

ENTOMOLOGICAL SOCIETY OF AMERICA
SHARING INSECT SCIENCE GLOBALLY

INTERNATIONAL PROCEEDINGS OF THE ENTOMOLOGICAL SOCIETY OF AMERICA

2026

April 27–29, 2026
INTERNATIONAL BRANCH VIRTUAL SYMPOSIUM
https://www.entsoc.org/membership/branches/international/virtual-symposium

ISBN: 978-0-938522-60-7

© The Author(s) 2026, unless otherwise noted.
Published by the Entomological Society of America.

Table of Contents

FRONTIERS IN IPM: SUSTAINABLE MANAGEMENT OF INVERTEBRATE PESTS IN A CHANGING WORLD 4

Aigbedon-Atalor, P. (PLENARY) Insect chemical communications and IPM under variable climates: The role of modulating temperature 4

Gonzalez Rodriguez, J. (PLENARY) Integrating RNAi into fruit fly IPM: Semi-field suppression of *Ceratitis capitata* (Diptera: Tephritidae) and unexpected boosts in parasitoid performance 4

Rondon, S. (PLENARY) Solve pest problems: Supporting Integrated Pest Management decisions 4

Avosani, S. Applied biotremology: How vibrational stimuli support pest management 4

Burgess-Akitt, Z., Retzlaff, J., Burak, R., Gavloski, J., Mori, B. Alfalfa weevil deltamethrin resistance on the Canadian Prairies 5

Cambronero-Heinrichs, J.C., Pepori, A., Pecori, F., Santoiemma, G., Cavaletto, G., Santini, A., Rassati, D. Rethinking Dutch elm disease ecology: The potential role of ambrosia beetles 5

Cantaros, H.C., Alviar, K. Impacts of oral DSRNA delivery on *Laccase* expression and survival of the sweet potato weevil *Cylas formicarius* Fabr. (Coleoptera: Brentidae) 5

Carter, A., Stewart, A., Zazra, D., Noor, I., Hussain, A., Richer, M., Scheel, M., Smith, R. Assessing new mosquito larvicide technology compatibility using a diffusion of innovation model 6

Fatukasi, O., Wijerathna, A., Thilakarathna, M., Evenden, M. Effect of *Rhizobium leguminosarum* strains on plant metabolites, and pea leaf weevil, *Sitona lineatus* (Coleoptera: Curculionidae) host selection 6

Gomez, J. How many *Hypothenemus hampei* can one parasitoid wasp, *Cephalonomia stephanoderis*, remove? 6

Houchat, J.-N., Cochenille, T., Six, A., Ruhland, F., Verheggen, F., Doury, G., Ameline, A., Tougeron, K. Insecticidal and repellent properties of garlic essential oil on the edaphic aphid *Pemphigus bursarius* 6

Kundu, P., Sattler, S.E., Louis, J. Differential abundance of sorghum flavonoids impedes fall armyworm feeding 7

Mc Donnell, R., Coulton, A., Howe, D., Denver, D. Lethality of three species of *Pellioditis* nematodes (Rhabditidae) to the pest slug *Deroceras reticulatum* (Agriolimacidae) in laboratory assays 7

Peñalba, J., Rourmec, C., Luna, M.G., Salas Gervassio, N. Effect of non-solanaceous plants for the conservation biological control of *Pseudapanteles dignus*, a parasitoid of *Phthorimaea absoluta* 7

Romain Gracia, D., El Fakhouri, K., Mhada, M., Ramdani, C., Lamiri, A., El Bouhssini, M. Optimizing planting dates and screening for host plant resistance for sustainable insect pest management in quinoa in Morocco 7

Saguez, J., Jochems-Tanguay, L., Lefebvre, M. Cutworm parasitism in the province of Quebec (Canada) 7

Sebitsang, S. Life-stage susceptibility of laboratory and field populations of *Phthorimaea operculella* (Zeller) (Lepidoptera: Gelechiidae) to South African entomopathogenic fungi 8

Shafi, I., Kariyat, R. Who bites first matters: Herbivore order drives transgenerational soybean responses 8

Tanner, S.C., Bridges, W. Crowdsourcing pest detection: A citizen science-informed approach to species distribution modeling of the muhly grass mealybug, *Stemmatomerinx acircula* Howell & Miller (Hemiptera: Pseudococcidae) 9

Vieira Santos, L., Watt, C., Retzlaff, J., Beaudoin, A., Mori, B. Beyond the target: Insecticide effects on beneficial predators in alfalfa 9

Volk, E. Influence of nitrogen application on western flower thrips populations in gerbera daisy production 10

INSECT TAXONOMY IN THE 21ST CENTURY 11

Evangelista, D. (PLENARY) How many Amazonian insects are there, and how many have gone extinct? 11

Fagan-Jeffries, E. (PLENARY) Insect investigators and community science: Making taxonomy relevant to the next generation 11

Meier, R. (PLENARY) From dark taxa to digital species: Scaling insect biodiversity discovery with novel technologies 11

Awad, J. Legacy data: A blessing and a curse 12

Bailey, E., Wiegmann, B.M. Revising calyptrate fly classification from genus to family level 12

Belloncle, P., Awad, J. An integrative taxonomic framework for *Inostemma* Haliday, 1833 (Hymenoptera: Platygastridae) 12

Dorey, J., Gilpin, A.-M., Johnson, N., Esquerre, D., Hughes, A., Ascher, J.S., Orr, M. Building a generalizable method for insect species estimation 12

Garcia Cordon, A.C., Bossert, S. Integrative taxonomy of Central American *Ptiloglossa*: Using whole genome sequencing for delimiting species 13

Oberski, J. Taxonomic advances in the ubiquitous yet challenging “pyramid ants” (Formicidae: *Dorymyrmex*) 13

VISUALIZING ENTOMOLOGY: FROM LENS TO CANVAS 14

Bay, N. (PLENARY) The living canvas: Narrating insect ethology through macro photography 14

Iserman, M. (PLENARY) From specimen to symbol: How insects move between science and art 14

Ojo, D. (PLENARY) Reframing insects through the lens: Visual storytelling for entomology and conservation 14

Roe, A. (PLENARY) Scientific observation through brush and pen 14

INVITED SOCIETY: IOBC-NTRS (INTERNATIONAL ORGANIZATION FOR BIOLOGICAL CONTROL, NEOTROPICAL REGION SECTION) 15

Cingolani, F. (PLENARY) IOBC-NTRS: Neotropical Region Section of the International Organization for Biological Control 15

Luna, M. (PLENARY) Scaling biological control across Latin America: Advancing the IOBC NTRS legacy 15

de Oliveira, R. (PLENARY) Strategies in Integrated Pest Management in tropical agriculture 15

GENERAL 10-MINUTE PRESENTATIONS AND POSTERS 16

Ahsan, J. Ionotropic receptors mediate olfactory learning and memory in *Drosophila melanogaster* 16

Bidart, M.G., Hill, E. Milkweed species influence fitness-related traits of the monarch butterfly *Danaus plexippus* 16

Brar, G., Ngor, L., McFrederick, Q., Torson, A.S., Rajamohan, A., Rinehart, J.P., Singh, P., Bowsher, J. High abundance of lactobacilli in the gut microbiome of honey bees during winter 16

Cohen, H., Scordato, E., Lambert, A., Blakey, R., Questad, E. Impact of non-crop habitat on pests and their natural enemies in citrus and avocado 17

Deschodt, P., Ogilvie, D., Cory, J. Gut microbiome disruption decreases caterpillar susceptibility to baculovirus 17

East, S. Entomology For All - ESA's Diversity, Equity and Inclusion Committee 17

Geest, E. Butterfly diversity and community dynamics among gardens in an urban zoo 17

Jean, O.S., Shelomi, M. Tracing OrPV: From the coconut rhinoceros beetle to its sympatric neighbors 18

Kaur, A., Chakroborty, N. Temporal constraints on competing memories in the western honeybee, *Apis mellifera* 18

Kvedaraitė, F. The influence of nutritional substrates on the growth of *Tenebrio molitor* L. 18

Olszewski, P., Budrys, E., Orlovskytė, S., Wiśniowski, B., Ljubomirov, T., Kaczmarczyk, P., Bogusch, P., Sparks, T. Functional link between foreleg spines and nesting behaviour in European *Oxybelus* (Hymenoptera: Crabronidae) 19

Pudasaini, R., Farrell, C., Li-Byarlay, H. Transcriptomic analysis of low and high biting honeybees (*Apis mellifera* L.) across different ages 19

Sconce, F., Weinhold, A. Careers in insect science 19

Shelomi, M. Ice nucleating bacteria associated with *Belgica antarctica* 19

Strachan, H., Kroh, D., Li-Byarlay, H. Screening for high hygienic behavior in honeybee (*Apis mellifera*) colonies in Ohio 20

Wyszyńska, A., Kubicka, A., Bajerlein, D. Functional morphology of the mandibles of *Margarinotus carbonarius* (Histeridae): modularity, asymmetry and sexual dimorphism 20

Frontiers in IPM: Sustainable Management of Invertebrate Pests in a Changing World

(PLENARY) Insect chemical communications and IPM under variable climates: The role of modulating temperature

Pascal Aigbedion-Atalor (atalor@hawaii.edu), Univ. of Hawaii at Manoa, Honolulu, HI

