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## **BOOK OF ABSTRACTS**



#### Impact of Symbionts on Insect Biology

#### PO559

#### GENOME REDUCTION IN THE MOSQUITO SYMBIONT ASAIA

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The genus *Asaia* represents a peculiar member of Acetic acid bacteria (AAB): it oxidizes acetate and lactate to carbon dioxide and water, but not ethanol to acetic acid. Several species and strains of the genus *Asaia* were firstly isolated from tropical flowers. The symbiotic mutualism between *Asaia* and mosquitoes. encompassing Anopheles, Aedes and Culex genera, well-known vectors of parasites and arboviruses causing some of the major infectious diseases in public health, including malaria, Dengue and Zika is widely accepted and its colonization within its hosts is characterized by a wide tissue tropism, harbouring in the gut, the salivary glands and the reproductive tracts of female and male individuals, corresponding to the mode of its horizontal transmission (co-feeding) within a population and its vertical transmission between host generations (paternal transmission). Studies aimed at understanding the features of AAB symbiotic alliances with their hosts focused on the investigation of possible benefits provided by the role of the potential advantages given by AAB to their respective hosts. Through the genome sequencing of several *Asaia* isolates from various mosquito species, we disclosed differences in the architecture of the strain isolated from field-collected specimens of the South-American malaria vector *Anopheles darlingi*, and in particulary its genome reduction in comparison with other isolates from mosquito species belonging to Anopheles within a single bacterial taxon evolving in the mosquito host that represents a good model to study the genome reduction dynamics within a single bacterial taxon evolving in the mosquito bots that represents a common biological niche.

Keywords: Asaia, endosymbiont, genome reduction

#### P0560

### EFFECTS OF LAB PROCEDURES ON THE TRANSFER OF *B. OLEAE* ENDOSYMBIONT, *CANDIDATUS ERWINIA DACICOLA*

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Bactrocera oleae (Rossi) is a key pest of the olive crops in the Mediterranean basin. An important issue regarding *B. oleae* on which scientists are focusing the most is its symbiosis with *Candidatus Erwinia dacicola*. This bacterium is considered essential for the olive fly. It is vertically transmitted through generations and it benefits both larvae and adults in field; whereas, it had been found rarely in lab colonies, probably because of preservatives in artificial diets. So that, in order to understand the reason of its loss during rearing lab procedures, we exposed eggs laid by wild females to three different treatments: a propionic acid solution, a mixture of sodium hypochlorite plus Tritonxand water as control. The symbiont load on eggs was evaluated by real-time PCR and SEM. In the same time, we also tried a horizontal transfer among adults, exposing lab flies to ripe olives and gelled water contaminated by wild flies, wax domes containing eggs laid by wild females, cages dirtied by faeces dropped by wild flies in cohabitation with wild adults. In the first experiment, real-time PCR of eggs showed a significant reduction in Ca. *E. dacicola* abundance on eggs treated with propionic acid solution or the mixture of sodium hypochlorite plus Tritonxcompared to the control. Secondly, PCR-DGGE highlighted that the horizontal transfer of the endosymbiont occurred in the case of cohabitation. Thus, our results indicate how the symbiont load could be decreased by the use of preservatives in lab rearing procedures and that cohabitation between wild flies and lab ones permits the horizontal transfer opening further possibilities to establish a permanent symbiotic colony, a strategic tool for future SIT applications. Moreover, PCR-DGGE performed with an appropriate primer set was proved to be a consistent method for Ca. *E. dacicola* screening.

Keywords: Olive fly, lab rearing, endosymbiont, Candidatus Erwinia dacicola, DGGE, SIT

#### PO561

#### DIFFERENTIAL GENE EXPRESSION IN WOLBACHIA INFECTED AND NON-INFECTED DROSOPHILA PAULISTORUM

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The neotropical superspecies *Drosophila paulistorum* (Diptera, Insecta) comprises at least six reproductively isolated forms, each harboring a closely related but bidirectionally incompatible mutualistic Wolbachia strain. Although wild type flies of each semispecies are known to be isolated from the others by both pre- and post mating incompatibilities, recent studies have shown that mating and successful offspring development can be achieved after insects are treated for reduction of Wolbachia titer. This suggests that in this system the bacteria not only prevents embryonic development through cytoplasmic incompatibility but also affect mate choice, possibly through interference in pheromone production and recognition. In the present study, RNA samples were collected from heads and abdomens of males and females of three semispecies of *D. paulistorum*. Both naturally infected wild type specimens and flies which had gone through antibiotics treatment and subsequent gut flora restoration were sampled so that the influence of Wolbachia on gene expression could be investigated. Differential gene expression analysis was done using reads mapped to a de-novo assembled transcriptome and revealed hundreds of genes with altered expression for twolbachia depletion. Several of these were involved in cell cycle and germ cell development, which possibly relates to Wolbachia's tropism for reproductive tissue and ability to maniputale host reproduction. However, a large number of genes related to other processes were also observed, including stress response, defense against microbes, pheromone production and reception, fatty acid metabolism, proteolysis, muscular and visual functions, among others which might be related to less studied phenotypes induced by the symbiont.

Keywords: Wolbachia, Drosophila, symbiosis