IWGO Digital Meeting

5 & 6 May 2022

The International Working Group on *Ostrinia* and other Maize Pests (IWGO)
is a Working Group of the International Organization of Biological Control – Global (IOBC - Global)

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Scientific Programme

Thursday, 5 May 2022

Swiss Time	Presenter	Title of Presentation
13:00	IWGO Convenors	Welcome
13:10	Qiulin WU	Migration routes of the invasive fall armyworm *Spodoptera frugiperda* in China
13:30	Yongzhi ZHONG	Pheromone binding protein identification for sex pheromone of fall armyworm
13:50	Zhenying WANG	Monitoring and management of fall armyworm, *Spodoptera frugiperda*, in China
14:10	Tao JIN	Biocontrol potential of *Trichogramma* species against *Spodoptera frugiperda* and their field efficacy in maize
14:30	Marc KENIS	Classical biological control of fall armyworm: should we choose the most efficient parasitoid or the safest?
14:50	Stefan TOEPFER	Steps to develop an effective nematode-based biological control solution for the fall armyworm
15:10	**Break**	
15:25	Lakpo Koku AGBOYI	Perspectives for sustainable management of fall armyworm in Africa
15:45	Kyeong-Yeoll LEE	Invasion of *Spodoptera frugiperda* into Korea and identification of entomopathogenic fungus *Metarhizium rileyi* as a potential biological control agent
16:05	Bruce TABASHNIK	Managing fall armyworm in Africa: can *Bt* maize sustainably improve control?
16:25	Juan-Luis JURAT-FUENTES	DNA-based screening and mechanisms of resistance to *Bt* corn in fall armyworm and corn earworm
16:45	IWGO Convenors	Wrap-up Day 1
16:55	IWGO Convenors	End Day 1

Friday, 6 May 2022

Swiss Time	Presenter	Title of Presentation
13:00	IWGO Convenors	Welcome
13:05	Yueqin WANG	Inheritance and fitness costs of Vip3Aa19 resistance in *Mythimna separata*
13:25	Jingfei GUO	Genotypic variation in field-grown maize eliminates trade-offs between resistance, tolerance and growth in response to high pressure from the Asian corn borer
13:45	Erik DOPMAN	Four genes underlie voltinism and sex pheromone use in the European corn borer moth
14:05	Dominic REISIG	Impact of maize seed mixtures on *Helicoverpa zea* (Lepidoptera: Noctuidae) phenotype and genotype
14:25	Anna BERECZKI	Integrating automated pest trapping and population dynamics modelling for optimising the timing of cotton bollworm control options
14:45	Dakota BUNN	Contribution of larvae developing on corn and dry beans to the adult population of western bean cutworm in Michigan
15:05	**Break**	
15:20	Brad S. COATES	The USDA-ARS Ag100Pest Initiative: developing chromosome-level genome assemblies for corn pest insects
15:40	Dimpal LATA	Genome size evolution in the beetle genus *Diabrotica*
16:00	Kyle PADDOCK	Western corn rootworm (*Diabrotica virgifera virgifera* LeConte) resistance to *Bacillus thuringiensis* is linked to altered bacterial community
16:20	Kyle BEKELJA	Intersections between chemicals and biopesticides: seed coatings may obstruct resistance management plan for GMOs targeting western corn rootworm (*Diabrotica virgifera virgifera* LeConte)
16:40	IWGO Convenors	Wrap-up Day 2
16:50	Ivan RWOMUSHANA	Nairobi, Kenya to host the 28th International Working Group on *Ostrinia* and other Maize Pests (IWGO) Conference in 2023
17:00	IWGO Convenors	End Day 2

