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Genetic and developmental basis of ovipositor sensory diversity in D. suzukii

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Unlike most *Drosophila* species, the spotted wing drosophila (*D. suzukii*) possesses the remarkable ability to pierce the skin of ripening fruits. Whereas related species typically oviposit in soft, decaying substrates, *D. suzukii* has evolved both a preference for firmer fruits and an enlarged, morphologically specialized ovipositor adapted to this ecological niche. Consistent with this diversification, the ovipositor exhibits substantial interspecific variation not only in size and trichome patterning but also in the number, density, and spatial arrangement of its sensory organs. These sensory structures have undergone pronounced evolutionary transitions that contrast sharply with the relative morphological conservation observed in thoracic and leg sensilla.

Despite limited knowledge about ovipositor sensory organ development, the overall cellular architecture of the ovipositor is largely conserved among *Drosophila* species. This suggests that the observed sensory diversification is not merely a byproduct of general tissue expansion but reflects targeted evolutionary modification.

To investigate the molecular basis of these adaptations and the emergence of *D. suzukii* as an agricultural pest, we conducted comparative transcriptomic analyses of developing genital tissues across closely related *Drosophila* species. Differentially expressed genes in *D. suzukii* were functionally tested through tissue-specific RNAi knockdown in *D. melanogaster*, revealing several promising candidates implicated in sensory organ development. Ongoing work integrates bioinformatic and developmental approaches to further characterize the genetic and cellular mechanisms underlying this evolutionary innovation.

Keywords: D. suzukii, female genitalia, ovipositor, sense organs

*Speaker

The Natural History of D. melanogaster in its Ancestral Range

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Here we give a brief description of our ongoing field work on aspects of the natural history and evolutionary ecology of the vinegar fly (Drosophila melanogaster) in its ancestral native range, i.e. in the Mopane and Miombo woodlands of southern central Africa.

Keywords: Drosophila melanogaster, natural history, evolutionary ecology, ancestral range, southern central Africa, wilderness habitats

*Speaker

Characterizing the cold acclimated phenotypes in Drosophila suzukii: from bioenergetics to multi-Omics

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The spotted wing drosophila, Drosophila suzukii, is an invasive fruit pest that, like many other species, can enhance its cold tolerance in response to various forms of cold acclimation. However, little is known about the underlying mechanisms of cold acclimation. Here we conducted various experiments to characterize cold acclimation responses and decipher their physiological correlates. We found that various forms of developmental acclimation (in both lab and field) promoted cold survival much strongly than acclimation at adult stage. Next we focused on cold-hardy flies, acclimated during development, and we compared their mitochondrial properties, mitochondrial proteome and metabolome with cold susceptible control flies. At low temperature, coupling between complex I electron transport and the phosphorylation process remained tight in cold acclimated flies, whereas it decreased drastically in control. Mitochondrial respiration in the presence of succinate or G3P increased significantly in control flies compared to cold acclimated flies at low temperatures. Measures of enzymes activities between both phenotypes (at both 20 and 10 ∘C) revealed strong differences in CS, PDH, G3PDH. The proteomic comparison of cold acclimated vs. control flies, using isolated mitochondria, showed substantial quantitative changes in the mito-proteome, with 288 and 56 proteins being up- and down-regulated respectively in the cold acclimated phenotype, including proteins involved in the organization and assembly of mitochondrial complexes (e.g. complexes I and III or ATP synthetase) as well as in mitochondrial enzymatic reactions. Collectively, these data show that mitochondria is a moldable system that likely underlies a part of cold adaptation. Finally, both target GC-MS and explorative GC-HRMS metabolomics showed that all flies acclimated under various cold conditions had markedly different metabolome than controls, with typical cryoprotectants being accumulated. Together, these data suggest a deep remodeling of metabolome during cold acclimation.

Keywords: winter phenotype, cold performance, mitochondria

*Speaker

Locus-specific, polymorphic transposable element expression in somatic tissues across Drosophila natural strains

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N/A

Keywords: Transposable elements, polymorphism, drosophila melanogaster, somatic tissue

*Speaker

Seasonal wing size variation in three Drosophila species in the tropics

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Seasonal wing size variation in three Drosophila species in the tropics

Keywords: ecology, phenotypic variation, temporal

*Speaker

Drosophila suzukii in Morocco: Population Dynamics and IPM Tactics in Raspberry Orchards

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Drosophila suzukii Matsumura (Diptera: Drosophilidae), is an invasive pest causing substantial economic losses in soft fruit production worldwide. In Morocco, infestations in raspberry orchards are increasingly threatening the competitiveness of the export sector, especially under stricter regulations limiting chemical pesticide use. This study aimed to support sustainable management by integrating field monitoring, laboratory biological assays, and sterile insect technique (SIT) evaluations into a comprehensive IPM program for *D. suzukii* in Morocco. Population dynamics were monitored weekly in raspberry cultivars using banana–yeast baited traps until the end of May. Infestation levels were consistently higher in the Yazmin cultivar, which exhibited three annual peaks of *D. suzukii* adult flies, while a total of six generations were predicted based on accumulated degree-days. SIT trials were conducted using cobalt-60 irradiation facility at INRA-Tangier. Reciprocal crosses at 180–210 Gy showed complete sterility in irradiated females, while males retained partial fertility, particularly at intermediate doses. Entomopathogenic fungi isolated from naturally infected individuals included several virulent strains. Isolate "L19" induced 100% adult mortality within five days. Laboratory assays confirmed high pathogenicity at 10–10 conidia/mL, with irradiated flies showing even greater susceptibility. Under greenhouse conditions and during field trials in Larache, a 0.02% fresh orange (*Citrus sinensis*) zest essential-oil formulation captured twice as many females as the control.This study provides the first integrated assessment of *D. suzukii* population dynamics in Moroccan raspberry systems and demonstrates the potential of biological control agents, attractant-based trapping, and SIT. These combined approaches offer promising components of an eco-friendly IPM strategy capable of reducing pesticide reliance and strengthening the resilience of Morocco's berry export sector.

Keywords: Degree day modelling, Sterile insect technique, Entomopathogenic fungi, Attractant based trapping, Integrated pest management

*Speaker

Synthetic Biology Platforms to Accelerate Functional Genomics and Genetic Control in Drosophila suzukii

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Drosophila suzukii has emerged as a key model for studying genome evolution, developmental genetics, and sex-determination mechanisms within the genus *Drosophila*, while simultaneously posing major challenges as an invasive agricultural pest. To advance functional genomics and genetic control such as the sterile insect technique (SIT) in this species, we have developed and optimized a suite of synthetic biology tools that enable precise genome engineering, conditional gene expression, and scalable phenotypic analyses.

Our recent reviews synthesised the state of the field, covering transposon-mediated germline transformation, recombinase-based genome targeting, and CRISPR-driven gene editing, as well as genetic control strategies including sperm-marking strains, sex-ratio distortion, neoclassical genetic sexing strains, transgenic sexing strains, a sex-sorting incompatible male system, precision-guided sterile insect technique, and gene drives based on synthetic Maternal effect dominant embryonic arrest (Medea) or homing CRISPR systems. Meanwhile, we developed two molecular conditional systems that facilitate the transition of engineered lines from laboratory proof-of-concept to potential field applicability. A temperature-inducible CRISPR system achieved up to 95.4% somatic mutation and 100% inheritance of induced mutations, while a tetracycline-repressible system produced 100% female elimination at the embryonic stage under restrictive conditions.

To support reproducible, community-wide application, we standardised and distributed experimental pipelines including an optimized microinjection workflow for high-efficiency embryo transformation and a non-lethal genotyping approachfor transgene and mutation detection. Collectively, these molecular platforms expand the genetic toolkit available for *D. suzukii*, enabling more sophisticated elucidation of gene function, regulatory networks, and reproductive biology, while providing a robust foundation for future synthetic-genomic interventions aligned with area-wide integrated pest management frameworks for this invasive species.

Keywords: functional genomics, genome engineering, CRISPR, conditional system, sex determina-

*Speaker

tion, genetic control

Evolution of genetic constraints on wing shape during D. suzukii's worldwide invasion

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The extent to which phenotypic evolution can be constrained by genetic correlations is an important question in evolutionary biology. To address this question, biological invasions are opportune models where derived, invasive populations can be compared to their extant ancestors, allowing to track the evolution of genetic correlations from the ancestor, throughout the invasion process. In this paper, we focused on the worldwide invasion of Drosophila suzukii (Matsumara, 1931), and investigated the evolution of the genetic covariance matrix G from wing shape measured in ancestral native, and derived invasive populations. Leveraging invasion history resolved by population genetics approaches, we tested how G evolved throughout potential periods of drift and selection and whether G remained stable during the invasion. Using a multivariate QST-FST approach, we further tested whether the observed phenotypic divergence in wing shape is greater than expected under a neutral scenario of evolution. Our results show moderate yet significant quantitative genetic differentiation of wing shape among D. suzukii populations and a relative stability in the structure of G, presenting a roughly spherical shape but slightly different volumes. These characteristics likely reflect the demographic history of populations and suggest a low level of genetic constraint on adaptive evolution. The divergence among populations was greater than expected under a purely neutral model of evolution, compatible with an effect of selection on wing shape. Overall, our study suggests that selection, drift but not ancestral genetic constraints affected the early stages of wing shape evolution during D. suzukii invasion.