(PLENARY) Integrating RNAi into fruit fly IPM: Semi-field suppression of *Ceratitis capitata* (Diptera: Tephritidae) and unexpected boosts in parasitoid performance

Jhonn Gonzalez Rodriguez (gonzalez_jho@gva.es), Instituto Valenciano de Investigaciones Agrarias (IVIA), Valencia, Montcada, Spain

RNA interference (RNAi) has emerged as a promising tool for species-specific pest control, yet its practical implementation in field-oriented delivery systems and its ecological safety remain major barriers for adoption.
Here, we present a novel bait-based dsRNA delivery strategy targeting *Ceratitis capitata,* applied as proteinaceous droplets under semi-field conditions. We evaluated the silencing efficiency of two genes (V-ATPase and RPS13) and quantified their impact on fruit infestation. Additionally, we performed biosafety assessment of dsRNA baits on two key non-target species, the parasitoid *Diachasmimorpha longicaudata* and the frugivorous fly *Drosophila suzukii.*
Our results demonstrate robust gene knockdown for both c-dsRNAs in adult medflies, but only **V-ATPase c-dsRNA** bait treatment translated into a significant reduction in pupal emergence and fruit damage under semi-field exposure. Non-target assays revealed no detrimental effects on survival, fecundity, or gene expression in either *D. longicaudata* or *D. suzukii*. Surprisingly, c-dsRNA bait formulation exposure increased parasitism rates in *D. longicaudata*, suggesting unforeseen physiological interactions with potential implications for integrated pest management.
Overall, this study provides the first evidence that dsRNA bait-droplet applications can effectively suppress medfly reproductive success in realistic conditions while maintaining high ecological safety for beneficial and non-target insects. These findings advance RNAi-based technologies toward field-ready, environmentally compatible fruit fly control strategies.
Keywords: RNAi, medfly, bait, non-target effects.

(PLENARY) Solve pest problems: Supporting Integrated Pest Management decisions

Silvia Rondon (silvia.rondon@oregonstate.edu), Oregon State Univ., Corvallis, OR

Pest management strategies across Oregon and the Northwest for both agricultural and non-agricultural sectors are diverse. Integrated Pest Management specialist across the west strive to connect through centers and belonging to central hubs for IPM research, extension. IPM centers provide resources, tools, and foster and encourage collaboration among university researchers, Extension agents, producers, and government agencies to advance pest management that is economically viable, environmentally responsible, and protective of human health. IPM designs offer professional IPM tools, resources, education and training, and news on events and initiatives that facilitate sustainable pest management practices.

Applied biotremology: How vibrational stimuli support pest management

Sabina Avosani (sabina.avosani@irda.qc.ca), IRDA, Saint-Bruno-de-Montarville,, QC, Canada

Biotremology explores how insects use substrate-borne vibrations to communicate, and this knowledge is increasingly being applied to develop innovative pest control strategies. In this short presentation, I will focus on how vibrational signals can be exploited to disrupt key behaviors of agricultural pests. I will present examples from my own work, illustrating how vibrational stimuli can interfere with mating and feeding processes in a pest species, the spittlebug vector of *Xylella fastidiosa* in Europe. This case study demonstrates the potential of vibrational approaches as sustainable, species-specific tools that can complement existing integrated pest management programs.

Alfalfa weevil deltamethrin resistance on the Canadian Prairies

Zachary Burgess-Akitt (zakitt@ualberta.ca)[1], Jennifer Retzlaff[2], Roger Burak[3], John Gavloski[4] and Boyd Mori[1], [1]Univ. of Alberta, Edmonton, AB, Canada, [2]Alfalfa Seed Commission of Alberta, Brooks, AB, Canada, [3]Manitoba Forage Seed Association, Arborg, MB, Canada, [4]Manitoba Agriculture, Food & Rural Development, Carman, MB, Canada

The alfalfa weevil, *Hypera postica* Gyllenhal (Coleoptera: Curculionidae), is an important pest of alfalfa, *Medicago sativa* L. (Fabaceae), especially in alfalfa grown for seed production. Cultural management strategies effective in forage alfalfa (e.g., harvest timing) are incompatible with seed alfalfa. Management of the alfalfa weevil in alfalfa seed production systems relies on insecticides, especially pyrethroids. In southern Alberta, resistance to the pyrethroids lambda-cyhalothrin and deltamethrin has been documented, but it is unknown whether this resistance extends across the Canadian Prairies. The objective of this study was to determine the distribution of alfalfa weevil deltamethrin resistance in the Prairie Provinces. Alfalfa weevils were collected from alfalfa seed production fields across Alberta, Saskatchewan, and Manitoba, and vial bioassays were used to determine deltamethrin susceptibility. Alfalfa weevil populations in Alberta and Saskatchewan showed resistance, while resistance was not detected in Manitoba. These findings will allow for more informed pest management decisions accounting for regional population differences.

Rethinking Dutch elm disease ecology: The potential role of ambrosia beetles

Juan Carlos Cambronero-Heinrichs (juan.cambronero.heinrichs@una.cr)[1,2], Alessia Pepori[3], Francesco Pecori[3], Giacomo Santoiemma[4], Giacomo Cavaletto[4], Alberto Santini[3] and Davide Rassati[4], [1]Programa de Investigación en Enfermedades Tropicales (PIET), Escuela de Medicina Veterinaria, Universidad Nacional de Costa Rica, Barreal, Heredia, Costa Rica, [2]Centro Nacional de Innovaciones Biotecnológicas (CENIBiot), CeNAT-CONARE, Pavas, San José, Costa Rica, [3]National Research Council, Institute for Sustainable Plant Protection (CNR-IPSP), Sesto Fiorentino, Firenze, Italy, [4]Laboratorio di Entomologia, Dipartimento di Agronomia, Animali, Alimenti, Risorse naturali e Ambiente (DAFNAE), Università di Padova, 35020, Legnaro PD, Italia., Padova, Italy

Dutch elm disease (DED), caused by *Ophiostoma novo-ulmi*, has severely affected elm populations across the Northern Hemisphere. Although *Scolytus* bark beetles are recognized as the principal vectors of the pathogen, the contribution of ambrosia beetles to its ecology remains poorly understood. We investigated whether biological features of four widespread ambrosia beetle species are compatible with a potential role in the movement of *O. novo-ulmi*. Females of *Anisandrus dispar*, *Xyleborinus saxesenii*, *Xylosandrus crassiusculus*, and *Xylosandrus germanus* emerging from experimentally colonized elm material were screened for the pathogen. *Ophiostoma novo-ulmi* DNA was detected in beetles originating from both diseased and apparently healthy elm logs, demonstrating that these insects can acquire or retain pathogen-associated material. We additionally evaluated interactions between *O. novo-ulmi* and microorganisms associated with ambrosia beetles. The pathogen did not negatively affect the fungal symbionts examined, suggesting that their coexistence within the beetle-associated microbial environment is possible. Conversely, *Dryadomyces* spp. and the bacterial isolate *Erwinia* sp. 1C4 reduced or constrained pathogen growth under experimental conditions, although neither interaction resulted in complete suppression. Together, these observations reveal microbial and ecological conditions compatible with ambrosia beetles carrying the DED pathogen. They broaden the conventional view of DED transmission beyond *Scolytus* beetles and highlight the need to determine experimentally whether ambrosia beetles can transfer viable *O. novo-ulmi* to susceptible elm hosts.

See published study:
Cambronero-Heinrichs JC, Pepori AL, Pecori F, et al. 2025. Microbial interactions support the role of ambrosia beetles as potential vectors of Dutch elm disease. *Microbial Ecology* 88:124. https://doi.org/10.1007/s00248-025-02624-y

Impacts of oral DSRNA delivery on *Laccase* expression and survival of the sweet potato weevil *Cylas formicarius* Fabr. (Coleoptera: Brentidae)

Hannah Corinne Cantaros (htcantaros@up.edu.ph)[1] and Karen Alviar[2], [1]Univ. of the Philipppines - Los Banos, Los Banos, Laguna, Philippines, [2]Univ. of the Philippines - Los Baños, Los Baños, Laguna, Philippines

Assessing new mosquito larvicide technology compatibility using a diffusion of innovation model

Alexandria Carter (almocart@iu.edu)[1], Akilah Stewart[2], Dave Zazra[3], Iffat Noor[4], Abrar Hussain[5], Martin Richer[1], Molly Scheel[6] and Rebecca Smith[7], [1]Indiana Univ. School of Medicine, Indianapolis, IN, [2]Indiana Univ. School of Medicine, South Bend, IN, [3]North Shore Mosquito Abatement District, Northfield, IL, [4]Univ. of Illinois Urbana-Champaign, Urbana, IL, [5]Univ. of Illinois Urbana-Champaign, Urbana, IN, [6]Univ. of Notre Dame, South Bend, IN, [7]Univ. of Illinois, Champaign, IL

New mosquito management techniques for reducing the transmission of arboviruses for the protection of human health are needed. An RNA-interference (RNAi) larvicide that was developed as a new mosquito control measure could enhance mosquito control in the North Shore Mosquito Abatement District near Chicago, IL. However, compatibility with the community attitudes and practices of the North Shore (NS) community should be evaluated before larvicide testing proceeds. A survey using the Diffusion of Innovation model was developed to assess public attitudes regarding mosquito control. Three different possible outcomes were considered: acceptance of a new larvicide, a new mosquito-specific larvicide, or a new GMO larvicide. Respondents (n=532) that reported greater mosquito nuisance were more likely to support new, and mosquito-specific larvicide technology. Beliefs that larvicide use could reduce the number of mosquitoes around one's property and that prevention measures will reduce the number of mosquitoes in one's home were associated with acceptance of all three different outcomes. Knowledge that mosquitoes can breed in stagnant pools of water or tires was also associated with support of the new larvicide technology. Larvicidal product factors, including human safety, correlated with support for the new larvicides and new mosquito-specific larvicides. Individual willingness to use larval insecticides was related to preventing mosquito bites not concern for arbovirus infection. Product factors such as mosquito specificity and environmental/human safety were critical factors for respondent support, suggesting that the new RNAi larvicide technology may be compatible with the NS-Chicago community depending on the manner in which its characteristics are communicated.