Migration routes of the invasive fall armyworm *Spodoptera frugiperda* in China

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Taking advantages of its long-distance migration capacity, omnivorous, high fecundity, and resistance to pesticides, the fall armyworm (FAW) *Spodoptera frugiperda* (J.E. Smith), a crop pest native to the Americas, has posed a serious threat to the nation's agriculture production since its first invasion into China in mid-December 2018. In China, maize is not only one of the most important crop plants with widest area but the most suitable host plant for the devastating FAW. Once the outbreak of invasive FAW happens, it will soon ravage the maize crops in China. In our project, the Asian monsoon-governed migration routes and patterns of FAW in maize-cropping regions of China were unveiled by systematic field surveys, long-term searchlight-trap monitoring, meso-scale numerical simulations of synoptic conditions, air-based trajectory analysis and statistical analysis *etc.* The studies indicate that FAW performs two major migration pathways, including the eastern and the western routes, to fly across the eastern and western China separately, which has caused regional severe infestation. Specifically, the western migration route of FAW originates from Myanmar and Yunnan, China and ends in north-western China in July, especially in Ningxia and Alxa Left Banner of Inner Mongolia, China, while the eastern pathway starts from the north-eastern Indo-China Peninsula and southern China and reaches the North China Plain and the south of Northeast China Plain by October. Our results provide scientific support for the early warning, green prevention, and ecological control of the widespread FAW populations in China.

Pheromone binding protein identification for sex pheromone of fall armyworm

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Spodoptera frugiperda among the China population employs a four-component sex pheromone blend to accelerate male-female allocation and mating behavior. The underlying molecular mechanism has been incompletely elucidated. In the current study, we showed that differences existed between genders toward the four sex pheromone components, including Z9-14:AC, Z7-12:AC, Z9-12:AC, and Z11-16:AC, in terms of electrophysiological responses and behavioral valences. Male adults were significantly more sensitive to all tested compounds than female adults. Furthermore, ecological outputs may be related to four pheromone-binding proteins, namely, SfruPBP1, SfruPBP2, SfruPBP3, and SfruPBP4. They formed four distinct clades within the lepidopteran phylogeny, and male adults expressed significantly higher levels of *SfruPBP1* and *SfruPBP2* than female adults. We observed the highest binding affinities of SfruPBP1 toward all four sex pheromone components. SfruPBP4 had moderate binding affinities for Z7-12:AC, Z11-16:AC, and Z9-12:AC, while SfruPBP2 showed binding toward Z9-14:AC. This observation suggests that SfruPBP1 plays a key role in sex pheromone discrimination and drives sexually biased behavioral decisions toward certain pheromone components. These findings will help to develop behavioral-mediating tools as part of integrated pest management approaches for this cross-border pest.

Monitoring and management of fall armyworm, *Spodoptera frugiperda,* in China

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The fall armyworm, *Spodoptera frugiperda* (Smith), is native to the tropical and subtropical regions in the Americas. It has been one of the most important insect pests of corn and another migratory pest that migrate north in spring and back south in autumn, since invaded in China in January of 2019. About 1.36 million ha corn infested by fall armyworm in 24 provinces in 2021. The annual generations of the fall armyworm were 1 to 7 from north to south of China. In order to manage of the invasive pest, a national monitoring and early warning system based on insect radar combined with searchlight traps and sex pheromone traps was set up to provide the information of population dynamics and the possible landing regions during migrating to the main corn growing regions. Strategies for fall armyworm, including the regionalization management strategy with different control measures, biological control with biopesticides and natural enemies, physical control, seed coating, resistance to insecticides monitoring, new application technique for insecticide of broadcasting tiny granules by drone. Technical specifications for forecast and control of fall armyworm issued by Ministry of Agriculture and Rural Affairs of China in 2021.

Biocontrol potential of *Trichogramma* species against *Spodoptera frugiperda* and their field efficacy in maize

Tao Jin[1]