Keywords: Drosophila suzukii, G, matrix, geometric morphometrics, biological invasion, quantitative genetics, QST, FST

*Speaker

Transposable elements modulate gene expression in response to oxidative stress in D. suzukii

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Transposable elements (TEs) are repetitive DNA sequences that can influence gene regulation and sometimes contribute to adaptive variation. In the invasive fruit fly *Drosophila suzukii*, TEs comprise nearly half of the genome (47%), yet their functional contribution to stress responses remains largely unexplored. Here, we investigated two polymorphic intronic TE insertions, Mrp4-TE and inaE-TE, located within genes involved in oxidative stress responses. We characterized these insertions across natural populations and assessed their impact on gene expression after paraquat-induced oxidative stress. Our results show that both *Mrp4* and *inaE* genes exhibit increased expression following oxidative stress, particularly in populations carrying the TE insertions. Allele-specific expression analysis revealed that Mrp4-TE drives cis-regulatory changes, though it did not enhance paraquat resistance. These findings demonstrate that specific TE insertions can modulate gene expression in response to oxidative stress in *D. suzukii*, highlighting TEs as a source of regulatory variation with potential relevance for adaptation and invasion processes.

Keywords: Transposable elements, oxidative stress, gene regulation

*Speaker

Drosophila suzukii glue as a new model to understand adaptation

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At the end of the larval stage, Drosophila larvae produce a proteinaceous glue that allows the animal to adhere to a substrate for several days during metamorphosis. Our general aim is to use Drosophila glue as a model to explore the mechanisms of adaptation. We developed a new assay to quantify Drosophila glue adhesiveness and compared adhesion between different Drosophila species. We found that D. suzukii produces a little amount of glue compared to other species. Nevertheless, the adhesion conferred by this glue appears to be sufficient to protect D. suzukii pupae from ant predation. We will discuss what makes *D. suzukii* unique compared with other *Drosophila* species during the understudied period of metamorphosis.

Keywords: bioadhesion, pupa

*Speaker

Local and regional variation in parasitoid resistance and cellular immunity of Drosophila melanogaster across Europe.

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Parasitoid wasps are important drivers of insect population dynamics, yet how host immune traits are structured within and among populations remains poorly understood. To defend against its aggressor, Drosophila melanogaster relies mainly on cellular encapsulation, a hemocyte-mediated response. We used common-garden assays on isofemale lines from nine European sites to measure parasitoid resistance and encapsulation ability against Leptopilina boulardi alongside hemocyte counts and phenoloxidase activity. We found that resistance and encapsulation ability varied strongly among lines within sites but showed little variation between sites. In contrast, hemocyte profiles differed significantly between sites, suggesting local selective pressures on immune cell composition. Intraspecific variation indicates that other factors, additional species of parasitoid or competitors, may drive different evolutive strategies at the local scale. Our findings show that immune traits evolve at different spatial scales, emphasizing the need for multi-level sampling to understand coevolution and to predict ecological outcomes of parasitoid pressure.

Keywords: Experimental evolution, selective pressures, evolutionary dynamics

*Speaker

Host–transposable element coexistence: Distinct ecological niches exploited by endogenous retroviruses

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Endogenous retroviruses (ERVs) represent a class of transposable elements (TEs) that remain active in genomes. Despite sharing replication mechanisms, ERVs occupy distinct cellular and developmental niches, partitioning their life cycles across different expression and integration domains. Using molecular approaches, we explore how ERVs uncouple transcription and integration to ensure efficient vertical transmission while minimizing host damage. In *Drosophila melanogaster*, infectious ERVs expressing an *env* gene are transcribed in somatic cells surrounding germ cells, but integrate within the germline. Moreover, ERVs differ in their developmental "insertion windows"-some integrate early in embryogenesis, while others target primordial germ cells. These strategies highlight the ecological diversification of ERVs, where spatial and temporal decoupling enables coexistence with the host by restricting deleterious steps to transient lineages. Altogether, these findings refine our understanding of TE–host coevolution by showing how active ERVs partition biological space to persist within host genomes.

Keywords: drosophila melanogaster, transposable elements, endogenous retrovirus, epression, integration

*Speaker

Genetic diversity of Drosophila in urban populations

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Keywords: ..

*Speaker

Genomic prediction of population level categorical traits: application to the host fruit of origin of Drosophila suzukii population samples

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Local adaptation is a process whereby populations develop characteristics that improve their fitness in their environment. This study explores the ability of supervised classification methods to predict the host fruit of Drosophila suzukii, a generalist pest that has rapidly invaded Europe and North America, and for which a pattern of local adaptation to fruit has been demonstrated by Olazcuaga et al. (2022). We analysed Pool-Seq data from 44 natural French populations, focusing on three economically significant fruits: blackberry, cherry and strawberry. First, we characterised the genetic structure of the populations and searched for genomic regions associated with the host fruit using C statistics-based genomic scans and related approaches. Second, we applied several supervised classification models (linear regression, random forest and neural networks) to link genomic profiles to host fruits. Although some alleles appear to be significantly associated with a given host fruit, these signals are not sufficient to reliably predict the fruit of origin from the genome. These results suggest that the genetic determinants of local adaptation to host fruit in D. suzukii are likely to be subtle, polygenic, or masked by complex selection dynamics.

Keywords: Local adaptation, Genomic prediction, Poolseq data

*Speaker

Genomic prediction of population level categorical traits: application to the host fruit of origin of Drosophila suzukii population samples

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Local adaptation is a process whereby populations develop characteristics that improve their fitness in their environment. This study explores the ability of supervised classification methods to predict the host fruit of Drosophila suzukii, a generalist pest that has rapidly invaded Europe and North America, and for which a pattern of local adaptation to fruit has been demonstrated by Olazcuaga et al. (2022). We analysed Pool-Seq data from 44 natural French populations, focusing on three economically significant fruits: blackberry, cherry and strawberry. First, we characterised the genetic structure of the populations and searched for genomic regions associated with the host fruit using C statistics-based genomic scans and related approaches. Second, we applied several supervised classification models (linear regression, random forest and neural networks) to link genomic profiles to host fruits. Although some alleles appear to be significantly associated with a given host fruit, these signals are not sufficient to reliably predict the fruit of origin from the genome. These results suggest that the genetic determinants of local adaptation to host fruit in D. suzukii are likely to be subtle, polygenic, or masked by complex selection dynamics.

Keywords: Local adaptation, Genomic prediction, Poolseq data

*Speaker

Role of detoxification in xenobiotic adaptation in Drosophila suzukii, the spotted wing

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Drosophila suzukii is an invasive drosophilid pest that attacks ripening, healthy fruits and has become a major pest of soft fruit crops worldwide. As a polyphagous species, *D. suzukii* is exposed to a wide diversity of plant defence compounds and synthetic insecticides, which creates a complex xenobiotic environment. In insects, xenobiotic detoxification is classically described as three phases: phase I functionalisation (cytochrome P450 monooxygenases, carboxylesterases), phase II conjugation (glutathione S-transferases, UDP-glycosyltransferases) and phase III excretion (ATP-binding cassette transporters). In this study, we specifically focus on phase I and phase II to investigate their contribution to the adaptation of *D. suzukii* to this chemically heterogeneous environment.

Our objectives are (i) to clarify the role of detoxification metabolism in xenobiotic adaptation of *D. suzukii*, with a particular focus on host-plant defence compounds; (ii) to determine whether adaptation to host plants can also confer pre-adaptation to chemical insecticides; (iii) to evaluate whether field populations have already evolved insecticide resistance. To address these objectives, flies were maintained for 48 h on fruit puree media differing in suitability (cherry, blueberry and grape), then toxicological tests and detoxification enzyme activities were performed, together with the expression of selected detoxification genes. Compared with the flies fed on standard cornmeal medium, flies reared on cherry, blueberry or grape puree exhibited increased tolerance to spinosad and lambda-cyhalothrin, consistent with differences in host secondary-metabolite profiles. For enzyme activity, there was no significant difference in glutathione S-transferases activity but a significant decrease in carboxylesterases activity. P450 activity showed a sex-specific pattern, with up-regulation in males and no significant change in females. Ongoing transcriptomic analyses will identify candidate detoxification genes across the three phases for subsequent functional validation.

This project aims to clarify how detoxification metabolism contributes to xenobiotic adaptation in *D. suzukii* and to provide basic information for insecticide resistance risk management.

Keywords: Drosophila suzukii, xenobiotic adaptation, detoxification metabolism

*Speaker

The role of endosymbionts in Drosophila host susceptibility to the trypanosomatid parasite

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Endosymbionts are well-known for protecting insect hosts from pathogens, however, their role in parasite defence remains understudied. Trypanosomatids are protozoan parasites highly prevalent in natural insect populations, including *Drosophila* species. We investigated two common *Drosophila* bacterial endosymbionts, *Spiroplasma* and *Wolbachia*, and their effects on *Jaenimonas drosophilae* trypanosomatid infection. The first study examined the fitness impacts of *Spiroplasma* in two *Drosophila* species, *Drosophila* melanogaster, where it causes male-killing, and *Drosophila* hydei, where this effect is absent, and assessed the endosymbiont effect on fecundity and longevity in both species. While *Spiroplasma* has a strong fitness effect on non-infected flies, there was no effect in the *J. drosophilae* infection treatment. However, we observed a different sensitivity to the parasite in the studied *Drosophila* species which suggests species-specific immune responses, potentially due to different evolutionary history. The *Wolbachia* study, using Drosophila Genetic Reference Panel lines, uncovered a weak but significant association between *Wolbachia* presence and trypanosomatid load. Further research into the underlying molecular mechanisms could elucidate the role of these endosymbionts in mediating infections in different *Drosophila* species. These findings can provide valuable insights into the evolution of insect-microbe interactions and potential implications for managing insect disease vector populations.