Effect of *Rhizobium leguminosarum* strains on plant metabolites, and pea leaf weevil, *Sitona lineatus* (Coleoptera: Curculionidae) host selection

Olajide Fatukasi (fatukasi@ualberta.ca), Asha Wijerathna, Malinda Thilakarathna and Maya Evenden, Univ. of Alberta, Edmonton, AB, Canada

Pea leaf weevil (*Sitona lineatus* L.) is a major pest of field peas and faba beans (Fabaceae). Economic damage to these legumes is caused by *S. lineatus* adults and larvae that feed on foliage and the rhizobia-containing root nodules, respectively, thereby causing reduced plant nitrogen and crop yield. The rhizobia-plant interaction may affect *S. lineatus* herbivory by influencing plant food quality and chemical defense. We tested the hypothesis that *Rhizobium*-field pea interactions influence *S. lineatus* herbivory and development. Field pea plants were treated with different *Rhizobium* strains (Wild-Type and Mutant Type) and compared to nitrogen-treated plants without *Rhizobium*, and a water-treatment control. Treatments significantly affected the plant metabolites produced in both below and above-ground tissues. There was no treatment effect on adult *S. lineatus* adult herbivory, which could be due to a trade-off between nutritional food quality and chemical defense. The wild-type, however, significantly supported *S. lineatus* larval host preference and development from egg to adult stage compared to the mutant-type, and other treated plants. Reduced development of *S. lineatus* on plants inoculated with the mutant *Rhizobium* could be due to smaller nodule size and a lack of fixed nitrogen compared to the wild-type treatment.

How many *Hypothenemus hampei* can one parasitoid wasp, *Cephalonomia stephanoderis*, remove?

Jesus Gomez (jesus.gomez3@upr.edu), Univ. of Puerto Rico at Mayaguez, San Juan, PR

Insecticidal and repellent properties of garlic essential oil on the edaphic aphid *Pemphigus bursarius*

Jean-Noël Houchat (jean.noel.houchat.7@gmail.com)[1], Thomas Cochenille[1,2], Audrey Six[3], Fanny Ruhland[4], François Verheggen[4], Géraldine Doury[1], Arnaud Ameline[1] and Kévin Tougeron[2], [1]UMR CNRS 7058 EDYSAN (Ecologie et Dynamique des Systèmes Anthropisés), Univ. de Picardie Jules Verne, 33 rue St Leu, F80039 Amiens Cedex, France, [2]EICG, Institut de Recherche en Biosciences, Université de Mons, Place du Parc 20, 7000 Mons, Belgium, [3]APEF, Association des producteurs

d'endives de France, 2 rue des fleurs, 62000 Arras, France, [4]Chemical and Behavioural Ecology, Gembloux-Agro-Bio-Tech TERRA, Université de Liège, Gembloux, Belgium

Differential abundance of sorghum flavonoids impedes fall armyworm feeding

Pritha Kundu (pkundu3@unl.edu)[1], Scott E. Sattler[2] and Joe Louis[3], [1]Univ. of Nebraska Lincoln, Lincoln, NE, [2]USDA - ARS, Lincoln, NE, [3]Univ. of Nebraska, Lincoln, NE

The Fall armyworm (FAW, *Spodoptera frugiperda*) remains a major constraint in sorghum production and a priority target for integrated pest management (IPM). We previously demonstrated that the *Brown midrib 12* (*Bmr12*) gene, which encodes the caffeic acid-O-methyltransferase (COMT) enzyme, confers enhanced, flavonoid-mediated resistance to FAW. Here, we investigated whether the central intermediate flavonoid, naringenin, mediates early resistance. Artificial FAW diet bioassays confirmed that naringenin indeed suppresses FAW larval growth. Our findings thus identify naringenin as the key COMT-dependent flavonoid underlying the previously reported FAW resistance in *Bmr12*-OE plants, thereby offering a mechanistic basis for leveraging flavonoid pathways in sorghum IPM strategies.

Lethality of three species of *Pellioditis* nematodes (Rhabditidae) to the pest slug *Deroceras reticulatum* (Agriolimacidae) in laboratory assays

Rory Mc Donnell (rory.mcdonnell@oregonstate.edu), Andrew Colton, Dana Howe and Dee Denver, Oregon State Univ., Corvallis, OR

Invasive slugs such as *Deroceras reticulatum* (Agriolimacidae) are among the most important pests of agriculture throughout North America. Current control measures such as the use of chemical pesticides are unreliable and have damaging non-target effects. This has resulted in increased research on biological control using nematodes in the genus *Pellioditis* (=*Phasmarhabditis*) (Rhabditidae) which have been commercialized in the U.K. and Europe. Surveys for these nematodes in the U.S. have resulted in the discovery of three gastropod-killing species (*P. hermaphrodita*, *P. californica*, and *P. papillosa*) throughout the west coast. Subsequent laboratory trials demonstrated for the first time the lethality of these U.S. strains at two inoculation rates against *D. reticulatum*. Data show that all three of the nematode species are lethal to *D. reticulatum* but the extent of and time to cause complete mortality varied. In terms of slug survival (LT 50) and percentage slug mortality (median), *P. papillosa* demonstrated the most lethality in the assays. Nevertheless, before a decision can be made on the use of these nematodes as safe biological control agents in the U.S., it will be necessary to fill remaining knowledge gaps. Of particular importance will be comprehensive host range testing with native non pest gastropod species.

Effect of non-solanaceous plants for the conservation biological control of *Pseudapanteles dignus*, a parasitoid of *Phthorimaea absoluta*

Julieta Peñalba (julietapenalba@cepave.edu.ar)[1], Catalina Roumec[1], Maria G. Luna[1,2] and Nadia Salas Gervassio[1,2], [1]CEPAVE (CONICET-UNLP-CICPBA), La Plata, Buenos Aires, Argentina, [2]Universidad Nacional de San Antonio de Areco, San Antonio de Areco, Argentina

Optimizing planting dates and screening for host plant resistance for sustainable insect pest management in quinoa in Morocco

Dachena Romain Gracia (dechena.gracia@um6p.ma)[1], Karim EL Fakhouri[2], Manal Mhada[2], Chaimae Ramdani[2], Abdeslam Lamiri[3] and Mustapha El Bouhssini[1], [1]Univ. Mohammed VI Polytechnic, Benguerir, Marrakesh-Safi, Morocco, [2]Univ. Mohammed VI Polytechnic, Benguerir, Morocco, [3]Hassan 1st Univ., Settat, Casablanca-Settat, Morocco

The cultivation of quinoa (Chenopodium quinoa Willd.) in Morocco has seen a marked increase in recent years, driven by its high nutritional value and capacity for adaptation to challenging environmental conditions. However, the cultivation of this crop is constrained by insect pests that can cause significant yield and seed quality losses. This study provides a comprehensive assessment of the main insect pests associated with quinoa in the Benguerir and Merchourch regions, focusing on the most abundant hemipteran species. Damage assessments revealed that pest pressure varies across crop development stages, with flowering and grain filling being the most vulnerable. Infestations reduce plant growth and yield, highlighting the need for effective management strategies. Screening of quinoa genotypes showed differential responses to Campylomma sp., Nysius sp., and Aphis sp., indicating promising tolerance and resistance traits. These traits will be

further validated using an automated phenotyping system under controlled conditions. Winter sowing limits the build-up of major hemipteran populations but may expose plants to aphid attacks, whereas early-ripening crops can face higher false bug infestations. Therefore, careful timing of planting, combined with the selection of resistant or tolerant genotypes, is critical for mitigating pest damage. In conclusion, integrating optimized sowing dates with resistant or tolerant genotypes represents the most effective strategy to reduce insect pest impacts throughout quinoa's growth stages. This approach supports sustainable quinoa production in Morocco while maintaining yield and seed quality.

Keywords: Chenopodium quinoa; insect pests; Hemiptera; host plant resistance; planting dates.

