a commercial SIT programme

Megan Mulcahy[1], Sean Thackeray[1], Khalipha Dambuza[1], Emma Stirk[1], Sean Moore[2]

[1]River Bioscience, Port Elizabeth, South Africa. [2]Citrus Research International, Port Elizabeth, South Africa

Categories

- Agricultural Entomology

Abstract

The sterile insect technique (SIT) programme against *Thaumatotibia leucotreta* (Lepidoptera: Tortricidae) in South African citrus, relies on two methods of releasing sterile adults into the environment. Aerial releases are conducted using Robinson-R22 Helicopters, and manual releases are conducted using quadbikes. To provide farmers with more flexibility and to increase sustainability of SIT, a project has been initiated to reposition SIT as a preventative practice that forms the basis of a systems approach for integrated management of *T. leucotreta*. A key aspect of the project is to investigate the possibility of reducing the number of moths released per ha (from 2000 moths/ha to 1000 moths/ha) and to determine whether alternative release methods can be used effectively. A point release method, whereby moths are hand released at a single point per ha, was identified as an alternative to aerial and manual releases. Point release was tested in small-scale field trials in the Eastern Cape during the 2021-2022 citrus season. Results were favourable and large-scale commercial trials were initiated in 2022-2023. Two valleys were selected for commercial trials. These were the Sundays River Valley (SRV), where moths are typically released at a rate of 2000 moths/ha, and the Gamtoos River Valley (GRV), where the release rate is 1000 moths/ha. The commercial point release trials were conducted on 313 ha in the GRV and 595 ha in the SRV at a release rate of 1000 moths/ha, in accordance with the projects repositioning objectives. Weekly pheromone trap data were collected from point release sites, and sites where aerial and manual releases were being conducted. The number of wild and sterile males caught in each monitoring trap was compared across all release methods to determine whether point releases performed favourably to aerial and manual release methods at the different rates.

APIS Bloom: A novel tool for improving honeybee pollination in kiwi crops

Megan Mulcahy[1], Jeannine du Plooy[1], Emma Stirk[1], Eben Mundell[1], Sipho Manqele[1], Jaimee Harris[2], Michiel Bruggeman[2], Sean Thackeray[1]

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Categories

• Agricultural Entomology

Abstract

Successful production of numerous crops hinges on adequate pollination by honeybees, *Apis melifera* (Hymenoptera: Apidae). Honeybee pheromones play a critical role in honeybee colony life, including development, reproduction, defense, and the provision of pollination services through foraging and resource orientation. Pheromones involved in foraging facilitate communication between worker bees, allowing them to locate areas with good sources of pollen and nectar. The Nasonov gland pheromone is a worker-exclusive pheromone that has an attractive effect on honeybees and is typically used to mark hive entrances, promote swarm clustering, and for the identification of foraging sites. Apis Bloom is a proprietary blend of terpenoids that mimics the Nasanov gland secretion. The product aims to harness the processes that bees use to identify and locate high value foraging sources. It was developed in the United States and has been used to increase bee activity and pollination services in crops such as almonds, blueberries and raspberries. The purpose of this study was to determine whether the product could be used in a South African context to pollinate kiwifruit, a cross-pollinated crop which relies on honeybee and hand pollination for the production of quality fruit. Four kiwi farms were selected for inclusion in the study near the city of George, Western Cape. Each block of kiwis was divided into a treatment block upon which Apis Bloom was applied 2-3 days prior to blooming of the flowers, and a control block, which was left untreated. Honeybee hives were provided by the Bee-Tech Group and deployed across both the treatment and control blocks. The number of flower visits, amount of pollen collected, percentage fruit set, overall yield and fruit quality was assessed in each block. The data was used to determine whether Apis Bloom improved bee activity and pollination of the kiwis, relative to control sites.

A comparison of x-ray and gamma irradiation for the sterilization of false codling moths (FCM) in a commercial SIT programme

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Categories

• Agricultural Entomology

Abstract

Sterile insect technique (SIT) is a population suppression mechanism used for the area-wide integrated pest management of the false codling moth (FCM) in citrus and other fruit crops in South Africa. This SIT programme has been implemented by XSIT since 2007 using a Cobalt-60 gamma irradiation source. A dose of 180Gy is used for sterilization of male and female moths, which are released in orchards to compete with wild moths. Although gamma irradiators are effective, reliable, and inexpensive to use and maintain, replacing an isotopic source is costly. Safety concerns, and the logistics of procuring a new source, are a barrier to the sustainability of SIT programmes. In contrast, X-Ray irradiators are safer to use, easier to obtain and do not require specialized licensing or installation. However, X-Ray machines have a lower penetration and throughput in comparison to isotopic irradiators. Despite this, X-Ray irradiators have been used successfully in several SIT programmes. The purpose of this study was to determine whether X-Ray irradiation could be used by XSIT to successfully sterilize FCM. This study formed part of a SANDIA funded project that was facilitated by the National Institute for Communicable Diseases (NICD) and the WITS University Health Consortium (WHC). A Rad Source (RS 2400 Series) X-Ray irradiator was used to assess the efficacy of using X-Rays for irradiation of FCM. Dose mapping was completed to determine the Gy/min and to ensure moths received an even X-ray dose of 180Gy. Sterility tests were then conducted to determine whether adequate levels of sterility were achieved in comparison to gamma-irradiated moths, and flight tests were conducted to compare moth quality. Results thus far show that the X-ray irradiator is comparable to the Gamma source in terms of sterility. Further experiments aimed at comparing throughput and irradiation at different doses are currently underway.

The use of an anthranilic diamide insecticide for mating disruption of false codling moth

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Categories

• Agricultural Entomology

Abstract

False codling moth (FCM), *Thaumatotibia leucotreta*, is an important pest of citrus and other crops. The egg and neonate larval stages of FCM are often controlled with sprays of chemical insecticides. These chemicals may have secondary effects against the adult life stages. *Chloratraniliprole (Coragen™)* and *cyantraniliprole (Exirel®)* are anthranilic diamide insecticides, being ryanodine receptor modulators, but possibly also having a mating disruption effect on FCM adults. A field trial was replicated over two seasons to examine this, with the addition of spinetoram (Delegate) in the second season, to determine whether an insecticidal effect was being misinterpreted as a mating disruption effect. Each chemical was applied at the registered recommended rate to identical and adjacent citrus orchards, replicated twice each season. Pheromone traps were hung in each orchard, including untreated orchards, and approximately 1000 sterile moths were released in the centre of each orchard each week for 3 to 4 weeks and recaptures compared. Simultaneously, five virgin females and one virgin male were placed into gauze nets in trees and gauze cages under trees. Moths were recovered after 48 hours and females dissected to determine spermatophore transfer. From the results obtained for both seasons it was determined that Coragen and Exirel had a mating disruption effect on adult FCM. Fewer males were caught in traps in treated than untreated orchards, but not for Delegate. Fewer spermatophores were transferred by moths in treated than untreated orchards. These results confirmed a 35 to 49% mating disruption effect.

Sentinel plant research reveals two cryptic cypress-feeding aphid species on *Widdringtonia* in South Africa

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Categories

• Invasive Insects

Abstract

A project monitoring plant health in South African botanical gardens and arboreta was initiated under the framework of the International Plant Sentinel Network (IPSN). The aim has been to use plant collections in botanical gardens and arboreta as sentinel sites to improve surveillance and identification of new and emerging pest and pathogen risks. As part of this project, aphid samples were collected from Widdringtonia spp. exhibiting severe aphid infestation and showing branch dieback in the Kirstenbosch National Botanical Garden (Kirstenbosch NBG), Cape Town. In this study, we identified the aphids collected in Kirstenbosch NBG using DNA sequence data for the mitochondrial cytochrome c oxidase (COI) gene. The results led to the identification of two cryptic aphid species, namely *Cinara cupressi* (Buckton) and *Cinara tujafilina* (Del Guercio). *Cinara cupressi* has become invasive on cypress in various parts of the world, including Africa and has led to significant economic losses and environmental damage. *Cinara tujafilina* has been previously reported on cypress in East and southern Africa and elsewhere in the world, but only as a minor pest. For South Africa, this is the first confirmed report of these aphids on Widdringtonia spp. The results form an important foundation for effective and sustainable management of these pests. They also highlight the value of sentinel projects in the detection and identification of cryptic pest species.

Keywords: *Cinara cupressi*, *Cinara tujafilina*, cypress aphid, Cupressaceae, alien invasive pests, conifers

Diversity and trophic interactions between Acari and Collembola in agroecosystems: Variation through space and time

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Categories

- Agroecology

Abstract

Despite a broad appreciation of the need for healthy soils in agroecosystems, relatively little is known in South African fruit orchards about key role players, inter-organismal linkages within soil food webs, and the extent to which they contribute to above-ground ecosystem function. Higher-order consumers such as predators regulate herbivory, decomposition, and nutrient cycling in these systems. Soil-borne predators (such as Acari) can decrease biodiversity loss from anthropogenic change by strengthening food web links over space and time. The aim of this study was to document and identify the main species of Acari and Collembola found, assess their variation in space and time, and infer their likely trophic interactions in agroecosystems in deciduous fruit orchards in the Western Cape. Samples were collected in Barrydale, the Warm Bokkeveld and Koue bokkeveld. A total of 20 working row and tree row samples were collected at each farm, for two years, collected four times a year (mid-season). Invertebrates were extracted using Tullgren funnels and identified to morphospecies level. The diversity for each orchard was determined and to infer functional roles we performed stable elemental isotope analysis (Δ13C and Δ15N ratios) and estimated trophic niches on the collected Acari and Collembola samples. In the lab, we also assessed the temperature-dependence of locomotor performance of the most common predator and prey species to better understand trophic interactions. Preliminary results show that heavily managed orchards are less diverse than less intensely managed orchards. Future work will investigate if there are any correlations between stable isotope estimates of trophic levels and lab assays of potential predator prey relationships. Trophic interactions are expected to vary between orchards implementing different management strategies.

Susceptibility of false codling moth eggs from different sterile: fertile release ratios to parasitism

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Categories

• Agricultural Entomology

Abstract

Sterile insect technique (SIT) and the augmentative releases of egg parasitoids *Trichogrammatoidea cryptophlebiae* Nagaraja have been used in the control of false codling moth (FCM) *Thaumatotibia leucotreta* Meyrick in South Africa. FCM control can be improved when releases of irradiated moths and egg parasitoids are conducted simultaneously and where these techniques do not negatively affect one another. A laboratory study was conducted to investigate the susceptibility of FCM eggs resulting from different irradiated to non-irradiated moth pairings to parasitism by *T. cryptophlebiae*. The release ratios of sterile to fertile FCM used were: 0:1, 10:1, 20:1, 40:1 and 60:1. Parasitoids emerging from the release ratios were tested for their fitness using a flight chamber to determine host egg searching capability. Male and female moths treated (T) with 150 Gy of gamma-radiation were out-crossed with normal untreated (N) counterparts, and eggs produced offered to *T. cryptophlebiae* for parasitism. Parasitism of newly laid (24-h-old) eggs, as well as eggs that were 48- and 72-h-old was evaluated. In general, eggs from the different release ratios were acceptable for oviposition and suitable for parasitoid development. However, significant differences in the number of parasitized eggs were detected when the T: N release ratios increased and when the egg age was greater than 24 h. Similarly, more parasitoids emerged in higher release ratios where the sex ratio was in the favour of the female parasitoids. Our results suggest that *T. cryptophlebiae* would accept and hatch from FCM eggs laid from different release ratios with a higher proportion of female parasitoids. This would aid in parasitoid development indicating that a synergistic suppressive effect can be achieved when both SIT and augmentative releases of *T. cryptophlebiae* are used together for the control of FCM. However, further studies combining releases of irradiated moths and parasitoids in the field are warranted.

Development and optimisation of a qPCR assay for the enumeration of *Cryptophlebia leucotreta granulovirus (*CrleGV) used for commercial applications.

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Categories

• Invertebrate Pathology

Abstract

Thaumatotibia leucotreta (Meyrick) (Lepidoptera: Tortricidae), is an important agricultural pest in South Africa. Its classification as a phytosanitary pest by many international markets promotes the need for strict control of *T. leucotreta*. This is achieved through an integrated pest management (IPM) programme which uses the baculovirus *Cryptophlebia leucotreta granulovirus (CrleGV*) as a component. Although this virus has been successfully applied as a biopesticide for nearly two decades, further research and development is necessary. One aspect of interest is the quantification of viral particles which is required for both field and laboratory-based applications. While dark field microscopy is traditionally used for the quantification of baculoviruses, this method is subjective and time-consuming. This study aimed to develop and optimise a qPCR technique to accurately quantify *CrleGV-SA OBs.* Oligonucleotides were designed to amplify regions within the *lef-8, lef-9*, and granulin genes. Three sets of DNA plasmids (*pJET1.2-Gran, pJET1.2-lef-9, and pJET1.2-lef-8)* were constructed, each containing one of the target regions. These were evaluated for use as standards in a qPCR assay. To ensure optimal quantification of samples, different gDNA extraction methods were also evaluated. A range of *CrleGV-SA* samples were evaluated using the qPCR assay and under dark-field microscopy, with data obtained statistically compared. The results showed general agreement between the two methods. This indicates that the qPCR assay developed in this study can be used as an alternative to dark-field microscopy for the quantification of *CrleGV,* offering a rapid and reliable method for use in laboratory and commercial settings.

Dragonflies on oceanic and sky islands face similar challenges

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Oceanic islands often have signature endemic odonates. This assumes that the islands have a deep history and are isolated from the mainland. The same can happen among odonates that live on sky islands that have experienced a long geologically stable history. Isolated oceanic and sky island area, topography, and moisture levels all play a role in determining local odonate assemblages. Here we compare oceanic island geology, topography, area, and climate of Indian Ocean islands with that of sky islands in the ancient Cape Fold Mountains at the southern tip of Africa in terms of their odonate faunas. We relate the findings to islands globally. Both oceanic and sky island odonates are experiencing great challenges in the face of direct human activity and climate change, not least because the highly adapted local species have nowhere else to go.

An introduction to male-male agonistic behaviours in sympatric species of *Heliophanus* Jumping Spiders

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Antagonistic encounters between con- and heterospecific males of the jumping spider genus *Heliophanus* C.L. Koch found in South Africa were examined for the first time. These interactions may occur when males enounter one another while searching for mates. Such encounters may lead to increased male-male bouts of aggression. The genus *Heliophanus* is one of the largest genera of jumping spiders globally (>170 spp.), and the largest in South Africa (44 spp.), with various sympatric species with distinctly similar ornamentation and/or coloration. Here we paired males of three species of *Heliophanus* (*H. debilis*, *H. fascinatus*, and *H. pistaciae*), which are sympatric and visually similar jumping spiders, to determine whether males would exhibit higher frequencies of antagonistic behaviour s towards either conspecific or heterospecific males. A total of 69 pairings were conducted among two conspecific (*H. pistaciae* vs. *H. pistaciae*; *H. fascinatus* vs. *H. fascinatus*) species of *Heliophanus*. From these 69 pairings, we found differences in sizes and weights among the three species, with 1) *H. fascinatus* males being larger in size compared to *H. debilis* and *H. pistaciae*, and 2) *H. pistaciae* males weighing less than either *H. debilis* or *H. fascinatus*. We described and quantified a total of eleven distinct agonistic behaviour s, with two "escalated" behaviour s performed by males. Additionally, no differences were found in the frequency of agonistic behaviour s performed by con- or heterospecific males towards opponents. Here we discuss these results in the context of male-male competition among sympatric and visually similar species.

Timber plantations differ in soil arthropod assemblages, but not diversity, compared to natural systems

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Timber plantations are often seen as a significant threat to biodiversity. We assess whether this is true in the case of soil arthropod biodiversity when compared to nearby natural ecosystems. We compared the alpha-diversity, beta-diversity and assemblage composition of two important soil arthropod taxa, ants and springtails, between plantations (Eucalyptus and Pinus) and natural systems (indigenous forest and grassland). Our study was conducted in two different climatic regions (the Midlands and Zululand) in KwaZulu-Natal, South Africa. Surprisingly, plantations had equal amounts of alpha-diversity compared to the natural systems, and beta-diversity within the plantations was unexpectedly high. Nevertheless, although many species were shared between the systems, we found that the assemblage composition of these taxa differed between all biotopes, showing complementarity within this type of production landscape. Our results, therefore, show 1) the conservation of natural areas within these production landscapes is crucial for unique below-ground biodiversity, 2) environmental variation within the plantations may be driving the high species turnover between the plantations through small-scale resource and habitat diversification, and 3) that conservation recommendations for above-ground biodiversity within these production landscapes may differ from those aimed at below-ground biodiversity, as soil biodiversity is not affected by plantations to the degree that above-ground biodiversity can be affected.

Thermal tolerance of the *Leptocybe invasa* (Hymenoptera: Eulophidae) gall community and the potential impact of climate change

Michelle Schröder, Bernard Slippers, Brett Hurley

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Categories

• Physiological Ecology

Abstract

Parasitoids of insect pests, often used in biological control programs, tend to have a lower thermal tolerance than their herbivore hosts. This will have significant impacts on their ability to manage insect pests in a changing climate. The frequency of extreme weather events such as heat waves are expected to increase with global climate change. Increased temperatures even for short periods can result in herbivore populations being favoured due to a decrease in parasitoid activity or death of the parasitoids, which can lead to sporadic insect outbreaks. We examined the thermal thresholds of the invasive blue gum chalcid wasp *Leptocybe invasa*, and two if its biological control agents, namely the parasitoid wasps *Selitrichodes neseri* and *Quadrastichus mendeli*, to gain insight in how climate change will influence the management of this pest. Insects were exposed to a ramping heating and cooling temperature protocol in a water bath to determine critical thermal limits by observing when the insect loses locomotory function (CTmax / CTmin) and to determine lethal thermal limits by observing death of the insects 24 hours after exposure (ULT50 / LLT50). Preliminary results indicate *L. invasa* has a higher thermal tolerance than the parasitoid species, *Q. mendeli* and *S. neseri*. This indicates that *L. invasa* populations will be favoured at high temperatures and that climate will play an important role in the population fluctuations of the two parasitoid species. This is an important consideration for the development of climatically robust pest management programmes for *Eucalyptus* pests such as *L. invasa*.

The journey thus far: A taxonomic and systematic evaluation of the Afrotropical wasp genus *Netelia* (Tryphoninae, Ichneumonidae)

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Categories

• Systematics and Taxonomy

Abstract

The genus *Netelia* is a globally distributed koinobiont ectoparasitoid wasp of lepidopteran larvae and contains approximately 38 described Afrotropical species. They are uniformly testaceous and morphologically similar in appearance, and best distinguished by evaluating morphological specializations found on the inner surface of the male genitalia. This makes species identifications challenging and as a result, the genus has not had any modern taxonomic assessment. The most recent evaluation of the world fauna considered that the multitude of subgenera defined within *Netelia* are not well-supported. Also, that the available species key and the subgeneric descriptions have excluded assessment of characters associated with the male genitalia. Therefore, all described Afrotropical *Netelia* are still only defined by their original species descriptions, some of which date back to the mid-1800's. By making use of approximately 2000 specimens collected from a range of Afrotropical habitats and housed in both the Natural History Museum in London and the Iziko South African Museum, the main aim of this project is to: reassess species delimitations and describe new species; explore evolutionary relationships between species using the COI barcoding gene; and make use of DNA metabarcoding techniques to identify parasitoid-host relationships. To date, there are approximately 35 undescribed species housed within the Iziko collection alone, however with further sample processing, this number is expected to increase exponentially. The project will provide novel character assessment supporting species delimitations, determine parasitoid-host relationships and describe many new Afrotropical *Netelia* species, with provision of well-illustrated keys to all African species. Since parasitoid wasps have been effectively used in South African agricultural and water resource management, this project will enable the discovery of potentially new bio-control agents of agricultural pests, and subsequently have a positive input into the bioeconomy and sustainability of South Africa's food production and security.

Risk analysis for invasive *Bactrocera invadens* and *Prostephanus truncatus* in South Africa

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Categories

• Invasive Insects

Abstract

Prostephanus truncatus is a species that is naturally found in southern and central America and is particularly abundant in Mexico. However, it has also been detected and identified in the Kruger National Park, which is situated near the border of Mozambique, South Africa, and Zimbabwe. Meanwhile, *Bactrocera invadens*, which is native to Asia, is also present in South Africa, where it is found in abundance in Limpopo. Both *B. dorsalis* and *P. truncatus* are listed as Category 1a species under the National Environmental Management: Biodiversity Act (Act No 10 of 2004) and Alien and Invasive species list in South Africa. In a planned study, our aim is to assess the potential risks associated with these two species in South Africa. We utilized the Risk Analysis for Alien Taxa (RAAT) to quantify the associated risks and found that both species have high risk scores. *B. invadens i*s known to displace native fruit flies through competition and has a negative impact on the agricultural sector by damaging fruits in farms and storage facilities. On the other hand, inter-specific competition studies have shown that *P. truncatus* can displace maize weevil (Sitophilus spp) and severely damage stored dry agricultural crops and timber products. The prospects for successful management of these two species are at a medium level, in terms of ease of management. Therefore, we recommend and support the current NEMBA listing for *B. invadens* and P. truncates, primarily because they do not have any environmental or socio-economic benefits. A surveillance strategy should be developed for *P. truncatus*, and further research and monitoring is highly recommended.

Patterns of foraging for protein by fruit fly pests in South African citrus orchards

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Categories

• Agricultural Entomology

Abstract

The application of protein baits as sprays or stations forms the core of fruit fly control measures in orchards. Protein baits target adult flies in search of protein as a food source for reproductive maturation. Protein baits limit insecticide use and its negative effects on beneficial insects. In order to increase the effectiveness of proteinaceous baits, a proper understanding of the protein foraging behaviour of fruit flies is required. In this study, the spatial and temporal foraging patterns of three fruit fly species (*C. capitata, C. cosyra, and B. dorsalis*) in response to protein baits was investigated. A series of trials using laboratory reared flies in field cages erected over lemon trees within an orchard were undertaken. The effects of fly age, sex and nutritional status of the three fruit fly species, and the placement of a protein bait station at different heights in the canopy were determined. The location of protein bait in the canopy affected responses by *C. capitata, C. cosyra, and B. dorsalis*, with more flies foraging on protein in the mid to upper canopy. Nutritional status, sex and age also affected protein foraging, with 1-day-old flies with prior access to protein being less responsive to protein bait, while 10-day-old protein-deprived flies foraged intensely for protein. Protein deprived females were more attracted to protein than males of the same nutritional status, and foraging for protein peaked in the warmer part of the day when temperatures were between 20-25 ^{o}C. The results show that protein baits should not be applied on the ground, and that protein baits may be less effective for fruit fly control in environments where natural sources of protein are available.

Keywords: Protein bait, fruit flies

Elevation influences turnover in generations of the two-spotted stink bug, *Bathycoelia distincta* (Hemiptera: Pentatomidae) in the Levubu area, South Africa

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Categories

• Physiological Ecology

Abstract

Understanding pest population dynamics requires knowledge of thermal physiology of a species and the climatic conditions where they occur. Climate change affects insect physiologically and climatic conditions globally, with mountainous agricultural landscapes most threatened. The macadamia orchards near Levubu in the Limpopo Province of South Africa are situated across different climatic zones that vary along an elevational gradient. Orchards in this area are prone to pest damage by the two-spotted stink bug, *Bathycoelia distincta* (Hemiptera: Pentatomidae), a major pest of macadamia in South Africa. This study aims to quantify the effects of three climatic zones namely, the Cwa (Monsoon-influenced humid subtropical climate), Cwb (Subtropical highland climate or Monsoon-influenced temperate oceanic climate), and Bsh (Hot semi-arid steppe climate) on generation turnover, heat and cold thermal stress, thermal safety margin (TSM), and relative fitness of *B. distincta* throughout an annual cycle. Four macadamia orchards were selected along an elevational gradient within the three climatic zones (Arbor, Welmac, Neuhof, and Highfield). Overall, climates observed in the four climatic zones along the elevational gradient significantly impacted the population turnover of *B. distincta*. The number of generations increased with increasing elevation: Arbor (2 generations), Welmac and Neuhof (1.3 generations), and Highfield (0.9 generations). The models suggest that *B. distincta* populations are not thermally (heat and cold) stressed and encountered high TSM and relative fitness at Highfield throughout the season. Collectively, *B. distincta* performed best at orchards at lower elevations sharing the Cwa climate zone. Macadamia orchards at lower elevations in the Cwa climate zone and closer to the Bsh climate zone could experience increased nut damage because increased temperatures will increase the number of pest generations. The consequence of climate warming could also result in expanding the geographical range of *B. distincta* and pose management challenges in orchards at lower elevations.

Using presence-only modelling to quantify the suitable habitat of a communally exploited edible insect (*Gonimbrasia belina*).

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Edible insects remain a key resource for many African communities. In southern Africa, the mopane larvae (larval stage of the mopane moth; *Imbrasia* = *Gonimbrasia belina*), are harvested annually by communities for food and trade. Harvesting remains informal, largely unregulated, and mainly occurs on communal land. However, recent increases in demand have raised concerns about sustainability. The first step in evaluating the sustainability of harvests is to quantify suitable habitats. In this study, we aim to quantify the extent of suitable mopane larvae habitat; second, estimate each country's contribution towards total suitable habitat; third, estimate the effectiveness of conservation areas to capture suitable habitat; and finally, explore variables affecting suitable habitat. We generated a presence-only ensemble model by contrasting several algorithms (generalized linear models (GLM), BIOCLIM, and Random forests [RF]). The model was calibrated over South Africa, Botswana, Namibia, Zimbabwe, Mozambique, Malawi, and Zambia. We found that 71% of the model landscape is classified as suitable habitat. Suitable habitat differs among countries, with the highest in Botswana (32%), 24% in Namibia, 20% in Zimbabwe, 12% in Mozambique, 10% in South Africa, and 2% in Zambia. While a large percentage of suitable habitats fell within some land with protection status (37%), the majority were in non-protected areas (62%). In terms of protected areas, less than one percent of suitable habitats were contained in IUCN I and II categories (7%). Our study suggests that only a small percentage of suitable mopane larvae's habitat is contained in formally protected areas. As such, the population's persistent dependence on non-protected areas suggests that conservation planning should strive for community co-developed sustainable harvest strategies.