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We evaluated egg parasitoids of the genus *Trichogramma* (Hymenoptera: Trichogrammatidae) in the biocontrol of *Spodoptera frugiperda* (Smith), a recently invaded pest in China. To compare host selection and fitness, the parasitization capacity of seven *Trichogramma* species were measured with different aged-adults, as well as allowed to parasitize *S. frugiperda* eggs at different host egg densities in the laboratory. The field trials involved the release of *T. chilonis*, *T. ostriniae*, *T. confusum*, and *T. pretiosum*, in a maize plantation in Danzhou, Hainan. The results showed that the numbers of eggs parasitized by ten female *T. chilonis*, *T. ostriniae*, and *T. confusum* within the initial 24-hours were 101.5, 87 and 93, respectively. The total number of eggs parasitized by *T. chilonis*, *T. ostriniae*, *T. confusum*, and *T. pretiosum* within the first 96 h were 180, 139, 191.3 and 169, respectively. The most effective egg densities were 35, 30, 40 and 40 eggs/tube (84.8 cm^3), with *T. chilonis*, *T. ostriniae*, *T. confusum*, and *T. pretiosum* affecting 21.7, 18.8, 23.8 and 16, respectively. After *T. chilonis*, *T. ostriniae*, *T. confusum*, and *T. pretiosum* were released, the parasitism rate on the egg masses ranged from 61.5% to 87.5%. The rate that the egg masses did not hatch were 41.7%, 12.5%, 15.4% and 15.4%, respectively. Moreover, the rate of plant damage ranged from 36.1% to 59.7%. The larvae density on the plants ranged from 0.43 to 0.83 individuals/plant, which was significantly lower than untreated control (95.6% and 1.37 individuals/plant). Our results are encouraging, the four *Trichogramma* species are viable biocontrol candidates for *S. frugiperda*.

Classical biological control of fall armyworm: should we choose the most efficient parasitoid or the safest?

Marc Kenis[1]

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Classical biological control (CBC) is one of the options considered for the management of fall armyworm (FAW) (*Spodoptera frugiperda*) in invaded regions. Several parasitoid species attack FAW in its native range and could be introduced into Africa, Asia and Oceania. Nowadays, the two most important criteria for the selection of natural enemies in CBC programmes are their efficiency and their specificity for the target pest. In the Americas, the most frequent and abundant parasitoid of FAW is the egg-larval braconid parasitoid *Chelonus insularis*. However, it is an oligophagous species known to parasitize several other species of Lepidoptera. Furthermore, other *Chelonus* species in Africa and Asia have adopted this new host. Among the other common parasitoids of FAW in the Americas, the ichneumonid larval parasitoid *Eiphosoma laphygmae* is probably the most specific one. There are only two doubtful records on other hosts and recent laboratory tests have confirmed its specificity for FAW. We hope that the presentation will generate a discussion on whether the risk of non-target effects related to the release of an oligophagous parasitoid against FAW is acceptable, given the importance of the target pest, or whether we should focus only on specific parasitoid species presenting a very low risk for non-target species.

Steps to develop an effective nematode-based biological control solution for the fall armyworm

Patrick Fallet[1,2], Didace Bazagwira[3], Lara De Gianni[1], Julie Guenat[4], Joelle Kajuga[3], Ishimwe Primitive Mukundwa[3], Bancy Waweru[3], Carlos Segura Bustos[1], Ted C.J. Turlings[1] & Stefan Toepfer[2,5]

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The fall armyworm (FAW), *Spodoptera frugiperda* (Lepidoptera: Noctuidae), is an important pest of maize originating from the Americas. It recently invaded Africa and Asia, where it causes severe yield losses. To fight this pest, tremendous quantities of insecticides are being used. As a safe alternative, we explore the possibility to control FAW with entomopathogenic nematodes (EPN). First, we tested in the laboratory whether EPN isolated from the invasive range of FAW can be as virulent on FAW larvae as EPNs from FAW`s native range or as commercial EPN. Among 40 tested EPN strains, representing 12 species, some EPN isolated from Rwanda were found to be as effective as commercial EPN or EPN from Mexico. At only 125 EPN per larva, the Rwandan *Steinernema carpocapsae* RW14-G-R3a-2 caused rapid 100% mortality of second- and third-instar and close to 75% of sixth-instars. Virulence varied greatly among EPN strains, underlining the importance of thorough screening (Fallet et al., 2022. *Insects*, 13). Secondly, we tested in laboratory eight different formulations to apply EPN into the whorl of maize where the larvae mostly feed. Treating maize plants with only 3000 EPN in a carboxymethyl cellulose (CMC) gel formulation caused 100% mortality of larvae and prevented plant damage considerably. EPN applied in water or in a surfactant-polymer-formulation (SPF) caused 72% and 94% mortality. Thirdly, we tested the use of EPN against FAW under field conditions. One-time treatments with EPN applied in water, SPF or CMC gel were all able to prevent heavy plant damage; but only the EPN-gel formulation reduced FAW infestation to a similar extend as a standard dose of cypermethrin (Fallet et al. 2022 *BioRxiv*). Fourth, we currently study whether repeated applications may be needed to reduce re-infestations by FAW across a cropping season depending on local maize phenology and pest dynamics. Up to now, findings clearly demonstrate that EPN are excellent candidates for the biological control of FAW and are a safe alternative to chemical insecticides.