Keywords: host, parasite interactions, endosymbionts, Wolbachia, Spiroplasma

*Speaker

The genetic regulation of phenotypic variance across the Drosophila G-P map

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Keywords: Population Genomics, phenotypic noise, G, P maps, complex traits

*Speaker

Natural Selection and Invasiveness in Drosophila suzukii

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Understanding how natural selection acts on invasive species is not only a central goal in invasion biology, but also provides broader insights into how species adapt to rapid changes in their environment. Genomic analyses of Drosophila suzukii, an invasive Drosophilid of global agricultural importance, has found genetic variants associated with invasiveness. I aim to characterize if and how selection acts on invasiveness-associated variants in D. suzukii collected across the growing season. Using a dataset of individually-sequenced D. suzukii, I will determine the overlap between these variants and regions of the genome showing signatures of directional and balancing selection, and will characterize basic allelic properties such as allele age and linkage disequilibrium. To this end, a total of 70 wild adult D. suzukii were collected every _˜1-2 weeks in Vermont from July to November, then individually sequenced with whole-genome sequencing to _˜15x coverage. This analysis will provide an in-depth view of the genetic architecture of invasiveness in a cosmopolitan, seasonally-adaptive invasive Drosophilid, providing a resource for both evolutionary and management-based studies.

Keywords: Drosophila suzukii, seasonality, invasive species, invasiveness, natural selection

*Speaker

Divergence of Ejaculate Female Interactions Across Populations of Drosophila melanogaster

Emma Whittington * [1]

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How species are formed and maintained is a fundamental question. Classically, populations diverge in geographic isolation, such that populations are (at least partially) incompatible upon secondary contact. Within isolated populations, interacting traits coevolve. Specifically, elevated evolutionary rates suggest that coevolving traits that interact after mating (i.e. postmating) and before zygote formation (i.e. prezygotic) rapidly codiversify between the sexes. Consequently, these may contribute to incompatibilities and reproductive barriers in crosses between species or populations. To understand these barrier mechanisms, first we must characterise the players involved (i.e., male and female proteins that interact after mating) and second, ask how the genes encoding these proteins codiversify and evolve. In *Drosophila melanogaster*, previous work has characterised the genes encoding sperm, seminal fluid, and female reproductive fluid proteins, and I am utilising the DEST 2.0 database to assess patterns of evolutionary rate and divergence in reproductive genes across populations of *D. melanogaster.*

Keywords: reproductive islation, sexual selection, divergence

*Speaker

Interactions between ecology and sexual conflict across european D. melanogaster populations

R. Axel W. Wiberg * [1]

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NA

Keywords: sexual conflict, temperature

*Speaker

DESTv3 – Updates & Goals

Alan Bergland * [1], Martin Kapun [2], Joaquin Nunez [3], Mathieu Gautier [4]

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Continued advances in the scale of DNA sequencing have enabled the generation of vast quantities of population genomic data across the species range, through time, and across closely related species. Our goal is to integrate population genomic datasets for Drosophila flies using a robust and reproducible mapping and variant calling steps. DEST version 3.0 improves upon previous versions of DEST by (1) the ability to perform SNP calling simultaneously with Pool-Seq and individual sequencing, (2) the capacity to work with any species and mixtures of species, (3) improved containerization of the mapping and SNP calling steps. We have used the DESTv3 pipeline to generate population genomic datasets combining PoolSeq, individuals, and isofemale lines for multiple drosophila species. We compare these datasets with previous releases of DEST.

Keywords: DEST, Drosophila, bioinformatics

*Speaker

When larvae feed adult flies: unexpected facilitation between life-stages

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Although insects with complete metamorphosis usually exploit different ecological niches at different life-stages, the fate of larvae and adults can be tightly interlinked. Here, we show for the first time that the abundance of larvae determines the fitness of adults, in the pest fruit-fly *Drosophila suzukii*.
Our microcosm experiment revealed that the presence of strawberries infested with larvae, and their shear numbers, can increase both adult survival and female fecundity. By contrast, mimicking farmers' prophylaxis and removing infested berries diminished parasitic pressure by a three-fold factor. These effects are explained by the effect of larvae on yeast multiplication in fruit flesh, and the reliance of adult females on yeast for protein acquisition and ovogenesis.
The study hence demonstrates an unexpected ecological relationship between the life-stages of a same insect species, and reveals why prophylaxis is so efficient at protecting crops.

Keywords: prophylaxis, symbiosis, ontogenetic niche, shift

*Speaker

The molecular axis of endemism is governed by the opposing forces of purifying and balancing selection

Luke Proud * [1], Jingqi Liu [2], Julia Beets *

[3], Dylan Hyland [2], Emily K. Longman [1], Courtney Tern [2], Paul Schmidt [4], Thomas Flatt [5], Joaquin Nunez *

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Understanding the forces that shape genetic variation in nature is a central goal of evolutionary biology. The prevailing "Standard Model" of population genetics posits that genome-wide variation is governed primarily by mutation-selection balance, with genetic drift as the dominant force and adaptation occurring through rare selective sweeps. Under this framework, most standing variation is expected to be nearly neutral or deleterious, and adaptive change is viewed as "slow" and infrequent. However, recent large-scale genomic analyses challenge this view. Using the largest global dataset of wild *Drosophila melanogaster* assembled by the DrosEU consortium (i.e., DEST, https://dest.bio/), spanning samples collected across six continents and more than a decade, we analyzed over 21 million variants to test the spatial distribution of functional polymorphism. Consistent with the Standard model, non-synonymous mutations are abundant among mutations that are found in a limited number of populations (endemic). The abundance of endemic deleterious mutations among populations is negatively correlated with mean annual temperature, consistent with theoretical predictions that effective population size determines the strength of purifying selection. However, contrary to predictions from the Standard Model, the abundance of nonsynonymous mutations displays a noticeable uptick among the most cosmopolitan mutations. The enrichment of cosmopolitan nonsynonymous variants is associated with older allele ages, suggesting these mutations are not incomplete recent sweeps. Cosmopolitan variants explained more variance in complex traits than endemic ones across hundreds of phenotypes, and nonsynonymous cosmopolitan variants were less likely to be classified as harmful based on integrative functional scores. These variants were also more likely to be shared with

*Speaker

D. simulans and are enriched among immunity-related genes. We show using simulations that the enrichment of non-synonymous cosmopolitan SNPs can only be explained by models where balanced polymorphisms are common, rather than models relying solely on unconditional beneficial mutations sweeping across metapopulations. Together, these findings suggest that natural selection is pervasive across genomes in the wild and that the opposing action of purifying and balancing selection jointly contributes to the distribution of genetic variation across the species range.

Keywords: balancing selection, purifying selection, standard model, drosophila, population genetics

Interspecific larval interaction may mask the primary damage by Drosophila suzukii

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Several studies have shown that the proportion of *Drosophila suzukii* captured in traps in different orchards often does not match its proportion in fruit samples collected at the same site. This discrepancy may arise from multiple factors, for example, the characteristics of the host plant or interactions among drosophilid species. In our study conducted on grapes, we observed a striking pattern: *D. suzukii* represented a much higher proportion of the drosophilids emerging from individually isolated berries than from pooled berries taken from the same clusters, where melanogaster-type drosophilids (*D. melanogaster* and *D. simulans*) were overwhelmingly dominated. An obvious difference between the two sample types is that in the pooled samples, larvae from different berries could encounter one another, which may have influenced their survival. Our laboratory experiments conducted on artificial medium with controlled larval densities supported this interpretation. Both same-aged and younger *D. melanogaster* larvae were able to prevent the successful development of *D. suzukii* larvae. We attribute this effect to the predatory tendencies of *D. melanogaster* larvae. This phenomenon has an important practical implication: predation by melanogaster-type larvae, even when oviposited later, may mask the primary damage initially caused by *D. suzukii*.