Cutworm parasitism in the province of Quebec (Canada)

Julien Saguez (saguezj@yahoo.com)[1], Laurence Jochems-Tanguay[2] and Maxime Lefebvre[2], [1]CÉROM, Saint-Mathieu-de-Beloeil, QC, Canada, [2]IRDA, Saint-Bruno-de-Montarville, QC, Canada

Cutworms (Lepidoptera: Noctuidae) are significant early-season crop pests. Their larvae are susceptible to attack by various natural enemies, which could represent valuable biological control agents. However, their actual contribution to cutworm population control remains poorly documented in Quebec. The effectiveness of parasitism in cutworms depends on the parasitoid species and host involved, the life stage of the parasitized host, environmental conditions, and the synchronicity between the host and its natural enemies. The objectives of this study are to (1) identify the natural enemies associated with the black cutworm (*Agrotis ipsilon*) and the darksided cutworm (*Euxoa messoria*) in Quebec, (2) assess parasitism rates and (3) map the distribution of hosts and their natural enemies.
In 2025, cutworm larvae were collected from different crops and regions of the province. They were individually reared on an artificial diet, under controlled conditions and observed regularly to determine the causes of mortality and identify the organisms involved. The project allowed us to identify various natural enemies present in Quebec. However, the results indicate low rates of parasitism across all sampled sites, suggesting that the impact of natural enemies on cutworm populations was limited during the study year.

Life-stage susceptibility of laboratory and field populations of *Phthorimaea operculella* (Zeller) (Lepidoptera: Gelechiidae) to South African entomopathogenic fungi

Setho Sebitsang (sebitsangs@arc.agric.za), Agricultural Research Council–Vegetable, Industrial and Medicinal Plants, Pretoria, Gauteng, South Africa; Stellenbosch Univ., Stellenbosch, Western Cape, South Africa

Phthorimaea operculella, remains one of the most persistent pests in South African potato production, yet there is still limited local information on how its life stages respond to entomopathogenic fungi (EPF). This study assessed the susceptibility of eggs, first-instar larvae, and pupae from a long-term laboratory colony and a field-derived population to three South African fungal isolates (*Beauveria bassiana* BB3, *Metarhizium anisopliae* MA2 and *Verticillium* sp. VIMPB) including a mixture containing all three isolates (CBMV). Laboratory bioassays were used to measure cumulative mortality and mycosis after 120 hours, while glasshouse trials on potato plants were used to evaluate egg hatch, larval survival and infection, feeding damage, and survival patterns over time. Life stage strongly influenced susceptibility, with larvae consistently showing the highest mortality and infection, followed by eggs and then pupae. Susceptibility patterns did not differ between the laboratory and field populations, suggesting that both populations responded similarly under the test conditions. In the laboratory assays, BB3 and the CBMV mixture produced the strongest effects across life stages, while VIMPB showed lower activity. In the glasshouse trials, EPF treatments reduced larval survival and feeding damage, although egg hatch remained largely unaffected. Overall, the results show that larval susceptibility is robust across populations and environments, and that BB3 and the CBMV mixture have the greatest potential for further development in South African potato integrated pest management. This work provides the first detailed local assessment of EPF activity against multiple life stages of *P. operculella* under laboratory and glasshouse conditions.

Who bites first matters: Herbivore order drives transgenerational soybean responses

Insha Shafi (i002@uark.edu) and Rupesh Kariyat, Univ. of Arkansas, Fayetteville, AR

Plants often undergo biotic and abiotic challenges, that occur either simultaneously or sequentially, insect herbivory, being a major challenge. Most studies on plant-herbivore interactions focus on pairwise comparisons, examining one or two herbivores attacking a single crop, or a single herbivore species that attacks multiple crops. However, sequential herbivory, where herbivores arrive and attack in a sequence, is poorly studied in crops like soybean (*Glycine max*). To address this gap, we examined the effects of the sequential attack of two chewing herbivores, fall armyworm (FAW) (*Spodoptera frugiperda*) and soybean looper (SL) (*Chyrysodeixis includens*) on soybean. We hypothesised that herbivory by FAW and SL

under differential sequence of incidence would result in distinct effects on morpho-physiological and yield traits in soybean. We found that initial herbivory resulted in strong morpho-physiological response; however, there was no difference during sequential attack. And, both FAW and SL performed poorly on FAW fed plants, indicating strong priming by FAW. No effects were observed across yield traits, suggesting strong tolerance of soybean. However, progeny from alternating sequential attacks (FAW-SL and SL-FAW) displayed strong transgenerational response. FAW-SL progeny resulted in strong physiological response compared to SL-FAW progeny. Interestingly, in terms of progeny fitness traits, SL-FAW outperformed FAW-SL progeny, suggesting strong sequence-specific effects. Taken together, these findings highlight that sequential herbivory can result in distinct morphophysiological response in soybean. More importantly, these effects transcend across generations, shaping soybean physiology and fitness.

Crowdsourcing pest detection: A citizen science-informed approach to species distribution modeling of the muhly grass mealybug, *Stemmatomerinx acircula* Howell & Miller (Hemiptera: Pseudococcidae)

S. Cory Tanner (shannt@clemson.edu) and William Bridges, Clemson Univ., Clemson, SC

Stemmatomerinx acircula Howell and Miller (Hemiptera: Pseudococcidae), a mealybug native to Florida, has undergone rapid range expansion across the southeastern United States since approximately 2018. Documenting the distribution of mealybugs and scale insects presents a significant challenge using traditional survey methods alone. This study leveraged citizen science observations alongside museum records to compile occurrence data for species distribution modeling, representing what may be the first documented use of citizen science data in mealybug distribution research. Maximum entropy (MaxEnt) modeling incorporating bioclimatic variables and fine-scale urban density data--capturing both climatic constraints and anthropogenic landscape influences--revealed that *S. acircula* currently occupies approximately 125,000 km^2 of core habitat area concentrated along the Atlantic and Gulf coastal plains. Urban density emerged as a significant predictor, reflecting the species' association with ornamental landscape plantings of muhly grass (*Muhlenbergia capillaris*) in urbanized areas. Isothermality and coastal proximity were identified as fundamental niche constraints, restricting core habitat to maritime-influenced climates with reduced diurnal temperature fluctuation. These findings advance our understanding of the ecological drivers shaping this species' current distribution while demonstrating the value of citizen science data as a tool for detection, monitoring, and proactive management of range-expanding pests.

Beyond the target: Insecticide effects on beneficial predators in alfalfa

Leonardo Vieira Santos (vieirasa@ualberta.ca)[1], Caitlin Watt[2], Jennifer Retzlaff[3], Adele Beaudoin[1] and Boyd Mori[1], [1]Univ. of Alberta, Edmonton, AB, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]Alfalfa Seed Commission of Alberta, Brooks, AB, Canada

Alfalfa (*Medicago sativa* L.) is an economically important forage crop worldwide, yet its production is threatened by the alfalfa weevil (*Hypera postica* Gyllenhal), a key defoliating pest capable of causing substantial yield losses, especially in seed production systems. In Canada, management of *H. postica* mainly depends on insecticide applications. This approach has contributed to insecticide resistance and has negatively affected non-target arthropods, including natural enemies that may help regulate weevil populations. These concerns generate a need to better understand predator communities within alfalfa seed systems and their potential role in biological control. This study investigates predator abundance in commercial alfalfa seed fields in southern Alberta. It evaluates how insecticide use impacts these communities to aim for a more sustainable integrated pest management (IPM) approach. Field surveys were conducted during the 2025 growing season across multiple fields differing in insecticide management. Foliage-dwelling predators and *H. postica* larvae were sampled using sweep nets and counted in both treated and untreated fields. Preliminary findings reveal a diverse predator community, primarily composed of coccinellidae, nabidae, and anthocoridae. Initial analyses show that although insecticide applications reduce *H. postica* densities, they also significantly decrease predator abundance. This suppression of natural enemies may compromise biological control during critical stages of weevil development. Final analysis is ongoing; however, current results highlight important trade-offs associated with insecticide use. Improved knowledge of predator community structure and dynamics will support IPM strategies that effectively manage *H. postica* while conserving beneficial arthropods.

Influence of nitrogen application on western flower thrips populations in gerbera daisy production

Emma Volk (evolk@ucanr.edu) and Hamutahl Cohen, Univ. of California Cooperative Extension, Camarillo, CA

Frankliniella occidentalis, commonly known as Western flower thrips (WFT), and species of the *Aphididae* family (aphids) are significant pests in gerbera daisy production. Gerbera daisy production is valued at $32 million in California, USA. Research shows that high nitrogen (N) application levels can increase WFT and aphid population abundance in cut flower production, so we conducted a study to determine the N application level that decreases WFT and aphid populations while maintaining marketable flower yields. We applied four N treatments from February to October 2025 in a greenhouse in Camarillo, CA (4 reps per treatment; 6 plants per rep): 225 ppm N, 200 ppm N, 175 ppm N, and 150 ppm N. We harvested blooms twice weekly and used 5-second shake counts to determine the number of WFT and aphids. We then compared the median number of insects between each treatment group. The 150 and 225 ppm N treatments had the highest median aphid counts, with 22 and 15 aphids per bloom, respectively. WFTs had no significantly different counts between any of the N treatments. The 200 ppm N treatment had a median of 16 bloom counts per plant, a significantly higher count compared to the other N treatments . Our study suggests that conventional N treatments that exceed 225 ppm may exacerbate pest pressure. N levels at 200 ppm may maximize harvest while minimizing pest pressure. Decreasing N application to 200 ppm has the added benefit of potentially reducing input costs while minimizing water pollution.

Insect Taxonomy in the 21st Century

(PLENARY) How many Amazonian insects are there, and how many have gone extinct?