Perspectives for sustainable management of fall armyworm in Africa

Lakpo Koku Agboyi[1], Dirk Babendreier[2] & Marc Kenis[2]

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The fall armyworm (FAW), *Spodoptera frugiperda* (Smith), has become one of the major threats to maize production in Africa. To achieve sustainable management of FAW, research was carried out in Ghana, focusing on biological control based on locally-occurring parasitoids. Over 12 parasitoids of FAW were identified in Ghana including two major larval parasitoids, *Coccygidium luteum* (Brullé) and *Chelonus bifoveolatus* Szépligeti and one major egg parasitoid, *Telenomus remus* Dixon. On-station trials with *T. remus* against FAW showed similar parasitism rate compared to non-release fields located between 150-400 m round, indicating a high dispersal potential of this parasitoid in a short time. Studies on *Coccygidium luteum* indicated that it can provoke 89% mean reduction of maize leaves consumption in parasitized FAW larvae. Additional field experiments conducted in Ghana showed that some products based on azadirachtin, *Bacillus thuringiensis* and maltodextrin were effective against FAW, without significantly affecting the parasitism rate displayed by the principal parasitoids occurring in the field. These results open a way for developing effective IPM strategies against FAW, based on biocontrol agents and bioinsecticides compatible with locally occurring parasitoids.

Invasion of *Spodoptera frugiperda* into Korea and identification of entomopathogenic fungus *Metarhizium rileyi* as a potential biological control agent

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The fall armyworm (FAW), *Spodoptera frugiperda,* is one of the important invasive pest species in Africa and Asia. Since 2019 FAW has invaded Korea and damaged many corn fields over the country. Molecular diagnosis using nucleotide sequences of *triose phosphate isomerase* (*Tpi*) gene indicated that at least three genetic groups (Tpi-Ca1, Tpi-Ca2a, and Tpi-Ca1/Ca2) were invaded Korea. Natural enemies of FAW were surveyed in the cornfields of Yeoncheon Country, Korea in August 2021. One of the major control agents of larvae was the entomopathogenic fungus *Metarhizium rileyi*. We isolated its Korean strain and identified morphological and molecular characteristics. The Korean strain was highly pathogenic to FAW larvae causing 89% mortality after 7 days post-treatment. Manufactured products of *M. rileyi* can be used for biological control of FAW in the fields.

Managing fall armyworm in Africa: can *Bt* maize sustainably improve control?

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The recent invasion of Africa by fall armyworm (FAW), *Spodoptera frugiperda*, a lepidopteran pest of maize and other crops, has heightened concerns about food security for millions of smallholder farmers. Maize genetically engineered to produce insecticidal proteins from the bacterium *Bacillus thuringiensis* (*Bt*) is a potentially useful tool for controlling FAW and other lepidopteran pests of maize in Africa. In the Americas, however, FAW rapidly evolved practical resistance to maize producing one *Bt* toxin (Cry1Ab or Cry1Fa). Also, aside from South Africa, *Bt* maize has not been approved for cultivation in Africa, where stakeholders in each nation will make decisions about its deployment. Here we address strategies to make *Bt* maize more sustainable and accessible to smallholders in Africa. We recommend mandated refuges of non-*Bt* maize or other non-*Bt* host plants of at least 50% of total maize hectares for single-toxin *Bt* maize and 20% for *Bt* maize producing two or more distinct toxins that are each highly effective against FAW. The smallholder practices of planting more than one maize cultivar and intercropping maize with other FAW host plants could facilitate compliance. We also propose creating and providing smallholder farmers access to *Bt* maize that produces four distinct *Bt* toxins encoded by linked genes in a single transgene cassette. Using this novel *Bt* maize as one component of integrated pest management could sustainably improve control of lepidopteran pests including FAW.