Keywords: pest management, intraguild predation, grape, vineyard, SWD, melanogaster

*Speaker

Investigating Mating Dynamics and Polyandry in Drosophila suzukii: Integrating Behavioural Assays and Stable Isotopes

Gerardo Roselli * [1], Marco Valerio Rossi Stacconi [2], Rachele Nieri [1], Silvia Schmidt [3], Gianfranco Anfora [1]

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[2] Edmund Mach Foundation – Italy
[3] Laimburg Research Centre – Italy

The spotted wing drosophila (SWD), *Drosophila suzukii* (Matsumura) (Diptera: Drosophilidae), is an invasive insect pest that poses a serious threat to small and stone fruit production worldwide, causing substantial economic losses. Native to East Asia, it exhibits high ecological plasticity and adaptability to a wide range of environmental conditions, facilitating its rapid spread across Europe and North America following its introduction as an alien species. Conventional insecticide-based control strategies have proven costly and often ineffective, underscoring the need for more sustainable, environmentally friendly alternatives. In recent years, attention has increasingly focused on integrated pest management (IPM) approaches. Among these, the Sterile Insect Technique (SIT) and CRISPR-based genetic technologies, such as gene drive systems, have emerged as promising tools. Both strategies aim to suppress wild populations by releasing sterile males or males carrying heritable mutations that, by competing with wild males for mating opportunities, reduce fertility or offspring production in the target population. Consequently, in-depth knowledge of reproductive dynamics is essential for accurate modelling, optimisation, and planning of release programmes. While field conditions may influence the effectiveness observed in laboratory studies, they remain crucial for determining the biological parameters necessary for successful field implementation. In the present study, the mating behaviour of SWD, including mating propensity, latency time, copulation duration, and remating, was evaluated under varying oviposition substrates, light conditions, sex ratios and arena volumes. Polyandry was then investigated using stable isotopes (^{1}N and ^{13}C) for sperm labelling and its detection in spermathecae by mass spectrometry.

Keywords: remating, polyandry, behaviour

*Speaker

The temporal dynamics of a balanced inversion polymorphism

Harshavardhan Thyagarajan * [1]

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The selective maintenance of balanced inversion polymorphisms represents a classical puzzle in evolutionary genetics. Numerous inversion polymorphisms have been found to persist at intermediate frequencies and are thus thought to be maintained by strong selection. Yet, despite decades of study, the precise modes of balancing selection responsible for their persistence remain incompletely understood. A classical example is the cosmopolitan In(3R)Payne inversion polymorphism of Drosophila melanogaster. Previous work suggests that this long-term polymorphism is subject to strong spatially varying selection along latitudinal gradients on several continents, always being at intermediate frequencies in tropical or subtropical low-latitude areas but absent in cool high-latitude areas. As spatially varying (divergent) selection is expected to generate frequency clines that approach fixation of the alternative alleles at the cline ends, it is unclear why the inversion does not locally fix at one end. An intriguing possibility is that the loci captured by the inversion are subject to local balancing (e.g., negative frequency-dependent) selection independent of temperature yet at the same time happen to render the inversion susceptible to cool temperatures. Here, we have sought to explore this hypothesis by manipulating and tracking the dynamics of inversion frequencies in (i) outdoor mesocosms in Philadelphia from late summer through early winter, and (ii) laboratory cages with factorial variation in starting frequency and temperature. We find that the polymorphism is amenable to multiple equilibria, consistent with maintenance by negative frequency-dependent selection; in conjunction with selection against the inverted arrangement in cooler environments, along latitudinal gradients. These results indicate that the In(3R)Payne polymorphism is affected by multiple forms of balancing selection across space and time.

Keywords: Balancing selection

*Speaker

Drosophila suzukii alters food quality and affects fruit removal by European native birds

Jana Collatz * [1], Adrian Weidmann [2,3], Martin Gossner [4], Irene Bühlmann [4], Mike Werfeli [5], Urs Kormann [3]

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Interactions between frugivorous birds and fruit-bearing plants are crucial for ecosystem functioning. We hypothesized that the presence of the polyphagous invasive *Drosophila suzukii* impacts these interactions by altering the nutritional quality and visual appearance of the wild berries that it uses for development.
In laboratory experiments we infested berries of blackberry, black elder, blackthorn and dogwood with *D. suzukii* eggs. During larval development, we quantified fruit sugar content using Brix values and assessed changes in fruit coloration through measurements of reflectance spectra combined with an avian visual perception model. To evaluate behavioral consequences, we offered infested and uninfested fruits simultaneously to free-living birds in field choice experiments.

Infestation led to a rapid reduction in sugar content in three of the four berry species and produced detectable differences in chromatic contrast between infested and uninfested fruits. These changes in fruit quality corresponded with a 60% reduction in fruit removal by songbirds. Our results provide the first experimental evidence that *D. suzukii* exerts dual ecological impacts on fruit–frugivore interactions. By decreasing both the nutritional value and availability of fruit resources during late summer and autumn, when many songbirds depend on wild fruits to accumulate migratory reserves, the species may negatively affect bird populations. Moreover, reduced fruit removal represents a disruption of the initial step in seed dispersal, suggesting that spotted wing drosophila may compromise avian seed dispersal services for native plants. Our findings highlight that an invasive species known for its agricultural impacts also poses a substantial threat to critical ecosystem functions.

Keywords: ecological impacts, wild fruit, mutualism, trophic interactions

*Speaker

Heat-induced fertility loss in males of the DrosEU Phenotyping Panel

Julian Mensch * [1], Nicolás Flaibani [1], Pablo Schilman [1], Rhonda Snook [2], Hervé Colinet [3], Sonja Grath [4], Michael Ritchie [5], Astrid Bavay [6], Solene Morelle [5], Luis Castañeda [7], Claudia Fricke [8], Olexandra Protsenko [9], Nadiia Morozova [9], Pedro Simões [10]

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[9] National University of Kyiv – Ukraine
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In this talk, we will present the protocol and preliminary results from an ongoing collaborative project investigating heat-induced male fertility loss across lines from the DrosEU Phenotyping Panel. This collaborative effort brings together multiple Consortium groups focused on understanding climate adaptation.

Keywords: fecunduty, fertility, heat stress

*Speaker

The winning combination of traits: unraveling male phenotypes favored by multivariate sexual selection in Drosophila suzukii

Allan Debelle * [1], Joris Froissard [2], Anne Xuereb [2], Yann Le Poul [3], Patrice David [3], Simon Fellous [2], Julie Collet [4]

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[4] Biologie des Oiseaux et Aviculture [Nouzilly] – Université de Tours, Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement – France

Characterising the mating behaviour of pest species is key to develop targeted and sustainable pest management strategies. Yet, traits affecting male mating success are still largely unknown for a key invasive pest species like *Drosophila suzukii*. In this study, we used a male competition experimental design on a recently established population to characterize multivariate sexual selection on male phenotypes, including morphological (body size, wing shape, wing pigmentation and wing interference patterns; WIP) and olfactory traits (cuticular hydrocarbons; CHCs). Data analysed from 1254 males show that wing pigmentation, WIP and CHC all influence male mating success. Specifically, males with large dark spots on dark wing backgrounds are strongly positively selected. Nevertheless, neither male body size nor wing shape have a significant effect on male mating success. These results can be of critical use for emerging sterile insect technique programs on *D. suzukii*, to improve sterile male quality, select wild individuals used for colony enrichment, or design targeted selection protocols.

Keywords: sexual selection, multivariate selection, wing interference patterns, cuticular hydrocarbons, sterile insect technique

*Speaker

Dynamics of embryonic mortality rates in different Drosophila melanogaster stocks under chronic consumption of thiamethoxam-based insecticide at sublethal concentration

Natalia Volkova * [1], Serhii Serbo [1], Kostiantyn Shchogolev [1]

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Today, insecticides continue to be used in various areas of the economy, particularly in the agricultural sector, to combat sucking and leaf-eating insects on many grain, fruit, vegetable, fodder crops, and medicinal herbs, as well as to control insects that transmit diseases to humans, livestock, and domestic animals. In recent years, the use of pesticides (particularly neonicotinoids) has attracted increasing attention because they may have long-term effects on pollinating insects. In addition, as they accumulate in ecosystems, they become a separate factor affecting the stability of the latter. The aim of this study was to analyze embryonic mortality in different *Drosophila* laboratory stocks under conditions of chronic consumption of thiamethoxam-based insecticide at residual concentration. Embryonic mortality in the *Canton-S*, *radius incompletus*, and *26701* (*para(ST76)*) *Drosophila melanogaster* stocks was quantitatively characterized in the control and under conditions of chronic consumption of thiamethoxam-based insecticide at residual concentrations. The wild-type *Canton–S* stock is characterized by a stable level of embryonic mortality over 5 consecutive generations. The proportion of embryos that die in the first 9 hours of development does not exceed 10%, and the proportion of embryos that die later does not exceed 5%. Chronic consumption of insecticide at residual concentration does not affect embryonic mortality in this stock. Mutant stock *26701* (*para(ST76)*) is characterized by a high level of embryonic mortality in the first 9 hours of development, which fluctuates in the control from 20% to 40% over several generations. Under conditions of insecticide consumption, a decrease in the indicator is observed in a number of generations (r=-0.61; $p< 0.05$). The proportion of embryos that die at later stages, on the contrary, increases in a number of generations (r=0.83; $p< 0.05$) under conditions of insecticide consumption in residual concentration. The mutant stock *radius incompletus* is characterized by a high level of both early and late embryonic mortality. The values of the indicators fluctuate widely across generations in both the control and experimental groups. There is no linear dynamics of change.