The expression and evaluation of CrpeNPV GP37 as a formulation additive for enhanced infectivity with CrleGV and improved *Thaumatotibia leucotreta* control.

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Categories

• Invertebrate Pathology

Abstract

False Codling Moth, *Thaumatotibia leucotreta,* is a serious agricultural pest causing damage to fruit crops in South Africa. Two *baculoviruses*, *Cryptophlebia leucotreta granulovirus* (*CrleGV*) and *Cryptophlebia peltastica nucleopolyhedrovirus (CrpeNPV)* infect *T. leucotreta*, causing larval mortality. CrleGV-SA is currently one component of an integrated pest management programme for the control of *T. leucotreta* in the field. To initiate primary infection, baculovirus proteins such as GP37 facilitate the penetration of virions through the peritrophic membrane. The genome of *CrpeNPV* encodes *GP37*, while that of CrleGV-SA does not. A previous study reported that bacterial-expressed GP37 encoded by *Cydia pomonella granulovirus (CpGV)* resulted in a 13.98- and 20.20- fold improvement in LC_{50} when combined with *Spodoptera exigua* NPV or Autographa californica NPV respectively, indicating that GP37 significantly enhanced the infectivity of NPVs and the lethality of *Bacillus thuringiensis* in *S. exigua* larvae. The aim of this study was to express CrpeNPV GP37 in a bacterial system and then evaluate its effect on larval mortality when combined with CrleGV-SA in laboratory bioassays. Oligonucleotides targeting the *GP37* gene from *CrpeNPV* genomic DNA were designed, enabling the subsequent amplification and cloning of the gene into the pCA528 vector for expression in *E. coli* Rosetta cells. A time course induction study was performed in which transformed cells were induced at 25 ºC for 0 h, 3 h, 5 h and 24 h post-induction (*hpi*). *SDS-PAGE* and Western blotting of samples collected at various time points showed that GP37 was visible at 3 *hpi*, with maximal expression at 24 *hpi*. Solubility analysis experiments indicated that the expressed protein is mainly in the insoluble fraction at 5 *hpi*. Ongoing experiments include improving protein solubility in preparation for purification and quantification, which will be followed by bioassays to evaluate the effect of the protein on larval mortality when combined with *CrleGV*-SA.

Selection of a South African *Heterorhabditis bacteriophora* isolate for in vitro liquid mass production for the biocontrol of *Thaumatotibia leucotreta*.

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Stellenbosch University, Stellenbosch, South Africa

Categories

• Agricultural Entomology

Abstract

The *in vitro* liquid mass production of entomopathogenic nematodes (EPNs) is a highly advanced biotechnological process that is critical for EPN commercial success as a biocontrol product. EPNs have a complex bacto-helminthic relationship with their associated bacteria, which is critical to the successful production of high concentrations of infective juvenile yields. *Heterorhabditis bacteriophora* is the most common EPN species found in South African soils, with previous research having shown its high pathogenicity against a variety of soil-borne insects. Currently, a foreign isolate of *H. bacteriophora* are registered in South Africa as a biopesticide product for the control of false codling moth (FCM), *Thaumatotibia leucotreta*, which is a key pest of citrus. Four isolates of *H. bacteriophora*, obtained from previous field surveys conducted across South Africa, was used in this study. Each *H. bacteriophora* isolate, together with their associated *Photorhabdus* symbiotic bacteria, was identified, using molecular techniques, with the bacteria concerned being tested for bioluminescence. Four *H. bacteriophora* isolates were laboratory-screened to determine the best candidate in terms of pathogenicity against FCM and in terms of their ease of in vitro culture. The screening was conducted by means of doing bioassays, along with the production of monoxenic nematodes and bacteria. The *H. bacteriophora* isolate chosen for having the highest pathogenicity, also showed strong bioluminescence. The study indicated that two of the *H. bacteriophora* isolates involved showed no bioluminescence, while two showed luminescence, indicating that it could be two different symbiotic bacterial species that are associated with the same nematode species. The *H. bacteriophora* isolate with the highest pathogenicity and ease of culture was chosen for the development of the *in vitro* liquid production protocol.

Comparison of physiological traits of phylogenetically diverse thermophilic *Ocymyrmex* species (Formicidae, Hymenoptera).

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Categories

• Physiological Ecology

Abstract

Temperature and scarcity of water are the main constraints to the activity of small organisms living in desert regions, as they are exposed to high day temperatures and need to evolve adaptations to these harsh conditions. Several insects living in arid regions have evolved physiological adaptations that enable them to survive dry conditions. Ants in the genus *Ocymyrmex* are most diverse in the arid regions of southern Africa. Some of the species in this group have adapted to forage when ground temperatures exceed 50ºC. The physiological traits that enhance thermotolerance across phylogenetically distinct *Ocymyrmex* species exposed to different thermal regimes across different climatic zones in South Africa were investigated in this study. Desiccation resistance, critical thermal limits and cuticular hydrocarbon composition of these ants were measured, to test whether these physiological traits were evolutionary conserved or labile, and whether thermophilic adaptations in *Ocymyrmex* were conserved through evolutionary constraints or driven by environmental influences. These assessments demonstrated that these ants have relatively high thermal limits and desiccation resistance. The latter is explained by the prevalence of long chained cuticular hydrocarbons and high abundance of linear alkanes, which are believed to promote waterproofing.

Assessing the competitive ability of *Lagarosiphon major* against *Egeria densa* in the presence and absence of biological control by Hydrellia flies: A Reciprocal Yield Model approach

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Categories

• Biological Interactions

Abstract

Invasive aquatic plant species pose a significant threat to freshwater ecosystems, causing environmental and economic harm globally. *Lagarosiphon major* and *Egeria densa* are two such invasive species that have rapidly spread in freshwater ecosystems worldwide. These invasive species are known to have a competitive advantage over native aquatic plants. Reciprocal yield models have previously been used to study plant competition in the presence of herbivory, in the context of biological control. The aim of this study was to use Spitters' reciprocal-yield models to evaluate the competitive ability of these two invasive species, *L. major* and *E. densa* in the presence and absence of their respective biological control agents, *Hydrellia lagarosiphon* and *Hydrellia egeriae*. The experimental design consisted of eight different factorial combinations of planting densities of *L. major*: *E. densa*, with and without biological control agents. The experiment was conducted in a controlled environment, and herbivore inoculation initiated four weeks after the setup using two neonate larvae per plant. The experiment was run for a total of 10 weeks, and height of the longest shoot, dry weight, and the number of new shoots were measured at the end of the experiment. Preliminary results showed that *L. major* is superior competitor to *E. dense* due to its more rigid yet versatile structure. When both species are exposed to biological control, this competitive edge was exacerbated by the addition of herbivory, due to the destructive nature of *H. egeriae* relative to *H. lagarosiphon*. The results of the study provide valuable insights into the competitive ability of *L. major* against *E. densa* and the role of biological control in mediating this competition and therefore should be taken into consideration when trying to manage these plants.

Larval performance of a specialist herbivore *Pareuchaetes insulata* (Lepidoptera: Erebidae: Arctiinae) on an invasive alien shrub *Chromolaena odorata* from four locations in South Africa

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Categories

• Weed Biological Control

Abstract

The Evolution of Increased Competitive Ability (EICA) hypothesis posits that specialist herbivores will demonstrate improved performance on plant individuals from an adventive range, compared to their performance on individuals of the same plant species from its native range, because the adventive plants have diverted resources from defence against natural enemies, towards growth and reproduction. To indirectly test EICA, an experiment was conducted on newly hatched *Pareuchaetes insulata* larvae fed on leaves of *Chromolaena odorata* plants that were collected from locations where *P. insulata* has established in South Africa (Umkomaas and Komatipoort) and locations where the moth has not been recorded (Thohoyandou and Pietermaritzburg). Insect performance metrics measured were larval, pupal and total development time, pupal weight, growth rate and overall survival. Consistent with EICA, immature stages that fed on leaves from Umkomaas had prolonged development compared to larvae that were fed on leaves from Thohoyandou and Pietermaritzburg, and Komatipoort, a location in which *C. odorata* has only recently been reassociated with *P. insulata*. Larvae that fed on leaves from a shaded habitat from Komatipoort had developmental time intermediate between larvae feeding on leaves from the shade from Thohoyandou and Umkomaas. Overall survival was lowest on leaves of plants obtained from Komatipoort. Pupae of the larvae which fed on the leaves from a full-sun habitat from Komatipoort showed an intermediate trend of development between pupae of the larvae that fed on leaves from Umkomaas and Thohoyandou. Location did not appear to influence pupal mass, but this variable was higher in full-sun plants from Umkomaas, Thohoyandou and Pietermaritzburg. The existing reassociation time may not be enough for evolutionary changes to have occurred in *C. odorata* defence and *P. insulata* response to plant evolution and could explain the inconsistency in some *P. insulata* performance parameters on infested and uninfested populations of *C. odorata*.

Impact of the gut microbiome on life history, body composition and stress resistance in False Codling Moth (*Thaumatotibia leucotreta*)

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Categories

• Agricultural Entomology

Abstract

Bacterial diversity and abundance within the gut can have a profound influence on host performance and fitness. For False Codling Moth (FCM), *Thaumatotibia leucotreta*, a major pest of citrus in South Africa, little work has been undertaken on gut bacterial diversity or its influence on FCM physiology. The aims of this study were to: 1. Characterize the gut microbiomes of both field and laboratory reared FCM. The laboratory-reared insects were either reared using normal SIT methods or had the egg chorion stripped to see whether microbiota was maternally transmitted to offspring. 2. Measure a suite of physiological traits in field, standard laboratory-reared and microbiome-altered laboratory-reared specimens to determine the link between the gut microbiome and individual performance. Microbiome characterization revealed the most abundant bacterial genera were *Bradyrhizobium*, *Methylobacterium* and *Burkholderia-Caballeronia-Paraburkholderia*. Larvae from the dechorionated treatment had the lowest counts of species richness compared to the control and field FCM, indicating maternal transfer of microbes at the egg stage. Analysis of physiological traits revealed that larvae from the field had a greater mass than laboratory reared FCM. However, FCM with an altered gut microbiome had a greater adult mass, with the highest dry mass. There was no difference in macronutrient content between treatments. When exposed to cold stress, FCM with altered microbiomes were less likely to suffer mortality than control and field-specimens. These results provide evidence that FCM may have a systematic association with specific bacterial genera essential to their development. Most importantly, specific genera identified in the control and field FCM treatments were pathogens present at sublethal levels that have the potential to impact insect mass and cold tolerance. Integration of microbiome analysis has the potential to enhance the rearing practices of FCM for SIT and biopesticide production via probiotic application and pathogen monitoring practices.

Host-specificity testing of the leaf-feeding flea beetle, *Phenrica guerini*, a biological control agent for the invasive alien cactus, *Pereskia aculeata*

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Categories

• Weed Biological Control

Abstract

Pereskia aculeata Miller is an invasive alien cactus that is problematic in both South Africa and Australia. In South Africa, the flea-beetle, *Phenrica guerini* Bechyné was released as a biological control agent 30 years ago and it plays an important role in reducing the invasive potential of the weed. Meanwhile, the plant has become increasingly problematic in Australia, where no biocontrol agents have been released to date, so *P. guerini* is being considered by the Australian authorities. Host-specificity testing was conducted before *P. geurini* was released in South Africa, but protocols and testing methods have improved since the early 1980s when it was conducted. Updated host-specificity testing was required to determine if *P. guerini* is suitably host specific for release in Australia. No-choice larval survival tests were conducted on 26 test plant species from 11 families, with survival to the adult stage only being recorded on *P. aculeata*. Some larval development was recorded on three plant species, two Portulacaceae (*Talinum caffrum*, *Portula oleracea*) and one in the Basellaceae (*Anredera cordifolia*), but the larvae could not successfully pupate. No-choice oviposition testing with adult *P. guerini* was conducted on six test plant species. No adult feeding was recorded on any test plants and significantly more eggs were oviposited on *P. aculeata* (158.8 S.E. ± 21.4) than on *Talinum caffrum* (5.2 S.E. ± 5.2), which was the only test plant on which they oviposited. In a multiple-choice trial that included all three test-plant species that supported any larval feeding as well as *P. aculeata*, oviposition, and feeding was only recorded on the target weed. *Phenrica guerini* is therefore a *P. aculeata* specialist and is suitably host-specific for consideration for release in Australia as a biological control agent.

Smallholder farmer's knowledge, perception and management practices of the fall armyworm, *Spodoptera frugiperda*, in Limpopo

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University of Pretoria, Pretoria, South Africa

Categories

• Agroecology

Abstract

The arrival of the fall armyworm, *Spodoptera frugiperda*, during the 2016 cropping season is currently causing devastating damage on maize in Limpopo, South Africa. The present study investigated knowledge, perception and management practices of *S*. *frugiperda* by smallholder farmers at Dzindi and Tshiombo irrigation schemes of Limpopo Province. The study was conducted from 28 June to 8 July 2022 in 16 focus group discussion interviews, 12 at Dzindi and four at Tshiombo irrigation scheme. Although farmers failed to identify *S*. *frugiperda* eggs and pupal stages, they positively identified the pest by its larval stage and refer to it by several local names. All farmers relied extensively on insecticides *for S. frugiperda* control. In exception to Dzindi irrigation scheme farmers, who have adopted Bt maize, almost all farmers have not yet adopted alternative methods to chemical control such as mechanical control (crushing egg and handpicking of larvae), biological control, cultural practices (such as Push Pull Technology), indigenous knowledge, or the use of monitoring tools (traps), for the management of S. *frugipierda*. The present study provided valuable information to support extension services and researchers when designing sustainable management practices to control *S. frugiperda* on maize in smallholder farmer communities.

Key words: Fall armyworm, focus group discussion, insect pest management

Transgenerational responses to heat and fasting acclimation in the Angoumois grain moth

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Categories

• Physiological Ecology

Abstract

The Angoumois grain moth *Sitotroga cerealella* (Olivier) is a one of the main grain pests in Africa that mostly affects staple cereal grains such as sorghum and maize. While its economic importance is well established, little is known about its thermal responses, particularly how heat pretreatment affects fitness in subsequent generations, regardless of the pest experiencing sub-lethal heat stress bouts during storage that may elicit acclimatory responses. Using laboratory reared *S. cerealella*, we examined the effects of heat and fasting acclimation on physiological heat tolerance (i.e., critical thermal maxima [CTmax] and heat knock down time [HKDT]). We investigated whether pre-exposure to heat stress (static or fluctuating temperatures) and fasting stress would result in fitness costs and/or benefits in the subsequent generations (i.e., transgenerational plasticity). Our findings demonstrated that both CT_{max} and HKDT were reduced by dynamic temperature acclimation (28–38°C), especially at lower ramping rates (for CT_{max}) and that acclimation had significant interactions with temperature ramping rates on CT_{max}. We did not find fasting acclimation to significantly affect CT_{max}, indicating a lack of evidence for cross tolerance/susceptibility in the next generation. All acclimation treatments for HKDT (including fasting) demonstrated significantly lower HKDT than controls, with most of these differences occurring in dynamic acclimation (28-38°C) treatments, indicating a fitness cost of acclimation. This is the first study on the costs of transgenerational plasticity in stored products pest and has broader implication on the improvement of heat-based phytosanitary grain treatments. We thus conclude that prior heat stress reduces heat tolerance in subsequent generations of *S. cerealella*, suggesting that heat-based phytosanitary controls may have cross-generational additive consequences.

The impact of *Trichilogaster* wasps and *Melanterius* weevils on the reproductive fitness of two Australian invasive acacia species in South Africa.

Pride Mudavanhu

Agricultural Research Council - Plant Health & Protection (ARC-PHP); Alien Weed Biocontrol, Entomology Department, Vredenburg Campus, P/Bag X5017, Stellenbosch, South Africa

Categories

• Weed Biological Control

Abstract

The use of bud galling wasps from the genus *Trichilogaster* and seed feeding weevils from the genus *Melanterius* against two alien invasive Australian acacia species positioned South Africa amongst the leaders in biological control of invasive perennial woody tree species. The research dates back to the 1970s, and biocontrol has been permanently present on Acacia longifolia and *A. pycnantha* for more than 40 years. As part of long-term post release monitoring and evaluation of the efficacy of the technique, this study sought to determine whether the long-term presence of biocontrol is reflected in the curtailment of the reproductive fitness of these invasive woody tree species. Due to conflicts of interest associated with Australian acacias that form the mainstay of the South African forestry industry, biocontrol has been limited to the use of insect agents that only preclude or reduce their reproductive capacity while allowing the commercial utilization of the woody parts of the plants. In spite of the presence of dense stands of the infestations in some mountain and riparian habitats, we report findings on the performance of the biocontrol agents as reflected in galling extent, seed damage, seed rain, soil seed bank density, post-fire seedling recruitment and survival. Results are discussed within the context of determining whether there is a need to update the current management strategy.

Key Words: bud galling wasps, seed feeding weevils, invasive perennial weedy trees, biocontrol.

Host specificity of *Psyllaephagus* species (Hymenoptera: Encyrtidae) towards four invasive eucalypt psyllids (Hemiptera: Aphalaridae) introduced in South Africa

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Categories

• Invasive Insects

Abstract

Global eucalypt production is threatened by invasive insect pests native to Australia. Among these invasive insects, eucalypt-feeding psyllids constitute the majority. South Africa eucalypt plantations host two free-living psyllids, *Blastopsylla occidentalis* and *Ctenarytaina eucalypti*, and two lerp-forming psyllids, *Glycaspis brimblecombei* and *Spondyliaspis* cf. *plicatuloides*. In order to reduce their economic impact and further dispersal, classical biological control has been employed and worked successfully as co-evolved parasitoids, *Psyllaephagus* wasps are highly specific in their parasitisation. Upon the unintentional introduction of the psyllids in South Africa, some came along with their co-evolved *Psyllaephagus* species. A previous study showed that the parasitoid of *G. brimblecombei*, namely, *Psyllaephagus bliteus*, also parasitised S. c.f. plicatuloides, demonstrating that the host specificity of the psyllid parasitoids requires investigation. The objective of the study was to determine the host specificity of *Psyllaephagus blastopsyllae, P. pilosus* and *P. bliteus* using eucalypt-feeding psyllids, *Blastopsylla occidentalis*, *C. eucalypti*, *G. brimblecombei* and *S.* cf. *plicatuloides*. To determine host specificity, the three different species of *Psyllaephagus* were collected from their respective hosts locally, and five-day-old parasitoids were exposed to non-host psyllid nymphal instars in both choice and non-choice setting. In both tests, the parasitoids were exposed to various stages of the psyllid nymphal instars. *Glycaspis brimblecombei* was identified as a potential new host for *P. blastopsyllae*, and *S*. cf. *plicatuloides* was confirmed as an alternate host for *P. bliteus*. *Psyllaephagus pilosus* was the only parasitoid to show no interest in the other psyllids tested. All female parasitoids preferred specific nymphal stages that promote parasitoid larval development. Our findings indicate that some *Psyllaephagus* spp. attack hosts within an ecological niche, whereas others are highly host specific.

Key words: Biological control, choice test, forest pest, no-choice test, psyllid

Psylloid community structure and diversity in and adjacent to citrus orchards

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Categories

• Agricultural Entomology

Abstract

Psylloids (Hemiptera: Psylloidea) constitute a group of sap-sucking insects that include species of economic concern. These insects have the ability to transmit a Gram-negative bacteria *Candidatus* Liberibacter spp. The two known psylloid vectors of these bacteria species are the African citrus triozid (ACT), *Trioza erytreae* and Asian citrus psyllid (ACP), *Diaphorina citri*. The latter has great world economic concern with the ability to vector '*Candidatus* Liberibacter asiaticus' (CLas), which has the ability to kill trees rapidly. ACP and CLas are currently not present in southern Africa. The aim of this study is to determine the diversity and community structure of indigenous psylloid species in citrus environments. Yellow sticky traps and sweep nets were used to collect psylloids at 12 different commercial citrus environments in Limpopo and Mpumalanga provinces. Statistical analyses were conducted using R (Version 4.2.2) and species accumulation curves (SAC) were used to estimate the sampling efforts. The results indicated that psylloids' community structure is significantly different between plant species and the trap methods (i.e., trapping vs sweep-netting) in citrus environments. The diversity of psylloids was high in different citrus environments in both provinces, with Limpopo being the highest, and most species were collected using the trapping method. The most abundant and widely distributed species were *Diaphorina punctulata*, *Diaphorina virgata*, *Retroacizzia mopanei*, *Acizzia* sp.1, *Psylla loranthi*-group, *Euryconus* sp. and *Pauropsylla trichaeta*. Several plant families adjacent to citrus orchards were recorded as hostplants of these psylloid species. However, citrus is not a host to any of the psylloid species surveyed in the citrus orchards and their threat is therefore not known.

Phylogenetic analysis of the bacterial microbiome of *Rhipicephalus sanguineus* ticks in the Mnisi community, South Africa

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

Many emerging communicable diseases amongst humans can be ascribed to tick-borne zoonotic pathogens arising from animals. *Rhipicephalus sanguineus* ticks are ideal vectors of zoonotic pathogens and, although capable of parasitizing most vertebrates, they are most prevalent on dogs, especially in rural resource poor communities. The Mnisi community in Mpumalanga, South Africa is one such rural, impoverished community. This community sits at the wildlife-livestock-human interface creating an ideal situation for the spread of zoonotic pathogens. The aim of this study was to analyse the bacterial microbiome of *R. sanguineus* ticks collected from dogs in the Mnisi community.

To achieve this, we collected ticks in 2016, 2017 and 2019 from a total of 23 community dogs. From each dog, 10 male *R. sanguineus* ticks were collected and the midgut (MG) and salivary gland (SG) tissues were dissected and pooled per tissue. We processed 19 MG pools and 19 SG pools. Genomic DNA was extracted and amplified using universal 16S rDNA barcoded primers. Samples were then sequenced using Pacific Bioscience's circular consensus sequencing strategy.

The microbiome analysis revealed 19 genera, including *Anaplasma, Ehrlichia* and *Coxiella*. Further phylogenetic analysis showed two *Anaplasma* species. *Anaplasma platys*, which causes canine thrombocytopenia, was detected in in 2017 (2.53%) and 2019 (1.05%). Although it is a canine pathogen, human infection with *A. platys* has been previously recorded. *Anaplasma centrale*, which causes bovine anaplasmosis, was detected in all 2019 samples (17.80%). The *Coxiella* genus was classified as a *Coxiella*-like endosymbiont, specific to *R. sanguineus* ticks, and was detected in all samples from 2016 (74.54%), 2017 (84.29%) and 2019 (42.78%). These results highlight the importance of *R. sanguineus* and the role it plays in the possible transmission of pathogens within the community.

The recovery of arthropods after pine removal in Table Mountain National Park

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Table Mountain National Park is a significant protected area within the Cape Floristic Region where highly diverse, endemic, and fire-adapted fynbos is dominant. A major threat to biodiversity arises from alien invasive plants such as areas of non-indigenous pine plantation. Although some have been cleared, pine plantations support low indigenous plant and arthropod diversity, and alien plant invasions threaten natural ecosystems and their processes. Clearing and restoration of these areas may allow for the recovery of fynbos plant species, but there is limited information on the response of arthropods after pine clearing. Between 2005 and 2007, arthropods were sampled at sites with varying land use changes across Table Mountain. Since then, some pine plantations have been cleared, thus some previous plantation sites are now recovering fynbos. Furthermore, some plots have burnt in the interim, and at different times with varying burn frequencies. Arthropods were resampled in 2022 and 2023 at the same sites which have varying categories of recovery from pine plantation, less than 5 years post pine removal, approximately 30 years post pine removal to pristine fynbos. This was done to investigate arthropod recovery post pine removal in terms of species composition, diversity, and functional richness. Increased knowledge of arthropod recovery post pine removal may inform management strategies for this biodiversity hotspot and allow for the assessment of land transformation influences on arthropod assemblages.

Habitat diversity in remnant grassland and expansive open grassland together conserve diverse butterfly traits.

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Habitat loss threatens insect diversity, but heterogeneity in remaining habitat can buffer these impacts by increasing opportunities for species survival. Wooded biotopes, such as indigenous forest and woodland, may benefit grassland insects by providing complementary resources, resource continuity and refuge. We assess whether the presence of indigenous forest patches in grassland ecosystems alleviate the impact of afforestation with exotic tree plantations on butterflies in northern Zululand, South Africa. We sampled butterflies in grassland conservation corridors among plantations and in an adjacent protected area. We selected sites that were situated along uncorrelated gradients of indigenous forest and plantation cover in the landscape and accounted for variation in local-scale plant composition. Butterfly groups that differ in habitat preference, larval diet, and mobility were assessed separately. Large-scale conservation corridors among plantations supported equally high butterfly diversity as the adjacent protected area. Despite this, there were subtle shifts in butterfly taxonomic and trait composition with increasing plantation cover. Grassland butterflies that are naturally associated with high forest cover were unaffected by plantation cover and were well-supported in conservation corridors with forest patches. Across all sites, indigenous forest cover benefited butterflies with woody larval host plants. However, butterflies with certain traits were underrepresented in the grassland corridors between plantations. These traits are associated with intrinsic vulnerability to landscape transformation, such as low mobility and habitat specialization. We show that conservation corridors are a valuable mitigation measure in afforested landscapes and demonstrate the added contribution from indigenous forest patches towards maintaining butterfly diversity. In addition, the preservation of expansive, unwooded grasslands is critical to ensure the persistence of the widest diversity of species and traits.