DNA-based screening and mechanisms of resistance to *Bt* corn in fall armyworm and corn earworm

Juan Luis Jurat-Fuentes[1]

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Larvae of the corn earworm (*Helicoverpa zea*) and fall armyworm (*Spodoptera frugiperda*) are relevant pests of corn and other crops in the Western Hemisphere, yet the fall armyworm is quickly expanding its range and becoming a global super pest threatening corn production. In their native range, larvae of fall armyworm and corn earworm have been controlled using transgenic corn producing insecticidal proteins (IPs) from *Bacillus thuringiensis* (*Bt*). However, the evolution of practical resistance threatens sustainable use of IPs and *Bt* corn in controlling these pests. Together with collaborators, our research team is focused on advancing novel control technologies for armyworm and earworm and the use of DNA-based tools in screening for resistance to IPs produced in *Bt* corn. This presentation will include an update of our activities, implications of available data, and emerging opportunities for control of fall armyworm and corn earworm populations.

Inheritance and fitness costs of Vip3Aa19 resistance in *Mythimna separata*

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The "high-dose/refuge" strategy is expected to work most effectively when resistance is functionally recessive and the fitness costs are present. In the present study, a laboratory selected *Mythimna separata* strain that have evolved >634.5-fold resistance to Vip3Aa19 was used to determine the mode of inheritance. Besides, the fitness costs associated with the resistance were also characterized among resistant (RR), -susceptible (SS) and -heterozygous (R♂S♀ and R♀S♂) strains on nontoxic diet. The LC_{50} values of R♀S♂ was significantly higher than that of R♂S♀ (254.58 µg/g vs 14.75 µg/g), suggesting that maternal effects and sex linkage were present. The effective dominance h of F_1 offspring decreased as concentration increased, suggesting the resistance was functionally dominant at low concentration and recessive at high concentration. The analysis of observed and expected mortality of the progeny from a backcross suggested that more than one locus is involved in conferring Vip3Aa19 resistance. No significant differences were observed among the four insect genotypes with few exceptions. In short, resistance to Vip3Aa19 in *M. separata* was inherited as maternal and multigene. And the resistance in the strain was not associated with significant fitness costs. The results described here provide useful information for understanding resistance evolution and for developing resistance management strategies.

Genotypic variation in field-grown maize eliminates trade-offs between resistance, tolerance and growth in response to high pressure from the Asian corn borer

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Plant constitutive resistance, induced resistance, and tolerance are assumed to be alternative strategies, and are often accompanied by growth reduction. How maize coordinates the interactions between three types of defenses and growth in the field is fundamental knowledge for maize breeding. Field experiments with inbred maize lines, five resistant to and five susceptible to Asian corn borer (ACB), combined with larvae bioassays and analysis of agronomic traits, defensive chemicals, nutritional compounds, plant hormone, and gene expression were used to test whether and how these defenses and growth result in trade-offs. We found a trade-off between maize constitutive resistance and induced resistance to ACB, which is related to levels of benzoxazinoids, but not jasmonates. Moreover, maize resistance and tolerance to ACB were not correlated, and neither of them showed correlation with growth. The genotype-specific variation in metabolites and gene expression resulted in the absence of trade-offs between resistance, tolerance, and growth. These results provide evidence that we could simultaneously breed maize with higher defenses and better yield in the complex field conditions.

Four genes underlie voltinism and sex pheromone use in the ECB moth

Erik Dopman[1]

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Understanding the genetic basis for voltinism and sex pheromone use in pests is important because details about when and how insects breed can influence the size, frequency, and geographic distribution of outbreaks. In my talk I will describe recent results that identify four genes that underlie this trait diversity in the ECB moth.