Keywords: insecticide resistance, life history traints, adaptation

*Speaker

Optimising X-ray irradiation protocols for the Sterile Insect Technique in Drosophila suzukii: development and regional adaptation for Trentino–Alto Adige

Asia Colmagro * [1,2], Marco Valerio Rossi Stacconi [3], Gerardo Roselli [1,2], Silvia Schmidt [2], Gianfranco Anfora [1]

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The Sterile Insect Technique (SIT) is a promising biological control strategy for *Drosophila suzukii*, a pest of major importance in Italy and particularly in the Trentino–Alto Adige region, where it poses a serious threat to berry and cherry production. The successful implementation of SIT depends on the development and optimisation of irradiation protocols that are adapted to specific experimental and applied conditions, and capable of inducing high levels of sterility while maintaining insect quality and reproductive performance.
This study investigates the effects of X-ray irradiation on survival, morphology, and reproductive behaviour of *D. suzukii* under laboratory conditions. Insects have been irradiated using high-energy photons produced by a clinical LINAC (linear accelerator) normally used in medical radiotherapy. Across irradiation doses, insect quality has been assessed through adult emergence and longevity, fertility and fecundity, mating propensity and success, copulation duration and latency, remating frequency, and male–male mating competition. Morphological parameters have been evaluated through qualitative assessments of deformities affecting wings, legs, antennae, mouthparts, and ovipositor, as well as quantitative morphometric measurements including tibia length and wing venation.
The resulting dataset provides a detailed characterisation of sterile insects' performance and supports the selection of irradiation doses that balance induced sterility with insect quality. These findings will inform subsequent semi-field trials and contribute to the development of an efficient, ecologically informed SIT programme tailored to fruit-growing systems in the Trentino–Alto Adige region.

Keywords: Sterile Insect Technique, Integrated Pest Management, X, ray irradiation, reproductive behaviour, Trentino–Alto Adige

*Speaker

Reproductive and life-history dynamics of a Drosophila suzukii population from northern Patagonia

Julian Mensch * [1], Lucas Kreiman [1], Nina Saroka [1], Andrés Martínez [2], Verónica Chillo [2], Mónica Germano [2], Deborah Fischbein [2]

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The spotted-wing *Drosophila* (*D. suzukii*) is an invasive pest species whose establishment in temperate regions exposes populations to strong seasonal environmental fluctuations. In northern Patagonia, where winter minimum temperatures frequently drop below 0 ∘C, populations persist year-round despite the absence of crops and limited food availability. Here, we characterize seasonal variation in reproductive and life-history traits in a natural population of *D. suzukii* over two consecutive years. We quantified seasonal changes in reproductive status and morphology, including ovarian maturation, wing length, and body pigmentation. Pronounced seasonal shifts were observed, with darker and larger individuals predominating during colder months. During winter, females were reproductively arrested, while reproductive maturity increased sharply in spring and declined again in autumn. Reproductive activation was only detected when monthly maximum temperature exceeded 10 ∘C and occurred prior to the availability of berry crops, indicating that temperature, rather than host presence, drives seasonal reproductive dynamics. These patterns are consistent with plastic phenotypic responses commonly described as a winter phenotype and suggest seasonal reallocation of resources between reproduction and survival. Our results highlight the role of life-history plasticity in facilitating persistence of *D. suzukii* in temperate environments and provide insights into how reproductive timing may respond to ongoing climate change.

Keywords: ovarian maturation, winter phenotype, South America

*Speaker

Population Genomics and Local Adaptation of European Drosophila Melanogaster Populations

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Keywords: popgen, evolution, drift, gwas, adaptation, phenotype, genotype

*Speaker

Sex & Germs & Speciation: The Wonderful World of Neotropical Wolbachia and other influential bugs

Wolfgang Miller * [1]

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Selfish genetic elements (SGEs) like transposons, viruses, and bacteria are universal life entities with the capacity to replicate faster than the host and to coevolve tightly by fluctuating waves of conflict and cooperation. In the light of the Holobiome concept, the phenotype of an organism is formed not only by its nuclear and organelle genomic compounds but also by the genomic entities of its cohabitating SGE symbionts. Thereby, SGEs are now considered as important factors to drive along the genetic diversity and speciation of their hosts, even within short evolutionary periods of time. As shown by the latitudinal diversity gradient, tropical organisms have a much higher diversification and speciation rate than temperate ones, and thereby are ideal systems for studying the tempo and mode of SGE-driven host speciation under experimental conditions. *Drosophila paulistorum* spp. is a neotropical species complex belonging to willistoni group that became famous since the 1960s by Dobzhansky and Ehrman as a reference model system to study the causes and consequences of incipient speciation in nature, but also under lab-controlled conditions. We show that the maternally-transmitted endosymbiotic *Wolbachia* bacteria are fixed mutualistic entity of all *D. paulistorum* flies, which are restricted to defined functional host tissues by autophagy, and importantly, direct sexual mating behavior of both sexes and hence drive reproductive isolation between closely related neotropical fly species. Finally, the potential role of another hidden passenger that is also fixed in all neotropical Drosophila hosts like Male-killing *Spiroplama* will be also discussed.

Keywords: neotropical Drosophila model system, symbiosis, selfish genetic elements, speciation

*Speaker

Population-scale genome analysis in Drosophila reveals heterogeneity in TE activity

Artem Ilin * [1]

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Transposable elements (TEs) are ubiquitous genomic parasites and major contributors to genome variation across eukaryotes. To persist over evolutionary time, TE lineages must replicate while facing host repression. In *Drosophila melanogaster*, TE activity is limited by genome defense pathways including piRNAs, yet transposition rates are known to vary across TE families and genotypes.

We analyzed TE insertion heterogeneity across 14 DSPR (The Drosophila Synthetic Population Resource) founder genomes, focusing on insertions unique to individual lines. This revealed substantial line-specific variation in recent TE activity. The LTR retrotransposon **roo** showed high activity across all genomes. In addition, three founder lines showed pronounced expansion of distinct TE families representing the three major TE classes: **copia** in **A5** (LTR retrotransposon), **Doc** in **B2** (LINE), and **Hopper** in **A6** (DNA transposon). In B2, many Doc insertions carried amino acid substitutions in gag relative to the consensus. In A6, increased Hopper activity was unexpected because short Hopper copies are not thought to be autonomous; however we also detected expansion of longer Hopper variants carrying an intact transposase-coding ORF, suggesting the presence of mobilization-competent copies. To our knowledge, such long Hopper elements have not previously been identified, although the Hopper2 transposon shows homology to the longer version we detected.

These results show that despite host silencing mechanisms, TE activity remains high and strongly heterogeneous among founder genomes. Different populations may therefore experience distinct TE-driven mutational pressures, but the factors underlying this heterogeneity remain to be determined.

Keywords: drosophila, transposable elements, population genomics

*Speaker

Scalable, Biosafety-by-Design Genetic Control for Drosophila suzukii

Gerard Terradas * [1], Andrea Deantoni [1], Daniela Mayorga [1], Alice Santi [1], Giulia Morselli [1], Alessandra Gatti [1], Eugenia Pignataro [1], Matteo Rucco [1], Anna Strampelli [1], Andrew Hammond *

1,2,3

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Gene drive and genetic control technologies hold considerable promise for suppressing harmful insect pests, but their wider application has been limited by a combination of biological, operational, regulatory, and biosafety challenges. In particular, systems designed to spread and persist indefinitely in the environment raise substantial concerns that complicate risk assessment and deployment.
Biocentis is a biotechnology company developing genetic control solutions for Drosophila suzukii and other invasive pest species. We are developing a self-limiting genetic control approach designed to enable effective population suppression while avoiding long-term persistence or uncontrolled spread of engineered traits. By restricting trait persistence in time, this strategy aims to reduce regulatory and biosafety barriers, while also supporting practical deployment strategies that minimise release frequency and operational complexity.
By integrating biosafety-by-design with a focus on scalability and implementation, this work highlights how non-spreading genetic control systems may offer a pragmatic pathway toward responsible use of genetic technologies in invasive pest management, with potential benefits for the long-term sustainability of soft-skinned fruit production.

Keywords: genetic control, self, limiting, population suppression

*Speaker

Multiple stressors in invasion success: thermal physiology and insecticide-mediated metabolic responses in Drosophila suzukii

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The success of invasive insect pests is increasingly shaped by the interaction between climatic and chemical stressors. In agricultural landscapes, temperature variation and insecticide exposure act simultaneously, yet their combined effects on physiological traits that determine performance and survival remain poorly understood. Addressing this gap is essential for predicting invasion dynamics and improving integrated pest management under climate change.
We examined how thermal tolerance and energy metabolism vary among *Drosophila suzukii* populations distributed along a _˜700 km latitudinal gradient in Chile, and how these traits are modulated by chronic exposure to sublethal insecticide concentrations. Flies from five populations were reared under common garden conditions, acclimated to different developmental temperatures, and exposed to environmentally relevant insecticide doses. Thermal tolerance was quantified using time–temperature survival assays, while standard metabolic rate (SMR) was measured using flow-through respirometry.

Preliminary results indicate strong population-level variation in metabolic performance and thermal tolerance, with clear geographic structuring. Flies from cooler southern populations exhibited higher metabolic rates at benign temperatures, consistent with metabolic compensation, but this pattern was altered under insecticide exposure. Moreover, insecticides shifted thermal safety margins in a temperature-dependent manner, suggesting that chemical stress can modify physiological responses to climate.
By integrating geography, thermal physiology, and insecticide stress, this study provides a mechanistic framework for understanding how multiple stressors interact to shape invasion success in *D. suzukii*. Our findings highlight the importance of incorporating physiological responses into climate-smart integrated pest management strategies.