Thermal stress exposure of pupal oriental fruit fly has strong and trait-specific consequences in adult flies

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Categories

• Physiological Ecology

Abstract

Global climate change is projected to increase the incidence of heat waves, their magnitude and duration resulting in insects experiencing increasing environmental stress in both natural and managed ecosystems. While studies on insect thermal tolerance are rapidly increasing, variation across developmental or juvenile stress cross-stage effects within and across generations remain largely unexplored. Yet in holometabolous insects, heat stress at an early developmental stage may influence performance and survival during later stages. Here, we investigated the effects of pupal mild heat stress on the performance of laboratory reared adult *Bactrocera* dorsalis (Hendel) (Diptera: Tephritidae) measured as longevity, critical thermal maximum (*CTmax*), critical thermal minima (*CTmin*), heat knockdown time (HKDT) and chill coma recovery time (CCRT). Pupal heat stress significantly influenced performance of B. dorsalis adults resulting in impaired longevity and heat tolerance (*CTmax* and *HKDT*) in both sexes with improved and compromised cold tolerance (*CTmin and CCRT*) in females and males, respectively. These findings highlight the role of juvenile stages in mediating stress responses at adult stages. For B. dorsalis, pupal heat stress largely compromised thermal tolerance implying that the species has limited potential to shift its geographic range in heat prone areas. Significant benefits in cold tolerance in females following heat stress may help in improving survival in the cold in the short-term despite restricted activity to the same traits in males. This study suggests that basal heat tolerance and not short-term compensatory thermal plasticity following heat stress may have aided the recent invasion of B. dorsalis in African landscapes.

Understanding *thelytoky* in the Cape honeybee: how ideas and technology evolved to give a more complete understanding of this biological phenomenon.

Robin Crewe

University of Pretoria, Pretoria, South Africa

Categories

• Physiological Ecology

Abstract

Thelytoky in the Cape honey bee (*Apis mellifera capensis*) was experimentally demonstrated for the first time by a beekeeper in 1912. This discover was greeted with incredulity at the time, but subsequently shown to be correct. The Cape honey bee remains the only subspecies of honey bee in which thelotoky in workers is present.

In the intervening century since this discovery, the Cape honey bee has been the subject of increasingly intensive investigation, because thelytoky does not simply determine that laying workers can produce female offsping without fertisation. The presence of thelotoky has major effects on the production of key social pheromones and on ovary morphology. Furthermore, the presence of these laying worker individuals can lead to their establishment as social parasites in other honey bee subspecies.

The biological understanding of the nature of thelotoky in the Cape honey bee will be examined from the time of its discovery in 1912 to current understanding of the *phenmenon* up to 2022. The discussion will explore evolving ideas about the nature of thelotoky and the way in which advancment in analytical technology has made a richer understanding of the phenomenon possible. The review will cover developments in social behaviour, histology of cell division in the ovary, analysis of social pheromones, and the insights provided by genomic analysis in the quest for the identification of the thelotoky gene.

Invasion success of *Vespula germanica* is dependent on haplotype match to thermal refuges within a Mediterranean climate

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Categories

• Invasive Insects

Abstract

The invasive wasp *Vespula germanica Fabricius* is widely distributed can have major environmental and socio-economic impacts. In South Africa this species is still limited to a relatively small geographic range and has spread slower compared to other invaded countries. *Vespula germanica* in general has poor dispersal abilities (>1000m per annum). Previous work in the Western Cape has identified that the distance between climatically suitable habitat fragments is a major constraint on invasive spread. This restricts natural dispersal to other suitable locations with further expansion solely dependent on human mediated jump dispersal. To investigate this further, we quantified the mitochondrial diversity of 72 representative nests and the average environmental conditions at these nest locations. We found two haplotypes that were significantly different in the mean annual summer maximum temperature that nests were exposed to. The more common haplotype (H1) had a mean of 28°C compared to the rarer haplotype (H2) had a mean of 26°C. H2 is therefore far more constrained than H1 by high summer maximum temperatures to fragmented thermal refuges in the landscape. This suggests that the two invading haplotypes have come from two different climatic regions in their native range. Where H1 is more heat tolerant in its distribution than H2, it suggests a more southerly (warmer) origin for the former and more northerly (temperate) for the latter. The slow invasion of *V. germanica* in the Western Cape since its detection in 1972, followed by sudden expansion from 2000, suggests an initial invasion of a poorly climatically matched (temperate) haplotype followed by a second invasion of a more meso-Mediterranean heat tolerant one. A global analysis of haplotype diversity in the native and invaded range can confirm this hypothesis. The country of origin is thus less important than the prevailing native climatic conditions from where haplotypes originate.

Southern *afrotemperate* forest tree flowers are visited by a diverse array of diurnal and nocturnal insects

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

The largest indigenous forest in southern Africa is confined to the eastern regions of the mega-diverse Cape Floristic Region, between the Outeniqua mountains and the Indian Ocean. Here, large stretches of continuous and fragmented forests form a mosaic landscape with fynbos, farmlands, urban areas and plantation forestry areas. Despite an abundance of work on pollination in the fynbos biome, indigenous forests have been largely overlooked, with the most comprehensive notes on forest tree pollination dating back to 1926. These notes, however, are mostly anecdotal and were concluded from ground observations by a single researcher. The canopy layer height in southern Afrotemperate forests typically ranges between 12-25 metres. Despite divergent phylogenies, ca. 60% of canopy tree species produce a strikingly similar flower morphology of small, white flowers. Here, we accessed flowering tree canopies, using rope pulling techniques, and observed insect flower visitors of four common canopy tree species. A total of 144 hours of day- and night-time observations were captured. The most common flower visitor was the Cape honeybee (*Apis mellifera capensis*). However, Dipteran, Lepidopteran and non-bee Hymenopteran species contributed significantly to flower visitation rates, with respective tree species showing unique assemblages of flower visitors. Here, I give an overview of this diversity. Interestingly, temporal segregation in flowering phenology was noted for focal tree species, as well as differences in petal colour.

Dose mapping of an X-ray irradiator with application to Sterile Insect Technique (SIT) for the control of *Eldana saccharina* Walker (Lepidoptera: Pyralidae) in sugarcane

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Categories

• Agricultural Entomology

Abstract

In South Africa, the stalk borer *Eldana saccharina* significantly reduces sugarcane yield. The application of the sterile insect technique (SIT) as a proof of concept for the control of *E. saccharina*, and ways to incorporate this strategy into an AW-IPM system are under consideration. Gamma irradiation is widely used in SIT programmes. However, the high costs and strict safety regulations associated with housing and acquiring radioactive isotopes are major factors limiting accessibility to gamma sources. X-ray irradiation has gained a lot of attention in recent years due to its safety, minimal training regulations, and low transportation costs. A study was conducted to determine the dose distribution of a 6-canister X-ray irradiator (RAD Source 2400 Q4) for sterilization of *E. saccharina* moths. The dose uniformity was assessed, and the absorbed dose was measured using 2ml ampules filled with a Fricke dosimeter solution with standard G-value for Fe3+ = 15.5/100 eV. *Eldana saccharina* moths were placed in plastic containers alongside Fricke dosimeters and irradiated inside canisters to achieve absorbed dose values of 100, 150, 180, 200, and 250 Gy. Results showed that the average minimum dose rate of 18.30 ± 0.06 Gy/min was obtained near the base of the plastic container facing towards the back of the canister, while the maximum dose rate of 20.46 ± 0.08 Gy/min was observed at the cap periphery of the container. It was evident that the relative dose distribution pointed to a significant drop in absorbed dose at the back of the canister compared to the maximum dose measurement at the front. Irradiating *E. saccharina* moths at a position towards the front of the canister was found to be a viable option. A dose rate of 19.30 Gy/min was recommended to achieve minimal overexposure and deliver the target dose to sterilize E. saccharina moths.

The first fossil *staphylinid* from Africa supports an ancient ecosystem reconstruction of a Cretaceous crater lake at Orapa, Botswana.

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University of the Witwatersrand, Johannesburg, South Africa

Categories

• Systematics and Taxonomy

Abstract

The fossil record of insects is rich temporally and spatially, and insects preserved in lacustrine deposits are found as far back as the Late Carboniferous (360 Ma). Coincidentally, the fossil record of Coleoptera dates back to the Early Permian (300 Ma) or Late Carboniferous (360 Ma). *Staphylinidae* is a hyper-diverse family with over 65 561 extant and 450 extinct species, making it the most speciose in the animal kingdom. It includes four informal subgroups, viz. *omaliine, tachyporine, oxyteline, and staphylinine*, encompassing 1 extinct and 33 extant subfamilies. A new genus and species of rove beetle, *Afristenus orapensis* gen. et *sp. nov*., is described and figured based on one well-preserved compression fossil from the African, Upper Cretaceous fossil insect deposit, Orapa Diamond Mine in north-east Botswana. *Afristenus* is definitively placed in the extant subfamily *Steninae* based on its harpoon-like labial feeding apparatus. *Afristenus* differs from all other *Steninae* by its head and neck behind the eyes being broader than eyes that cover two-thirds of the side of the head and a transverse prothorax, which is distinctly broader than the head. The new specimen from Orapa Diamond Mine possibly has unique antennae with a compact 5-segmented-club, and a stem composed of elongated antennal segments. This is the first *stenine* compression fossil with a preserved labial feeding mechanism. It confirms the widespread distribution of *stenines* with this feeding apparatus in the Cretaceous; supporting the hypothesis that this feeding mechanism was part of the ground plan of the Steninae, and the Lower Cretaceous, but probably not Jurassic origin for the group. It also demonstrates morphological conservatism dating back to the Cretaceous. In the Cetaceous, Orapa is reconstructed as being strongly seasonal, with a warm, high humidity, wet summer, and a dry, cold winter.

Building a better baculovirus biopesticide: improving control of tree fruit Lepidoptera

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Categories

• Invertebrate Pathology

Abstract

Baculoviruses have been used for control of tree fruit Lepidoptera for several decades, with the first being Cydia pomonella granulovirus (CpGV) for *Cydia pomonella* (codling moth) control. Subsequently, pest species, such as *Grapholita molesta* (oriental fruit moth), *Thaumatotibia leucotreta* (false codling moth) and *Helicoverpa armigera* (bollworm) have been targeted. Despite the obvious benefits and efficacy of virus-based biopesticides, they do present certain shortcomings. For example, although host specificity is an advantage, so is it a disadvantage; baculoviruses are also UV-sensitive and degrade rapidly in direct sunlight; although not common, pest resistance can occur; and speed of kill is slow. Consequently, a multi-faceted research programme is being driven to develop solutions to these deficiencies and to optimize efficacy of baculovirus biopesticides. This includes bioprospecting for novel baculoviruses, selection for UV-resistance, various forms of synergism, virulence selection and formulation. For example, bioprospecting for new baculoviruses has identified alternative *CrleGV* isolates in the event that resistance by *T. leucotreta* may develop. A novel *CpGV* isolate with potential to overcome codling moth resistance to *CpGV* has also been found. A novel virus species, the *Cryptophlebia peltastica nucleopolyhedrovirus* (CrpeNPV), with a relatively broad host range, being virulent against several species of tortricids, has also been found and characterized. We have also successfully selected a UV-resistant *CrleGV* isolate, with more than 1000-fold improved virulence after UV-exposure, compared to the wild-type isolate and are pursuing the same for *CrpeNPV*. Combining different species of virus and a virus with another microbe, has also resulted in synergistic responses, increasing virulence. Passaging of a virus through a closely related heterologous host can result in selection of more virulent genotypes, thus improving virulence against the heterologous host. Lastly, novel delivery system formulation is being pursued. These and other strategies present tremendous opportunities for improvement of efficacy of baculovirus biopesticides.

A novel baculovirus based biopesticide for tortricid management

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Categories

• Agricultural Entomology

Abstract

Baculovirus based biopesticides are well known for their favourable toxicological profile, consistent efficacy, IPM compatibility and host specificity. However, host specificity can limit their broader use against non-host insect pests. *Cryptophlebia peltastica nucleopolyhedrovirus* (*CrpeNPV*) is a novel baculovirus that was isolated from litchi moth, *Cryptophlebia peltastica* (Lepidoptera: Tortricidae), which is endemic to sub–Saharan Africa. Unlike other known baculoviruses isolated from the Tortricidae, CrpeNPV offers a unique spectrum of action due to it being a nucleopolyhedrovirus as opposed to a granulovirus (GV). Initial studies highlighted the meaningful potential for CrpeNPV to contribute towards sustainable agriculture in two ways: through resistance management of Cydia pomonella granulovirus (CpGV) resistant *Cydia pomonella* populations and through virulence against several non-homologous economic pests within the Grapholitini tribe, with global importance. From a South African perspective many of these tortricids are phytosanitary pests in export markets. This study focused on moving towards field development of *CrpeNPV* as a biopesticide. Multiple field trials were conducted using a randomised single plot experimental design to establish field efficacy of *CrpeNPV* at various rates against several *trotricid* crop pests, as well as comparing the different treatment combinations against existing standards. Therefore, each crop-pest combination had different treatment regimens, based on their current commercial spray programmes, with the inclusion of untreated controls across the board. Reduction in pest infestation on crops was calculated as a percentage compared to the untreated control. Field trials were conducted both in South Africa and across several European countries. Results in litchis against *C. peltastica* and *Thaumatotibia leucotreta*, showed *CrpeNPV* to provide pest control of up to 87% at the highest field rate. Studies in pome fruit, targeting *C. pomonella*, achieved up to 92% control at the highest rates. In macadamias, targeting *T. leucotreta* and *T. batrachopa*, control of up to 93% and 89% was recorded.

Prospects for Classical Biological Control of papaya mealybug using its parasitoid *Acerophagus papayae* in Africa

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Categories

- Invasive Insects

Abstract

Papaya mealybug (PMB) (*Paracoccus marginatus*) is an invasive pest from Mexico and Central America that was first reported in East Africa between 2016 and 2020. The pest has been reported to cause 57% yield losses and £2,224/ha household economic losses annually. Majority of papaya farmers manage PMB using highly hazardous pesticides, thus harming native insect biodiversity. To reduce on pesticide reliance, conserve biodiversity and protect the environment, Classical biological control (CBC) of PMB using its parasitoid, *Acerophagus papayae* provides the most ecologically sound and climate-smart approach. Consequently, CAB International in partnership with Kenya Agricultural and Livestock Research Organization, Kenya Plant Health Inspectorate Services and National Museums of Kenya are implementing the classical biological control of PMB using *Acerophagus papayae* parasitoid that was imported from Ghana to Kenya in 2020 for efficacy testing in quarantine facilities. A release dossier was subsequently prepared and approval granted by the Kenya Technical Standing Committee on Imports and Exports (KSTCIE) for the release of *A. papayae* in Kenya in 2021. Field releases of *Acerophagus papayae* adults commenced in December 2021 at 6 research sites in three coastal counties of Kenya i.e. Kilifi, Mombasa and Kwale) to evaluate the efficiency of the parasitoid to establish and parasitize papaya mealybug under field conditions. A total of 5725 adults were supplied at different time and numbers at the research sites in three supplies. The parasitoid was able to establish within the first month of introduction after collection of papaya infested fruits and monitored for emergence of *A.papayae*. Parasitism levels varied across the sites with the highest parasitism of 72% being recorded at Kwale. *Acerophagus papayae* establishment in the field and parasitizing the mealybug to levels not detectable in the field has proved to be the most effective control strategy that should be implemented in Kenya and Africa beyond.

The role of landscape context, vertebrate predators, and pesticide application on nut quality and invertebrate community composition across macadamia orchard landscapes

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Categories

• Agroecology

Abstract

The South African macadamia industry is amongst the fastest growing industries, and currently the largest producer of macadamia in the world. The industry depends on syngenetic pesticides to control major economic pests such as stink bugs. Land use change and agricultural intensification have led to a decrease of farmland biodiversity and its ecological functions. Here we assessed invertebrate diversity and composition within the macadamia landscape in the sub-tropical fruit growing region of South Africa. We were specifically evaluating a) the role played by landscape context and elevation in shaping invertebrate community composition, b) impact of arboreal vertebrate predators on insect community composition in macadamia orchards and their surrounding natural landscape and c) estimating the relationship between pesticide application and nut quality metrics. The study was stratified across six macadamia farms along an elevational transect and included exclusion experiments (cages) at the edge and interior (50m from edge). The cages enclosed two macadamia trees and excluded vertebrates from accessing the trees. Invertebrates were sampled using a portable thermal fogger at each of the treatments and 50m into the surrounding matrix of remnant natural vegetation. The response of taxonomic and functional diversity (size) to landscape context and treatments were modelled using Generalized Linear Mixed Models. Species richness increased with elevation and with landscape context, increasing from the interior towards the edge and into the remnant natural vegetation. Insect size increased with elevation and elevation effects were more pronounced in the interior and least pronounced in remnant natural vegetation. Farms in the lower elevation varied in species composition compared to higher elevation. Pesticide applications did not influence the amount of damage observed caused by insects, while there was weak negative evidence for sound kernel increases with the decreased application of pesticides. The study highlights the potential of ecological intensification to enhance ecosystem services.

Larval exposure to detergents and acids alters the life history of the major malaria vector *Anopheles arabiensis* Patton (Diptera: Culicidae).

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

Anopheles arabiensis Patton is a member of the *An. gambiae* complex. It is the major malaria vector of South Africa. This complex tends to breed in clean, clear, sunlit bodies of water. However, there are various examples throughout Africa of this species adapting to breeding in polluted water. The effect of various pollutants have been characterised for this species. However, these have largely been associated with agricultural activities. *Anopheles arabiensis*, in particular, has been associated with the adaptation to urban areas. As such, it would be useful to understand the effect of urban pollutants on this particular malaria vector. In this study, we examined the effect of the opposite ends of the pH scale. The effects of larval exposure to hydrochloric and nitric acid were examined as well as that of detergents with and without phosphate was assessed. This was performed on the insecticide-susceptible SENN strain and the insecticide-resistant SENN-DDT strain. Hydrochloric acid and phosphate-containing soap were more toxic than nitric and phosphate-free soap. Both acids resulted in faster larval development in SENN, but only nitric acid increased larval development rate in SENN-DDT. Detergents had a generally negative effect on larval development. Larval acid exposure did not alter adult longevity, but soap exposure generally resulted in increased adult longevity. Larval nitric acid exposure increased deltamethrin tolerance the most, and phosphate free soap the least. This study demonstrates species-specific effects of these pollutants on this major malaria vector. These findings have epidemiological significance and may be able to affect diseases transmission.

Thirty years of sampling effort and status quo of African Darwin wasp diversity (*Ichneumonidae, Hymenoptera*)

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Species richness of Afrotropical *Hymenoptera* is poorly known. Most African vegetation types have been inadequately sampled and many wasp species remain to be collected. Effective species discovery requires implementation of long-term, continuous inventory surveys, using a diverse range of sampling methods with a high degree of spatial and temporal coverage. This is a critical need, particularly given the rapid escalation in habitat transformation, largely as the result of anthropogenic impact. Over the last 30 years I have conducted continuous surveys across a range of habitats in South Africa and further afield in Africa (totaling 94 000 Malaise trap days = 257 Malaise trap years), which have produced an estimated 39 million insect specimens, the Hymenoptera comprising an estimated 5.4 million specimens, and the Ichneumonidae an estimated 470 000 specimens from Malaise trap samples alone. There are, however, major challenges associated with mobilizing the specimen data, including logistical bottle-necks associated with curation, digitization and description of species to elevate the data through the value chain for the benefit of science and society. As part of the Afrotropical *Hymenoptera* Initiative (www.waspweb.org) we are slowly addressing this paucity of data. As an example, the Darwin wasp family has 363 described genera and 2 102 described species in the region, but I estimate there are c. 20 000 species, hence we know about 10% of the fauna. Historically about 800-900 species have been described every 50 years since the first African species was named in 1758, but in the last 20 years we have only described 162 species. However, these contemporary revisions have allowed for an assessment of the degree of the undiscovered fauna, with revisions at generic level resulting in a 10-100 fold increase in species richness, supporting the contention that we only know a small fraction of the existing species richness.

Medicinal, religious, and cultural use of invertebrates by traditional communities in Africa: A systematic review

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

Zootherapy describes the use of animals and their products as medicine to heal human diseases and includes their use in religious and cultural activities. Invertebrates have also been used for medicinal uses for decades. For instance, several studies have scientifically proven that certain insects' bodies have antibacterial, antirheumatic, anesthetic and immunological properties, which can be useful in healing humans. Invertebrates are not only medically important for humans but also religiously and culturally significant for humans. Therefore, this study aims to review existing literature on the medicinal, religious, and cultural uses of invertebrates in Africa. The PRISMA guidelines were used to systematically search Science Direct, Sabinet African Journal, Web of Science and Google scholar databases for studies from 2000 to 2022 on the medicinal, religious, and cultural use of invertebrates in Africa and South Africa. Articles were selected based on the relevance of the title and abstract. Information that was extracted and collected was the year, study area, study invertebrate, reported medicinal, cultural, and religious use, primary findings, and conclusions. Preliminary findings show that in African countries such as Nigeria, Cameroon, Ethiopia, Republic of Benin and Burkina Faso, zootherapy is prevalent and commonly used. Over 30 species of invertebrates were found to have medicinal, religious, and cultural uses in these countries. The most common invertebrates' classes used for medicinal purposes include Insecta, Arachnida, Myriapoda, Crustacea and Gastropoda. Termites, bees and ants were the most quoted insects with medicinal significance. For instance, the most prevalent ailments cured by these invertebrates include sickness in children, skin problems, infections, wounds, respiratory issues, stomachache, rheumatism, headaches and preventing bleeding from pregnant women. Insects are dominantly used in traditional practices such as a lucky charm for business or romance, protection against evil, initiation during traditional practices, attracting good fortune, and prediction of change in season.

Evaluating baculovirus mixtures against false codling moth *Thaumatotibia leucotreta* Meyrick. (Lepidoptera: Tortricidae)

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Categories

• Invertebrate Pathology

Abstract

The false codling moth (FCM), *Thaumatotibia leucotreta*, is an important pest of citrus, stone fruit, avocados, peppers, and other important agricultural crops in southern Africa. Baculovirus based biopesticides are components in an integrated pest management (IPM) programme to manage the pest in the field. Despite these viruses being relatively host-specific and safe to humans and animals in comparison to chemical insecticides, their application is hindered by their slow speed of kill, sensitivity to UV light, and the potential for insect resistance. Previous studies using a combination of two baculoviruses infecting *T. leucotreta* demonstrated a reduction in lethal concentration in laboratory bioassays, indicating that such mixtures may have the potential for application in the field. The aim of this study is to evaluate baculovirus mixtures of *CrleGV-SA, CrpeNPV, CpGV-M and HearNPV*, to determine whether synergistic or antagonistic interactions occur against *T. leucotreta* neonate larvae, measured by lethal concentrations. Preceding this, genome analysis was conducted. A set of oligonucleotides targeting unique regions in each viral genome were designed to distinguish between the virus present in the samples. Occlusion bodies were extracted from larval cadavers infected with *CrleGV, CrpeNPV, CpGV and HearNPV* and the genomic DNA was extracted from purified occlusion bodies from each sample. The genomic specific oligonucleotides were used together with universal primers targeting regions of the *polh*, *lef-8* and *lef-9* genes in PCR assays. The results of the universal primers confirmed the presence of baculovirus in the viral samples. The genomic specific oligonucleotides confirmed the target viruses in the samples with the expected amplicon sizes generated. qPCR assays are currently underway to generate melt curves to analyse any differences in the DNA sequences. Surface-dose response biological assays are in progress to evaluate lethal concentration of each virus alone and in combination against *T. leucotreta* neonate larvae.

Effect of sublethal doses of glyphosate herbicide on water hyacinth (Pontederia crassipes Mart.) (Pontederiaceae) and its biocontrol agent, *Megamelus scutellaris* Berg. (Delphacidae: Hemiptera).

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Categories

• Weed Biological Control

Abstract

In South Africa, the integrated management of the water hyacinth (*Pontederia crassipes*) using chemical and biological control has become necessary as biological management alone is deemed too slow to control the weed's invasiveness. However, herbicidal control is not sustainable as plant populations rapidly recover when spraying stops, and is detrimental to the biocontrol agents. This study was designed to evaluate the influence of sublethal doses of a routinely-used glyphosate herbicide KILO MAX® on water hyacinth and its biocontrol agent, *Megamelus scutellaris*. Mesocosm studies were designed where four different treatments of herbicides were applied to water hyacinth plants; Control (no herbicide), 0.4%, 0.6% and 0.8%, with and without the biocontrol agent. This study discovered that a concentration of 0.4% slows the vegetative growth of water hyacinth (ramets, flowers, leaves) without killing the weed and *M. scutellaris*. *Megamelus scutellaris* populations were significantly higher on plants treated with 0.4% compared to plants treated with 0.6%, 0.8%, and surprisingly the control plants ($F_{12}= 16.11$, $P < 0.001$). Nitrogen (N) content of plants treated with low dose of KILO MAX® herbicide was significantly higher than the untreated control plants ($F_3 = 9.685$, $P = 0.025$), with C: N ratio significantly higher in control plants than the treated plants ($F_3 = 36.74$, $P < 0.001$). The high N content may be responsible for enhanced *M. scutellaris* populations on sublethal herbicide-treated plants. Consequently, the sublethal dose enhanced feeding by *M. scutellaris*. This suggests that the sublethal dose of KILO MAX® is compatible with *M. scutellaris* and can therefore be recommended for integrated management approaches of water hyacinth.