Dominic Evangelista (dominicev@gmail.com), Univ. of Illinois Urbana-Champaign, Champaign, IL

Amazonia is the world's largest rainforest, predicted to house 25% of all terrestrial species. While there is much deserved concern about ongoing and future loss of amazonian biodiversity, there are few reliable estimates of how many species there may be and how many have already gone extinct due to human activity. I use publicly available biodiversity and GIS data to model amazonian insect biodiversity and extinction due to habitat loss. To tie habitat loss to extinction rates, I model endemism across the continent. I start by modelling cockroach diversity patterns for the whole Amazon basin. Cockroaches, while not often considered ecologically important, are colloquially thought of as resilient to extinction. This makes them useful for communicating the dire state of insects generally to a broader audience. I then expand to predict extinction in more charismatic, and diverse, insect groups. For cockroaches alone, the most conservative preliminary estimate suggests that there are ~4X more Amazonian species than are currently described and habitat loss has resulted in extinction of hundreds of species.

(PLENARY) Insect investigators and community science: Making taxonomy relevant to the next generation

Erinn Fagan-Jeffries (erinn.fagan-jeffries@adelaide.edu.au), Univ. of Adelaide, Adelaide, Australia

There are many ways to invite people to care about insect taxonomy – one way is to get them personally involved in the process. The Insect Investigators project worked with 50 schools around regional Australia to survey insects using Malaise traps and DNA barcoding in 2022. In the years since the specimens were collected, we have been working with schools to name new species from their samples, directly involving young people with the process of documenting and describing their local biodiversity. In this talk I'll give an overview of the project and how we hope to make taxonomy relevant to school students, give some tips and tricks for naming species with the community, and discuss some of the challenges of combining community science with rigorous taxonomy.

(PLENARY) From dark taxa to digital species: Scaling insect biodiversity discovery with novel technologies

Rudolf Meier (Rudolf.Meier@hu-berlin.de), Museum für Naturkunde Berlin, Berlin, Berlin, Germany

Insects dominate terrestrial biodiversity, yet most insect species remain undescribed. This gap is not caused by a lack of material, but by workflows that were designed for low-throughput taxonomy and remain poorly aligned with modern digital infrastructures. As a result, biodiversity research continues to generate an expanding analog legacy that is difficult to reuse for large-scale ecological analysis, monitoring, and conservation. This talk presents a framework for accelerating insect biodiversity discovery by treating species as digitally native entities from the outset. The approach combines high-throughput DNA barcoding using nanopore sequencing, robotic specimen handling and imaging, and artificial intelligence for data extraction and description. Large specimen sets are first screened using cost-effective "megabarcoding" to generate transparent and testable species hypotheses. These hypotheses then guide targeted morphological validation rather than exhaustive specimen-by-specimen study. AI-assisted tools support image analysis, character documentation, and the generation of standardized, structured species descriptions. Each processed specimen becomes the anchor for a persistent digital record integrating sequences, images, metadata, and trait information in open repositories. These records are FAIR-compliant, machine-readable, and immediately reusable for biodiversity monitoring and conservation. By shifting insect taxonomy toward scalable, interoperable workflows, the vast "dark taxa" that dominate insect diversity become visible and tractable in a digital age.

Legacy data: A blessing and a curse

Jessica Awad (jessica.awad@naturalis.nl), Naturalis Biodiversity Center, Leiden, South Holland, Netherlands

As an information system, Linnaean taxonomy was not designed to handle 21st century big data, dark taxa, mOTUs, and "known unknowns". Under the rules of the ICZN, it is easy to generate new names with minimal detail, while revising these names is much more difficult and time-consuming. For most dark taxa in Europe, an abundance of superficial descriptions makes species-level identification impossible without comparison to primary types. In some cases, it may make sense to ignore such superficial descriptions. However, many names link to valuable ecological information and historical observations which are essential to the study of biodiversity loss and global change. By integrating traditional taxonomy with advanced technological methods, it is possible to efficiently extract legacy data that was previously locked in literature and collections. Such efforts are currently underway at Naturalis Biodiversity Center, with a newly established research program focusing on insect dark taxa, primarily gall midges (Diptera: Cecidomyiidae) and their parasitoids (Hymenoptera: Platygastridae).

See published study:
Awad J, Reinisch R, Moser M, Vasilița C, Krogmann L. 2025. Untangling host specialization in a "double dark taxa" system. *Annals of the Entomological Society of America* 118(3): 206–219. https://doi.org/10.1093/aesa/saaf003

Revising calyptrate fly classification from genus to family level

Ezra Bailey (ezra.bailey@tamu.edu)[1,2] and Brian M. Wiegmann[2], [1]Texas A&M Univ., College Station, TX, [2]North Carolina State Univ., Raleigh, NC

The calyptrate flies (Diptera: Calyptratae) are a diverse clade with approximately 23,000 species, including economically and medically important taxa such as the New World screwworm, tsetse flies, bot flies, and stable flies. Despite decades of morphological and molecular study, many higher-level relationships within Calyptratae remain uncertain, and even some familial boundaries remain under debate. Building on previous phylogenetic efforts, we leverage phylogenomic data to assess relationships with historical uncertainty, comprising hundreds of loci from anchored hybrid enrichment to thousands of loci from whole genomes. Datasets include a broad sampling of calyptrate families using exclusively genomic data, a genera-rich sampling of muscoid grade taxa Anthomyiidae and Scathophagidae, and the first sampling of the Calliphoridae subfamily Luciliinae to include all genera. Analyses reveal paraphyly in key genera and families, identify lineages requiring extensive sampling, and support certain revisions to existing classifications. Our results highlight the value of genome-scale data in resolving uncertainties in classification and provide a framework for robust comparative genomic studies on calyptrate evolution.

An integrative taxonomic framework for *Inostemma* Haliday, 1833 (Hymenoptera: Platygastridae)

Pierre Belloncle (bellonclep@gmail.com)[1] and Jessica Awad[2], [1]Sorbonne Univ., Paris, Ile-de-France, France, [2]Naturalis Biodiversity Center, Leiden, South Holland, Netherlands

Inostemma Haliday, 1833 (Hymenoptera, Platygastridae) is a genus of parasitoid wasps targeting Cecidomyiidae (Diptera), with 112 described species currently known to science. Most of these species are not discernible from one another while basing ourselves on species descriptions, making their identification close to subjective. This makes *Inostemma* a dark taxon, and prevent any taxonomical or ecological study to be made with this taxon without revising it first. This presentations aims at explaining past and current challenges encountered by taxonomists while studying this genus, and how integrative taxonomy helps us to better compute these species with a combination of morphological and molecular data analysis along with ct-scanning. A focus is made on the type species of the genus *Inostemma boscii* (Jurine, 1807) to illustrate this presentation's point.

Building a generalizable method for insect species estimation

James Dorey[1], Amy-Marie Gilpin[2], Nikolas Johnson[1], Damien Esquerré[1], Alice Hughes[3], John S. Ascher[4] and **Michael Orr** (michael.christopher.orr@gmail.com)[5], [1]Univ. of Wollongong, Wollongong, NSW, Australia, [2]Western Sydney Univ., Penrith, NSW, Australia, [3]Univ. of Hong Kong, Hong Kong Island, Hong Kong, [4]National Univ. of Singapore, Singapore, Singapore, [5]Staatliches Museum für Naturkunde Stuttgart, Stuttgart, Germany

Robust species richness estimates are critical for meaningful conservation prioritization, understanding ecosystem resilience, and studying evolutionary processes. Yet, they remain elusive even for some of the best-studied groups and regions. As keystone pollinators, bees are crucial for the maintenance of healthy ecosystems, yet what estimates exist are haphazard and derived from guesswork. We statistically estimated global, continental, and country lower bounds of species richness. Globally, we estimated 24,705–26,164 bee species, an 18–25% increase, representing at least 32–45 years of taxonomic research. Particularly high undescribed biodiversity is expected from Asia, Africa, and the Americas. Taxonomic gaps correlate with gross domestic product per capita (GDPc), observed species richness, number of occurrence records, and completeness of occurrence databases. Our statistical R-package framework promises to progress understanding lesser-known groups, downstream consensus and, at long last, estimate the number of species on Earth.

Integrative taxonomy of Central American *Ptiloglossa*: Using whole genome sequencing for delimiting species

Ana Cristina Garcia Cordon (garciacordon.anacristina@gmail.com)[1] and Silas Bossert[1,2], [1]Washington State Univ., Pullman, WA, [2]Smithsonian Institution, National Museum of Natural History, Washington, DC

The genus *Ptiloglossa* (Colletidae: Dipaglossinae) comprises 56 described species throughout tropical America and parts of southwestern United States. Like other diphaglossine bees, the genus *Ptiloglossa* includes crepuscular or nocturnal bees. Historically, studies on the genus are limited to species descriptions, an unpublished taxonomic revision, and the description of a few nest aggregations. Bees of the genus *Ptiloglossa* are challenging to identify at the species level due to a lack of diagnostic features. Many species are only known from one single sex or a single specimen. Our research aims to delimit and identify *Ptiloglossa* species from Central America using genome sequencing. Additionally, a new species is described from Guatemala and Honduras. We use molecular data to reconstruct a phylogeny of *Ptiloglossa*, delimit species, and pair males with corresponding females of the same species. This study focuses on Central American bee species to help illustrate the richness and diversity of the region.