Keywords: Drosophila suzukii, invasion biology, thermal physiology, metabolic rate, insecticide exposure, latitudinal gradient, climate change, integrated pest management, physiological adaptation

*Speaker

Evolution and Plasticity of Testis Colour in Drosophila: Comparative Patterns, Environmental Drivers, and Genetic Mapping using DPP lines

Bahar Patlar * [1], Sabine Noebel [1], Tim Christ [1], Patrick Mueller [1]

[1] Martin-Luther-Universität Halle Wittenberg - Martin-Luther-University Halle Wittenberg – Germany

The colour of the testis varies strikingly across Drosophila, ranging from white to yellow to red, yet its evolutionary history, ecological factors affecting it, and genetic basis remain poorly understood. We combine comparative, experimental, and population-genomic approaches to establish testis pigmentation as an evolvable and environmentally sensitive reproductive trait. Using standardized imaging across $>$ 30 drosophilid species, we detected extensive interspecific divergence in testis lightness, showing a strong phylogenetic signal, indicating that shared ancestry explains much of the among-species variation. Within species, we tested environmental drivers in *D. melanogaster* and found pronounced plasticity: a high-sugar diet yielded lighter testes, testes darkened with age, and cooler developmental temperature (18∘C) produced lighter testes than warmer conditions (25–28∘C). Building on these results, we are now quantifying testis colour variation in the *Drosophila Phenotyping Panel* (DPP) lines to test for latitudinal differentiation and to identify candidate loci underlying pigmentation differences.

Keywords: Drosophila Phenotyping Panel, testis colour, male mating

*Speaker

Quantifying the impact of insect host genotype on Wolbachia titer

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Wolbachia are the most abundant endosymbiotic bacteria found in arthropod species, known to induce a wide variety of phenotypes on their hosts, with strong evidence indicating that some fitness-associated host traits depend on bacterial load.
Here we quantify how *Wolbachia* titer is influenced by the genome of its host, in *Drosophila melanogaster,* using the *Drosophila Genetic Reference Panel* (DGRP).

We first found a large variation in *Wolbachia* titers among 90 DGRP lines, using read mapping coverage data to estimate titers *in silico*.

We found high broad-sense heritability ($h^2 = 0.76$) for *Wolbachia* titer, suggesting that variations in this phenotype are mostly due to variations in the host genotype.

To identify the host loci associated with this phenotype, we performed a genome-wide association study using 1,202,368 biallelic SNPs.

Finally, we validated our estimation of *Wolbachia* titers in silico using direct estimation with qPCR.

We discuss our results in light of previous studies in *D. melanogaster* and *D. simulans*, and we conclude that our research brings further evidence of *Wolbachia* titer regulation by the host genome, illustrating the complexity of host-endosymbiont relationships.

Keywords: Wolbachia, Drosophila melanogaster, titer, host genotype

*Speaker

Speciation with gene flow, assortative mating, and chemical senses: insights from genomics

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How reproductive isolation evolves and persists despite ongoing gene flow remains a central question in speciation research. In this talk, I present a comparative synthesis of recent work investigating the evolution and genomic architecture of assortative mating barriers under gene flow, with a particular focus on chemosensory-mediated behaviours. Building on the genic view of speciation, I examine how divergent selection can promote the emergence, maintenance, and coupling of barrier loci despite the homogenising effects of recombination.
I focus on two complementary systems: the two European house mouse subspecies (*Mus musculus domesticus / M. m. musculus*), which met secondarily after a prolonged period of divergence in allopatry and currently form a hybrid zone, and the pea aphid (*Acyrthosiphon pisum*) host-race complex, characterised by host-plant-adapted populations that presently coexist in sympatry. In both systems, assortative mating plays a key role in reducing gene flow and is mediated by chemical cues involved in mate or habitat choice.
Using whole-genome sequencing and population genomic analyses, I show that assortative mating traits and, more generally, reproductive isolation have a highly polygenic basis but exhibit non-random genomic architectures. In mice, genomic signatures of reinforcement highlight clusters of olfactory and vomeronasal receptor genes associated with assortative mate preferences. In aphids, analyses across a divergence continuum reveal the accumulation of barrier loci with divergence, with chemosensory genes enriched among barrier loci and often clustered, sometimes within chromosomal rearrangements. Together, these results underscore the importance of chemosensory systems and clustered genetic architectures in facilitating divergence with gene flow.

Keywords: speciation, population genomics, chemical senses, genetic architecture, gene flow

*Speaker

Exploiting the demographic past of natural populations to understand the adaptive architecture

Christian Schlötterer * [1]

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alternative topics could be:
Frequency dependent selection revisited - evidence from experimental evolution

The importance of purifying selection for the TE landscape in Drosophila

The first two would be on unpublished data, the last one has already been published. Feel free to pick the topic which you feel to be of most interest to the DrosEU community.

Keywords: Drosophila, adaptation, experimental evolution

*Speaker

Evaluation of Metarhizium anisopliae ICIPE 78 as a biopesticide candidate for the management of Drosophila suzukii

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The invasive *Drosophila suzukii* is a major economic pest that inflicts significant damage on soft-skinned fruit crops, including berries and grapes. The recent establishment of this pest in Africa jeopardizes the stability of the growing berry industry, while heavy reliance on chemical insecticides for control threatens biodiversity and environmental health. Here, twenty fungal isolates, including *Metarhizium anisopliae*, *M. brunneum*, *Beauveria bassiana* and *Paecilomyces isaria*, were screened for pathogenicity at 1 × 10ˆ8 conidia/mL against this pest. Dry conidia of the most potent isolates were further evaluated for development as a biopesticide for *D. suzukii* management, by assessing both their direct pathogenicity and indirect effects via fungal volatile-mediated behavioral responses. The screening identified five highly pathogenic *M. anisopliae* isolates (ICIPE 7, ICIPE 18, ICIPE 20, ICIPE 30, ICIPE 78), and their dry conidia led to high mortality in diet and raspberry-reared *D. suzukii*. ICIPE 78 exhibited the fastest lethal action with an MLT50 of 4.75 ± 1.03 days, followed by ICIPE 7, 18, 30, and 20 with mortality occurring between 5-8 days. Additionally, ICIPE 78 was horizontally transmitted by donor-flies, causing premortem reduction in fertility of recipient-females. Furthermore, conidia of ICIPE 78 induced significant attraction to *D. suzukii*, and sporulating cadavers colonized by the isolate effectively attracted and infected healthy flies. The high pathogenicity of ICIPE 78 and its attraction to *D. suzukii* render this isolate a promising candidate for pest suppression. Moreover, its existing commercial status against other pests offers a strategic advantage, potentially facilitating rapid deployment via label extension.

Keywords: biopesticide, virulence, horizontal transmission, horticulture

*Speaker

Genetic architecture of host susceptibility to Wolbachia-induced cytoplasmic incompatibility in Drosophila suzukii

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Wolbachia-induced cytoplasmic incompatibility (CI) is the most prevalent bacterial manipulation shaping host reproduction and evolutionary trajectories and is increasingly exploited in pest control strategies. CI manifests as embryonic lethality in crosses between *Wolbachia*-infected males and uninfected females, and its intensity can vary substantially. Host genetic background is one of the factors contributing to incomplete CI, as hosts may harbor alleles that reduce susceptibility to CI. The spread of such suppressor alleles may ultimately reduce or eliminate CI expression and potentially lead to *Wolbachia* extinction. However, the genetic architecture underlying this suppression remains poorly understood. The *Wolbachia-Drosophila suzukii* system represents an excellent model to investigate this question, as the strength *of* CI is largely driven by host genetic background in this species. Using two lines of *D. suzukii* with extreme CI phenotypes (0 vs. 70% embryonic mortality), we performed reciprocal crosses and measured embryonic mortality in crosses involving F and F hybrid males mated with uninfected females. To model the observed patterns, we tested several genetic models, including dominance, additive, autosomal, X-linked or cytoplasmic effects. Based on AICc, the best models included autosomal and dominance effects or autosomal, dominance, and cytoplasmic effects. Our findings highlight the key role of host genotype in modulating CI strength. Further investigations are required to identify the specific genes responsible for host susceptibility to symbiont-induced CI.

Keywords: symbiotic bacteria, reproductive manipulation, Wolbachia, pest control

*Speaker

Dissecting the Metabolic and Regulatory Basis of Cold Adaptation in Drosophila

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Keywords: ...

*Speaker

From wild host plants to crop plants: the domestication of a fly born to be wild?

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As with any crop pest, the immense scientific interest in the spotted wing drosophila, *Drosophila suzukii*, is largely motivated by the damage it causes to agricultural production of fruits such as cherries, strawberries and other small fruits. But beyond crop systems and anthropised areas (gardens, urban spaces), this invasive fly is capable of infesting the fruits of a large number of wild plants and finding refuge in natural habitats. What is the true nature of *Drosophila suzukii* today: wild like a wolf or domesticated like a dog? Here, we will present the results of several studies conducted in France with the aim of understanding and quantifying the relative influences of multiscale environmental factors on the fruit infestation rates of wild, ornamental and crop host plants. Our various studies invariably show that three sets of factors

*Speaker

influence the success of fruit infestation: (i) local factors related to resource quality and ecological niche, (ii) landscape factors related to dispersal or reflecting the presence of favourable habitats, and (iii) macro- and micro-climatic factors affecting the activity and survival of individuals. From a temporal perspective, as winter ends, the fly successively uses native wild and ornamental host plants, then cultivated cherries, and finally wild cherries and other fruits. *Drosophila suzukii* was clearly born to be wild and systematically returns to the forest, probably its ancestral habitat, during periods of harsh weather. However, it also uses key plants and habitats associated with humans, suggesting a dynamic towards domestication similar to the common fly *Drosophila melanogaster*, somewhere between 'dog and wolf'. A better understanding of its pendular migrations between natural and anthropised ecosystems would make it possible to better predict the risk of infestation of cultivated fruits, such as cherries, particularly by winter fruit-bearing plants (sentinel plants).