Towards a comprehensive biosecurity masterplan for the citrus industry of Southern Africa

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Categories

• Agricultural Entomology

Abstract

The citrus industry of southern Africa including producers in South Africa, Zimbabwe and Eswatini exports more than 2 million tons of fresh fruit to major markets in Europe, the Middle East, the Far East and United States to the value of R30 billion annually. This makes citrus one of the region's top fresh produce export commodities. However, the citrus industry faces an ever-increasing threat from invasive pests and diseases due to global trends in the movement of people and goods in international trade, and the impact of climate change shifting the dynamics of pests and diseases establishing and spreading into new regions. Consequently, the risk of invasive pests and diseases threatening the continued success of the citrus industry has increased significantly in recent years. Biosecurity entails the management of risks due to introduction, establishment or spread of pests and diseases on an industry, the economy, the environment and the community. Biosecurity has attracted significant attention in recent years, prompted by high-profile outbreaks of plant pests and diseases affecting livelihoods and economies. To address the challenges CRI has developed a masterplan with the aim to establish an effective biosecurity system that includes actions ranging from assessment of biosecurity risks on an ongoing basis, to implementation of pest detection and rapid response procedures, and development of strong local, regional, and international collaborative networks, as well as promoting awareness about biosecurity issues. Biosecurity objectives can only be achieved through partnerships with multiple stakeholders. Among the key stakeholders of southern Africa's citrus biosecurity are commercial citrus growers represented by the Citrus Growers Association (CGA), Citrus Research International (CRI), the Department of Agriculture, Land Reform and Rural Development (DALRRD), South Africa's Citrus Nurserymen Association (SACNA), the Agricultural Research Council (ARC), as well as the general public.

Biological Control of the Banded Fruit Weevil (Coleoptera: Curculionidae) Species Complex.

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Categories

• Invertebrate Pathology

Abstract

The banded fruit weevils, *Phlyctinus callosus* Schönherr and *Phlyctinus xerophilus* Haran (Coleoptera: Curculionidae) are native *entimine* weevils of economic concern to the deciduous fruit and grapevine industry of South Africa. The use of entomopathogenic nematodes (EPNs) and entomopathogenic fungi (EPF) as inundatively applied biological control agents of these weevils is a potentially sustainable alternative to broad-spectrum insecticides that are currently used in their management. Two EPN species and two EPF isolates were screened in the laboratory on the target life stages of *P. callosus* and *P. xerophilus*, using 24-well bioassay plates as test arenas. Entomopathogens were inoculated onto 12.7 mm filter papers in wells, to which an individual insect was added. Concentrations of 50-200 infective juveniles (IJs)/insect, and 5 ×105 conidia/insect were applied in separate bioassays. Mortality and infection were recorded 48–96 h post inoculation for EPNs, and for 18 days post inoculation for EPF. A semi-field trial was conducted in an apple orchard using *Steinernema yirgalemense* against *P. callosus* and *P. xerophilus* larvae. A concentration of 60 IJs/cm2 was applied, and field cages removed 96 h post inoculation. Mortality and infection were assessed after further 48 h incubation in the laboratory. A control group, not inoculated with entomopathogens, was included in each bioassay. Poor and variable results (often < 50% mortality) were obtained in adult laboratory bioassays for EPNs and EPF. Potential differential susceptibility of *P. callosus* and *P. xerophilus* adults to EPF was shown. Larvae and pupae showed ≥ 50% mortality to *S. yirgalemense* in laboratory bioassays. Under field conditions, *P. xerophilus* larvae (48%) were found to be more susceptible than were *P. callosus* larvae (25%) to *S. yirgalemense*. These results highlight the importance of taxonomic work to refine pest management. Natural infection of different life stages of *Phlyctinus* by native EPNs and EPF in agro-ecosystems was demonstrated.

Is darker better? Phenotypic colour variation in a beetle reveals performance costs and sex-specific responses to developmental plasticity

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Categories

• Physiological Ecology

Abstract

Dark pigmentation resulting from cold rearing temperature is ubiquitous in insects. Yet, the costs associated with this developmental plasticity have only been explored for a handful of species despite the broad implications of colour variation for evolutionary responses to climate change. We explored two competing hypotheses relating to colour plasticity of insects. First, if melanin is costly to synthesize and requires allocation of resources, increased melanisation should be negatively associated with performance traits or other aspects of fitness. Second, given the positive association between melanisation and traits such as immunity and desiccation resistance, we expect a positive coadaptation between melanisation and performance. We assessed whether temperature-induced melanisation of the globally invasive beetle *Harmonia axyridis* f. *succinea* (Pallas) (Coleoptera: Coccinellidae) was related to resting metabolic rate and flight performance parameters while accounting for rearing temperature regime and parental affiliation.

The percentage melanisation and number of black spots of cold-reared beetles explained little variation in resting metabolic rate at most temperatures tested (15, 20, 25, 30 and 35 °C). For beetles reared at the warm regime, darker beetles tended to have lower resting metabolic rate, but the strength of this relationship varied depending on the temperature tested, body mass and sex investigated. For flight performance after the cold rearing regime, larger and lighter-coloured beetles travelled further than small beetles, but this relationship was not found for darker individuals. In addition, in warm-reared beetles, darker individuals had lower mean flight speeds. These results indicate that there are performance costs associated with developmentally induced melanisation but also reveal complex interactions with sex and body size. Finally, we found substantial variation in the extent of melanisation for warm-reared females compared to equally treated males. We propose new hypotheses that underlie the differential selection for diverse colour phenotypes between sexes in the wild.

Genetic analysis and semi-field assay of a UV-tolerant strain of CrleGV for improved control of *Thaumatotibia leucotreta*

Tahnee Bennett[1], Martin Hill[1], Sean Moore[2,1], Michael Jukes[1,3], Caroline Knox[1,3], Gill Dealtry[4]

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Categories

• Invertebrate Pathology

Abstract

The moth, *Thaumatotibia leucotreta* is indigenous to sub-Saharan Africa and a pest of citrus. Currently, *Cryptogran*^{TM}, a commercial formulation of CrleGV-SA, is the preferred product to use in South Africa for the control of *T. leucotreta*. One of the major factors affecting the baculovirus efficacy in the field is UV irradiation. A UV-tolerant *Cryptophlebia leucotreta granulovirus* (CrleGV-SA-C5) isolate was isolated after consecutive cycles of UV exposure. This UV-tolerant isolate is genetically distinct from the CrleGV-SA isolate and has potential as a biological control agent for improved control of *T. leucotreta*. Thus, the study aimed to determine the biological and genetic stability of CrleGV-SA-G5 following bulk-up in fourth instar *T. leucotreta* larvae. A *de novo* assembly was conducted to reassemble the genome of CrleGV-SA-C5 followed by a sequence comparison with the CrleGV-SA genome, and seven SNPs were detected. Two methods of screening were conducted to differentiate between CrleGV-SA-C5 and CrleGV-SA genomes and confirm the presence of the SNPs. The first was the construction of six plasmids, and sequencing and the second was a quantitative PCR melt curve analysis. Following the differentiation, the genetic integrity of the CrleGV-SA-C5 isolate after two virus bulk-ups was determined by PCR amplification of the target regions in the bulk-up virus followed by sequencing. Sequencing results confirmed the presence of the target SNPs in the CrleGV-SA-C5_BU2 (bulk-up 2) genome. The UV-tolerance of the CrleGV-SA-C5 isolate in comparison to the CrleGV-SA isolate was evaluated by detached fruit bioassays under natural UV irradiation. Statistical analysis indicated that there was no significant difference between the virus treatments, possibly indicating the need for a revised experimental protocol.

Developing a biological control programme for a challenging target weed, *Trichocereus spachianus.*

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Centre for Biological Control, Rhodes University, Grahamstown, South Africa

Categories

• Weed Biological Control

Abstract

Trichocereus spachianus is an invasive cactus species in South Africa and poses various challenges as a target for biological control, including confusion around its taxonomy and origin. Adapted to arid environments, this cactus is of particular concern in dry savannah and Karoo biomes, where its invasion of rangelands reduces grazing areas for indigenous wildlife and livestock. While previous records indicate that *T. spachianus* is indigenous to Argentina, recent field surveys have failed to verify its presence. Establishing the origin of the target weed is important in developing a biological control programme since it enables the collection of host-specific insects directly from the wild populations of the target plant. Due to the absence of native cacti in the Old World, successful biological control programmes against cacti species in South Africa have involved utilising both new associations and oligophagous insects. As wild populations of this particular cactus could not be located, direct collection of insects from these populations was not possible, and thus the possibility of using new associations between the cactus and several oligophagous insects collected off cacti species closely related to *T. spachianus* was explored. The suitability of multiple *Hypogeococcus* (mealybug) entities and a cochineal species, *Dactylopius confertus*, as potential agents was determined by determining their potential efficacy on various cacti species, including *T. spachianus*. The findings revealed that the *Hypogeococcus* entities would not be effective biocontrol agents, as very few established and persisted on *T. spachianus*. On the other hand, *D. confertus* demonstrated potential as a biocontrol agent, as the results showed that it had a relative high fecundity and survival rate on *T. spachianus.* Host specificity testing and further efficacy trials are underway, but the preliminary results suggest that the cochineal is likely to be suitably specific and damaging g enough for release

Bait and bait presentation in the management of the fruit-piercing moth, *Serrodes partita,* in Citrus orchards

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Categories

• Agricultural Entomology

Abstract

The fruit-piercing moth, *Serrodes partita* (*Fabricius*) (Lepidoptera: Erebidae), is a polyphagous, multivoltine pest of citrus. The adult moth pierces the skin of ripening or ripe citrus fruit and sucks the juices, facilitating the entry of secondary fungal pathogens and fruit fall. In the Eastern Cape, the population dynamics of *S. partita* have evolved over the years, with recent observations showing recurring occurrences as opposed to usual seasonal outbreaks approximately five to 10 years apart. Current pest management practices are limited, lack specificity and are only useful for small orchards, with significant drawbacks for large-scale production. This study aimed to develop an effective trapping system for monitoring and controlling *S. partita*, by creating effective bait and bait presentation techniques. Four different trap designs (funnel, bucket, delta, and disc traps) were evaluated against *S. partita*, with the funnel trap being the most effective. Although the most effective, it was clear that the funnel trap could be further improved as a monitoring tool. Therefore, further studies were conducted to improve the design, using an electronic trap to exploit the nocturnal moth's visual and olfactory cues - with promising results. Alternatives to banana baits, based on an Australian proprietary recipe and banana essence have also been tested. An efficient trap design combined with synthetic bait will significantly improve the management of *S. partita* in susceptible citrus orchards.

The genus *Amphoterus*: taxonomic notes on a rare Afrotropical hover fly genus

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Categories

• Systematics and Taxonomy

Abstract

The genus *Amphoterus* Bezzi, 1915 is a rare group of hover flies restricted to the Afrotropical Region. Three species are recognized, *Amphoterus cribratus* Bezzi, 1915, known from only one male and one female, *Amphoterus braunsi* van Doesburg, 1956, described from a single male and *Amphoterus londti* Midgley *et al*, 2023, described from a single female. While not often collected, a large series of *A. braunsi* has been accumulated over time at the KwaZulu-Natal Museum. Apart from the usual sexual dimorphism, patterns of pilosity on the face can be used to differentiate males from females in the genus. High quality photographs, DNA barcodes and notes on useful taxonomic features will be presented.

Fruit fly species composition, seasonality, and fruit infestations in avocado orchards in Limpopo and Mpumalanga

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Categories

• Agricultural Entomology

Abstract

Several fruit fly species (Diptera: Tephritidae) are known to attack different types of commercially grown fruit. The economic impact includes direct yield losses and indirect losses resulting from quarantine restrictions that are imposed by importing countries. The South African avocado industry consists of 15 439 ha of commercial avocado plantings, the majority of which are situated in the Limpopo and Mpumalanga provinces. The industry is export orientated and under increasing pressure to access new markets. The avocado is known to be a poor host for the development of fruit flies. However, fruit flies can develop in the fruit under certain conditions. Various indigenous *Ceratitis* spp. and the invasive Oriental fruit fly, *Bactrocera dorsalis* (Hendel) are associated with avocado production in South Africa. Fruit flies were monitored in different avocado production areas (Limpopo and Mpumalanga) in four cultivars ('Carmen Hass', 'Hass', 'Lamb Hass' and 'Maluma Hass'). Five monitoring systems were used in order to trap the different fruit fly species. Fruit was inspected for the presence of fruit fly lesions during the fruiting period. High *B. dorsalis* numbers were trapped in bucket traps with Invader-Lure™ (contains methyl eugenol) in 'Maluma' orchards prior to harvest in both Limpopo and Mpumalanga. 'Maluma' was the only cultivar where fruit fly lesions were found. The data gathered are especially important in developing a systems approach (as detailed in ISPM 14, ISPM 35) that integrates different measures for pest risk management, in order to meet a predetermined level of protection. In terms of host-pest relationships, a systems approach for fruit flies is particularly attractive on avocado which is a poor host and where low fruit fly infestation levels are present.

Role of developmental plasticity in tethered flight performance of the oriental fruit fly (*Bactrocera dorsalis*)

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Categories

• Agricultural Entomology

Abstract

Insect dispersal is a key component in the population ecology and dynamics of insects, and it is crucial to understand insect dispersal in a range of disciplines such as invasion biology and integrated pest management. Variation in dispersal ability between individuals is influenced by differences in individual phenotypes as a result of dietary intake. The oriental fruit fly, *Bactrocera dorsalis* (Hendel) (Diptera: Tephritidae) is an invasive pest of fruit that is established in the northern regions of South Africa. However, there is a high possibility for future expansion of *B. dorsalis* further west- and southward into areas where it is currently absent in part due to its reported strong flight capacity. We investigated the effect of development in different host fruit (mango, guava, orange, grapefruit, papaya and apple) on adult body condition, wing morphology and flight of *B. dorsalis*. One day after adult emergence, tethered flight of flies of known weight was assessed using computerised flight mills and the wings were included in an assessment of wing morphology using geometric morphometrics. Additional flies were assessed for flight muscle mass and lipid content. Our results show significant differences in the larval and pupal developmental time and survival, flight performance, wing morphology, and lipid content and flight muscle mass of *B. dorsalis*, with flies reared on mango being the best overall performer. There was a significant difference between female and male wing shapes, indicating the presence of sexual dimorphism. Our results show variation in flight performance of *B. dorsalis* between individuals can be associated with changes in individual phenotypes that are associated with developmental host. There is a risk of *B. dorsalis* spreading to infest mango trees in the Northern and Western Cape region as they are susceptible to damage by *B.dorsalis* because of their high larval development and adult survival.

Expanding the South African sterile insect technique project's toolbox of sex separation systems for the malaria vector *Anopheles arabiensis*.

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Categories

- Medical, Veterinary and Forensic Entomology

Abstract

The South African mosquito sterile insect technique (SIT) project targeting the primary malaria vector *Anopheles arabiensis* is at an advanced developmental stage. Numerous technical aspects of the technology including sex separation strategies have been optimized. However, the current systems to exclude female mosquitoes from the production line before irradiation and field releases remains an "Achilles heel" of the project. Females must be excluded because, unlike males, they are capable of transmitting diseases. The present system for separating sexes to exclusively obtain *An. arabiensis* males for releases is proving to be operationally challenging and need further optimisation to ensure an efficient field pilot-trial. Thus, a proposal was made to expand the South African SIT project's toolbox of sex separation systems by developing additional genetic sexing strains (GSSs) using classical genetics and transgenic approaches. An *An. arabiensis* strain in which males are produced under temperature conditions that genetically favour their production due to the temperature sensitivity lethality (*tsl*) mutation is being developed. So far, a *tsl* mutant strain has been isolated. However, for this strain to be useful, a visible selectable marker linked to both the sex-determining locus and the *tsl* mutation is required. Insecticide resistance and morphological body/colour variations are being investigated as selectable markers that can be linked to the *tsl* mutation. If these markers are isolated, they will be translocated to the sex-determining chromosome, allowing males and females to be distinguished. Furthermore, a report on the successful creation and evaluation of two An. arabiensis transgenic strains based on a fluorescent marker will be discussed. The one strain has the fluorescence linked to the X-chromosome while the other is linked to the Y-chromosome. Combining these sexing strains enables the sorting and release of non-transgenic males. These advancements have laid a solid foundation for the South African SIT project.

The biological control agents *Carvalhotingis Visenda* (drake and hambleton) (Hemiptera: Tingidae) and H*edwigiella Jureceki* (obenberger) (Coleoptera: Buprestidae), as vectors of the adventive pathogen C*ercosporella Unguis-cati* speg. (M*ycosphaerellaceae*) in South Africa

Thabo Moabi[1], Wijnand Swart[1], Nontembeko Dube[1], Anthony King[2], Alec Edwards[1]

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Categories

• Weed Biological Control

Abstract

Dolichandra unguis-cati, an invasive vine in southern Africa, can only be effectively controlled biologically; chemical and mechanical control proved to be either ineffective or harmful to the environment. Two host-specific natural enemies, *Carvalhotingis visenda* and *Hedwigiella jureceki* were imported to control *D. unguis-cati*. However, the persistence and establishment of these biocontrol agents have been influenced by the appearance of an adventive leaf-spot pathogen *Cercosporella unguis-cati*. This study aimed to determine if *C. visenda* and *H. jureceki* are vectors of *C. unguis-cati* on *D. unguis-cati* in South Africa. Insect specimens were collected from the quarantine facility at the Agricultural Research Council-Plant Health and Protection (ARC-PHP) and from two field sites where *C. visenda* has been established, and *C. unguis-cati* is present. Individual specimens of *C. visenda* and *H. jureceki* were plated on potato dextrose agar (PDA) and malt extract agar (MEA) using sterile procedures. Additionally, leaves of *D. unguis-cati* infected by *C. unguis-cati* were collected and plated on a PDA. Several pure fungal cultures differentiated according to morphological characteristics were isolated from *C. visenda* and *H. jureceki*. A part of these displaying characteristics associated with plant pathogens was subjected to further testing to determine their pathogenicity on *D. unguis-cati*. Molecular sequencing of the ITS gene region (internal transcribed spacer, with ITS1 and ITS2) showed that these isolates were in the genera of *Neopestalotiopsis, Fusarium, Pestalotiopsis, Nigrospora*, and *Alternaria*. Pathogenicity results indicated that none of the isolated fungal pathogens displayed lesions similar to the ones caused by *C. unguis-cati* on *D. unguis-cati*. Contrary to what was assumed, *C. unguis-cati* was not present in any of the isolated cultures, leaving no conclusive evidence to prove that *C. unguis-cati* dispersal is aided by either *C. visenda* and/or *H. jureceki.* Therefore, *C unguis-cati* may be dispersed by other unknown agents.

Impact of the gall-inducing fly *Polymorphomyia basilica* Snow (Diptera: Tephritidae) on the growth and reproduction of *Chromolaena odorata* (L.) R.M.King & H.Rob (Asteraceae) in the laboratory

Thandeka Mahlobo[1,2], Nontembeko Dube[1,2], Costas Zachariades[3], Caswell Munyai[2]

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Categories

• Weed Biological Control

Abstract

Gall-inducing insects are a classic example of how insects can impact the morphology and physiology of their host plants by forming galls which act as nutrient sinks. An eight-month laboratory study was conducted to determine the impact of the galls induced by *Polymorphomyia basilica* oviposition and or the subsequent larval feeding on the growth and reproduction of *Chromolaena odorata*. Three treatment levels were used, viz. control: 0% of the shoots were exposed, low infestation: 50% of shoots were exposed, and high infestation, where 100% of the shoots were exposed for *P. basilica* to oviposit for 48 hours each month. Results showed that *P. basilica* oviposition and or the subsequent feeding by larvae reduced the height and flower production of *C. odorata* plants but promoted lateral growth by increasing the number of shoot tips. Basal stem diameter was not affected by the presence of the galls. The presence of galls also decreased the leaf and root dry biomass on the treated plants but had no significant impact on stem biomass. The difference between the low- and high-infestation treatments was only significant for root biomass, suggesting that more galls are required for the roots to be affected. Overall, the study showed that *P. basilica* meets the requirements of an effective biocontrol agent against *C. odorata* in South Africa. Its release should complement the already released agents in reducing the fitness and productivity of *C. odorata*.

Keywords: Galls, efficacy, biocontrol, biomass

Investigations into the unsuccessful attempts to control *Leptospermum laevigatum*, using a leaf-mining moth, *Aristaea (Parectopa) thalassias*

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Categories

• Weed Biological Control

Abstract

Biological control of *Leptospermum laevigatum* has been implemented since the 1980s with limited success to date. *Aristaea (Parectopa) thalassias* is one of two poorly-performing biological control agents of the plant. A study was carried out over 32 months to investigate factors which may be contributing to the low efficacy of the moth, and larval mortality factors due to parasitism, predation, overcrowding and season were considered. The developmental biology of the moth, which was unknown was also studied. The results demonstrated that the moth is abundant in the field and the rapid development of immature stage permits several generations a year. Although parasitism and overcrowding was low, mortality was ± 50% for all of the immature stages and was significantly impacted by season. Despite this, the moth was still abundant in the field suggesting that mortality was not the sole reason for low efficacy of this agent. Factors such as plant compensation, leaf quality as well as adult mortality, combined with egg mortality may have contributed to survival and efficacy of A. thalassias as a biological control agent against *L. laevigatum*. While findings from this study have given insights into the survival and population dynamics of *A. thalassias* on *L. laevigatum* in South Africa, the evidence presented in this study could not explain the low field efficacy of the agent. Determining why a biocontrol agent is ineffective is a common problem in several biocontrol programmes, and often, is a result of complex issues which may not be easily discernible.

The effects of acclimation temperatures on larval stages of macadamia nut borer, *Thaumatotibia batrachopa* (Meyrick) (Totricidae: Lepidoptera)

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Categories

- Agricultural Entomology

Abstract

Thermal biology studies reveal the thermal breadth of insects, and thermal tolerance studies are key to understanding the effect of climate change on insect population abundance and distribution. The macadamia nut borer (MNB), *Thaumatotibia batrachopa* (Meyrick) is one of the major insect pests of macadamia. The aim of this study was to investigate the effects of acclimation on critical thermal limits (CTLs) of *T. batrachopa* larval stages. We investigated the CTLs of larval stages of MNB by determining the critical thermal minima (CT_{min}) and critical thermal maxima (CT_{max}) at 20, 25, and 30°C acclimation temperatures. An ANOVA was used to determine the effects of acclimation temperature on CTLs of MNB larval stages. Preliminary analysis showed the amount of variation in CTmin and CTmax of all larval stages in response to acclimation. Instar 4 had significantly? higher CT_{min} compared to all other instars, and all larval stages had a similar 20 and 25°C acclimation response to CT_{min}. All instars showed significantly higher CT_{max} in response to acclimation at 30°C. Multiple comparisons using Tukey's HSD test showed that the CT_{max} of all instars increased from 25 to 30°C. The results suggest that different larval stages can adapt to fluctuating high temperatures. This information is important for understanding the baseline responses that shapes the population dynamics of MNB in the orchards.

Keywords: MNB, CT_{max}, CT_{min}, acclimation, instars

The effect of biological control agents on the population dynamics of *Pontederia crassipes* (C. Mart) Solms (Pontederiaceae) and *Salvinia minima* Baker (Salviniaceae)

Tressia Chikodza, Martin Hill, Julie Coetzee

Rhodes University, Grahamstown, South Africa

Categories

• Weed Biological Control

Abstract

The planthopper, *Megamelus scutellaris*, was released in South Africa for the biological control of *Pontederia crassipes*. Inundative releases of *M. scutellaris* has been shown to control the weed even in high elevation, eutrophic sites, such as Hartbeespoort Dam. However, subsequent to the control of *P. crassipes* on Hartbeespoort Dam, in 2021, the water surface was covered by *Salvinia minima*, in what is termed an invasion cascade. In Florida, USA, a strain of the control agent, *Cyrtobagous salviniae* has successfully managed *S. minima*. This strain has been imported to South Africa and is undergoing host-specificity testing. This study investigated the competitive ability of *P. crassipes* under *M. scutellaris* herbivory against *S. minima* to determine the impact of biological control when the two plants are competing for resources. The impact of the planthopper was evaluated using an additive series analysis of competition between *P. crassipes* and *S. minima*. Competitive abilities of *P. crassipes* and *S. minima* were determined using an inverse linear model with plant weight as the yield variable. In the absence of herbivory, *P. crassipes* was 4 times more competitive than *S. minima*, but only 1 times more competitive when exposed to *M. scutellaris* feeding. *Salvinia minima* was 1.2 times as aggressive as *P. crassipes* that was free of herbivory, but 2.6 times as competitive when *M. scutellaris* were established on *P. crassipes*. In the presence of herbivory on *P. crassipes*, interspecific competition coefficients from *P. crassipes* on *S. minima* were no longer statistically significant. These results provide insight into the competitive ability of *P. crassipes* when grown with *S. minima* and the impact of the biological control on its competitive ability, and thus establishing which species should receive most attention from invasion control organizations, and when.

Temporal partitioning of *Bullacris unicolor* (Orthoptera: Pneumoridae) calling activity to avoid predation

Vanessa Couldridge, Robyn Manuel, Rekha Sathyan, Tarné Johannes

University of the Western Cape, Bellville, South Africa

Categories

• Biological Interactions

Abstract

Ecological interactions, including competition, predation, and environmental conditions, may significantly impact acoustic signalling behaviour. Here we characterise nocturnal signalling patterns in the bladder grasshopper *Bullacris unicolor* and relate this to biotic and abiotic factors, thus providing insights into ecological drivers of acoustic signalling behaviour. Passive acoustic recorders monitored nocturnal calling activity of the focal species, competitors and predatory bats across the distribution of *B. unicolor*. Results indicate that *B. unicolor* calls preferentially at certain times of the night, but that peak activity period varies across the geographic range. There was a strong relationship between *B. unicolor* activity and bat activity. *Bullacris unicolor* populations further north showed an overall avoidance of bat echolocation call period, whereas further south an overlapping of call periods between *B. unicolor* and bat echolocation was observed. Bats at northern sites showed a distinct activity period early in the night and *B. unicolor* may thus reduce predation risk by shifting signalling activity to later in the night. In contrast, bats were active throughout the night at southern sites and *B. unicolor* did not delay calling activity in this region of its distribution, although the species did shift signalling slightly to reduce peak overlap with co-existing pneumorid species.