Impact of maize seed mixtures on *Helicoverpa zea* (Lepidoptera: Noctuidae) phenotype and genotype

Pezinni Daniela Pezzini[1], Dominic Reisig[1], David Buntin[2], Megan Fritz[3], Francis Reay-Jones[4] & Katherine Taylor[3]

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[4]*Clemson University, Florence, South Carolina, USA*

Most successful insecticide resistance management approaches rely on refuges to provide a source of insects to mate with insects that have been exposed to an insecticide. In the southern United States, due to biological constraints and the lack of refuge adoption, species have evolved *Bt* resistance. One way to increase refuge is to mix *Bt* and non-*Bt* maize seed in the bag prior to planting. However, ear-feeding insects can be exposed to sub-lethal levels of *Bt* when plants cross pollinate, potentially accelerating the rate of resistance relative to block refuges (the differential survival hypothesis). Our study focused on analyzing *Helicoverpa zea* survival and their phenotype (pupal depth, weight, sex, adult eclosion time, and flight distance) from block and seed mixture *Bt* maize in the field. We linked the phenotype to the genotype from survivors of interest (those that flew after developing on maize expressing Cry1Ab + Cry1F + Vip3Aa20 in a seed mixture, compared to those using non-*Bt* maize as a host) using whole genome sequencing. While there were major impacts on survival in the seed mixture, the most consistant impacted phenotype in response to *Bt* exposure was reduced pupal weight. However, results of discriminant analysis of principal components and FST distances showed several genomic regions that have undergone statistically divergence of alleles, providing strong evidence for the differential survival hypothesis. Our future analysis will focus on trying to link regions of genotypic deviation to loci associated with resistance.

Integrating automated pest trapping and population dynamics modelling for optimising the timing of cotton bollworm control options

<u>Anna Bereczki</u>[1,2] & Mark Szalai[1]

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Data-driven plant protection is crucial to prevent yield losses caused by insect pests, as well as optimise the pesticide use and therefore make agriculture more sustainable. This is particularly true for controlling cotton bollworm (*Helicoverpa armigera* Hübner, CBW; Lepidoptera: Noctuidae), the worldwide pest being responsible for serious damage in several crops, including maize, because its population continuously spreads further to new areas and is affected by climate change, i.e. the proper timing of possible control options is becoming more challenging. Traditional pheromone traps are precise and widely used tools for monitoring CBW population, however, data collection with them is time consuming and labour intensive. Therefore, we integrated automated smart trapping with population dynamics models to provide sufficient information about adult population levels in close real-time. The model simulates the adult population in daily time steps and it is based on weather data as growing degree day thresholds drive changes between life cycle stages. Automated pheromone trapping data enables us to refine our model during the season with daily information, i.e. adjust model parameters with current CBW adult captures and local weather data directly from the investigated fields. The number of adults was determined using machine learning driven image recognition. Our research can contribute to data-based plant protection decisions on CBW control and management by providing sufficient information on pest pressure.

Contribution of larvae developing on corn and dry beans to the adult population of western bean cutworm in Michigan

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The western bean cutworm, *Striacosta albicosta* (Smith) (Lepidoptera: Noctuidae), is historically a pest of both corn (*Zea mays* L. (Poales: Poaceae)) and dry beans (*Phaseolus* sp. L. (Fabales: Fabaceae)) in the western Great Plains. However, it has recently undergone an eastward range expansion establishing itself across the Corn Belt in 25 states and 4 Canadian provinces. To mitigate the effects of infestation in Michigan, foliar insecticides are used in dry beans, whereas management of the pest in corn relies more heavily on the use of *Bt*-expressing hybrids. In this study stable carbon isotope analysis was used to determine what crop adult moths developed on as larvae with analysis showing that very few of the adult moths developed on dry beans. These results suggest that beans and corn are not suitable as co-refuges and that mainly adults which developed on corn are contributing to the next generation of western bean cutworm in Michigan.