Keywords: Drosophila suzukii, biological invasions, anthropisation, landscape composition, climatic gradient

The Rise and Fall of the P-Transposon in Neotropical Drosophila Reservoirs

Stéphane Ronsseray * [1], Aurélie Hua-Van [2], Bruno Da Silva [1], Guilherme Baiao [3], David Gassner [4], Clément Carré [1], Lisa Klasson [3], Laure Teysset [1], Wolfgang Miller [4]

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The canonical *P* transposon has invaded natural *Drosophila melanogaster* populations pandemically between 1950 and 1970 after its arrival by horizontal transfer, most likely from neotropical *Drosophila willistoni* flies. We analyzed the *P* element status in willistoni group species (*D. willistoni, D. equinoxialis, D. paulistorum, D. insularis, D. nebulosa, D. tropicalis*) by sequencing to investigate the functional and evolutionary status of *P* family members in their ancestral reservoir hosts (still mobile or not). We found that potentially autonomous *P* elements exist in most of the *D. willistoni* and *D. equinoxialis* populations from Central and South America, whereas the majority of *D. paulistorum* and *D. tropicalis* populations apparently lack complete *P* copies. In addition, we discovered in all willistoni group species, except the most distant one (*D. nebulosa*), the presence of numerous *P*-MITEs (around 200bp) with conserved sequences capable for being *trans*-mobilized. Moreover, all the willistoni group species carry an ancestral *P* element variant, named "protocanonical *P* element" (pc*P*), which differs from the canonical *P* element (c*P*) of *D. melanogaster* by three diagnostic marks including a four bp intronic insertion and a SNP in the 3' Transposase Binding Site (TBS), thereby becoming fully symmetrical with the 5' TBS, not present in c*P* elements. Finally, small RNA sequencing in *D. willistoni, D. equinoxialis* and *D. tropicalis* ovaries showed the existence of sense and antisense *P*-homologous piRNAs, indicating an epigenetic *P* repression based on a classical germline double-strand piRNA mechanism. Additionally, we found that neotropical willistoni host species can be classified into four evolutionary *P* element stages, *i.e.*, EXTINCTION (only highly defective pc*P* copies corresponding to *P*200-MITEs in *D. insularis*), EROSION (only degenerative full size and deleted pc*P* copies in *D. paulistorum* and *D. tropicalis*), ACTIVITY (still active pc*P* copies in *D. equinoxialis*) and REPLACEMENT (complete loss of pc*P* copies in *D. willistoni*, except *P*200-MITEs, replaced by c*P* copies of unknown origin). The evolutionary perspectives of the *P* family in the willistoni group species will be discussed.

Keywords: P transposable elements, Drosophila willistoni, epigenetics, long term homeostasis.

*Speaker

Tracking the invasion and geographic expansion of Drosophila suzukii along a latitudinal gradient in Chile

Luis E. Castañeda * [1], Francisco Pinilla [1], Moisés Valladares [1], Paula Irles [2], Christian Figueroa Caro [3], Mathieu Gautier [4], Arnaud Estoup [5]

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Invasive biology is a major driver of global change with adverse effects on human health, food security, and biodiversity. At the same time, invasive species are a key model for studying the mechanisms of rapid adaptation to heterogeneous environments. The rapid spread of invasive species across environmental gradients provides an important opportunity to assess whether rapid adaptive responses of populations to local environmental conditions result from local adaptation, phenotypic plasticity, or both. The spotted wing drosophila (*Drosophila suzukii*) is an excellent model to explore contemporary invasion and geographic expansion across environmental gradients. *Drosophila suzukii* is a highly invasive species native to Asia that is currently distributed across several countries in Africa, Europe, North America, and South America. It has been present in Chile since 2017 and is currently distributed across a latitudinal gradient of 3,000 km. Here, we use a combination of mitochondrial and microsatellite markers, as well as whole-genome sequences, to determine the genetic diversity and demographic processes of Chilean populations, as well as their putative source populations. We found strong genetic continuity between Brazil, Argentina, and Chile, as well as low differentiation among Chilean populations, which cluster tightly with Argentina. Further analyses revealed that the Chilean populations have a unique southern Argentinean source population. This finding supports the idea of a single introduction into Chile, followed by a stepwise latitudinal expansion. Further analysis using Pool-seq data will be valuable to test the invasion route of *D. suzukii* in Chile, analyze the population structure among introduced populations, and evaluate candidate genes under spatial selection along the latitudinal distribution of *D. suzukii* in Chile.

Keywords: invasion genetics, pest insects, distribution range expansion

*Speaker

D. suzukii harbour a niche-specific fungal community and a core bacterial community in natural conditions

Sido Dunis-Quarré * [1], Marie Lapègue [2], Benoit Facon [3], Nicolas Rode [3]

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Insects harbour diverse microbial communities that play key roles in host ecology and evolution. While the concept of a core microbiota has been conceptually widely adopted and documented in specialist phytophagous insects, much less is known about how microbiota vary across developmental stages (holometabolous species) and host plants (polyphagous species). Drosophila has been a well-established model to study microbiota, yet data regarding microbiota from natural conditions over the life cycle and host plants remain scarce.
Here, we characterized the gut-associated fungal and bacterial communities of *Drosophila suzukii* across developmental stages and host fruits using a metabarcoding approach by sequencing 16S and ITS markers. We artificially infested fresh cherries, blackberries and strawberries with lab-reared flies. We extracted larvae from fruits and transferred to a pasteurized fruit medium until pupation. We sampled larvae, pupae and emerging adults, as well as fruits before and after infestation.
Our results revealed that fungal communities, but not bacterial, were strongly structured between host fruits with a clear differentiation between blackberry-associated microbiota and those associated with cherry and strawberry. In contrast, bacterial communities were conserved across developmental stages, especially one taxa shared over host fruits, whereas fungal communities varied more strongly. In addition, we did not identified stage-specific bacterial nor fungal taxa. These results indicate the existence of a niche-specific fungal microbiota on blackberry and cherry/strawberry, and provide great candidates for core bacterial species naturally associated with *D. suzukii*.

Keywords: D. suzukii, niche specific microbiota, stage specific microbiota, core microbiota

*Speaker

A model to evaluate control strategies against Drosophila suzukii in cherry orchards

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The use of pesticides in cherry orchards against *Drosophila suzukii* has shown clear limitations, both in terms of environmental cost and long-term efficacy. In this context, understanding how alternative control measures, such as insect-proof nets, the sterile insect technique, or prophylactic measures, can be optimised and used effectively is crucial.
To this end, we develop a deterministic population dynamics model of *D. suzukii* based on its physiological characteristics, using a stage-structured formulation based on the linear chain trick. Development time, fecundity, and adult survival are modelled as functions of temperature, which allows the model to explicitly account for seasonality. The model represents the geographical configuration of cherry production landscapes, including orchards, surrounding wild resource patches, and the movement of populations between them. This spatially explicit framework allows us to capture variation in resources, population dynamics across patches, and the spatial application of control measures.
After detailing the main modelling assumptions, we consider several control problems, explore different scenarios, and determine the optimal solution under ecological and economic constraints. In the long term, this model will be deployed on a user-friendly online platform, enabling users to create schematic landscapes composed of multiple orchards and adjacent wild habitats, and to predict the effects of different control measures under realistic spatial configurations.

Keywords: cherry orchard, pest managment, sterile insect technique, control strategies, spatially explicit model, stage structuded model

*Speaker

Synthetic biology approaches to generate temperature-sensitive alleles for the Sterile Insect Technique

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The Sterile Insect Technique (SIT) is a pest control approach, which involves the release of only male sterile insect, as female insects are usually the cause of damages to crops and humans through egg-laying and bites. To separate the males from the females for the SIT, genetic sexing strains (GSSs) has been developed for several pest species to facilitate the sex separation process by genome-editing-based means. However, no GGS has been developed for the invasive agricultural pest *Drosophila suzukii* to date. This project aims at using different strategies to develop GSSs based on temperature-sensitive lethal (tsl) mutations for *D. suzukii*, which can facilitate the male selection of the species, which can then be subjected to the subsequent sterilisation and released to the wild to control the *D. suzukii* population.