Taxonomic advances in the ubiquitous yet challenging “pyramid ants” (Formicidae: *Dorymyrmex*)

Jill Oberski (jtoberski@gmail.com), Senckenberg Institute for Nature Research, Frankfurt, Hesse, Germany

The “pyramid ants” or “cone ants,” genus *Dorymyrmex,* are found widely throughout the Americas in arid and semi-arid open landscapes. Despite their conspicuous ground nests and daytime foraging habits, both of which contribute to the abundance of these ants in museum collections, the challenging nature of their taxonomy has long stymied research efforts. Recent work shows that the rapid Nearctic radiation is a young lineage (~3 Ma) that is actively speciating, often with three or more species in sympatry—a rich setting for the evolution of species interactions and social parasitism. To clarify species boundaries in Nearctic *Dorymyrmex*, I am taking an integrative approach that combines phylogenomics with classical morphological methods, field observations, and most recently, population genetics. To establish major species-group relationships, I sequenced partial genomes of *Dorymyrmex* by targeting ultra-conserved elements (UCEs) and inferred phylogenies under ML and Bayesian frameworks. Additionally, I generated a morphometric dataset of 24 measurements and 22 indices for 150 specimens, totaling 6,854 individual observations. Together, these results indicate the presence of at least 27 *Dorymyrmex* species in North America, more than doubling the currently valid 13. Here, I present an overview of the Nearctic radiation and discuss (1) how species have evolved and co-evolved, (2) how field observations of *Dorymyrmex* have improved our understanding of their socially parasitic relationships, and (3) how taxonomy can benefit from examining population genetics to detect introgression and hybridization.

Visualizing Entomology: From Lens to Canvas

(PLENARY) The living canvas: Narrating insect ethology through macro photography

Nicky Bay (nicky@bay.to), Independent macro photographer, NickyBay.com, Singapore, Singapore, Singapore

The transition from "lens to canvas" offers a unique opportunity to document more than just the form of a subject; it allows us to record its life history. This presentation explores the aesthetic beauty and scientific value of in situ macro photography across global biodiversity hotspots. While laboratory staging excels in morphological clarity, field photography captures "authentic moments"—behaviors and ecological interactions that are often difficult to observe or accurately represent in a controlled environment. By prioritizing the subject within its natural niche, we can visualize the complex, unscripted lives of insects, creating a "canvas" that complements taxonomic documentation with the vivid reality of behavioral art.

(PLENARY) From specimen to symbol: How insects move between science and art

Martha Iserman (bigredsharks@gmail.com), MarthaIserman.com, Dandenong Ranges, VIC, Australia

Insects are among the most intensely observed organisms in science, yet they are also powerful cultural and symbolic objects. This talk explores how insects move between scientific documentation and artistic interpretation, drawing on my background as a trained scientific illustrator and my current practice as a fine artist.
I will briefly outline how entomological illustration functions as a tool for accuracy and knowledge-building, then show how artists can use the same visual language- anatomy, segmentation, pattern, life cycles, scale-to create meaning beyond documentation. Through examples from my own work, I will discuss how insects become structures for storytelling, metaphor, and ecological thinking, rather than simply subjects to be recorded.
The presentation will also touch on practical aspects of observing and drawing insects, including how artists study specimens, photographs, and field notes, how scientific conventions influence composition and color, and where artists deliberately choose to diverge from accuracy.
By positioning insects as both biological realities and imaginative frameworks, this talk aims to offer a different perspective on how scientific knowledge can be translated, re-interpreted, and expanded through visual art.

(PLENARY) Reframing insects through the lens: Visual storytelling for entomology and conservation

Dara Ojo (dara@explorewithdara.com), ExploreWithDara.com, Edmonton, AB, Canada

This talk explores how macro photography can serve as a powerful tool for visualizing entomology beyond traditional scientific documentation. By combining field-based observation, artistic composition, and ecological context, photography can help translate complex entomological concepts into compelling visual narratives that resonate with broader audiences. Drawing from fieldwork across multiple ecosystems and collaborations with entomologists and conservation partners, this presentation examines how images can foster curiosity, challenge misconceptions about insects, and support conservation through storytelling. The talk will also touch on the ethical responsibilities of visual communicators working with living organisms and the role of imagery in shaping public understanding of entomology.

(PLENARY) Scientific observation through brush and pen

Amanda Roe (amanda.roe@nrcan-rncan.gc.ca), Natural Resources Canada, Sault Ste. Marie, ON, Canada

Observation lies at the heart of both science and art. Being able to effectively weave creative expression through a scientific lens can be a powerful communication tool. Scientific field notes are a prime example of this interplay between art and science. Field notes are a valuable tool in the entomologist's tool kit. They capture important pieces of data, observations, and a sense of place that can be vital to understanding natural systems. Moving beyond words, field notes can be richly illustrated and effectively communicate complex observations – in ways that still cannot be effectively replicated with still images or videos. Here, I will present my process, field kit, and examples of field notes that capture diverse entomological encounters from my travels.
© His Majesty the King in Right of Canada, as represented by the Minister of Natural Resources, licensed under the Open Government Licence - Canada. Reproduced here with permission.

Invited Society: IOBC-NTRS (International Organization for Biological Control, Neotropical Region Section)

(PLENARY) IOBC-NTRS: Neotropical Region Section of the International Organization for Biological Control

Fernanda Cingolani (fernandacingolani@cepave.edu.ar), Centro de Estudios Parasitologicos y de Vectores CEPAVE, Provincia de Buenos Aires, La Plata, Argentina

The IOBC-NTRS is the Neotropical Region Section of the International Organization for Biological Control (IOBC), a non-for-profit organization whose mission is to promote the development of biological control, and its use in integrated pest management programs all over the world. In particular, the IOBC-NTRS fosters connection and cooperation among people interested in biological control in Latin America and the Caribbean. We greatly appreciate the interdisciplinary work with institutions for educational and research purposes as universities and academic societies, government entities, extension services, NGOs, growers and private companies which pursue similar objectives. We promote the establishment of contact with representatives from the different countries in the region, for the exchange of information, building of cooperation, and working on joint initiatives.

(PLENARY) Scaling biological control across Latin America: Advancing the IOBC NTRS legacy

María Luna (lunam@cepave.edu.ar), CEPAVE (CONICET-UNLP) and National Univ. of San Antonio de Areco UNSAdA, La Plata, Provincia de Buenos Aires, Argentina

This presentation analyzes the implementation and expansion of biological control in Latin America and the Caribbean, tracing its evolution from classical introductions to modern augmentative and conservation-based approaches. Grounded in the landmark 2020 IOBC publication and recent syntheses (van Lenteren et al. 2025; Gontijo et al. 2025), we evaluate the region’s historical foundations and the current innovations driving the field forward. Data show that the region has the world's largest area under biocontrol and it is scaling through emerging technologies, regional policy alignment, and community-led adoption. Key drivers of this expansion include the optimized adoption of microbial agents, improved biopesticide registration protocols, and shifting farmer attitudes toward integrated pest management (IPM). However, significant challenges remain, including climate change and pesticide industry lobbying, which highlight the need for interdisciplinary collaboration to improve the application of biological control in the Latin America and the Caribbean region.

(PLENARY) Strategies in Integrated Pest Management in tropical agriculture

Regiane de Oliveira (regiane.cristina-oliveira@unesp.br), São Paulo State Univ. (UNESP), Botucatu, Botucatu, Brazil

Integrated pest management in tropical agriculture has progressed through the coordinated use of multiple complementary tactics rather than the substitution of one tool for another. Advances in biological control, ecological understanding of pest dynamics, and the refinement of selective chemical, behavioral, cultural, and biotechnological approaches have strengthened the resilience of production systems. As biological control becomes more consistently integrated into management programs, it contributes to system sustainability while also supporting the long-term effectiveness of other strategies. The combined use of natural enemies, monitoring, selective inputs, and resistance-management principles helps slow the evolution of pest resistance and maintains the functional diversity of control options available to growers. Research on parasitoid biology, mass-rearing, compatibility among tactics, and field-release technologies has expanded the applicability of integrated approaches across diverse tropical agroecosystems. These coordinated strategies enhance productivity, reduce vulnerability to pest outbreaks, and align agricultural practices with long-term environmental and economic sustainability.

General 10-minute presentations and posters

Ionotropic receptors mediate olfactory learning and memory in *Drosophila melanogaster*

Jawaid Ahsan (jahsan@cub.ac.in), Central Univ. of South Bihar, Gaya, Bihar, India

Phenylacetaldehyde (PAH), an aromatic compound, is present in a diverse range of fruits including overripe bananas and prickly pear cactus, the two major host fruits for *Drosophila melanogaster*. PAH acts as a potent ligand for the Ionotropic receptor 84a (IR84a) in the adult fruit fly and it is detected by the IR84a/IR8a heterotetrameric complex. Its role in the male courtship behavior through IR84a as an environmental aphrodisiac is of additional importance. In *D. melanogaster*, two distinct kinds of olfactory receptors i.e., odorant receptors (ORs) and ionotropic receptors (IRs) perceive the odorant stimuli. They display unique structural, molecular, and functional characteristics in addition to having different evolutionary origins. Traditionally, olfactory cues detected by the ORs such as ethyl acetate, 1-butanol, isoamyl acetate, 1-octanol, 4-methylcyclohexanol, etc. classified as aliphatic esters and alcohols have been employed in olfactory classical conditioning using fruit flies. This underlines the participation of OR-activated olfactory pathways in learning and memory formation. Our study elucidates that likewise ethyl acetate (EA) (an OR-responsive odorant), PAH (an IR-responsive aromatic compound) too can form learning and memory when associated with an appetitive gustatory reinforcer. The association of PAH with sucrose (PAH/SUC) led to learning and formation of the long-term memory (LTM). Additionally, the $Orco^{1}$, $Ir84a^{MI00501}$, and $Ir8a^{1}$ mutant flies were used to confirm the exclusive participation of the IR84a/IR8a complex in PAH/SUC olfactory associative conditioning. These results highlight the involvement of IRs via an IR-activated pathway in facilitating robust olfactory behavior.