The USDA-ARS Ag100Pest Initiative: developing chromosome-level genome assemblies for corn pest insects

Brad S. Coates[1], Amanda R. Stahlke[2], Sheina B. Sim[3], Scott M. Geib[3], O.P. Perera[4], Brian Scheffler[4], Kevin J. Hackett[1], Anna K. Childers[1] & Marcé D. Lorenzen[5]

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The United States Department of Agriculture Agricultural Research Service (USDA-ARS) Ag100Pest Initiative is generating high-quality reference genome assemblies for the "top 100" arthropod pests of agricultural significance in the United States; https://scinet.usda.gov/working-groups/ag100pest. The corn pest species currently being sequenced include: the corn earworm, *Helicoverpa zea*; western bean cutworm, *Striacosta albicosta*; ecotypes of the European corn borer, *Ostrinia nubilalis*; southwestern corn borer, *Diatraea grandiosella*, corn plant hopper, *Peregrinus maidis*; corn silk flies, *Euxesta* sp.; and the corn rootworms, *Diabrotica barbari*, *D. undecimpunctata,* and *D. virgifera virgifera*. Assemblies for *H. zea* and *P. maidis* are complete and at chromosome-level using assembly of continuous long read (CLR) or circular consensus sequence (CCS) read data, and high-throughput chromosome conformation capture (Hi-C) scaffolding. The 375.2 Mbp *H. zea* assembly was made from a single male pupa from a *Bacillus thuringiensis* (*Bt*) Cry1AcR resistant strain, and comprised of 30 autosomes and the Z sex chromosome that ranged from 7.2 to 18.8 Mb. The 759.6 Mbp *P. maidis* genome is scaffolded onto 15 chromosomes that are 16.6 to 88.9 Mbp. A new *D. v. virgifera* genome assembly is underway in the Ag100Pest Initiative, which contains 2,178 contigs with a median size (N50) of 1.3 Mbp and maximum length of 25.7 Mbp have been assembled. Hi-C scaffolding of *D. v. virgifera* contigs may improve the assembly to near chromosome scale. These and future genomes will be resources for investigating variation and population dynamics that contribute to the evolution of resistance to control tactics, and may contribute to efforts to develop sustainable insect resistance management and integrated pest management strategies.

Genome size evolution in the beetle genus *Diabrotica*

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Diabrocite corn rootworms are one of the most economically significant pests of maize in the United States and Europe and an emerging model for insect-plant interactions. Genome sizes of several species in the genus *Diabrotica* were estimated using flow cytometry along with that of *Acalymma vittatum* as an outgroup. Genome sizes ranged between 1.56 and 1.64 gigabase pairs and between 2.26 and 2.59 Gb, respectively, for the *Diabrotica* subgroups fucata and virgifera; the *Acalymma vittatum* genome size was around 1.65 Gb. This result indicated that a substantial increase in genome size occurred in the ancestor of the virgifera group. Further analysis of the fucata group and the virgifera group genome sequencing reads indicated that the genome size difference between the *Diabrotica* subgroups could be attributed to a higher content of transposable elements, mostly miniature inverted-transposable elements and gypsy-like long terminal repeat retroelements.

Western corn rootworm (*Diabrotica virgifera virgifera* LeConte) resistance to *Bacillus thuringiensis* is linked to altered bacterial community

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Management of western corn rootworm (WCR) is complicated by the insect's ability to evolve resistance to control tactics. Resistance to transgenic crops expressing toxins derived from *Bacillus thuringiensis* (*Bt*) can develop quickly and threatens the sustainability of the technology. Previous studies have shown the microbiota is crucial for susceptibility to *Bt* in Lepidopteran species. Thus, we hypothesized that resistance to *Bt* would alter the microbiome composition of the WCR In our study, we characterized the associated bacterial communities of *Bt*-resistant and -susceptible WCR using 16S rRNA sequencing. We found resistant insects harbor a bacterial community that is less rich and distinct from susceptible insects. After feeding on *Bt*-expressing corn, susceptible insects exhibited dysbiosis of the microbiome, whereas the microbial community of resistant insects remained relatively unchanged. These results suggest resistance to *Bt* produces alterations in the microbiome of WCR that may contribute to resistance. We further demonstrate that by itself, feeding on *Bt*-toxin expressing seedlings caused a shift in the microbiota. Improving our understanding of what factors affect the WCR microbiome is important to developing management practices that help control this damaging pest.

