

ENTOMOLOGY WITHOUT BORDERS



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ABSTRACT BOOK

Author Name: Helena Johansson

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Session Title: Contributed Papers: Genetics and Evolutionary Entomology: Populations and Spatial Diversity

Date of Presentation: Monday, September 26, 2016

Abstract Number: 1085

DOI: 10.1603/ICE.2016.114205

CANCELLED

Paper (Oral) Presentations

Presentation Title: Mitochondrial *tRNA-Ser* secondary structure modeling across *Lucilia* species (Diptera:Calliphoridae)

Author Name: Luz Gomez

Author Institution: Tecnologico de Antioquia

Session Title: Contributed Papers: Genetics and Evolutionary Entomology: Populations and Spatial Diversity

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Abstract text:

The blowfly genus *Lucilia* comprises at least 23 species distributed in the Neotropical region, some of them with medical and forensic importance. Previous systematics studies emphasized that a reliable methodology to delimit *Lucilia* species are needed, due to the possible existence of cryptic group species within the genus; the classic taxonomical traits are scarcely useful to identify formal species because of their little morphological variation. We modeled the secondary structure for the mitochondrial *tRNA-Ser* gene from several *Lucilia* specimens from Colombia and records available at NCBI. This marker and its adjacent regions (*Cytochrome B*, *Intergenic Spacer* and *NADH subunit I*) had proven to be useful distinguishing formal and closely related cryptic biological entities in species complex such as mosquitoes (Diptera: Culicidae) and Satyrinae butterflies (Lepidoptera: Satyrinae). We sequenced several specimens of *L. eximia* and compared to other species from NCBI. To test evolutionary patterns of this gene

and adjacent regions we calculated Neighbor Joining and Bayesian trees. Our results from K2P and Bayesian trees shows two groups: one including only specimens from *L. eximia* (group I) and the remaining *Lucilia* specimens (including some *L. eximia*) and *Calliphora* spp on group II. These two groups were in agreement with modeled secondary structure. Such differences remain only in *D* arm, and *T* arm with no changes in the anticodon. Tree topology and the distribution of *L. eximia* in the two groups suggests a possible mitochondrial introgression in relation to other *Lucilia* and *Calliphora* species.

Paper (Oral) Presentations

Presentation Title: Strong community structuring of defensive heritable symbionts is shaped by context-dependent transmission rates

Author Name: Jacob Russell

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Session Title: Contributed Papers: Genetics and Evolutionary Entomology: Populations and Spatial Diversity

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Abstract text:

Maternally transferred bacteria are prevalent across the insects where they have major impacts upon host nutrition, defense, and reproduction. A diverse range of bacteria have evolved such lifestyles, and opportunities for co-infection exist in a number of insects harboring multiple maternally transferred symbiont species. In this study we present evidence for strong structuring of maternally transferred symbiont communities within individual hosts of the pea aphid, *Acyrtosiphon pisum*. Extensive sampling over time and across the United States reveals consistent pairwise partnerships between a number of bacteria, while showing that several community types are much rarer than expected. A field-based study on transmission rates provides a partial explanation for these findings, as symbionts' rates of maternal transmission are impacted by the identities of co-infecting bacterial species. These discoveries have implications for our understanding of symbiont function within the model pea aphid system, due to a lack of research on symbiont-induced phenotypes for hosts with multiple symbionts. They also suggest the potential for active cooperation and competition in the within-host arena, raising questions