Keywords: CRISPR/Cas, genome editing, insect pest management, N, degron, protein design

*Speaker

On the importance of taxon proximity in pest phylogenomics: data from sister species helps redefining some evolutionary traits in Drosophila suzukii and other Drosophila

Omar Rota Stabelli * [1], Cristina Crava [1], Rupinder Kaur [1], Riccardo Piccinno [1], Gianfranco Anfora [2], Lino Ometto [3]

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[2] Fondazione Edmund Mach – Italy
[3] Department of Biology and Biotechnology, University of Pavia – Italy

A poor taxon sampling, especially the absence of sister species, is likely to reduce the resolution of genome studies aimed at improving our understanding of pests biology and management. We explored this issue in the fruit fly *Drosophila suzukii* by studying its evolution in the presence of new genome data from *D. lucipennis* and *D. subpulchrella*. Updated phylogenies indicate that the former is not a member of the suzukii subgroup, while the latter is the actual sister species of *D. suzukii*. Updated molecular clocks allowed reconstructing with more precision the origin of these species and of their harbored *Wolbachia*. The addition of the sister species to the phylogenetic framework allows us to redefine ecological scenarios: genetic signatures of cold adaptation are not peculiarities of *D. suzukii* as previously reported, but of its common ancestor shared with *D. subpulchrella*. Our enhanced comparative genomics identify a progressive turnover of chemosensory genes in the lineage leading toward *D. suzukii* only and support a new scenario for Or22a/b evolution in the melanogaster group. We finally drew a first picture of redox genes evolution on the Drosophila phylogeny. Our results allow us to interpret ecological considerations for *D. suzukii* more in detail and showcase how a sister species improves the accuracy of comparative genomics when studying the evolution of pest novel traits.

Keywords: genomics, phylogenomics, phylogeny, D. suzukii, odorant receptors

*Speaker

Wings of Change: the invasion ecology of Drosophila suzukii

Marco Valerio Rossi Stacconi * [1]

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The invasion success of *Drosophila suzukii* is driven by the tight coupling of behavioral flexibility, seasonal physiology, and population-level responses to heterogeneous environments. Drawing on long-term field studies, experimental work, and demographic modeling, this contribution synthesizes how ecological processes across scales shape the dynamics of this globally invasive pest. Temperature-driven development and reproduction strongly structure seasonal population growth, with degree-day–based models revealing key phenological transitions and periods of heightened sensitivity to management interventions. Overwintering biology further plays a central role: evidence for reproductive diapause, sex-specific seasonal dynamics, and long-term sperm storage indicates that overwintering females act as a demographic reservoir, and their abundance provides an early predictor of summer population outbreaks. Spatial and behavioral processes add an additional layer of complexity. Mark–release–recapture experiments and population genetic analyses demonstrate seasonal, long-distance movements across landscapes, linking crops, non-crop hosts, and overwintering habitats. At finer scales, reproductive site selection is mediated by chemical cues associated with prior infestation, promoting aggregation and rapid local population buildup on suitable hosts. Together, these results show how dispersal, reproductive plasticity, host use, and seasonal connectivity jointly underpin the invasion ecology of *D. suzukii*. Integrating these processes provides a framework for improving population forecasting and developing sustainable, diapause-aware pest management strategies.

Keywords: Biological invasion, Seasonal phenology, Host use, Dispersal, Overwintering

*Speaker

Field Evaluation of Sterile Drosophila suzukii Males for SIT Application in Cherry Orchards

Ghais Zriki * [1], Lisa Haddad [1], Jugurtha Ouzzir [1], Christine Fournier [1], Sarah Quemin [1], Capucine Perrey [1], Jeanne Monnier [1], Can Deschamps [2], David Monnin [1], Nicolas O. Rode [2]

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Keywords: Fruit flies, Spotted, Wing Drosophila, reproductive competitiveness, Sterile Insect Technique

*Speaker

Evaluating the Synergy Between the Incompatible and the Sterile Insect Technique to control D. suzukii

Benjamin Kaltenbach [1], Emilie Mendes [1], Julien Gélus [1], Hannah Lefort [1], Svitlana Serga [2], Ghais Zriki [3], Mathieu Gautier [2], Nicolas Rode * [4]

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We propose combining two complementary techniques to limit the reproduction of Drosophila suzukii. The first, known as the sterile insect technique (SIT), involves releasing males sterilised by irradiation. The second, known as the incompatible insect technique (IIT), harnesses *Wolbachia*, a bacterium naturally present in fruit flies, to sterilise males. Combining these two approaches may allow for a lower radiation dose to sterilise males, thereby preserving the performance of released males and enabling them to compete more successfully with wild males. The OPTIMISTII project aims to overcome several scientific and technical obstacles. A primary goal is the mass production of males that are both sterile and competitive, while keeping costs low. The project also aims to implement the genetic marking of males to facilitate field monitoring, and to use modelling to simulate the impact of this strategy in cherry orchards. This project could therefore provide a sustainable solution for protecting small fruit crops while reducing the use of chemicals and preserving the balance of agricultural ecosystems.

Keywords: irradiation, sterility, population control, IIT, SIT

*Speaker

Adaptive Challenges of Past and Future Invasion of Drosophila suzukii: Insights From Novel Genomic Resources and Statistical Methods Combining Individual and Pool Sequencing Data

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Global change is accelerating biological invasions, making it crucial to understand how species adapt in new environments to improve management strategies. Genomic data provide valuable insights into adaptation through genotype-environment association (GEA) studies, which identify genes and biological processes tied to invasion success, and through geometric genomic offset (gGO) statistics, which estimate genetic (mal)adaptation to new environments. Here, we investigate genetic adaptation in the invasive pest *Drosophila suzukii* using novel genomic resources and statistical methods. We use a new chromosome-level genome assembly and data from 37 populations, combining publicly available and newly generated pooled and individual sequencing data, analysed with an enhanced version of BayPass software, tailored for such hybrid datasets. First, we identify genomic regions showing genetic differentiation between native and invasive populations. Then, using a GEA with 29 environmental covariates, we estimate the gGO between the source environments and the invaded areas, shedding light on the potential adaptive challenges *D.suzukii* faced during previous invasions. In addition, we estimate gGO for geographical areas not yet invaded to predict future invasion risks, and identify regions from which preadapted populations may originate. Our results reveal numerous genomic regions associated with the invasive status from genome scans. However, when considering broader patterns of adaptation to specific environmental variables through gGO analyses, we find that *D.suzukii* populations likely faced only limited adaptive challenges across their major invasion range, while certain uninvaded regions still remain at high risk of future invasion. Our study offers significant insights into *D.suzukii* adaptation and provides a practical population genomics framework to predict biological invasions, applicable to various species.

Keywords: Biological invasions, Genomic Offset, Local Adaptation, GEA, Baypass

On the tracks of chromosomal variation in the invasive pest Drosophila suzukii

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Inversion polymorphism has been observed in many dipteran species, with *Drosophila* being particularly well studied in this regard. The adaptive importance of inversion polymorphism is well documented; in some species, there is a repeatable cline in inversion frequencies influenced by ecological variation. However, inversion polymorphism is also shaped by neutral processes and can provide insights into past demographic expansion. In the case of *Drosophila suzukii*, a native pest species from Asia, chromosomal variation has not been well studied. A chromosomal map from a homokaryotic line from Trento, Italy has been published. So far, only one inversion from a single location in Spain has been described.

Analysis of whole genome sequencing data from several isogenic strains suggests the presence of inversion arrangements on the 2R and 3R chromosomal arms. Polytene chromosomes from salivary glands were analysed from larvae belonging to these strains, and inversion loops were indeed observed in some, indicating heterokaryotypic state. To describe inversion arrangements, we crossed individuals from the respective lines with a homokaryotic line for which a chromosomal map has been published. These crosses confirmed our findings regarding the presence of inversions on the 2R and 3R chromosomal arms. Particularly interesting is the discovery of two separated but linked inversions on the 3R chromosome arm.

Our work suggests that the line from Trento, Italy, can be used as tester line for studying inversions in both laboratory lines and natural populations. Further analyses should shed light on whether inversion polymorphism in *D. suzukii* is shaped by adaptive (e.g. rapid adaptation to new environments) or non-adaptive (spread from its original range) processes.

*Speaker

Keywords: Drosophila suzukii, polytene chromosomes, inversion polymorphism, chromosomal map

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Key Initiative CLAPAS - University of Montpellier

The CLAPAS initiative from the University of Montpellier proposes to explore plant health through a broader approach, inspired by the concept of the exposome, which encompasses all interactions between plants and their environment (soil, microbiota, pests, beneficial organisms, etc.). This approach is fully in line with the One Health perspective, linking plant, environmental, animal, and human health.

INRAE

INRAE is a French public research institute working for the coherent and sustainable development of agriculture, food and the environment.

CNRS
CNRS is the French state research organisation and is the largest fundamental science agency in Europe.

CBGP
CBGP is an INRAE research unit based in Montpellier.

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IGH is a CNRS research unit based in Montpellier.

French Genetics Society
The French Society of Genetics is a private association that brings together researchers, and, anyone interested in genetics in any of the many areas in which this scientific discipline is developped or being applied. Its roles are to promote genetics, stimulate interaction among French-speaking geneticists and their foreign colleagues, assist young people who wish to pursue a career in genetics, and represent French-speaking geneticists at the national and international levels.

University of Montpellier

The University of Montpellier is a public research university located in Montpellier. Established in 1220, the University of Montpellier is one of the oldest universities in the world.

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Pole AEB serves as a hub for synergizing research and scientific consultation structures in order to develop joint initiatives among members of the University of Montpellier's I-SITE program of excellence.

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GIS Fruits (Scientific Interest Group for Fruits) brings together 22 partners from the French fruit industry involved in research, development, training, and professional organization in order to implement a long-term integrated strategy, ranging from research to the transfer of innovations to economic players.

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