Milkweed species influence fitness-related traits of the monarch butterfly *Danaus plexippus*

M. Gabriela Bidart (gbidart@bgsu.edu)[1] and Emily Hill[2], [1]Bowling Green State Univ., Bowling Green, OH, [2]BGSU, Bowling Green, OH

High abundance of lactobacilli in the gut microbiome of honey bees during winter

Gagandeep Brar (gagandeep.brar@bayer.com)[1], Lyna Ngor[2], Quinn McFrederick[3], Alex S. Torson[4], Arun Rajamohan[5], Joseph P. Rinehart[5], Preetpal Singh[6] and Julia Bowsher[7], [1]Bayer Crop Science, Union City, TN, [2]Univ. of California, Irvine, CA, [3]Univ. of California, Riverside, Riverside, CA, [4]USDA-ARS, Fargo, ND, [5]USDA - ARS, Fargo, ND, [6]Univ. of Toronto, Toronto, ON, Canada, [7]North Dakota State Univ., Fargo, ND

Honey bee gut microbiota support host development and physiology by influencing immune function, metabolism, behavior, and neurological processes. Although the gut microbial communities of honey bee queens, workers, and larvae have been extensively characterized, less is known about the microbiota of overwintering worker bees. This study examined gut microbiota dynamics in adult worker bees during overwintering, focusing on two commercial honey bee strains, Bolton™ and Mann Lake™. Colonies were maintained either in temperature-controlled indoor storage (6 °C) or under natural outdoor conditions and sampled during October, November, and December. Whole-gut microbial communities were characterized using 16S rRNA gene amplicon sequencing. Members of the genus Lactobacillus dominated the gut microbiota across all overwintering bees. An unclassified *Lactobacillus* taxon was significantly more abundant in November, whereas *Lactobacillus apis* was more abundant in October. Bolton bees exhibited significantly greater relative abundances of uncultured *Bartonella* and *Bifidobacterium*, as well as the unexpected presence of *Wolbachia*. In contrast, Mann Lake bees showed higher abundance of *Commensalibacter*. Microbial diversity analyses indicated that Shannon diversity was significantly associated with sampling month but not with bee strain or storage conditions. Similarly, significant monthly differences were detected using Bray-Curtis community dissimilarity metrics. Overall, gut bacterial composition was not substantially affected by overwintering method, whether colonies were stored indoors or outdoors. However, several bacterial taxa varied in abundance among sampling months, with minor differences observed between bee strains. Given the important role of the gut microbiome in honey bee health and nutrition, these findings suggest that *Lactobacillus* species may contribute to maintaining bee health during winter and overwintering storage.

See published study:
Brar G, Ngor L, McFrederick QS, Torson AS, Rajamohan A, Rinehart J, Singh P, Bowsher JH. 2025. High abundance of lactobacilli in the gut microbiome of honey bees during winter. *Scientific Reports* 15:7409. https://doi.org/10.1038/s41598-025-90763-0

Impact of non-crop habitat on pests and their natural enemies in citrus and avocado

Hamutahl Cohen (hcohen@ucanr.edu)[1], Elizabeth Scordato[2], Adam Lambert[3], Rachel Blakey[4] and Erin Questad[4], [1]Univ. of California Cooperative Extension, Camarillo, CA, [2]California State Polytechnic Univ., San Luis Obispo, CA, [3]Univ. of California, Santa Barbara, CA, [4]Cal Poly Pomona, Pomona, CA

We investigated how non-crop habitat enhancements at local and landscape scales influence insect communities in citrus and avocado in Ventura, California, a region characterized by a mosaic of agricultural land use, urban development, and natural areas. This project examines how proximity to natural habitat (riparian restorations) and the presence of on-farm vegetation (hedgerows) affects the diversity of insect communities. We targeted key citrus and avocado pests, including avocado thrips, red scale, and Asian citrus psyllid, while comparing how their predators and parasitoids respond to habitat mosaics.
We sampled insect communities using sticky traps and PCA scouting reports at 16 citrus and avocado orchard sites varying in their proximity to restored riparian areas and in the presence of hedgerows. We found that farms closer to riparian areas hosted fewer pest species and more beneficial insect species. We used generalized linear mixed models to examine the relationship between habitat and beneficial insect populations. In lemon, a higher percentage of non-crop habitat within 1000 meters of each site was associated with a greater abundance of parasitoids and predators and a reduction in pest species richness ($p<0.05$). Interestingly, non-crop habitat was not associated with reductions in avocado pest abundance and richness, possibly due to the lack of natural enemies for the major non-native avocado pests in our region. These findings suggest that small-scale habitat enhancements and broader landscape features play important roles in shaping pest control dynamics, but the impact varies by the type of crop and insects considered.

Gut microbiome disruption decreases caterpillar susceptibility to baculovirus

Pauline Deschodt (pauline.deschodt@ubc.ca)[1,2], Danielle Ogilvie[2] and Jenny Cory[2], [1]Univ. of British Columbia, Vancouver, BC, Canada, [2]Simon Fraser Univ., Burnaby, BC, Canada

Entomology For All - ESA's Diversity, Equity and Inclusion Committee

Stacie East (seast@entsoc.org), Entomological Society of America, Annapolis, MD

The Entomological Society of America (ESA) is committed to actively promoting diversity, inclusion, recruitment, and retention to cultivate a scientific society of excellence, tolerance, and mutual respect. The Diversity, Equity and Inclusion (DEI) Committee has made significant strides in driving this commitment forward, actively working to promote diversity and inclusion within the society. As of 2025, the DEI Committee operates as an open committee, structured into several sub-committees, that focus on various initiatives aimed at supporting under-represented communities and creating a more inclusive society. Over the past five years, the DEI Committee has achieved significant achievements, including the introduction of two new awards: the Alate Student Award, aimed at stimulating interest in entomology and encouraging attendance of students from minority-serving institutions at the ESA Annual Meeting, and the Distinguished Achievement Award, which recognizes outstanding contributions to diversity and inclusion in the field of entomology. Additionally, the committee has facilitated mentorship through programs like EntoMentos and Public Health Entomology for All, launched a new column in the American Entomologist to highlight diverse experiences and perspectives and regularly hosts webinars and annual meeting symposia featuring speakers from various backgrounds. The committee continuously seeks to develop new initiatives that address the needs of ESA members. Collectively, these initiatives demonstrate the DEI Committee's active commitment to making “entomology for all” a tangible reality, promoting a diverse and inclusive environment within ESA and the broader scientific community.

Butterfly diversity and community dynamics among gardens in an urban zoo

Emily Geest (egeest@okczoo.org), Oklahoma City Zoo & Botanical Garden, Oklahoma City, OK

Urbanization has reshaped landscapes worldwide and is known to strongly impact biodiversity. Butterflies are useful ecological indicators of urbanization because of their short lifespans, diverse habitat requirements, and sensitivity to temperature and microclimates. Butterfly gardens provide habitat patches within urbanized landscapes by including both larval hostplants and adult nectar plants, and thus are regularly recommended as a conservation action. To evaluate the effectiveness of butterfly gardens as urban conservation tools, it is essential to understand the dynamics of butterfly colonization and community change over time. To better understand how butterfly communities respond to different stages of urban gardens we examined three complementary datasets from gardens at the Oklahoma City Zoo and Botanical

Garden. Butterflies were detected immediately post garden planting but after 28 survey weeks community diversity differed with landscape context: the garden adjacent to a woody-shrub habitat accumulated more species and individuals than the garden embedded in an impervious surface matrix. Species richness was similar among gardens, but butterfly community compositions remained distinct, with some overlap observed in newly established gardens during the first summer post-planting. Finally, butterfly communities were distinctly separate by time period with beta diversity driven primarily by species turnover rather than species nestedness. Together these complementary results highlight that butterfly gardens can make meaningful conservation contributions, but their success is strongly dependent on both context and time. Further studies are needed to determine how plant selection, weather variability, seasonal timing, and position within the surrounding landscape matrix influence colonization trajectories and long-term butterfly community dynamics.

Tracing OrPV: From the coconut rhinoceros beetle to its sympatric neighbors

Ok Shin Jean (osmj41597@gmail.com)[1] and Matan Shelomi[2], [1]National Taiwan Univ., Taipei, Taiwan, Taiwan, [2]National Taiwan Univ., Taipei, Taipei, Taiwan

Oryctes rhinoceros picornavirus (OrPV) is a novel virus identified in the coconut rhinoceros beetle (CRB). Despite its high prevalence across CRB populations in Taiwan, the virus does not appear to significantly affect the lifespan of the host. This study investigates whether OrPV is a specialized resident of the CRB or if it has moved out into the local habitat to infect other local arthropods. We expanded our search across Taiwan and screened different CRB populations along with several species that share the same environment, including stag beetles, various scarabs, and other arthropods. Using an RT-qPCR pipeline, we measured viral levels to determine the extent of virus spread. Our initial sequencing confirmed the presence of the virus in some beetle species, and we are currently preparing samples from other groups to assess the degree of sequence similarity across different hosts. This research provides the first look at the social network of this novel virus and how it persists across a wide range of arthropod communities. The data suggests it is a common, background infection for CRB, but the full extent of its possible reservoir hosts remains to be determined.