Two new species of the wormlion genus *Vermilynx* Stuckenberg (Diptera: Vermileonidae), from the Northern and Western Cape Province, South Africa

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Categories

• Systematics and Taxonomy

Abstract

The Vermileonidae (Diptera), commonly known as wormlions, are an enigmatic group of flies, distributed throughout most of the world with the exception of Antarctica, South America, Australia and some oceanic islands. The greatest diversity of Vermileonidae, nine genera and 31 species, is found in the Afrotropical Region. Six of these genera occur in Southern Africa: *Lampromyia* Macquart, 1835, *Leptynoma* Westwood, 1876, *Namaquamyia* Stuckenberg, 2002, *Perianthomyia* Stuckenberg, 1996, *Vermilynx* Stuckenberg, 1995 and *Vermipardus* Stuckenberg, 1960. Four of these genera are endemic to Southern Africa and three are restricted to the arid western parts of the subregion. *Vermilynx vansoni* (Stuckenberg, 1965) was described from the Richtersveld (in the genus *Lampromyia*) based on a single female. Later, with the discovery of male specimens, the new genus *Vermilynx* Stuckenberg, 1995 was erected for this species. A second species, *Vermilynx jasoni* Stuckenberg, 1996 was described from the Springbok District of Namaqualand based on male and female specimens. In 2000, Stuckenberg reported two undescribed species in the holdings of the KwaZulu-Natal Museum but passed away before describing them. We present these two undescribed species here, one from the Gamkaskloof (Western Cape) and one from Pofadder (Northern Cape) in South Africa.

Commercial banana and macadamia plantations in a savanna matrix support high levels of arthropod diversity

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Categories

• Agroecology

Abstract

Expansion and intensification of agroecosystems is one of the major causes of habitat loss in the savanna biome in South Africa. As such, this study sought to determine the influence of commercial subtropical fruit plantations (banana and macadamia) on species richness, abundance, and composition of surface-active arthropods compared to the savanna biome. Given that pesticides and herbicides are applied from spring to early autumn in banana and macadamia plantations, we sampled in winter to reduce the potential impact of pesticides and herbicides. Surface-active arthropods were sampled using pitfall traps. Habitat type did not affect species richness and abundance of ants and spiders, as well as species richness of beetles. However, significantly greater abundance of beetles was recorded in the macadamia plantation compared to the banana and savanna. This could have been due to greater abundance of herbivorous beetles and other insects, which would have increased the diversity of predatory beetles. Furthermore, unlike the banana plantation, the macadamia plantation was characterised by a deep leaf litter layer and the presence of weeds and grasses, which probably increased abundance of beetles. Species composition indicated that the studied arthropod taxa associate with specific habitats, as demonstrated by the three habitats supporting different species composition. Despite savanna habitat not supporting high species richness nor abundance of surface-active arthropods, we recorded the highest number of unique species of ants and spiders in the savanna rather than in the plantations. These results highlight the importance of natural landscapes in conservation of surface-active arthropods.

Monitoring and forecasting false armyworm (*Leucania loreyi* Duponchel) in barley

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Categories

- Agricultural Entomology

Abstract

Barley (*Hordeum vulgare* L.) is grown in two distinct production regions in South Africa, the rainfed Southern Cape Rûens and irrigated areas in the Northern Cape, North West Province and Limpopo. Primarily used as malt for brewing beer, this is an important crop for local maltsters and the consumers who enjoy their product. In 2010, following unexpectedly low yields, false armyworm, was detected in irrigation areas from Douglas to Viljoenskroon. This was the first time that false armyworm was recorded as a pest of barley in South Africa and the damage was severe with some farmers losing up to 50% of their yield. This paper explains the work done to set up a network of pheromone traps to monitor this pest which is nocturnal and therefore difficult to detect. Importantly, a model that uses the life history data of this species was developed to forecast moth flights and set up an early warning system to notify farmers when they should scout for fall armyworm damage in their fields. Soil living pupae can remain viable in soil for up to five years. The larvae emerge under conducive conditions to feed on leaves, but more importantly, on the soft barley stems just below the awns, which then break off and fall to the ground. Multiple years data have identified areas where false armyworm occurs more regularly. Data over multiple years also clearly shows the large difference a relatively small change in climatic conditions can have on this crop pest. This paper will also reflect on the value of this kind of project and its methodology for monitoring other pests in future as a way to deal with the influence of climate change on crop production.

Dactyloipus tomenstosus 'californica var parkeri' (Hemiptera: Dactylopiidae): A successful biocontrol agent against *Cylindropuntia pallida* (Cactaceae) in Australia, but unsuccessful in South Africa?

Wade Sexton, Iain Paterson, Phillippa Muskett

Rhodes University, Makhanda, South Africa

Categories

• Weed Biological Control

Abstract

Cylindropuntia pallida FM Knuth, is an invasive alien species in Australia and South Africa. The plant becomes overabundant and has large spines that are harmful to livestock and reduces yields of wool and mohair for local farmers as well as reduceing access to grazing, shade, and water sources. Recently, *Dactylopius tomentosus* 'californica var parkeri', a cochineal species, was released in Australia as a biocontrol agent and dramatically reduced *C. pallida* densities. This came after host specificity testing in Australia showed that the agent was suitably host specific to *C. pallida*. Given this success, the agent was approved for release in South Africa. After three unsuccessful attempts to rear the agent in quarantine on South African plants, the possibility of the South African plants being unsuitable hosts was considered. A fitness bioassay was conducted by inoculating the agent on both Australian and South African *C. pallida* plants and recording survival, duration of development, and fecundity. The results indicated that the agent could develop and reproduce effectively on Australian plants but has significantly lower survival rates, longer duration of development, and lower fecundity on the South African *C. pallida*. Due to the host-specific nature of *Dactyloipius* species, these results suggest that there must be a genetic misidentification of *C. pallida* plants between the two countries and that this agent will not bring about effective control in South Africa. Therefore, a new agent is required, and field studies as well as the collection of other cochineal biotypes in its native distribution of Hidalgo, Mexico are necessary for biological control. During this project, we will hopefully find an effective biocontrol agent for the target weed and also help improve our understanding of how to select the most effective cochineals as biocontrol agents for cactus weeds in the future.

The current status of Asian citrus greening and its primary vector the Asian citrus psyllid in Africa, and preparation by the Southern African citrus industry for their imminent arrival

Wayne Kirkman[1], Solomon Gebeyehu[2], Elma Carstens[3], Paul Fourie[4], Aruna Manrakhan[2], Evans Mauda[2], Glynnis Cook[2], Vaughan Hattingh[3]

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Categories

- Invasive Insects

Abstract

In Africa, Asian citrus greening, or Huanglongbing (HLB) is known to occur in Ethiopia and Kenya, and the primary vector, the Asian Citrus Psyllid (ACP), *Diaphorina citri* is present in Kenya, Tanzania, Ethiopia, Nigeria and Benin. To prepare the southern African citrus industry for the imminent arrival of ACP and HLB, and to address other biosecurity risks, Citrus Research International (CRI) established a Biosecurity division that spearheads the advancement of the citrus industry's biosecurity needs, along with diagnostics and research. In South Africa, a comprehensive national HLB Action Plan and an HLB Safe System for nurseries have been developed that set out the necessary preparedness and incursion response actions. These have been officially adopted by the Department of Agriculture, Land Reform and Rural Development (DALRRD) and undergo periodic updates. In addition to ongoing surveillance and monitoring efforts in South Africa, Zimbabwe and Eswatini, CRI is working with collaborators in various African countries to track the movement of HLB and ACP into southern Africa. Surveys have been conducted in Mozambique in 2019, 2020 and 2022 around Maputo, in Inhambane province, and the Beira-Chimoio-Machipanda corridor, respectively. As yet no ACP or HLB have been detected. Surveys and visits have also been conducted in Ethiopia, Angola, Tanzania and Namibia. To determine the most likely incursion pathway of HLB and ACP into South Africa, CRI has developed a risk heat map of southern Africa to indicate strategic areas to focus surveillance and monitoring efforts. A modelling project is currently underway to validate and refine the current risk heat map.

Managing augmentative releases of *Anagyrus vladimiri* (Triapitsyn) for successful biocontrol of the citrus mealybug, *Plannococcus citri* (Risso)

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Categories

• Agricultural Entomology

Abstract

Mealybug populations remain problematic in commercial citrus orchards, thus motivating researchers to investigate efficacy of commercially available biocontrol options, particularly since insecticide residues are under constant review. In 2014, Citrus Research International reported promising efficacy levels of *Anagyrus vladimiri (Triapitsyn*) augmentation to control citrus mealybug *Plannococcus citri (Risso*). In this study, the efficacy of A. vladimiri was compared in open and netted citrus orchards in Burgersfort over two consecutive seasons. The predominant mealybug species was P. citri. In the 2020 season, mealybug infestation was considered low, not exceeding 25% infested fruit in trial orchards. This corresponded with high levels of parasitism of 3rd instars, inspected on fruit samples from each orchard, every two weeks. In the following season, mealybug infestation was far higher, and we were unable to record efficacy from releases, despite following a strict IPM programme for low-impact to beneficial insects. Parasitoids were collected from *eclosing* mummies to see if *A. vladimiri* augmentation was successful. In 2020, *A. vladimiri* made up 39% of parasitoids collected, however, only amounted to 19% the following year. Previously, timing of releases and insecticide residues were considered to be the major factors influencing efficacy. However, a compelling number of hyperparasitoids were collected from samples, including a new discovery of *Pseudaphycus sp. eclosing* from mealybug mummies, which indicated parasitoid-host interaction was also an important contributing factor. This could explain the variable mealybug levels. The role and cyclical occurrence of hyperparasitoids warrants further research over the long-term.

Effect of geographical location, insect type, and cooking method on the nutritional composition of insects consumed in South Africa

Zabentungwa Hlongwane[1], Muthulisi Siwela[2], Rob Slotow[2], Thinandavha Munyai[2]

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Categories

- Insects as Feed and Food

Abstract

Edible insects may be a sustainable source of protein and some other nutrients, especially for low-economic-status communities. The current study determined the influence of insect type, geographic location, and cooking method on the nutritional composition of insects. The investigation would contribute to maximal derivation of the nutritional benefits of insects. Dried samples of four insect types, *Gonimbrasia belina* (mopani worm), *Gynanisa* caterpillar, termite soldiers/workers, and termite alates, were procured from different street vendors across Vhembe district in Limpopo Province, South Africa. *G. belina* samples were cooked by frying, boiling with and without salt added. Generally, nutrient content varied significantly with insect type and geographic location ($p<0.05$). Protein content varied from 40 g/100 g in termite alates to 69.75 g/100 g in termite soldiers/workers. Termite soldiers/workers had the highest iron content (range: 496.33- 690.33 mg/kg), whilst *Gynanisa* caterpillar had the highest zinc content (range: 116.67-155.67-mg/kg). Similarly, the Gynanisa caterpillar had the highest levels of lysine (range: 0.80-4.53 g/100g), threonine (range: 0.79-2.64 g/100g), and isoleucine (range: 0.63-2.33). On the other hand, termite soldiers/workers had the highest levels of valine (range: 2.20-3.47 g/100g), leucine (range: 2.49-3.87 g/100g), and phenylalanine (range: 1.38-3.55 g/100g). The cooking method significantly affected nutrient retention. Boiling with salt added resulted in the highest retention of protein and total mineral content (ash), and, therefore, seems a suitable method for cooking insects. The findings indicate that, if optimally selected and cooked, edible insects can contribute significantly to the alleviation of protein, zinc, and iron deficiencies in target communities.

Rewriting the Forensic Entomology Case Report

Zanthe Kotze

University of Pretoria, Pretoria, South Africa

Categories

- Medical, Veterinary and Forensic Entomology

Abstract

The advancement of research in forensic entomology over the last two decades has opened numerous avenues for the way in which entomological evidence is handled and, more specifically, how data are reported. These data deal with larval insect age and the estimated time of colonization of vertebrate remains and can thus be used to assist law enforcement agencies in legal proceedings. When entomological case reports are compiled, the format varies greatly between law enforcement agencies, as well as between countries. This disparity poses a challenge for the unification of data for research and review purposes, as well as the standardization of data representation for scientific reports. It is crucial that these data are reported accurately and in an accessible manner for comparative studies, as well as to allow for the updating of distribution records. The template proposed outlines the minimum sections that should be considered when compiling an entomological evidence report, with focus on terminology used in such reports.

Phylogeography and genetic diversity of mopane worms (*Gonimbrasia belina*) in southern Africa

Zwannda Nethavhani[1], Ruan Veldtman[1], Rieze Straeuli[1], Casper Nyamukondiwa[2], William Versveld[3], Barbara van Asch[1]

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Gonimbrasia belina (Lepidoptera: Saturniidae) is an Emperor moth mostly found in *Colosphermum mopane* woodlands across southern Africa. The caterpillars (mopane worm) of *G. belina* are ecologically, nutritionally and economically important to many rural communities. The exploitation of this resource is largely unregulated, and concerns about population decline in many areas have emerged over the last two decades due to high demand. Despite its significance, the genetic diversity, phylogeographical structure, and demographic history of *G. belina* are unknown. We sequenced a total of 2033 bp in three mitochondrial genes (584 bp of ATP6-COX3, 813 bp of ND6-CYTB and 636 bp of COX1) to assess the genetic diversity, phylogeographical structure and demographic history of *G. belina* (n = 160) collected from 24 sites in South Africa, Namibia and Botswana. The total dataset included 33 haplotypes with most haplotypes clustering into three phylogenetic groups corresponding to the three countries. Only one haplotype was shared by Botswana and South Africa, and none were shared with Namibia. *Gonimbrasia belina* from the three countries had high levels of genetic divergence (Fst), ranging from 0.52 to 0.98 ($P < 0.05$). The analysis of molecular variance (AMOVA) showed that the most of genetic variation is among countries (81.75%). The genetic diversity of *G. belina* was higher in South Africa and Namibia compared to Botswana. A significant signature of population expansion was detected in *G. belina* from Botswana and Namibia, but not in South Africa. We provide genetic baseline data that will potentially allow for the identification of genetic diversity hotspots and coldspots with utility for informing sustainable harvesting practices. Future studies should include analyses of nuclear genetic markers across the full geographic range of *G. belina* where the species is harvested in large-scale for a more complete perspective on the genetic diversity of the species in Southern Africa.

High incidence of non-monophyletic species and incongruence between classic taxonomy and DNA barcoding data in African Saturniidae

Zwannda Nethavhani[1], Ruan Veldtman[1], Kayleigh Anske Hiscock[1], Rolf G Oberprieler[2], Barbara van Asch[1]

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Categories

• Systematics and Taxonomy

Abstract

African Saturniidae includes approximately 400 species, some of which are harvested and traded at large-scale as edible caterpillars. The taxonomy in this group is imperfect and often leads to difficulties in documenting and recording of species, despite their ecological, cultural and economic relevance. This study analyses new and publicly available DNA barcodes to contribute to cataloguing the biodiversity of African Saturniidae. We generated data for 17 species (n = 170) across 12 genera collected in South Africa and Namibia and assessed their diversity in the context of publicly available data for 137 species in the same genera (n = 1587). Based on the monophyly criterion, we also tested DNA-based species delimitation by comparing Molecular Operational Taxonomic Units (MOTUs) recovered by one distance-based method (Neighbor-joining) and two tree-based methods (Maximum Likelihood and Generalized Mixed Yule-Coalescent) against Operational Taxonomic Units (OTUs) records. We recovered a total of 139 OTUs, of which 63% were non-monophyletic. Half of these OTUs had high intraspecific genetic divergence (> 3%) incompatible with conspecificity. The three DNA-based methods were largely congruent and resulted in 120 MOTUs which overlapped with only 34% of the OTUs. The remaining OTUs are likely affected by taxonomic inconsistencies (i.e., misidentifications, synonyms, oversplitting and lumping of species), clerical errors and geographic differentiation that challenges the monophyly criterion. However, the majority of issues appear to be resolvable through the integration of classic taxonomy and DNA-based methods. The new sequences correctly represent the 17 species collected in South Africa and Namibia and can be used as a starting point for creating a highly curated library of DNA barcodes for the family. Due to the high incidence of operational issues detected in the public DNA barcode datasets, we suggest that curation is urgent and mandatory for improving the integrity and reliability of DNA barcode-based species identification in African Saturniidae.

The overwintering nature of the groundnut leaf miner (*Bilobata subsecivella*, Zeller 1852) in the greenhouse environment

Zwivhuya Leonard Ndou[1], Terence Nkwanwir Suinyuy[2], Godfrey Elijah Zharare[1]

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Categories

• Biological Interactions

Abstract

The groundnut leaf miner, *Bilobata subsecivella* (Zeller, 1852), is an important agricultural pest that infests groundnut and soybean in Asia, Africa, and Australasia's tropical and subtropical regions. The nocturnal adult moths congregate around the groundnut crop for mating activities. Larvae infest the crop after flowering to complete 5 instars, after which they pupate in webbed leaflets of the crop. All larval instars feed and live within the webbed leaf structure that serves as a refuge. However, little is known of how the pest overwinters and bridges the summer season in different agro-climatic regions. The study investigated the overwintering behaviour of *B*. *subsecivella* in the greenhouse environment during the warm and winter seasons in South Africa. Cultures of *B*. *subsecivella* in groups of 4 larvae per plant were introduced to cages with individuals or groups of 6 potted plants and kept in a greenhouse. Initial observations showed that more overwintering pupae were present in individually caged and potted plants than in group-caged plants. Larvae were observed to completely destroy crops in the individually caged plants and overwinter inside the webbed leaflets of the crop residues. The least infested potted plants in all seasons were those that were grouped. More puzzling was the observation that pupae from individual potted cages emerged as moths in high proportions within 3 days when transferred to a cage with a new growing plant in all seasons. Whilst in group-caged plants, they took over 5 days in the summer and 6 to 10 days in the winter season. We suggest that crop debris plays an important role in the overwintering of this species by sheltering the pupae. Understanding the overwintering behaviour of this species presents an opportunity to adopt integrated pest management approaches to limit the overwintering population through post-harvest cultivation or pupae busting.

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Poster Presentations

BI2

Can bats mitigate key insect pests in the citrus industry? An evaluation of bat activity-insect activity on a large-scale commercial citrus farm

Adam Khavheli[1], Dawn Toussaint[2], Stefan Foord[1,2], Lourens Swanepoel[1,2]

[1]University of Venda, Thohoyandou, South Africa. [2]African Institute for Conservation Ecology, Levubu, South Africa

Categories

• Biological Interactions

Abstract

Globally, bats have been recognised as one of the most important species in the biological control of several agricultural production systems. Bats achieve this feat through their wide geographical distribution, tolerance for human landscapes, and their fast-metabolic rates lead, resulting in high insect predation rates. While there is a growing list of agricultural systems benefiting from bat predation, the role of bats in controlling citrus insect pests remains to be explored. In this study, we use acoustic monitoring, with detailed pest insect monitoring, to investigate the activity of insectivores' bats in response to key insect pest emergence in a commercial citrus orchard. During a sampling effort of four 5-day surveys over a five-month period (August – December 2022), we recorded 23 bat species within an area less than 25 km2. We found that bat activity was affected by season and landscape variables. Bat activity generally peaks between 18h00 and 19h00 and monotonically decreases towards 20h00 after which they maintain a relatively low basal rate of activity, irrespective of landscape or season. However, bat activity remained higher over natural vegetation with close association with water (riparian edges). Similarly, bat activity increased from dry to wet season. Similarly, key pest insects like FCM increased in abundance from dry to wetter seasons, which coincided with increased bat activity. Furthermore, based on Bayesian ordination, distinct bat orchard versus and the natural landscape had distinct assemblages. Our results suggest that insectivorous bats occupy the same spatial and temporal extent as citrus pests, indicating a high potential for predation-mediated pest suppression. In conjunction with next generation genetic analysis of bat faecal pellets, we aim to shed further light on the extent of bat predation on citrus pests.

II4

Exploring novel techniques for managing and controlling Polyphagous Shot Hole Borer (*Euwallacea fornicatus*, Coleoptera: Curculionidae, Scolytinae) in South Africa using antimicrobial substances isolated from entomopathogenic nematodes.

Annelie Smit, John Terblanche, Francois Roets, Anandi Bierman

Stellenbosch University, Stellenbosch, South Africa

Categories

• Invasive Insects

Abstract

The polyphagous shot hole borer (*Euwallacea fornicatus*; PSHB) together with its fungal symbiont, *Fusarium euwallaceae*, incites Fusarium dieback disease on hundreds of tree species world-wide. As trees become infected, the pathogenic fungi block the xylem which then prohibits water and nutrient flow causing branches or whole trees to die off. The fungus acts as the main food source for this xylem-infesting pest. Control has proven difficult as no effective chemical control options have been found. Biological control options have not yet been intensively evaluated. Bacterial symbionts of entomopathogenic nematodes (EPNs) in the genus *Xenorhabdus* and *Photorhabdus* secrete antifungal secondary metabolites. These compounds act as a defensive mechanism for EPNs in their host and have the potential to kill or slow the growth of other fungi. In this study we evaluate the potential of these secondary metabolites in the control of pathogenic fungi associated with PSHB.

Fungal isolates were collected from beetles and beetle galleries. Isolates were cultured on malt extract agar (MEA) media and exposed to bacterial symbionts derived from EPNs, within the genus *Photorhabdus* and *Xenorhabdus* to verify inhibition of fungal growth *in vitro*. Possible antifungal metabolites derived from these EPN bacterial symbionts were tested against the pathogenic fungi at different concentrations and temperatures in an inhibition assay- based experiment. Treatments showing significant inhibition of fungal growth on MEA media were hereafter applied to inoculated wood sections of various tree host species.

This study showed that EPN-derived bacterial symbionts can serve as a viable biological control option for inhibiting the growth of pathogenic fungi symbiotic to PSHB and paves the way for the development of control options that are based on naturally derived antifungal compounds.

Keywords: *Euwallacea fornicatus*, Fusarium dieback, symbiotic fungi, bacterial symbionts, Entomopathogenic nematodes, antifungal, pathogenic fungus, biological control.

BI4

A genomic comparison of chromosome level assembled *Diuraphis noxia* biotypes reveal a dynamically shuffled architecture with evidence of numerous re-fusions.

Anna-Maria Oberholster, Francois Burger, Vittorio Nicolis

Stellenbosch University, Stellenbosch, South Africa

Categories

• Biological Interactions

Abstract

The aphid Diuraphis noxia (Russian wheat aphid), is a pest of wheat and other small grains which has successfully spread to all global wheat producing regions. Feeding damage of the aphid results in characteristic longitudinal streaking, leaf rolling, and head trapping which all contribute to a lowered crop yield. Following the commercial introduction of resistant wheat lines, select aphid populations have overcome resistance to develop new populations known as biotypes. As reproduction of the aphid is limited to cyclical parthenogenesis, thus lacking chromosomal crossover, the exact mechanism of this biotypification remains elusive. With the availability of the only known genealogically linked *D. noxia* biotypes, SA1 (wildtype) that developed into SAM and SAM2 (mutants), this study attempted to ascertain the genomic background to them occupying the extremes of the virulence scale. The ±500 Mb genome, containing just over ± 21,000 protein coding genes, appears to have many polymorphisms between biotypes in genes responsible for protein expression and turnover, which supports previous results indicating that biotypes differ in their ability to regulate their transcription. Interestingly, investigating the genomic synteny between the 4 sequenced aphid biotypes (2 genealogically linked laboratory biotypes and 2 field biotypes), revealed minimum levels of genomic synteny where it appears as if the individual chromosomes of the aphid biotypes have been shuffled. Unexpectedly, many of these syntenic breaks were shared between the biotypes despite their disparate development. As holocentric chromosomes (lacking centromeres) are quite common in aphids, this process may be common in holocentric insects that rely on parthenogenesis.

BBC6

Response of ground-dwelling terrestrial Arthropods to riparian disturbances: A systematic review

Asande Hadebe, Caswell Munyai, Sindiso Nkuna, Rob Slotow

University of KwaZulu-Natal, Pietermaritzburg, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Riparian zones play an essential role in the maintenance of biodiversity. Continuous disturbances such as river engineering, alien plant invasion and flooding have a devastating impact on these habitats. Arthropods are well-documented and known indicators of ecological disturbance. A systematic review was conducted to ascertain how arthropods respond to disturbances in riparian zones. In particular, we aim to examine the common drivers of riparian arthropods. Literature published from 1991-2022 was searched from the Web of Science and Scopus databases. Primary data literature was only retrieved for this evaluation if it specifically addressed terrestrial or semi-aquatic (have at least one of their life stages on land and water) arthropods in riparian zones and was published in English. The preliminary findings generally highlighted that disturbances in the floodplains reduce arthropod abundance. The presence of alien plant species drives arthropod assemblage. Furthermore, river channelization and dam construction reduce terrestrial arthropod species richness along the riparian zones by reducing the flow of nutrients. Studies have also distinguished that flood duration's structure arthropod communities. This results from the difference in flooding tolerance of various riparian arthropod species throughout the elevational gradient. Together these studies provide insight into what needs to be considered to sustain this endangered ecosystem.