Intersections between chemicals and biopesticides: seed coatings may obstruct resistance management plan for GMOs targeting western corn rootworm (*Diabrotica virgifera virgifera* LeConte)

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Nearly all maize seed (79-100%) in the United States (U.S.) includes a neonicotinoid seed treatment (NST) that is meant to provide insurance against sporadic, early-season insect pests. For key pests like the western corn rootworm (*Diabrotica virgifera virgifera* LeConte) (WCR), insecticidal proteins derived from a naturally-occurring soil bacterium, *Bacillus thuringiensis* (*Bt*), are expressed in plant tissues as an alternative to soil-applied insecticides. Maize expressing *Bt* proteins (i.e. *Bt* maize) is safe for applicators and non-target animals, and has dramatically reduced insecticide use for WCR and other pests. In response, the U.S. Environmental Protection Agency declared *Bt* technology a "public good" that should be preserved, and has since mandated the use of insect resistance management (IRM) strategies to prevent insect resistance, which poses the greatest threat to *Bt* technology. Current IRM strategies rely on non-*Bt* "refuge" plants, which are mixed with *Bt* plants at specified proportions (e.g. 5%). In theory, refuge plants allow enough *Bt*-susceptible insects to survive to overwhelm resistant phenotypes, prolonging the effectiveness of *Bt* traits. We know current refuge strategies are insufficient for WCR: instances of field-evolved resistance to all currently-available *Bt* traits have been documented, and others have shown that refuge plants produce small proportions of beetles relative to *Bt* plants. To make IRM worthwhile, it is necessary to determine why non-*Bt* refuges are failing to produce larger proportions of WCR. We conducted three years of field trials in two regions to test whether NSTs are interfering with beetle survival on refuge plants. While our results show that NSTs could affect refuge beetle proportions, likely depending on planting date, our principle finding was that refuge beetle proportions were extremely small, even in the absence of NSTs. We propose that IRM could be improved by increasing refuge size requirements in U.S. maize.

Nairobi, Kenya to host the 28th International Working Group on *Ostrinia* and other Maize Pests (IWGO) Conference, 2023

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The IWGO has been meeting since 1968, with the 27th Conference taking place in Switzerland in 2019. The city of Nairobi, Kenya, now welcomes all delegates to attend the 28th IWGO Conference in 2023. This would be the first time that the conference would be held in Africa since its inception and demonstrates this is a truly global event. Kenya hosts numerous centres of research excellence undertaking biological control which provides opportunities to showcase the excellent research being undertaken on the continent. Importantly, holding the event in Kenya would increase representation by African based scientists to IWGO at different career stages. Nairobi is a major airline destination hub in Africa with over 11 million passengers/year and has excellent infrastructure within the city to move around. The city also boasts of high-end hospitality facilities comprising 7,000+ hotel rooms, in 3 to 5-star graded categories with negotiated corporate rates for groups such as IWGO. Kenya offers easy visa applications to visitors such as e-visas or visas on arrival. With a warm tropical climate most of the year, and English speaking, warm, hospitable and peaceful people, Kenya is listed among the top 80 travel destinations worldwide. The proposed venue of the conference shall be Kenya's centre of phytosanitary excellence hosted at the headquarters of the Kenya Plant Health Inspectorate Service (KEPHIS), a quiet hub at Karen on the outskirts of Nairobi. KEPHIS is the regulator of biological control in Kenya and offers visitors a tour of their facilities for sharing lessons. Before and after the conference, delegates are invited to indulge in the exquisite dining facilities available around the city, offering a variety of multicultural cuisines. All the "big five" that wildlife has to offer can be found in Kenya and we encourage delegates to plan to take some time off to bask on the white sand beaches of Mombasa. Nairobi, Kenya welcomes you for IWGO 2023.

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