Temporal constraints on competing memories in the western honeybee, *Apis mellifera*

Antarjot Kaur (antarjot.aura@gmail.com) and Neloy Chakroborty, Thapar Institute of Engineering and Technology, Patiala, Punjab, India

Honeybees, *Apis mellifera*, routinely encounter multiple floral odors while foraging and must flexibly update memories without losing access to previously learned information. Understanding how sequential learning events interact during consolidation is critical for explaining how memory systems balance stability with adaptive updating. Rather than reflecting cognitive failure, interference between memories may represent an adaptive prioritization process during memory consolidation. Here, we examined when olfactory long-term memories in the honeybee are susceptible to Retroactive interference (RI) and Proactive interference (PI), and whether the temporal spacing of sequential learning modulates their expression. Using differential conditioning of the proboscis extension reflex (PER), honeybees were trained on two elementary learning tasks using odors, separated by 30-minute, 1-hour, or 2-h intervals, and retention tests at 24 hours. With 30-min interval, we found both RI and PI ($p<0.05$). Using 1-hr interval, interference effects were weaker and asymmetric. Although Task 1 retention showed within-subject reductions across time for the experimental group, between-group comparisons did not support strong interference at 24 h. Task 2 retention remained largely stable, suggesting temporally constrained and task-specific effects. With 2-h, Task 1 retention did not differ reliably from controls at 24 h, whereas Task 2 performance showed significant PI compared to controls ($p<0.01$). These results demonstrate that interference in honeybee olfactory memory is shaped by temporal competition during retrieval. It also highlights how bees adaptively regulate memory in fluctuating floral environments, stabilizing established foraging strategies while remaining sensitive to shifts in reward value, critical for adaptive foraging in rapidly changing agricultural landscapes.

The influence of nutritional substrates on the growth of *Tenebrio molitor* L.

Felicija Kvedaraitė (felicija.kvedaraite@gmail.com), Nature Research Centre, Vilnius, Lithuania

Functional link between foreleg spines and nesting behaviour in European *Oxybelus* (Hymenoptera: Crabronidae)

Piotr Olszewski (piotr.olszewski@biol.uni.lodz.pl)[1], Eduardas Budrys[2], Svetlana Orlovskytė[2], Bogdan Wiśniowski[3], Toshko Ljubomirov[4], Paulina Kaczmarczyk[1], Petr Bogusch[5] and Tim Sparks[6], [1]Natural History Museum, Faculty of Biology and Environmental Protection, Univ. of Łódź, Poland, [2]State Scientific Research Institute Nature Research Centre, Vilnius, Lithuania, [3]Faculty of Technology and Life Sciences, Univ. of Rzeszów, Poland, [4]Bulgarian Academy of Sciences, Institute of Biodiversity and Ecosystem Research, Sofia, Bulgaria, [5]Department of Biology, Faculty of Science, Univ. of Hradec Králové, Czech Republic, [6] Department of Zoology, Poznań Univ. of Life Sciences, Poznań, Poland.

The digger wasp genus *Oxybelus* (Hymenoptera: Crabronidae) exhibits considerable diversity in nesting behaviour, including variation in burrow architecture and prey transport. We investigated whether the length of female foretarsal spines is associated with these behavioural and architectural differences. Across six species, those with an oblique initial burrow section had longer foretarsal spines than species with a vertical entrance. These findings suggest an association between foreleg morphology and nesting behaviour and highlight the value of integrating morphological and behavioural data when investigating adaptations in *Oxybelus*.

Transcriptomic analysis of low and high biting honeybees (*Apis mellifera* L.) across different ages

Rameshwor Pudasaini (rpudasaini@centralstate.edu), Catherine Farrell and Hongmei Li-Byarlay, Central State Univ., Wilberforce, OH

Biting behavior is an important natural defense mechanism in honeybees (*Apis mellifera*) against *Varroa destructor*. Significant variation in this behavior exists across genetic lines of honeybees, with certain colonies exhibiting higher mite-biting activity than others. Selective breeding for enhanced biting behavior provides a promising strategy for sustainable mite control and overall colony resilience. However, successful implementation of such breeding programs requires a comprehensive understanding of the genomic mechanism underlying this trait. In this study, RNA-seq analysis of mandible transcriptomes of 1-day and 8-day old worker honeybees from high biting (HB) and low biting (LB) colonies were performed. A total of 9,345 genes (97.30%) showed a significant differential expression between LB and HB honeybees across different ages (one-way ANOVA, FDR < 0.05). Furthermore, the Weighted Gene Coexpression Network Analysis (WGCNA) exhibited the brown and yellow modules with significantly higher expression in HB compared with LB on both day 1 and day 8. Gene Ontology enrichment analysis showed over-representation of biological processes involved in neural signaling, sensory perception, muscle contraction, immune response, cellular respiration, metabolic processes, and structural organization. Kyoto Encyclopedia of Genes and Genomes **(**KEGG) pathways analysis identified significant enrichment of various pathways including oxidative phosphorylation, cytoskeleton-related pathways, motor proteins, ribosome-associated pathways, and citrate cycle (TCAcycle). In summary, the present findings provide valuable insight for understanding and improving mite-biting behavior in honeybees.

Careers in insect science

Francisca Sconce (fran@royensoc.co.uk)[1] and Anne Weinhold[2], [1]Royal Entomological Society, ST ALBANS, Hertfordshire, United Kingdom, [2]Royal Entomological Society, ST. ALBANS, Hertfordshire, United Kingdom

Ice nucleating bacteria associated with *Belgica antarctica*

Matan Shelomi (mshelomi@ntu.edu.tw), National Taiwan Univ., Taipei, Taipei, Taiwan

Belgica antarctica (Chironomidae) is the southernmost free-living insect. It tolerates the extreme conditions of Maritime Antarctica through cryoprotective dehydration, freezing at approximately -7 °C but surviving. Recent work on its larval gut microbiota identified ice nucleating bacteria. These could raise the supercooling point of the insect, freezing it at higher temperatures, which could be beneficial in reducing water loss, or deleterious by reducing time spent active. Alternatively, they do not affect the larval supercooling point at all.
To determine which option is true, *Belgica antarctica* larvae were collected from sites in the Antarctic Peninsula and taken to the Ukrainian Vernadsky Research Base on Galindes Island. Gut microbes were cultured, isolated, and tested for ice nucleating activity using a modified frozen drop test. The supercooling points of control and starved larvae were measured using a T-type thermocouple. Microbes were identified by barcode sequencing. The guts were dominated by a novel species of *Yersinia* and known, ice nucleating, Antarctic strains of *Pseudomonas.* Microbiome correlated with collecting

location. Starvation successfully cleared the gut of microbes, but had no effect on the supercooling point of the larvae. The conclusion is that, while the *Belgica* larval gut contains ice nucleating bacteria, these do not mediate the supercooling point of the insect. The factors that do remain uncertain.

Screening for high hygienic behavior in honeybee (*Apis mellifera*) colonies in Ohio

Heaven Strachan, Danielle Kroh and **Hongmei Li-Byarlay** (hli-byarlay@centralstate.edu), Central State Univ., Wilberforce, OH

Hygiene is essential to the health and productivity of honeybee colonies. Hygienic behavior a natural defense mechanism allows bees to detect and remove diseased or dead brood, reducing the spread of pathogens such as American Foulbrood, Chalkbrood, and *Varroa* mites. This behavior helps maintain brood health, improves queen performance, and supports strong population growth. Because hygienic traits are heritable, they are valuable in selective breeding programs aimed at creating more resilient colonies. This study focuses on Ohio honeybee colonies and explores the potential link between two resistance traits: mite-biting and hygienic behavior. Specifically, we ask whether colonies with high *Varroa* mite-biting behavior also exhibit increased hygienic behavior. We hypothesize a positive correlation between the two traits, suggesting that selecting one may enhance the other. To test this, we will use the Universal Bee/Odor (UBO) assay to measure hygienic behavior across all colonies, including feral, commercial, and Russian bees. Colonies will be grouped by known mite-biting behavior, and their UBO results will be analyzed statistically. We expect high-biting colonies to show stronger hygienic responses, indicating a possible genetic or behavioral link. This research supports pollinator health by informing breeding programs that strengthen natural resistance traits, reduce reliance on chemical treatments, and improve pollination services vital to agriculture and ecosystems.

Functional morphology of the mandibles of *Margarinotus carbonarius* (Histeridae): modularity, asymmetry and sexual dimorphism

Aleksandra Wyszyńska (alewys6@st.amu.edu.pl)[1], Anna Kubicka[2] and Daria Bajerlein[1], [1]Adam Mickiewicz Univ., Poznań, Wielkopolska, Poland, [2]Poznań Univ. of Life Sciences, Poznań, Wielkopolska, Poland