Keywords: arthropods, riparian zone, terrestrial, floodplain, disturbance, diversity

ST5

Molecular and morphological systematics of *Sycophila parasitoid* wasps (Hymenoptera: Eurytomidae) associated with *Ficus* (Moraceae)

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Categories

• Systematics and Taxonomy

Abstract

Sycophila Walker (Hymenoptera: Eurytomidae) is the fourth largest genus of Eurytomidae (Chalcidoidea) and comprises 117 valid species worldwide. While tropical and subtropical species of *Sycophila* are mainly associated with figs and are typically considered true parasitoids or inquilines, their diversity and biology are not well understood, especially in the Afrotropical region. In this study, adult fig wasps collected from 21 different African *Ficus* species were sorted and identified. As a result, five new species of *Sycophila* have been identified based on morphological characterization. The *Ficus* species from which adult fig wasps were collected include *F. abutilifolia, F. artocarpoides, F. bubu, F. burkei, F. chirindensis, F. conraui, F. fischerii, F. glumosa, F. ingens, F. lingua lingua, F. louisii, F. modesta, F. natalensis, F. ovata, F. petersii, F. polita, F. sansibarica, F. stuhlmannii, F. sur, F. sycomorus, and F. wakefieldii*. Molecular aspects of the study are yet to be pursued. Potential findings of molecular analyses will be used along with the morphological findings to provide a well-resolved phylogeny of this genus. By understanding the biology and ecology of *Sycophila* species it may be possible to develop more targeted and effective methods for controlling non-pollinating fig wasps, which can have a significant negative impact on pollination and hence fig propagation.

BBC1

Niche-modelling for Afrotropical hoverflies (Diptera, Syrphidae): a case study using the invasive species *Toxomerus floralis*

Burgert Muller[1], Kurt Jordaens[2], John Midgley[3,4]

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

Toxomerus floralis (Fabricius, 1798) is indigenous to the Nearctic and Neotropical Regions. The larvae are pollen-feeding and closely associated with the invasive plants *Mitracarpus hirtus* (L.) (Rubiaceae), a geographic contemporary, and the much more widely spread *Cyperus rotundus* (L.) (Cyperaceae). *Toxomerus floralis* was detected in 2013 for the first time in the Afrotropical Region and has since spread swiftly through large parts of the Afrotropical Region. The potential species distribution of *T. floralis* was modelled using MaxEnt and Worldclim Bioclimatic variables. The Bioclimatic variables were tested for collinearity using Variance Inflation Factor in the R package "usdm". This identified 9 correlated variables which were removed to improve upon estimations and to more accurately determine potential environmental variables that could have an influence on the species' distribution. The resulting models suggests that the distribution of *T. floralis* is potentially associated with the distribution of its host plant, *M. hirtus*, and also with *C. rotundus*, which is not native to its home range but does occur in almost all invaded areas.

ST7

Afrotropical *Athericidae* (Water Snipe Flies): Revision of the South African "Atherix" complex

Burgert Muller[1,2], Vaughn Swart[2], Louwrens Snyman[3]

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Categories

• Systematics and Taxonomy

Abstract

The family *Athericidae*, erected in 1973 by B.R. Stuckenberg, is a diverse sister-group to the Tabanidae (*Tabanomorpha*). They have a world-wide distribution, comprising 10 genera, 2 subfamilies and ca 100 species, of which 22 are known from the Afrotropical region, all belonging to the subfamily *Athericinae*. At present 5 genera are known from the region: *Pachybates Bezzi* and the monotypic *Trichacantha* Stuckenberg (both endemic to South Africa), *Atrichops* Verrall (Afrotropical, Oriental and Palaearctic Regions), and *Suragina* Walker (all regions, except Antarctica), the fifth, previously placed in *Atherix* Meigen are all endemic to South Africa, and have been considered incertae sedis since 1980, but have been referred to as being in the "*Atherix*" complex for the sake of identification. The 5 species of this complex are revised, with *Atherix barnardi*, *A. kar, A. peringueyi* and *A. androgyna* transferred to 2 new genera and *A. adamastor* transferred to Atrichops based on morphological characters and feeding biology. A new intermediary species of Atrichops is also described.

BBC2

The Diptera of Lesotho: A special issue in *African Invertebrates*

Burgert Muller[3], John Midgley[1,2], Kurt Jordaens[4], Terence Bellingan[5,2], Genevieve Theron[1], Mpho Phoofolo[6]

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

The Kingdom of Lesotho is a landlocked country, surrounded by the Republic of South Africa. While many vegetation types are shared between the countries, the extent of alpine vegetation is much greater in Lesotho, potentially holding a greater diversity of specialized species. Historic collecting in Lesotho has been limited, but some collections exist at various institutions. We undertook three field trips to Lesotho in December 2021, November 2022 and January 2023, visiting 30 sites and collecting over 6000 specimens. An overview of the recent collecting sites with habitat photographs is given. One new species has already been described from the 2021 fieldtrip. We invite contributions to a special collection of papers in African Invertebrates and provide an overview of specimens and families collected for this purpose.

II8

Early detection surveillance for Asian citrus greening (Huanglongbing) and its psylloid vectors along the North-Eastern borders of South Africa

Chuma Situnda[1], Tshepang Makitla[1], Xolani Sibiya[1], Aruna Manrakhan[1,2], Evans Mauda[1], Wayne Kirkman[3], Solomon Gebeyehu[1]

[1]Citrus Research International, Nelspruit, South Africa. [2]Stellenbosch University, Stellenbosch, South Africa. [3]Citrus Research International, Gqeberha, South Africa

Categories

- Invasive Insects

Abstract

The Asian citrus greening (Huanglongbing/HLB) is globally considered to be the most devastating citrus disease. The causative agent of the disease is a phloem-limited bacterium, *Candidatus* Liberibacter spp., which has two vectors, the Asian citrus psyllid (ACP), *Diaphorina citri* associated with *Candidatus* L. asiaticus causing HLB, and African citrus triozid (ACT), *Trioza erytreae* associated with *Candidatus* L. africanus causing African citrus greening. ACP and HLB were reported in the eastern and western parts of the African continent and are predicted to spread further south. Therefore, early detection of ACP in countries neighbouring South Africa and on the South African borders is critical for successful eradication/control of the pest. Eradication actions, if triggered for the pest along the South African borders would be crucial in delaying natural spread of the pest. In light of that, the Biosecurity Division of Citrus Research International (CRI) has developed and implemented a monitoring system for HLB and its vectors. Yellow sticky traps have currently been placed along the northern and eastern borders of the country to monitor ACP and ACT. The trapping network and density have been prioritised according to an ACP risk heat map. These traps are monitored on a monthly basis and read using a stereo microscope. The Department of Agriculture, Land Reform and Rural Development has also placed ACP traps throughout the country that are serviced regularly and read at CRI. Vectors identified from traps are isolated and verified by CRI Entomologists, before sent for molecular analysis to determine whether the vector carries any *Candidatus* Liberibacter species or not. To date, 165 traps are placed and serviced monthly along the north-eastern borders of South Africa and checked by the Biosecurity Division. No ACP and HLB has been detected. Trapping has been expanded to northern KwaZulu-Natal Province.

ST6

Morphological and molecular identification of a polyphagous grapevine pest, *Lobesia vanillana* (Lepidoptera: Tortricidae)

Eben Mundell, John Opoku-Debrah, Jeannine du Plooy, Megan Mulcahy, Sean Thackeray

River Bioscience, Port Elizabeth, South Africa

Categories

• Systematics and Taxonomy

Abstract

Lobesia vanillana is a sporadic pest of grapes in South Africa, which has the potential to cause significant economic losses. Accurate identification of this pest is thus crucial for accurate pest scouting and for the effective management of population levels in the field. For this purpose, species identification was investigated using both morphological and molecular genetic techniques. Late instar larvae and pupae are described and illustrated. Diagnostic characters are given, and keys are included to facilitate identification. In addition, as an alternative to morphological identification a diagnostic 658-bp region of the mitochondrial cytochrome oxidase I (COI) gene was amplified using Polymerase Chain Reaction (PCR) with the universal primers LCO1490 and HCO2198. We then sequenced the PCR products and used them to construct a phylogenetic tree. Our results showed that all morphologically identified samples belonged to the same species. The study demonstrates the effectiveness of using both molecular and morphological techniques to develop an identification system for *L. vanillana*. The accessibility of both morphological and molecular tools provides a reliable means of identifying *L. vanillana* from other tortricid species. This will be valuable for the early detection and management of this pest, which will ultimately help to reduce the economic losses caused by *L. vanillana* infestations in grape production.

II1

Beware!!! These biosecurity (exotic) pests can destroy the South African Citrus Industry

Elma Carstens, Solomon Gebeyehu, Wayne Kirkman, Lizeth Swart, Chuma Situnda, Xolani Sibiya, Tshepang Makitka, Biosecurity Advisory Committee Biosecurity Advisory Committee

Citrus Research International, Nelspruit, South Africa

Categories

• Invasive Insects

Abstract

Mitigation of biosecurity threats relies on regulations, procedures and actions designed to prevent the introduction, establishment and spread of exotic pests into regions and countries. Currently, the southern African citrus industry, which is worth more than ZAR 30 billion and employs 120 000 people, is free from many of the citrus pests that have been devastating in other countries and regions. The global increase in the movement of people and products, coupled with the absence of geographic isolation from most of the rest of Africa, means that the southern African citrus industry faces many potential biosecurity threats. Towards safeguarding the citrus industry, a list of the Top 10 pests which pose a threat to the southern African citrus industry has been compiled. This list includes three insects: the Asian citrus psyllid (*Diaphorina citri*), the peach fruit fly (*Bactrocera zonata)* and the melon fruit fly (*Zeugodacus cucurbitae*). Mini pest risk assessments for these insects will be presented, including global distribution, host range, possible pathways to southern Africa, and mitigation measures.

II2

Vectors (insects and mites) of Biosecurity (Exotic) Diseases of Citrus currently present in South Africa

Elma Carstens, Solomon Gebeyehu, Wayne Kirkman, Lizeth Swart, Chuma Situnda, Xolani Sibiya, Tshepang Makitka, Biosecurity Advisory Committee Biosecurity Advisory Committee

Citrus Research International, Nelspruit, South Africa

Categories

• Invasive Insects

Abstract

The southern African citrus industry, worth in excess of ZAR 30 billion, is under threat from several devastating exotic diseases that do not as yet occur in the country. The vectors of some of these diseases are already present in South Africa. If the diseases also enter, the presence of the vectors will increase the risk of establishment and spread and increase the potential impact. Five of the top 10 biosecurity (exotic) threats to citrus in South Africa are diseases for which there are insect or mite vectors present in South Africa. These vectors and the diseases include: *Trioza erytreae* (Huanglongbing); *Phyllocnistis citrella* (citrus canker); *Toxoptera citricida, Aphis gossypii* and *Aphis spiraecola* (sudden death disease); *Brevipalpus californicus, B. obovatus, B. phoenicis* and *B. yothersi* (citrus leprosis) and *Aphis craccivora* and *A. spiraecola* (yellow vein clearing disease). This poster serves to promote awareness about these pests and vectors of high biosecurity importance to citrus in South Africa.

BBC3

The status of soil macrofauna as bioindicators of soil health in agroecosystems

Emogine Mamabolo, James Pryke, René Gaigher

Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa

Categories

• Agroecology

Abstract

Regenerative and resource conserving agriculture has gained recognition as a sustainable substitute to intensive agricultural models to reduce soil degradation and loss of ecosystem services. However, the major stumbling block to the successful implementation of these practices by farmers is the difficulty in measuring their sustainability and effectiveness. Understanding the status of soil health in agroecosystems has been proposed as a fundamental step towards agricultural productivity and sustainability. In this research, different indicators were used to evaluate soil health and function within differently managed land uses with special emphasis on soil macrofauna as biological indicators. Soil physical, chemical and biological samples were collected using soil monoliths within four land uses: (1) conservation management, (2) livestock integration within the cropping systems, (3) conventional management, and (4) natural grasslands used as reference sites. The obtained data allowed for the identification of soil macrofauna bioindicator species which represented important features of soil health (biodiversity, chemical fertility, and physical quality). The integrated land use demonstrated the uppermost values of soil health according to the biological, chemical, and physical indicators. Most of the indicator variables which indicated poor soil health were greatly associated with the conventional land use. The biodiversity indicator was found to be closely linked with the overall indicator, suggesting that soil macrofauna might be the major drivers of soil health but importantly can be used to assess overall soil health. Twenty-five species were identified as bioindicators of soil health. The soil macrofauna bioindicators could greatly simplify the assessments of land use management effects by farmers within the study area, thereby encouraging them to actively participate in decision-making concerning land use management. The overall results demonstrated that regenerative practices could restore degraded soils and ecosystem services.

WBC2

Assessing the impact of the potential biocontrol, *Aphthona nonstriata Goeze* (Coleoptera: Chrysomelidae), on the invasive Iris *pseudacorus L.* (Iridaceae) in South Africa

Erin Boon, Julie Coetzee, Martin Hill

Rhodes University, Makhanda, South Africa

Categories

• Weed Biological Control

Abstract

Aquatic environments in South Africa are under continuous stress from alien invasive plants. *Iris pseudacorus L.* (Iridaceae) (yellow flag iris) is an emergent aquatic plant native to Eurasia and North Africa. In its non-native range, this plant is highly invasive. As an ecosystem engineer, it causes significant disturbance to aquatic ecosystems by altering the ecological function and services provided. *I. pseudacorus* was first recorded in South Africa in 2004 and has since proliferated. Mechanical and chemical control measures have proven ineffective against this invader, but biological control is a potential option. In 2016, the biological control programme for *I. pseudacorus* was initiated by introducing *Aphthona nonstriata Goeze* (Coleoptera: Chrysomelidae) to quarantine in South Africa. In its native range, *A. nonstriata* is only found in aquatic habitats associated with *I. pseudacorus*. The adults feed on the plant's leaves, whilst the larvae feed on the rhizomes. Here we conducted an impact study to determine the levels of damage caused by three different densities of *A. nonstriata* feeding on *I. pseudacorus*, viz. an insect-free control; a low-density treatment (10 adults per plant); and a high-density treatment (40 adults per plant). Several morphological and physiological parameters were measured to assess the impact of feeding damage based on the insect's different densities. This study aims to determine the efficacy of *A. nonstriata* as a biocontrol agent for *I. pseudacorus* and contribute to the release model. The number of dead leaves increased significantly between density treatments *($F_{2,15} = 18.98$, $P > 0.001$)*, and the length of the leaves decreased in the herbivory treatments *($F_{2,87} = 11.21$, $P < 0.001$)*. The leaf chlorophyll content was significantly reduced as herbivory density increased *($F_{2,15} = 22.08$, $P < 0.001$).* Feeding by *A. nonstriata* thus decreased the overall (morphological and physiological) performance of *I. pseudacorus*, even at low insect densities.

BBC4

Phytoplankton and littoral aquatic macroinvertebrate species composition from coastal and inland lakes of South Africa

Esethu Nkibi[1], Samuel Motitsoe[1], Musa Mlambo[2]

[1]Rhodes University, Grahamstown, South Africa. [2]Albany Museum, Grahamstown, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

South Africa has limited freshwater lake ecosystems and we know less about their biology. The National Biodiversity Assessment (NBA 2018) report identified eight important freshwater lakes in South Africa that have important socio-economic and ecological benefits. This study aims to document a biodiversity inventory for both phytoplankton and littoral aquatic macroinvertebrates species from six selected freshwater lakes collected during winter (July 2020) and summer (January 2021) seasons. From the six selected lakes, four were from the NBA 2018 target list. We hypothesize that the geographical location and related water chemistry will drive both phytoplankton and aquatic macroinvertebrates species composition. 122 phytoplankton and 87 aquatic macroinvertebrates species were collected and identified. Our results agreed with our hypothesis where both phytoplankton and aquatic macroinvertebrates species composition was sensitive to both the geographical location and physio-chemical lake characteristics. Phytoplankton and aquatic macroinvertebrate species composition were similar between coastal lakes (i.e., Lake Sibaya and Mzingazi), saline inland lakes (i.e., Chrissiesmeer and Banagher), and freshwater inland lakes (i.e., Terve Se Pan and Banagher), and completely different between lake types. Freshwater inland lakes were more species-rich and diverse followed by coastal and saline inland lakes. Our results provide empirical evidence on the biological composition of selected lakes which will inform policy and the development of management strategies for freshwater lakes in South Africa and will also contribute towards the next National Biodiversity Assessment 2024 with regards to biological data deficiency noted in the previous NBA 2018 report.

Keywords: Phytoplankton, aquatic macroinvertebrates, water quality, biomonitoring

AE10

Evaluations of susceptibility of *Busseola fusca* and *Spodoptera frugiperda* populations on Bt maize in South Africa

Ethel Xolile Magoso, Elrine Strydom

Agricultural Research Council-Grain Crops, Potchefstroom, South Africa

Categories

• Agricultural Entomology

Abstract

Maize production and productivity is currently under threat from lepidopteran pest such as *Busseola fusca* (Lepidoptera: Noctuidae) and *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in Sub-Saharan Africa. The use of genetically modified (GM) Bt maize was commercialized for the control of *B. fusca*, which have since then developed resistance against the single gene event expressing Cry1Ab toxins in various localities across South Africa. Ongoing studies to monitor resistance to Bt genes has been conducted by the Agricultural Research Council – Grain Crops since 2013. Geographically different populations of *B. fusca* and *S. frugiperda* were collected from the main maize production areas in South Africa to evaluate susceptibility levels of these species on Bt maize. Neonate larvae were inoculated onto whorl tissue of non-Bt iso-hybrid (control), Cry1Ab (Bt1) and Cry2Ab2+ Cry1A.105 (Bt2) to determine the survival and larval mass. All *B. fusca* larvae feeding on the Bt2 maize died within 7 days of inoculation. Survival of *B. fusca* larvae feeding on Bt1 was recorded at 40% 21 days after inoculation. *Spodoptera frugiperda* larvae feeding on Bt2 maize survived for 11 days at 40% compared to 70% survival on Bt1. Monitoring of susceptibility levels in maize remain an important part of insect resistance management (IRM). Through monitoring early signs of resistance development can be detected and managed timeously.

ST3

A new species of *Nyassamyia* Lindner 1890 (Diptera: Stratiomyidae) from South Africa

Genevieve Theron[1], John Midgley[1,2]

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Categories

• Systematics and Taxonomy

Abstract

Nyassamyia Lindner, 1980 is a small genus of Stratiomyidae endemic to the Afrotropical Region. Specimens are rarely collected but occur from South Africa to the Democratic Republic of Congo. The two described species are densely pilose, likely mimicking bees. Here we present a new species in this genus from KwaZulu-Natal, South Africa that closely resembles *N. deceptor* Curran, 1928. A brief diagnosis of the adults will be given, along with pictures of all species. Geographical distribution will be discussed, and biological observations of juvenile stages presented.

II6

Development of an egg activation and microinjection protocol for the application of CRISPR/Cas9 gene editing in the insect pest *Sirex noctilio*

Gudrun Dittrich-Schröder[1], Elmarie van der Merwe[1], Bernard Slippers[2],

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Categories

• Invasive Insects

Abstract

Sirex noctilio (Hymenoptera: Siricidae) is an invasive insect pest in South African pine plantations and considered as a model organism amongst forestry insect pests. Current pest management strategies for *S. noctilio*, such as the use of silvicultural practices or biological control, are not always efficient. A new, precise and potentially powerful approach has emerged using gene editing for genetic pest control. The discovery of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) with its associated Cas9 protein, has shown potential for precision genome editing and is therefore being explored as an alternative control strategy for *S. noctilio*. Gene editing in insects involves the microinjection of insect eggs and is the only feasible option to deliver CRISPR/Cas9 into the eggs but needs to be optimized for each species. Access to *S. noctilio* eggs is a challenge as eggs are laid singly under bark where they are difficult to extract, and dissection of the eggs from a female will not result in their development. Pressure exerted on the eggs during oviposition results in their activation and subsequent development. In this study a technique was developed to simulate the pressure experienced by the eggs during oviposition, so that the development of these eggs would be initiated. Furthermore, a microinjection protocol was developed and optimized specifically for *S. noctilio* focusing on identifying a method to keep the eggs stationary during microinjection. The egg activation technique was applied to eggs dissected from *S. noctilio* individuals collected from both winter and summer rainfall areas in South Africa and resulted in successful activation and subsequent development of eggs. A microinjection protocol was developed for *S. noctilio* and a mold was designed to allow quick positioning of the eggs in a secure manner for microinjection. The study lays an important methodological foundation for gene editing in *S. noctilio*.

II9

Development and application of CRISPR/Cas9 for gene editing in *Gonipterus* sp.2

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Categories

• Invasive Insects

Abstract

Gonipterus sp.2 (Coleoptera: Curculionidae) is one of the most important insect pests of *Eucalyptus* plantation forestry globally. This beetle defoliates trees thereby reducing tree growth and in turn wood production. Genetic-based pest management techniques provide a potentially environmentally friendly and precise alternative control method to chemical or biological control. The gene editing tool Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/CRISPR-associated protein 9 (Cas9) can be used to target genes involved in reproduction, development or feeding to ultimately reduce the damage caused by insect pests. The aim of this study was to develop a CRISPR/Cas9 gene editing protocol for use in the insect pest *Gonipterus* sp.2. *De novo* sequencing of the *Gonipterus* sp. 2 genome was conducted, followed by genome assembly and annotation. One approach to develop gene editing in non-model organisms involves knock out of a gene with an easily observable phenotype. For this purpose, the *Pale* gene, involved in melanin synthesis, was targeted as successfully transformed individuals were expected to have decreased amounts of black pigment, compared to the wild-type larvae. A number of single guides RNAs targeting the *Pale* gene were designed and the cleavage efficacy was confirmed in vitro. Various parameters, such as needle shape, pressure and method of securing the eggs for microinjection of *Gonipterus* sp. 2 embryos were optimised. *In vivo* work included microinjection of embryos with the Cas9-sgRNA ribonucleoprotein complex targeting the *Pale* gene, rearing of injected embryos as well as molecular confirmation of transformation. This study represents the first step in developing a gene editing protocol for the insect pest *Gonipterus* sp.2. Future work involves the targeting of a gene involved in reproduction, which could potentially be used in genetic pest control of this species.

AE8

An LC-MS/MS based method for rapid detection and identification of mites on traded plant commodities

Isabel Dhanani[1], Khyla Leeuwner[2], Maré Vlok[3]

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Categories

• Agricultural Entomology

Abstract

Developing reliable and rapid methodologies for detecting and quantifying mites of interest on a range of sample types is crucial for the support of agricultural pest control operations and the proper implementation of biological control efforts. This work describes the potential of a rapid and targeted protein-based method of detecting mites on traded fruit and propagation material. Specimens of the two-spotted spider mite, *Tetranychus urticae* (Acari: Tetranychidae), were collected from glasshouse propagated stone fruit foliage (Plant Quarantine Station, Stellenbosch) for peptide target evaluation. Species-level identification of the mites was morphologically confirmed using the taxonomic key of Smith Meyer (1987). After total protein extraction and tryptic digestion, the bottom-up proteome was acquired by liquid chromatography mass-spectrometry (LC-MS/MS) in data-independent acquisition mode. Peptide targets detected were evaluated based on their biological relevance to different life stages and their relative abundance and a subset of targets was selected for targeted method development. Protein targets were tested for the development of a rapid targeted LC-MS/MS acquisition method. Eight target peptides were monitored in multiple reaction monitoring mode and limits of detection were validated to determine the number of mites in a sample required to elicit a reliable detection signal. This proof-of-concept analysis demonstrates the potential of a protein-based method as a rapid and cost-effective way to detect mite species of quarantine importance.

AE11

Mass rearing of multiple tortricid species on a commercially produced artificial diet.

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Categories

• Agricultural Entomology

Abstract

Artificial diets have been used in many programs to rear insects for research, sterile insect technique (SIT), and the production of beneficial natural enemies and entomopathogenic viruses. A commercially produced artificial diet was found to support the growth and development of various tortricid species and may be used to facilitate successful mass rearing programmes. This diet was originally developed as a more cost effective and less labour-intensive diet for the mass rearing of *Thaumatotibia leucotreta* for SIT. To determine whether this diet could be successfully used for the mass-rearing of tortricid pests, a life-table study was conducted for several species reared on the diet. Larval development, pupal development, pupal mass, fecundity and fertility were evaluated for *T. leucotreta*, *Cryptophlebia peltastica*, *Lobesia vanillana* and *Cydia pomonella*. *Thaumatotibia leucotreta* larvae reared on this diet had an average developmental period of 15 days from egg to pupae, an average pupal weight of 0.029g, 353 eggs laid per pair, and a 64% hatch rate. Furthermore, a population of *T. leucotreta* had been reared for multiple successive generation on this commercial diet. The diet was also found to be suitable for the mass rearing of *Cryptophlebia peltastica* and *Lobesia vanillana*, which are important economic pests of litchis, macadamias, citrus and table grapes. It was observed that *C. peltastica* reared on this diet had an average developmental period of 20 days from egg to pupae, an average pupal weight of 0.065g, 92 eggs laid per pair, and a hatch rate of 69%. *Lobesia vanillana* reared on this diet develops in 20 days from egg to pupae, with an average pupal weight of 0.009g. *Cydia pomonella* had difficulties adapting to the commercial artificial diet and had prolonged developmental times. Further research is currently being conducted into making minor modifications to the diet for *C. pomonella*.

