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BOOK OF ABSTRACTS



mainly achieved by down regulation of OBPs related genes that switches off female host seeking behaviour. Innovative control approaches focusing on the semiochemical systems of mosquitoes could be used in the effort to disrupt undesirable host–insect interaction in order to reduce the transmission of arboviruses.

Keywords: Aedes aegypti, courtship, odorant binding proteins

CO143

THE SISTER-SPECIES APPROACH IN ENTOMOLOGY AND ITS IMPORTANCE IN DISENTANGLING GENOMICS, PHYSIOLOGY AND ECOLOGY OF SPECIES

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Current entomology utilizes a large array of analytical tools taken from different disciplines such as ecology, neurobiology, microbiology, genetics, and genomics; this interdisciplinary approach can generate robust knowledge, clarifying the biology of insect species. There is however one crucial aspect often neglected: the comparison between an insect and its closest related sister-species *i.e.* the closest species or group of species on a phylogenetic tree. In the absence of a sister-species, comparisons cannot discriminate characters that are unique to the pest from those shared with other members of its clade. While the availability of a sister-species makes it possible to polarize characters into the phylogeny, (1) allowing the identification of unique chemosensory genes useful for chemical ecological applications, (2) pin-pointing the estimate age of speciation and evolutionary patterns for paleo-ecological reconstructions as well as (3) identifying with more accuracy typical physiological and behavioural characters. Due to budget and/or logistic reasons, this knowledge is too often impaired by a pest being compared only with distantly related species. Here we present the rationale behind the sister-species concept and provide some successful examples about the benefit of comparing an insect biology with that of the closer related species. We advocate that entomology would benefit from from adding to its repertoire the sister-species concept by modifying current research agendas.

Keywords: Sister species, phylogenetics, insect pest management

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EXPLORING THE CHEMORECEPTOR REPERTOIRE AND THE ORCO-RNAI INDUCED BEHAVIORAL PHENOTYPES IN THE OLIVE FRUIT FLY, BACTROCERA OLEAE (DIPTERA: TEPHRITIDAE)

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The olive fruit fly (*Bactrocera oleae*) is the most destructive pest of the olive tree worldwide causing significant production losses and olive fruit impoverishment. The need to diminish conventional chemical approaches and develop efficient, specific control methods on the olive fly leads in the study of biological systems related to its harmful effect. Therefore, exploring the molecular basis of its chemoreception system will demonstrate the respective molecular targets that determine species-specific features on reproductive and sexual behavior, as well as host-plant recognition. To improve knowledge of olfactory perception and taste, we identified the complete olfactory receptor (OR) and gustatory receptor (GR) gene repertoires on the scaffolds of *B. oleae* genome. Gene structure, transmembrane helix prediction, and basic phylogenetic clustering were examined. Further interspecies comparisons were performed based on multiple sequence alignment of the entire OR protein sequence, to interpret similarities of orthologous copies, divergence or species-specific expansions among relative species. Furthermore, transient gene silencing of the olfactory coreceptor Orco was performed through dsRNA injections. Observation of copulation and oviposition rates demonstrated that silencing Orco plays a crucial role in the reproductive behavior of the olive fly, since pre- and/or post- mating processes were affected. These observed behavioral changes render this gene a potential target for the improvement of the olive fruit fly population control techniques. Screening and deorphanization of the chemoreceptors in the future, although still remain a challenging task, would allow the discovery of novel odorant-OR interactions to be tested towards the improvement and specialization of the olive fly control strategies.

Keywords: olfactory system, gustatory system, genomics, RNAi, oviposition, reproduction