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**BOOK OF ABSTRACTS**

Moths and butterflies (Lepidoptera) have sex chromosome systems with female heterogamety (WZ/ZZ or derived variants). Results of fluorescence *in situ* hybridization (FISH) with genomic, W-chromosome painting, and BAC (bacterial artificial chromosome) probes along with available sequence information suggest that lepidopteran W chromosomes are almost completely composed of repetitive sequences. The W chromosomes evolve rapidly and their molecular composition differs considerably even between closely related species, as we have recently shown in the magpie moth, *Abraxas grossulariata*, an iconic species in which the female heterogamety was discovered, and its congeneric species *A. sylvata*. On the contrary, Z chromosomes are highly conserved in Lepidoptera, as demonstrated by synteny mapping of Z-linked genes between distant species using BAC-FISH and linkage analyses. The W chromosome is an evolutionary novelty in Lepidoptera, as it is absent in the sister order Trichoptera (caddisflies) and in primitive moths such as Micropterigidae. Our recent data on the W presence/absence in lower Lepidoptera, together with conserved synteny of Z-linked genes, suggest the multiple origin of the W chromosome, although its single origin followed by repeated losses cannot be ruled out. Based on these new data, we have revised the hypothesis on the origin of the W chromosome.

Keywords: Lepidoptera, Evolution, Molecular differentiation, Sex chromosomes, Synteny mapping

## CO214

### THE GENOME OF *DROSOPHILA SUBPULCHRELLA* AND THE EVOLUTION OF FRESH FRUIT FEEDING IN *DROSOPHILA SUZUKII*: A COMPARATIVE GENOMICS APPROACH

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*Drosophila suzukii* is an invasive fruit fly pest that is spreading across temperate regions of North America and Europe. This species is characterized by a peculiar ecology, whereby females use a serrated ovipositor to lay eggs under the skin of fresh ripe fruits on which larvae feed. The genetic bases of such ecological and behavioral traits are starting to be investigated, for instance by combining genome-wide molecular evolution studies with ecological and behavioral observations. To increase the power of these analyses, we produced a draft genome and the transcriptome of *D. subpulchrella*, the closest known non-pest sister species of *D. suzukii*. Our comparative evolutionary analyses reveal a complex evolutionary history characterised by an initial speciation no older than 2 million years ago with past and possibly ongoing genetic admixtures between the two species. Moreover, the results indicate that two species share most of the chemosensory gene repertoire, indicating a progressive modification in the *suzukii* subgroup toward the peculiar *D. suzukii* feeding and oviposition behaviour. Finally, we could disentangle the evolutionary dynamics of Wolbachia symbionts in the two species. Our results indicate that comparative genomics between closely related species is particularly powerful when studying species-specific adaptations and ecological traits, which could be particularly relevant when defining management strategies for invasive species.

Keywords: *Drosophila suzukii*, *Drosophila subpulchrella*, comparative genomics, evolution

## CO215

### EVOLUTIONARY-FUNCTIONAL GENOMICS FOR ARTHROPOD CHARACTERISATION, CONTROL, AND CONSERVATION

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The increasingly thorough sampling of arthropod diversity through genomic sequencing offers new and powerful opportunities to explore links between gene evolution and gene function in an evolutionary systems biology framework. Sequenced genomes represent a logical framework for building comprehensive biological knowledgebases that support and drive biological research. However, these cannot exist in isolation, as cross-species comparisons detail the evolutionary histories of genomic elements and so inform their putative functions. To develop the best possible hypotheses on putative gene functions we must learn how to (i) use the accumulating data to meaningfully and quantitatively characterise the full evolutionary histories of genes and other genomic elements, and (ii) relate these evolutionary histories to assayable functions and thereby pave the way to exploiting real predictive power. Recent studies that combine detailed gene evolutionary characterisations with data from large-scale functional genomics experiments exemplify how this can enhance our understanding of the biological processes being studied. Thus, to substantially advance the biological characterisation, control, and conservation of arthropods, requires the joining of forces between evolutionary and functional genomics, and this should become the norm rather than the exception.

Keywords: Evolution, function, genomics, mosquito

## Evolution and Development of Functional Traits

## CO216

### SYMBIONTS AND PARASITES: YIN AND YANG SHAPING HOST PHYSIOLOGY

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Beneficial microbial symbionts serve important functions within their hosts, including dietary supplementation and maintenance and development of immune system homeostasis. We use the tsetse fly, *Glossina morsitans*, and its obligate mutualist, *Wigglesworthia glossinidia*, to investigate the co-evolutionary adaptations that influence multiple host physiological processes. The obligate symbiont *Wigglesworthia* is maternally transmitted to tsetse's intrauterine larvae, and provides a multitude of vitamins and co-factors that are essential for tsetse host physiology. We can produce flies that lack this symbiont by interfering with symbiont transmission process. Such offspring give rise to adults that exhibit a largely normal phenotype, with the exception being that they are reproductively sterile and also have a highly compromised immune system. Our results demonstrate that