BBC10

Assessment of Fine scale requirements for endangered Colophon beetles

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Categories

• Biodiversity, Biogeography and Conservation

Abstract

The genus Colophon (Cape stag beetles; Coleoptera: Scarabaeoidea: Lucanidae) is currently comprised of 21 species of flightless beetles that occur on disjointed peaks across the Western Cape. Consensus holds that the genus had a low altitude origin, and that the contemporary distribution of the species is a result of withdrawing up the mountain as temperatures began to warm and the conditions on the lowlands became unfavourable. Today these species only occur in refugial habitats on mountain peaks with no species being found below 800m elevation. Little to no information is currently known about the behaviour and ecology of the beetles other than the adults being crepuscular to nocturnal and only being active in summer months. Due to the lack of information, there could be currently undescribed species. These beetles are considered endangered with some species being considered critically endangered. The red listing however has yet to be done due to the current lack of knowledge about the fine scale habitat requirements of each species. This study aims to better understand the niche requirements by looking at the environmental factors across the mountains on which they occur as well as the documentation of any threats to the beetle. The fine scale requirements of the various species would allow for a predictive model which would indicate areas which are ideal for Colophon and could possibly help with the identification of new species. This will also allow for the red listing of the species and future population monitoring for to determine population sizes which remains crucial for red listing. The threats to the species can be logged and monitored in conjunction with the effects of climate change allowing for the more effective conservation of Colophon in the future.

WBC3

Suitability of *Pissodes validirostris* as a biological control agent for European pines in South Africa

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Categories

• Weed Biological Control

Abstract

The Cape Floral Area has unparalleled endemism, which is threatened by invasive pines, while pines in mountain catchments, chich substantially reduced runoff, worsening water shortages. Mechanical clearing of pines is costly, especially where the trees grow in difficult terrain. Pines seeds are the biggest hinderance to management as strong winds disperse seeds indiscriminately across the landscape often into difficult to clear and already cleared areas. A biological control agent that targets pine seed production may assist to limit the pine spread of invasive pine. With the support of the South African forestry sector biological control options for pine species are being reconsidered. The project aims to confirm the specificity of the European pinecone weevil, *Pissodes validirostris*, by determining the chemical ques driving host selection. European pines are being considered for biological control and the pine species planted commercially are mainly of North American origin, we aim to compare the volatiles chemical found in European and North American pine tissues. Results from ongoing work to identify the volatile compounds and bioassays to confirm behaviour will be presented. Confirming that specific plant volatiles in European Pines drive oviposition and therefore host specificity in *P. validirostris* will contribute significantly to the development of the biocontrol programme which may help reduce the significant negative impacts associated with wilding European pines in South Africa.

AE9

Investigating smother crops for the improvement of insect diversity in small grain cropping systems of the Western Cape

Kim Van Den Heever

Directorate of Plant Sciences, Programme: Research and Technology Development Services, Western Cape Department of Agriculture, Elsenburg, South Africa

Categories

• Agricultural Entomology

Abstract

There is limited knowledge on the direct and interactive effects of cover crop species at the research farms of Langgewens and Tygerhoek. A combination of pressures namely insecticide resistant insects, environmental concerns and cost containment prompted the need to develop new environmentally based methods of pest control. The main objective of this study was to determine how cover crop treatments affect arthropod diversity in the Western Cape cropping systems.

Monitoring of existing problem species as well as natural enemies took place at the Departmental Reasearch Farms namely, Langgewens (-33.279171, 18.715005) near Mooreesburg in the Western Cape Province of South Africa. The layout of the experiments was arranged in a randomised block design, with 11 treatments that included wheat, white mustard, lupine, rye, serradella, Saia oats and vetch planted as pure crop stands. In addition, the following crop combinations were planted: white mustard + lupine, rye + serradella and Saia oats + vetch. The control was an untreated plot of similar dimensions that allowed for natural weed germination. Yellow water traps were utilised to trap insects and sampled every second week. Samples were analysed in the laboratory. Data was analysed by an appropriated analysis of variance (ANOVA).

Results showed that parasitoids (*Diaeretiella rapae*), a parasite of aphids, were most active where white mustard or wheat occurred. Where mustard occurred two economically important pests of *brassicaceae*, particularly diamondback moth *(Plutella xylostella*) and cabbage stem weevil (*Ceutorhynchus pallidactylus*) were encountered. The control showed a more diverse composition of pestiferous insects across different arthropod orders.

Integrating smother crops as hedgerows within a current grain production system as a safe haven for natural enemies may assist in the reduction of problem insect species in a sustainable manner.

KEYWORDS: Smother crops, biodiversity, cropping systems, integrated pest management

AE6

Evaluation of stability and maintenance of ultraviolet tolerant strain of the *Cryptophlebia leucotreta granulovirus*-SA for the management of false codling moth

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Categories

• Agricultural Entomology

Abstract

Thaumatotibia leucotreta (Meyrick) (Lepidoptera: Tortricidae), commonly known as the false codling moth (FCM), is a serious pest of citrus in South Africa, mainly because of its phytosanitary status. This means that there is zero tolerance for FCM in consignments destined for exports, which has implications for foreign income should consignments be rejected. *Cryptophlebia leucotreta granulovirus-SA (CrleGV-SA)* is used as a commercial biopesticide aimed at suppressing the FCM population. However, the virus is sensitive to ultraviolet (UV) irradiation. Other studies have demonstrated differences in UV tolerance between different baculovirus species and that there is a chance of the selection of a UV-tolerant (UVT) *CrleGV* isolate that would allow for the development of a biopesticide that will persist longer in the field. This study assessed this by conducting bioassays of the UVT and wild-type (WT) virus against neonate FCM larvae. Passage of the UVT and WT virus was performed in the third or fourth instar FCM followed by another bioassay of the UVT and WT virus, with UV irradiation, against neonate FCM larvae. The dose-response bioassay showed that the UVT isolate caused higher mortality than the WT isolate. The LC50 and LC90 were 7.59 × 104 and 3.59 × 106 OBs/ml for the UVT, respectively, and 2.08 × 105 and 2.81 × 106 OBs/ml, for the WT, respectively. Both viruses were inactivated after 8 h of UV exposure, however, more replicates were needed for validation. The UVT virus shows potential and should be further investigated.

AE5

Exploring cold tolerance and fumigation treatments of mealybug (Hemiptera: *Pseudococcidae*) in pome fruit in South Africa

Liana De Araujo, Renate Smit, Matthew Addison, Pia Addison, John Terblanche, Minette Karsten

Stellenbosch University, Stellenbosch, South Africa

Categories

• Agricultural Entomology

Abstract

Mealybugs are important quarantine pests and strict phytosanitary standards are in place with regards to the use and residues of insecticides for export to foreign markets. Several mealybug species (Hemiptera: *Pseudococcidae*) are known pests on pome fruit in South Africa. *Pseudococcus viburni* (Signoret), the Obscure mealybug, is likely the most dominant with historic presence records of *Pseudococcus longispinus* (*Targioni-Tozzetti*), the Long-tailed mealybug, and *Pseudococcus calceolariae* (Maskell), the Scarlet mealybug. The exploration and implementation of alternative control options both pre- and post-harvest are critical to maintain current market access for South African pome fruit.

Here we aim to (1) identify the dominant mealybug species in pome orchards; (2) establish the thermal limits for different life stages of Obscure mealybug and (3) assess the efficacy of cold treatment and fumigation treatments on Obscure mealybug survival. To achieve the first objective, seven historically infested pome orchards in the Western Cape, South Africa were actively scouted for presence or absence of mealybug and a once-off fruit collection prior to harvest. The fruit was taken to the laboratory for destructive inspection to gauge whether a non-destructive visual inspection is a sufficient method for determining mealybug presence in an orchard. For the second objective, isofemale lines were started from field-collected individuals and will be identified morphologically by an expert prior to colony establishment. The colony will be used to measure cold tolerance traits in different life stages of the female: egg, crawler and adult. Finally, a combination of ethyl formate (C3H6O2) fumigation treatment and cold storage of fruit, adapted from the cold tolerance results, will be assessed against the aforementioned life stages.

Results from this work will feed into optimising field management and alternative post-harvest phytosanitary control measures for mealybug to ensure marketability of South African pome fruit.

AE2

The Wattle bagworm pheromone: analytical investigations and development of a pest management tool

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Categories

• Agricultural Entomology

Abstract

Pheromones are an important tool in integrated insect pest management programs. In bagworms, males must locate flightless females and are consequently inherently dependent on sex pheromones for mate location. The objective of this study is to characterize the sex pheromone of the Wattle bagworm (*Kotochalia junodi* Heylearts). This indigenous South African insect is a sporadic defoliating larval pest of Black Wattle (*Acacia mearnsii* De Wild.). Previous pheromone studies determined the female bagworm has two or three pheromone components in its pheromone blend by observing moth behaviour toward solvent fractions. In this study female Wattle bagworm samples were screened using Gas Chromatography Electro-Antennographic Detection (GC-EAD) and analytical validation was done via GC-MS. Moth behaviour trials were also performed.

We observed three repeatable electro-*antennographic* responses that correspond to three components in the headspace samples from virgin and feral females. Only two out of the three compounds were found in hexane-based samples. Titers of these two putative pheromone compounds were determined to range from 1.5 to 15 ng/µl after 2-minute surface washing of 16 female individuals with solvent. The pheromone blend ratio differed between female samples. On demand pheromone production is suspected, contrary to most other moths that store their pheromones in glands. Literature comparison of GCMS fragmentation patterns determined that all three antenna-active compounds are novel chemical structures. Despite attempting multiple different approaches toward structure elucidation at trace levels, the chemical identities of the three pheromone components remain unknown. Preliminary lab-based behaviour al assays showed that males can locate 1µl of solvent extracts within seconds of diffusion. A preliminary field trial with sticky traps showed that males can be trapped using female derived extracts. Further investigations are underway to identify and develop the application of this pheromone.

BBC8

Investigating Orthopteran Species Diversity Using Passive Bio-acoustic Monitoring

Maxine Laubscher

University of the Western Cape, Bellville, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Phytophagous insects make up a large amount of the globe's animal species. Insect diversity data is only available for a small portion of insects in South Africa. More than half of all insect species in South Africa are estimated to be unknown to science. Orthopteran species (grasshoppers, crickets, and katydids) have species-specific signals enabling researchers to find species using bio-acoustic methods. These recordings can be used to detect new species, endemics and mapping ranges, abundances, and species richness. Due to these unique sounds (mating calls), orthopteran species are perfectly suited for research using bio-acoustic monitoring to contribute towards greatly needed datasets. The aim of this project was to initiate biodiversity monitoring of acoustically signalling orthopteran species across different habitat types and seasons. Sampling sites were selected that represent different vegetation types across South Africa. Acoustic monitoring was done for one-week periods. Weather-proof, battery-powered recorders were mounted two meters above the ground. Both audible (up to 20 kHz) and ultrasonic (up to 128 kHz) sounds were recorded. Kaleidoscope Pro software (Wildlife Acoustics) was used for sound analysis. The number of species within each suborder was determined. Additionally, overall orthopteran species richness will be measured by counting the number of "*sonotypes*". *Sonotypes* were identified from spectrographic characteristics (frequency and temporal structure). *Sonotype* data was used to calculate an Acoustic Diversity Index (ADI), Normalized Difference Soundscape Index (NDSI) and a Bio-acoustic Index (BI) for each site. Preliminary data are presented.

II5

Detecting *Gonipterus* sp. n. 2 (Coleoptera: Curculionidae) defoliation levels using Unmanned Aerial Vehicle (UAV) imagery in commercial forests of South Africa.

Michelle Schröder[1], Phumlani Nzuza[1,2], Rene Heim[3], Bernard Slippers[4], Brett Hurley[1,5], Jolanda Roux[4,6], Ilaria Germishuizen[5], Benice Sivparsad[5], Wouter Maes[7]

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Categories

• Invasive Insects

Abstract

Invasive insect pests such as *Gonipterus* sp. n. 2 pose a significant threat to forest ecosystems. This economically important leaf-feeding beetle defoliates *Eucalyptus* trees. The presence of epicormic shoots and damage of growth tips are symptoms of defoliation. Early detection of *Gonipterus* sp. n. 2 is important for early intervention to prevent pest outbreaks. Conventional insect pest monitoring methods are time consuming and spatially restrictive. The use of remote sensing techniques such as imagery obtained with unmanned aerial vehicle systems presents the opportunity for rapid assessment at centimetre spatial resolution to detect damage levels of *Gonipterus* sp. n. 2. The aim was to develop a remote sensing damage detection model to use as a monitoring tool. *A Micasense* red-edge P sensor mounted on an unmanned aerial vehicle was used to take images of *E. dunnii* trees with varying levels of *Gonipterus* sp. n. 2 infestation. A random sampling approach was used to assess defoliated trees based on visual assessments of six severity classes. Multispectral images were analysed by extracting the mean spectral reflectance of a 0.5m buffer around the central tree crown. The model training and validation were implemented using support vector machines classification in Python, and hyperparameter tuning using grid search. Three classification modelling scenarios were investigated based on spectral reflectance bands, indices, and their combination. Recursive feature elimination was used to select the essential variables. The scenario using both spectral reflectance and vegetation indices had the highest classification accuracy of 0.92%, while spectral bands achieved 0.84%, and vegetation indices had a poor overall accuracy of 0.21%. The recursive feature elimination selected Red-edge717, near-infrared 842, and Enhanced Vegetation Index as the essential variables in classifying defoliation levels. This study

provides a baseline for developing an early detection system using UAV multispectral data for *Gonipterus* sp. n. 2.

II10

Seasonal Abundance and Infestation of Fruit Fly on Cucumber in Mozambique

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Categories

- Invasive Insects

Abstract

Fruit flies are pests of economic importance in cucurbits due to the enormous damage they cause. However, information on the abundance and infestation of fruit flies in cucurbits is scarce for Mozambique, thus, the present study was conducted.

The study was carried out in Maputo and Manica province from March 2020 to March 2022. Ten fields were selected containing cucumber, and 3 Tephritraps were installed with different attractants (cuelure, biolure and zingerone). The traps were inspected and emptied every week. To determine the incidence and infestation rate, 10 fruits were randomly collected per field. The fruits were weighed individually and placed in bowls for the emergence of fruit fly pupae and adults. All emerging insects were preserved in 70% alcohol and identified. The statistical package STATA 15 was used.

28 species were collected by trapping, of which 15 in Maputo and 23 in Manica belonging to the genus *Bactrocera* (1), *Ceratitis* (5), *Dacus* (20), *Zeugodacus* (1) and *Perilampsis* (1). *D. frontalis* (37%) and *D. bivittatus* (35%) were the most abundant in Maputo and *D. bivittatus* (69%) and *D. punctatifrons* (21%) were the most abundant in Manica. The invasive species *Zeugodacus cucurbitae* was collected only once in Manica. 13 fruit fly species were reared from cucumber. There was no significant difference observed in incidence between Maputo (30%) and Manica (44%). Also, no significant difference was observed in infestation rate between both provinces (39 and 44 pupae/kg respectively in Maputo and Manica); *D. ciliatus* was the most abundant fly in Maputo with about 93% of all emerged flies. The infestation rate showed the highest indices with 27,61 adults/kg in Maputo than Manica (1,07 adults/kg). Contrary, in Manica D. *bivittatu*s was the most abundant with about 68% and showed the highest indices with 32,63 adults/kg than Maputo (0,21 adults/kg).

AE3

The effectiveness of black soldier fly (*Hermetia illucens*) frass as a biopesticide of aphids (*Myzus persicae*).

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Categories

• Agricultural Entomology

Abstract

The risks of synthetic pesticides include pest resistance and impacts on the health of humans, non-target organisms, and ecosystems. Biopesticides are an alternative that reduces chemical pesticide use and improves health. *Myzus persicae*, the green peach aphid, is a sap-sucking insect pest that damages leafy vegetables, including Brassicas. This study aimed to evaluate the effectiveness of black soldier fly (*Hermetia illucens*), frass tea (BSFT) and frass residues incorporated in the soil as the potential biopesticides on *M. persicae* established on Brassica seedlings. The bioefficacy of BSFT at different concentrations (15g, 30g, and 60g) and frass soil amendment (50g) was experimentally compared to that of diluted dishwashing liquid (15g/L) as a positive control and distilled water as a negative control. Mortality and behavioural responses were observed over a 48-hour period. Responses were analysed using beta regression. *M. persicae* behaviour and mortality varied significantly between treatments. The highest mortality was 92% for nymphs and 82% for adults in diluted dishwashing liquid, 14% for nymphs and 20% for adults in frass soil amendment and 19% for nymphs and 18% for adults in 15g and 60g frass tea extracts. The lowest mortality was 3% and 4% for nymphs and adults, respectively, for distilled water and 30g of frass tea. In comparison, 30g and 60g of frass tea treatments had bio-repellent properties. Black soldier fly frass (BSFF) could be used within an integrated pest management strategy against aphids due to its biopesticide and bio-repellent properties.

Keywords: Bio-repellent, Bioefficacy, Brassica, Mortality.

BBC11

The insect research of Grootbos Nature Reserve

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Conservation and Research Unit, Grootbos Foundation, Gansbaai, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Since 2018, entomological research on Grootbos Nature Reserve has focused on four components; creating a monitoring framework by surveying the insect assemblages of the five vegetation types present on the Reserve, conducting research projects with applied ecological hypotheses, taxonomic revision in collaboration with experts and curation of insect specimens for these projects to create an insect collection and database for the Walker Bay region. To date, the Overberg Dune Strandveld has been surveyed for insect assemblages at different topographies during different seasons, visitation networks have been created for three vegetation types (Overberg Sandstone Fynbos, Elim Ferricrete Fynbos, Agulhas Sand Fynbos) to further understand insect plant interactions. Furthermore, a post-fire fynbos monitoring project is underway to identify insect successions after fire for five veld ages. In addition, one weevil has been described as a new species to science (*Phlyctinus grootbosensis*, Haran 2020) and a monkey beetle (*Diaplochelus spec. nov.*, Colville, in prep) taxonomic revision is underway. The current collection houses 32 000 specimens consisting of 17 orders and 208 families – with charismatic groups such as Odonata (n=22), Papilionoidea (n=32) and Formicidae (n=45) identified to species level through consultation with experts. With these data and this collection, the Conservation and Research Unit aim to further the understanding and knowledge of insects in the Walker Bay region, facilitate and promote the ecological research in the area to inform management decisions and identify new species, through collaboration with expert entomologists, to improve conservation action.

PE3

Diet development of the Cape fly *Ceratitis quilicii* (Tephritidae)

Pia Addison[2], Basson Nicolaas[1], John Terblanche[1]

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Categories

• Physiological Ecology

Abstract

Ceratitis rosa and *C. quilicii* (Cape fly) are two important fruit fly pests occurring throughout South and East Africa. The two species were still considered to be a single taxon (*C. rosa* or Natal fly) up until 2016, at which point sufficient data separated them into two taxa. For rearing of *C. quilicii*, various diets, supplements and protocols need to be adjusted to adapt rearing protocols for this species, which appears to have different requirements from *C. rosa*. Nutrition during early stages of fruit flies influence their development, which will affect their size, shape and fitness. This study evaluated the effect of different artificial larval diets with variable protein content on different physiological and morphological parameters of *C. quilicii*. The effect of three artificial larval diets containing dehydrated carrot powder and Brewer's yeast (4, 8 and 12% protein) were evaluated.

Results indicated that adult diets had a significant ($p<0.05$) effect on body water content, and macronutrient composition was significantly influenced by larval diets, except body carbohydrate content. There were significant differences among different larval diet treatments for both desiccation and starvation, with female flies from the 4% protein larval diet and male flies from the 8% protein larval diet surviving the best during desiccation, and males and females from the 8% protein larval diet surviving the best during the starvation assay. With geometric morphometrics it was found that there is a marked effect of sex and nutrition on the wing shape and size. Significant differences of the wing shape, not size, were found between male and female flies. There was furthermore a significant difference ($p<0.05$) of wing shape and size due to nutrition. The results point to developmental variations in flies reared from differing larval nutritional protein content, with the 8% protein larval diet treatment performing the best overall.

II3

Seasonal occurrence of the shell lerp psyllid, *Spondyliaspis* cf. *plicatuloides* (Hemiptera: Apharalidae), and other eucalypt psyllids in South Africa

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Categories

- Invasive Insects

Abstract

The invasive insect *Spondyliaspis* cf. *plicatuloides* (Froggatt) was first reported on ornamental eucalypts in South Africa in 2014. This marked the first report of the psyllid outside its native range of Australia, and little is still known on its seasonal occurrence, including the presence of different life stages. Such knowledge is important to inform monitoring and management interventions. To investigate the seasonal occurrence of *S*. cf. *plicatuloides* in South Africa, the immature life stages, namely eggs and five nymphal instars, were monitored in three distinct eucalypt growing areas over 12 months. Further, the abundance of *S*. cf. *plicatuloides* adults was monitored over a two-year period, using yellow sticky traps. Adults of other invasive eucalypt-feeding psyllids already established in South Africa, namely *Glycaspis brimblecombei*, *Blastopsylla occidentalis* and *Ctenarytaina eucalypti*, were monitored during the same period. All life stages of *S*. cf. *plicatuloides* were present throughout the year, suggesting that the psyllid has multiple overlapping generations. Abundance of *S*. cf. *plicatuloides* adults was highest in late spring at the cold temperate site, in early spring at the warm temperate site, and in winter at the subtropical site. Abundance of *G. brimblecombei*, *B. occidentalis* and *C. eucalypti* was highest in late spring / summer at all three sites. Results from this study are important for monitoring and development of integrated pest management programs for invasive eucalypt-feeding psyllids in South Africa.

Key words: Plantation Forest pests, population dynamics, invasive psyllid

BBC9

Novel species of *Lanurgus* bark beetles (Curculionidae: Scolytinae) infesting native cedar trees (Cupressaceae: *Widdringtonia*) in the Western Cape, South Africa

Renier Basson

Stellenbosch University, Stellenbosch, South Africa

Categories

- Biodiversity, Biogeography and Conservation

Abstract

Widdringtonia (Cupressaceae) cedar trees are native to southern Africa and two species occur in the mountains of the Western Cape province. *Widdringtonia wallichii* has a localised distribution and is critically endangered while *W. nodiflora* is rather widespread and common throughout its distribution. Very little is known regarding the pests and diseases of these trees. Bark beetles (Curculionidae: Scolytinae) are common pests of both native and exotic trees worldwide and are commonly associated with fungi. This study aimed to investigate the bark beetles and their associated fungi that occur on *Widdringtonia* species in the Western Cape. Bark beetles were sampled from infested *W. wallichii* trees at three different locations in the Cederberg, and from *W. nodiflora* at one site in Franschhoek Pass. Beetle identification was based on morphological examination and sequencing the CO1 gene region. Fungi were isolated from beetles, their frass and the walls of their tunnels and placed into morphogroups. Morphogroups were identified by sequencing the ITS region of two representative isolates. We identified four phylogenetically closely related and undescribed bark beetle species of the genus *Lanurgus* (Micracidini). Three were collected from *W. wallichii* bolts, twigs and cones, respectively, and one from *W. nodiflora* stems. Several yeast species (*Hyphopichia pseudoburtonii*, *Piskurozyma capsuligena* and *Yamadazyma mexicana*) were strongly associated with *Lanurgus* sp. 1 and *Lanurgus* sp. 2 beetles (45-80 % occurrence frequency), whereas *Geosmithia* species had a strong association with *Lanurgus cf. tsitsikammae* and *Lanurgus* sp. 3 (100% and 37.5%, respectively). This is the first comprehensive report of the bark beetles and their associated fungi infesting *Widdringtonia* and may reveal organisms with conservation implications for *W. wallichii*.

WBC1

How the Decay of Water Hyacinth, *Pontederia crassipes,* Impacts the Water Column

Rochelle Bessinger, Prof. Julie Coetzee

Rhodes University, Makhanda, South Africa

Categories

• Weed Biological Control

Abstract

Water Hyacinth, *Pontederia crassipes*, has become a significant burden to our waterways and the activities that rely upon them to function properly. With the implementation of inundative biological control methods, at Hartbeespoort Dam, water hyacinth populations have reduced significantly compared to when they were controlled manually or chemically. In addition, biological control has proven to be cheaper and more sustainable. However, public stakeholders around the Dam are concerned about increased detritus formation as a result of water hyacinth decay and believe that it is compromising the water more than when the plant was controlled manually or chemically.

Here we compare decomposition and sedimentation of water hyacinth under different control methods: herbicide application and biological control with *Megamelus scutellaris*, as well as no control, in a mesocosm study. Every two weeks, the water was strained, and detritus weighed, and water N and P were measured. Herbicidal control resulted in significantly faster rates of decomposition and detritus formation, followed by biological control, in comparison to no control.

In addition, a long-term field study at Hartbeespoort Dam is evaluating detritus formation under water hyacinth mats using quadrats and litter traps. Monthly monitoring will evaluate aquatic biodiversity, water chemistry as well as the mass of the detritus formed. The aim of these studies is to investigate the difference in water quality after water hyacinth has been controlled and to explore the consequences of these possible differences.

BI1

What is in the belly of the beast: The gut microbial community of *Gonipterus* sp. n. 2 in lab and field populations

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[1]FABI, Pretoria, South Africa. [2]CMEG, Pretoria, South Africa

Categories

• Biological Interactions

Abstract

In 1916, a weevil known today as the Eucalyptus snout beetle, *Gonipterus* sp. n. 2, was discovered in the Cape region of South Africa, feeding on *Eucalyptus* trees. Since then, the beetle's feeding habits have caused major economic losses in the forestry industry, leading to the discontinuation of several economically important *Eucalyptus* hosts. One possible reason for its success may be its ability to efficiently utilize resources and detoxify plant secondary metabolites. *Eucalyptus* trees produce varying levels of tannins and terpenoid essential oils, which are potent deterrents, antifeedants and insecticides for insect herbivores. Recent studies on insect-microbial interactions have revealed that gut microbial communities can play crucial roles in plant digestion, nutrient provision, and plant secondary metabolite detoxification. Based on these findings, we hypothesize that the beetle's ability to adapt to different *Eucalyptus* species may be attributed to its gut microbial community. Previously, a comparative metabolomic approach was performed on *Eucalyptus* leaves and beetle frass. From the analysis, we found that several *Eucalyptus* mono and sesquiterpenes were transformed into a range of oxidized products, many of which are known insect and microbial degradation products. To investigate the microbial members involved in detoxification, a 16s and ITS rRNA metabarcoding approach was utilised to explore the microbial diversity of the host plants and *Gonipterus* guts of field-collected and lab-reared beetles. Our results revealed that the gut of *Gonipterus* was enriched with Enterobacteriales and Saccharomycetales, which have members linked to plant secondary metabolite detoxification.

II7

Development time and reproduction rate of the invasive macadamia felted coccid, *Acanthococcus ironsidei* Williams (Hemiptera: Eriococcidae)

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Categories

- Invasive Insects

Abstract

The macadamia industry is one of the fastest growing tree crops in South Africa. The crop is however affected by a number of pests that can cause significant economic damage. *Pseudotheraptus wayi* Brown (Hemiptera: Coreidae), a polyphagous bug, was the first pest recorded on macadamia approximately 20 years after establishment of the first commercial orchards in 1957. Shortly thereafter, *Bathycoelia distincta* Distant (Hemiptera: Pentatomidae) were also recorded as a pest of macadamia. The latest pest recorded on macadamia was in 2017, namely *Acanthococcus* (formerly *Eriococcus*) *ironsidei* Williams (Hemiptera: Erioccocidae). This small (>1mm in size) scale insect, commonly known as macadamia felted coccid (MFC), is not a significant pest in its native range, Australia. However, it was recorded outside of its native range, in Hawaii in 2005, where it feeds on the branches, leaves and nuts of macadamia trees and has significant effects on nut yield and tree health. Information on the life cycle of MFC is limited, as its development was only investigated at one temperature (28°C, 64% RH). Our aim was to obtain an in-depth understanding of the life cycle of MFC to determine its invasion potential in South Africa. To do this, MFC was reared under controlled glasshouse conditions (23°C, 69% RH) on young macadamia trees. Development time from egg to adult, sex ratio and adult longevity was investigated at 15, 26, 29, 32°C; 70% RH in a laboratory study. In addition, the pre-oviposition period, fecundity and egg viability assays were investigated at 26°C. Here we present results from this study and discuss the implications for the macadamia industry in South Africa.

ST1

The cicada genus *Tugelana* Distant, 1912 (Hemiptera, Cicadidae): phylogenetic position and conservation status

Shelley Edwards, Martin Villet,

Rhodes University, Grahamstown/Makhanda, South Africa

Categories

• Systematics and Taxonomy

Abstract

The cicada genus *Tugelana* Distant, 1912 is monotypic and endemic to south-eastern Africa. Material was not available for a recent molecular phylogeny of its tribe, so its precise phylogenetic placement is unestablished. Consequently, a 627 bp sequence of the cytochrome oxidase gene was obtained and its candidate relatives identified as several species of *Platypleura* Amyot & Audinet-Serville, 1843 using the BOLD Identification System and NCBI Genbank's BLAST. Bayesian inference analyses indicated that the type species, the Maputaland Orangewing Cicada *Tugelana butleri* Distant, 1912, is closely related to the Dune Koko Orangewing Cicada *Platypleura zuluensis* Villet, 1989, which has a geographical distribution that is parapatric with *T. butleri* and which has aberrant genitalia for a member of *Platypleura*. This pair of species is placed fairly deep within the African clade of *Platypleura*. We therefore formally recognized *Platypleura* Amyot & Audinet-Serville, 1843 as a senior synonym of *Tugelana* Distant, 1912, syn. nov., and assign *T. butleri* Distant, 1912 to *Platypleura* as *Platypleura butleri* (Distant 1912), comb. nov. The species occurs on the wooded grasslands of the Maputaland coastal plateau east of Lebombo Mountains and south of Maputo Bay. Its Extent of Occurrence is about 6360 km2, which would qualify it as Vulnerable under the IUCN's classification criteria for conservation status.

AE7

Semi-field efficacy of the UV-tolerant *Cryptophlebia leucotreta granulovirus* isolate.

Sifundo Ngxekisa[1], Candice Coombes[1], Micheal Jukes[1], Sean Moore[1,2]

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Categories

• Agricultural Entomology

Abstract

Thaumatotibia leucotreta (Meyrick) (Lepidoptera: Tortricidae), is a key pest of citrus and other crops in South Africa, for which strict management plans are imposed. This includes the use of the FCM-specific baculovirus *Cryptophlebia leucotreta granulovirus (CrleGV). CrleGV* is a virus isolate used as a commercial biopesticide to suppress FCM populations. A challenge is that *CrleGV* is sensitive to UV irradiation which causes degradation of the virus in the field, reducing its efficacy. A UV-tolerant isolate, *CrleGV*-UVT, was developed via successive rounds of UV exposure and selection of viable viral occlusion bodies. This resulted in the development of an isolate that persists longer following UV exposure, when examined under laboratory conditions. This study investigated the efficacy and UV tolerance of the *CrleGV*-UVT isolate as compared to a wild-type isolate, *CrleGV*-WT, under natural UV exposure resembling conditions in the field. To accomplish this, detached fruit assays were conducted for both isolates including a control. The detached fruit assays included indoor and outdoor treatments to investigate the effect of UV irradiation on the *CrleGV* isolates. The detached fruit assays showed no differences by either of the *CrleGV* isolates regardless of UV exposure. An immediate assay was done to assess the viability of *CrleGV*-UVT and *CrleGV*-WT. This did not include any exposure time and the environmental conditions were kept constant throughout. The immediate assay showed that the two isolates can reduce FCM fruit infestation as compared to a control treatment. Consequently, certain factors might have affected the virulence of each isolate in the detached fruit assays indicating the need for additional research to optimise and improve the experimental procedures utilised.

BBC7

Ant (Formicidae: Hymenoptera) response to grazing lawns in Welgevonden Game Reserve, Waterberg mountains

Simphiwe Dlamini, Caswel Munyai

School of Life Sciences, University of Kwazulu-Natal, Pietermaritzburg, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Understanding where biodiversity is, how it is distributed and the response to disturbance is crucial for community ecologists. Across Africa, grazing lawns have recently been receiving considerable attention. However, most studies have focused on how plants and vertebrates respond to these habitats, with very few studies focusing on the response of invertebrates. Here we aimed to document how ant (Formicidae: Hymenoptera) diversity and assemblage composition vary between the grazing lawns and adjacent woodlands dominated by Terminalia sericea in Welgevonden Game Reserve, Waterberg mountains. The three-paired sampling sites were replicated four times (replicates 300 m apart) and sampled in three different elevational bands. In each replicate, pitfall traps laid in 2X5 were left open for five days. We collected a total of 10 351 ant specimens, representing 77 ant species in 23 genera and five subfamilies. Species richness was lowest in grazing lawns compared to adjacent woodlands, while abundance was highest in grazing lawns. Disturbance tolerant species, *Anoplolepis custodiens* and a generalist and dominant numerical species, *Phiedole megacephala*, dominated the ant assemblages in grazing lawns. Some notable predatory ant species were more common in adjacent woodlands. We infer that disturbance (grazing) and dominant ants shape diversity and assemblage across the Welgevonden landscapes associated with grazing by large mammals.

AE1

Challenges in rearing macadamia nut borer, *Thaumatotibia batrachopa*

Sinazo Nkomo, Tamryn Marsberg, Sean Moore

Citrus Research International, Port Elizabeth, South Africa

Categories

• Agricultural Entomology

Abstract

Thaumatotibia batrachopa, the macadamia nut borer, is an indigenous pest of macadamia in Africa. Information on the biology and management practices for *T. batrachopa* is limited, due to the insect's cultivated host range being almost exclusively macadamia nuts. This could be remedied to a large extent through the establishment of a *T. batrachopa* laboratory culture for research purposes, which is the aim of this study. Macadamia nuts were collected from various regions around South Africa. Several methods were used to extract *T. batrachopa* larvae from nuts. The first method involved cracking the husks and nuts open, and any larvae found were placed onto an artificial diet used for the closely related *T. leucotreta* (false codling moth). The second method involved placing the nuts in a large 2 x 2 m mesh cage and allowing *T. batrachopa* moths to emerge. Moths were then captured and placed into an oviposition cage. The second method proved to better, as it was less labour intensive and survival rate was higher. However, inducing mating and oviposition under laboratory conditions has proved challenging. Various methods have been used, with generally little success to date. This forms the major focus area of current research efforts. Finally, during collection and laboratory rearing, larvae showing symptoms of baculovirus infection were collected and stored for analysis. Suspected virus from these larvae was analyzed by sequencing the *PolH, Lef 8* and *Lef 9* gene regions

WBC4

The potential for biocontrol of the Brazilian cactus (*Brasiliopuntia brasiliensis*)

Sonwabise Maneli, Iain Paterson, Phillippa Muskett

Rhodes University, Makhanda, South Africa

Categories

• Weed Biological Control

Abstract

Brazilian cactus (*Brasiliopuntia brasiliensis*) is a new invasive alien plant species in South Africa that is currently only found at one site in Bonamanzi, KwaZulu-Natal. The cactus originated in Brazil, where it is a valued indigenous species. However, in South Africa, it has the potential to become a serious environmental pest. It has become invasive in an area of exceptionally high indigenous biodiversity and endemism (Sand Forests of KwaZulu-Natal), where it endangers and threatens indigenous plant and animal species. Biological control has successfully controlled several invasive cacti in South Africa, but no agents have been developed for the control of *B. brasiliensis*. This study aims to test some of the cochineal insects that are used for biological control of other cactus weeds in South Africa for their efficacy as control agents for *B. brasiliensis*. Trials to assess survival and fitness will be conducted by tracking the development of the five cochineal species/lineages (*Dactylopius opuntiae 'stricta', D. opuntiae 'ficus', D. austrinus, D. ceylonicus* and *D. tomentosus*) on *B. brasiliensis*. The number of offspring, weight, developmental time, and other fitness measures will be assessed for all five cochineal species of *B. brasiliensis* relative to their target weeds. The damage on *B. brasiliensis* will also be assessed relative to the damage done by cochineals on target weeds that they successfully control. These experiments will determine whether any of the cochineal species already used for biological control of cactus weeds in South Africa are likely to be effective against the Brazilian cactus. If any are suitably damaging, they will be considered as a potential management option for Brazilian cactus.

II11

Integrated pest management of B*agrada Hilaris* (Burmeister) (Hemiptera: Pentatomidae): what we need to know before we can control them

Susana das Neves[1], Pia Addison[1], René Sforza[2]

[1]Stellenbosch University, Stellenbosch, South Africa. [2]USDA-ARS-European Biological Control Laboratory, Montpellier, France

Categories

• Invasive Insects

Abstract

Bagrada hilaris (Bagrada bug) is a widespread pest on a variety of crops in South Africa, parts of Europe (most notably in France) and parts of North America (specifically California). It is primarily found on crops belonging to the family *Brasicaceae* and occurs secondarily on crops such as rooibos, in South Africa. Considerable damage is caused by *B. hilaris* sucking the sap of leaves and young plants, leading to plant death. Integrated Pest Management (IPM) is an environmentally friendly and multi-disciplinary approach to controlling pests on crops. Aim: to better understand the life history of *B. hilaris* to assist in creating informed IPM programmes.

Adults were placed into a small enclosure with sand and a food source. The sand was sifted every 24hours to collect eggs. Eggs were divided between four petri dishes with damp filter paper, one for each temperature, 15°C, 20°C, 25°C and 30°C. Petri dishes were checked daily. A change in life stage was recorded, 0=egg, 1-5=nymph instars, 6=adult. Non-parametric tests and the relevant post-hoc tests were performed using Statistica 13, Kruskal-Wallis and Mann-WhitneyU.

Preliminary data analysis indicated a negative correlation (r = - 0,83) between the number of days and life stage at 20 °C, in contrast there was no correlation found at 25 °C (r = 0,08). At 25 °C the mean number of days was highest in stage 6, however not significantly higher than stages 5, 2 and 0 which suggests that adults have more time to mate and lay eggs which allow for multiple generations in a year. Development at 15°C, and 30°C are also presented and results discussed. Information gleaned from studies like this can assist growers in developing informed IPM programmes when *B. hilaris* is most active.

AE12

Susceptibility of Potato tuber moth, *Phthorimaea operculella* (Lepidoptera: Gelechiidae) to four contact insecticides in South Africa.

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Unit for Environmental Sciences and Management, IPM Program, North-West University, Potchefstroom, South Africa

Categories

• Agricultural Entomology

Abstract

The potato tuber moth (PTM), *Phthorimaea operculella* (Zeller) (Lepidoptera: Gelechiidae), is a major pest of potato globally. It is extensively controlled with insecticides in South Africa, but potato producers complain of control failure with some of the insecticides applied. No data are available on the susceptibility of PTM to insecticides in South Africa. The aim of this study was to estimate the susceptibility of PTM populations collected in four potato producing regions, to four contact insecticides. These insecticides were identified by producers for susceptibility testing and belong to different mode of action groups, *viz. azinphos-methyl* (o*rganophosphate), indoxacarb (oxadiazine), lambda-cyhalothrin (pyrethroid),* and *lufenuron (benzoylureas*). Potato tuber moth infested tubers were collected from Douglas, Polokwane, Tom Burke and Velddrif. These populations were reared, and neonate larvae used for susceptibility testing within 24 hours after emergence. The standard testing method (number 022) recommended by the Insecticide Resistance Action Committee (IRAC) for *Phthorimaea absoluta* was adapted and used. Mortality data were analysed by means of probit analyses and the likelihood of control failure was assessed by comparing the estimated LC_{80}-values with its recommended, registered label rate. The recommended dosage for each of the respective insecticides was converted to concentration of the active ingredient applied at a tank water volume of 500 L/ha and expressed in parts per million (ppm). Reduced susceptibility, with LC_{80}-values higher than the recommended field application rates, was estimated for *azinphos*-methyl from the PTM populations at Tom Burke, Velddrif and Douglas. Higher LC_{80}-values for lambda-cyhalothrin and lufenuron, compared to the recommended field rates were recorded in the populations from all four localities and control failure with these insecticides is expected. Larvae from all four populations were susceptible to indoxacarb. Results from this study can inform decisions for spray programs to optimize chemical control and improve resistance management of this pest.

PE2

Biological observations of the larvae of *Meromacroides meromacriformis* (Bezzi, 1915)

Terence Bellingan[1,2], John Midgley[3,2], Georg Goergen[4], Kurt Jordaens[5]

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Categories

- Physiological Ecology

Abstract

Meromacroides meromacriformis (Bezzi, 1915) is an enigmatic hover fly, first collected in South Africa in the 1850s, but not again until 2020. A further collection in 2022 was also made in the country. While widespread in Africa, the species is rarely encountered and information about its biology is scarce. The recent collections in South Africa were associated with colonies of *Schedorhinotermes lamanianus* (Isoptera: Rhinotermitidae) found in rot-holes within the trunk of standing living trees, and in 2022 larvae were collected from a frass midden. The link between termites and *M. meromacriformis* requires further investigation, but this habitat specialization may explain why the species is encountered infrequently. Larvae collected in 2022 have been reared to adulthood in 2023. Efforts are underway to enhance conservation of both sites through education panels in collaboration with local wildlife authorities.

ST2

Spheginobaccha pamela Thompson & Hauser, 2015: additional locality records and description of the female

Terence Bellingan[1,2], John Midgley[3,2], Kurt Jordaens[4]

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Categories

• Systematics and Taxonomy

Abstract

Spheginobaccha de Meijere, 1908 is a rare genus of hover flies, restricted to the Afrotropical and Oriental regions. Only eight species are known from the Afrotropics, of which only three are known from both sexes. The recent discovery of a female *Spheginobaccha pamela* Thompson & Hauser, 2015 specimen as well as recent collections of the species in South Africa brings this number to four. We present photographs and taxonomic notes on the female of *Spheginobaccha pamela*.

BBC5

Arthropod diversity, distribution and drivers in a monoculture timber plantation of the Natal Midlands: A multi-taxon approach

Thembekile Mthimunye, Caswell Munyai

University of KwaZulu-Natal, Pietermaritzburg, South Africa

Categories

• Biodiversity, Biogeography and Conservation

Abstract

Timber plantations are rapidly expanding at the expense of native forests. This has implications for arthropods which facilitate essential ecological processes in forest ecosystems. Recent studies have suggested that timber plantations can form ecological networks for some forest invertebrate species. Additionally, evidence has shown that different arthropods may have unique responses to disturbance. Therefore, this study aimed to explore patterns of the multi-taxonomic response of arthropods to monoculture timber plantations. In particular, arthropod functional diversity was considered to indicate the ecosystem stability of timber plantations. To investigate the trends, ground-dwelling arthropods (ants, spiders, beetles, millipedes, centipedes, and orthopterans) were collected using pitfall traps in three habitat types (a native forest, Pinus plantation and Eucalyptus plantation) at the Umngenipoort research facility in the Natal Midlands. Each habitat was replicated seven times, with ten pitfall traps in each replicate. In total, 2 646 specimens were collected, with the most significant proportion (40% of total abundance) coming from the native forests. Detritivores represented by millipedes, were mainly dominant in the native forest, indicating a high abundance of organic matter. Spiders and centipedes, generalist predators, were more abundant in Pinus plantations, which may indicate insect prey availability since plantations are prone to insect pest attacks. Ants and beetles, which are representative of various trophic levels, were common across all the habitats. Ongoing analysis will focus on the species-level identification, how this varies between habitats and the specific environmental drivers that affect arthropod patterns in timber plantations and native forests. The outcomes of this study will highlight the importance of arthropod conservation in human-managed environments and the maintenance of the associated microhabitat environmental factors to enhance the conservation of the essential arthropod communities.

MVFE1

The effect of aldicarb on various fly species in a carrion ecosystem.

Tshepiso Motolo, Sonja Brink

University of the Free State, Bloemfontein, South Africa

Categories

- Medical, Veterinary and Forensic Entomology

Abstract

When calculating a postmortem interval (PMI) based on the developmental model, it is imperative to know whether the deceased was exposed to toxicants which can potentially influence the growth rate of forensic indicator species. This was the first study to test the effect of aldicarb (a carbamate insecticide that is acutely toxic to humans) on various fly species of a carrion ecosystem. The larvae of *Chrysomya chloropyga*, *Chrysomya albiceps* and *Sarcophaga cruentata* were exposed to a lethal dose of aldicarb. Larvae were measured and weighed at 24-hour intervals, pupal development was tracked by noting morphological landmarks and adult fitness was assessed based on the ability to reproduce. Aldicarb delayed the total development time of *C. chloropyga* by 48 hours, it accelerated the development time of *C. albiceps* by 24 hours but had no effect on the development rate of *S. cruentata*. It was furthermore noted that, the toxicant did not affect the reproductive fitness of any of the species examined. From the results it was evident that no generalizations can be made about the effect of a toxicant for forensic indicator fly species. This also underpins the notion that understanding the effects of drugs on the development of larvae is essential and that not taking it into consideration can lead to errors in determining a PMI. To ensure the forensic validity of entomological results, the presence of drugs in a corpse should be considered as part of the analysis.

Keywords: *Chrysomya chloropyga*, *Chrysomya albiceps*, PMI, *Sarcophaga cruentata*, toxicant.

AE4

Forewarned is forearmed: Pests of wheat not yet in South Africa

Vicki Tolmay

Agricultural Research Council: Small Grain, Stellenbosch, South Africa

Categories

• Agricultural Entomology

Abstract

Climate change, international commodity trading and the "global village" phenomena are unavoidable realities of life in 2023. The global population is increasing, and it is estimated that the world will need 1.5 times the amount of wheat currently produced, by 2050. This projected requirement must be met using the same or fewer hectares of crop land, under more volatile climatic conditions, with cultivars that still have to be developed to deliver these high yields under the predicted circumstances. The changing climate is already causing variations in prevalence and occurrence of known wheat pests in South Africa, with more regular outbreaks of so-called sporadic pests such as red-legged-earth-mite being reported. Furthermore, based on the rate at which new pest incursions are increasing, scientists estimate that crop-pest saturation could be a reality by 2050. In other words, all insect pests of a crop will be present throughout the world, wherever conditions are conducive for their survival. Knowing which pest insects could spread to South Africa from other wheat producing areas of the world, is therefore advisable. Prior knowledge of these pests with respect to identification, damage caused, and potential control can mitigate widespread damage and promote a coordinated response from the wheat value chain. This poster presents photographs and summarizes information regarding five arthropod pests of wheat, known to cause substantial damage elsewhere in the world. They are Hessian fly (*Mayetiola destructor* Say), Wheat stem saw fly (*Cephus cinctus* Norton), Orange wheat blossom midge (*Sitodiplosis mosellana* Géhin), Sunn pest (*Eurygaster integriceps* Puton) and Wheat curl mite (*Aceria tosichella* Keifer).

ST4

Development of a multi-entry identification key for economically important fruit fly (Diptera: Tephritidae: Dacinae) larvae

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Categories

• Systematics and Taxonomy

Abstract

Identification of fruit fly larvae is difficult due to the limited morphological characteristics present. However, this is the stage at which fruit flies are intercepted at ports of entry through horticultural imports. Molecular tools are useful, but DNA analyses take time and are expensive, compared to morphological identifications. This project aims to use available information from literature and our own research to build a multi-entry identification key for thirteen *tephritid* species and species-groups that are of economic concern for the European Union.

Third instar larvae were obtained from different regions and hosts, including South Africa, La Reunion, India, Spain, China, Greece, Israel, Australia and from the colonies maintained by the International Atomic Energy Agency in Austria. Thirteen species or representatives of species groups were obtained, based on availability, including *Ceratitis*, *Dacus*, *Bactrocera* and *Zeugodacus* spp.

The *cephalopharyngeal* skeletons were dissected out, cleared in a 10% NaOH solution, dehydrated with 70-100% alcohol and mounted in Euparal on glass slides. Images of at least 20 larvae/species were captured using a compound microscope fitted with a camera and 400x magnification and measurements taken of 1) distance between the ventral apodeme and apical tooth, 2) ventral angle between the apical tooth and ventral apodeme, 3) distance between the dorsal apodeme and the ventral apodeme, 4) the ventral apodeme and the pre-apical tooth, and 5) the apical tooth and pre-apical tooth. The number of tubules in the front spiracles were counted and the position of the spiracles in relation to the cephalic skeleton was noted. Differences between morphometric parameters were tested via ANOVA and verified using discriminant function analysis. A matrix was compiled including nine characters for which significant inter-specific differentiation was preliminarily detected.

The key was converted into a mobile application by LUCID, for both Android and Apple devices.

BI3

The importance of isolation, land use intensity, and habitat quality in conserving pollination networks within a grassland plantation forestry landscape

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Categories

- Biological Interactions

Abstract

Many areas of the world have been transformed due to urbanisation, agriculture, and plantation forestry. In these transformed landscapes, remnant natural patches are found with varying amounts of isolation, under different land use intensities and having different habitat qualities. Understanding which of these factors is most important for ensuring pollination networks will allow for informed conservation decisions. Much of the grasslands of the Midlands has been converted to commercial forestry, with conservation of the indigenous and endemic biodiversity taking place in conservation corridors (CCs). Although CCs have been implemented, these landscapes remain fragmented and largely threatened by intensive land use. This study examined the effects of land use intensity (LUI) and isolation, as a result of fragmentation, on flowering plant and pollinator biodiversity in CCs. Flower-visitation surveys were conducted within CCs under varying degrees of isolation and land use intensity as well as in the adjoining protected areas. Surprisingly, LUI did not have a significant impact on plant-pollinator communities and isolation had positive effects on biodiversity in these landscapes under low levels of LUI. At least one measure of local habitat quality predicted pollinator or flowering plant species richness indicating that local habitat quality is most important for pollinators and their interactions with flowering plants. In these fragmented landscapes quality of the patch is more important than landscape design. In particular, the proliferation of bramble (*Rubus cunefolius*) threatens the longevity of species interactions. This suggests for the protection of pollination networks in transformed landscapes, conservation efforts should focus on alien clearing and habitat management rather than addressing LUI and isolation issues.

PE1

When bad flies make good decisions: Experimental testing of *hygrosensing* behaviour of C*. capitata* compared to other Tephritidae to understand microsite selection and environmental responses

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Categories

• Physiological Ecology

Abstract

Background: Tephritidae, e.g., *Ceratitis capitata* and *C. rosa*, are major fruit fly pests in South Africa that affect market access for European crops. Despite many similar features shared between these species, *C. capitata* has greater environmental stress resistance and can markedly adjust its physiology and behaviour to better withstand hot and dry conditions compared to more range-restricted Tephritidae species, e.g., *C. rosa*, *C. quilici*, *C. cosyra*. These factors likely contribute to the invasion success and broader geographic distribution of *C. capitata* relative to more range-restricted congeners. However, the underlying mechanisms responsible for these differences are not well understood.

Aim: This study investigates the neuroethology and hygrosensing ability (ability to perceive and respond to small changes in environmental conditions) of *C. capitata* relative to other Tephritidae species to address this critical knowledge gap. This study therefore aimed to compare the hygrosensing ability and behavioural responses to changes in humidity of several tephritid species.

Methods: Experiments were conducted using behavioural free-choice and no-choice conditions, and functional assays assessing fly preferences for specific relative humidity and temperature conditions under controlled lab conditions.

Results: In general, we find some evidence that flies associated with greater geographic ranges (e.g. *C. capitata*) and hence, exposed to more climate variation, occupy a broader range of relative humidities under laboratory conditions. Species with pronounced desiccation resistance were more behaviourally responsive to changes in environmental moisture and temperature conditions. By contrast, the more niche specialised species (e.g., *C. rosa*), prefers moister environments in a free choice experiment, especially at warmer conditions, but also fails to recognize changes in conditions as rapidly as *C. capitata*. This suggests that sensing and responding to environmental humidity are coupled responses that link behaviour and physiology in profound ways.

Keywords: Tephritidae, *Ceratitis*, hygrosensing ability, neuroethology, humidity, fruit fly pests