



ID der Kurzfassung : 378

Effects of sugar and blood diets on the proteome of female *Lutzomyia longipalpis*

Inhalt

Introduction

Leishmaniasis is a vector-borne disease caused by protozoa of the genus *Leishmania* and remains a significant public health concern in tropical regions. In its vectors, blood feeding provides a suitable environment for parasite establishment in the female gut. Understanding the proteome associated with blood digestion may contribute to studies on vector competence and insect biology. Here, we compared the proteomes of different tissues from uninfected female *Lutzomyia longipalpis*, the main vector of visceral leishmaniasis in the Americas, subjected to blood and sugar feeding.

Methods

Blood-fed and sugar-fed *L. longipalpis* females were dissected, and their proteins were analyzed by LC-MS/MS using a bottom-up discovery proteomics approach. Proteins with differential metabolic functions in gut and body samples were identified using Perseus and UniProt annotations, and analyzed through orthology inference, multiple sequence alignment, and phylogenetic reconstruction using OrthoFinder, MAFFT, IQ-TREE, VectorBase, and NCBI Blast.

Results

Approximately 9,000 proteins were identified and grouped into four categories: blood-induced gut proteins, sugar-induced gut proteins, blood-induced body proteins, and sugar-induced body proteins. Comparative analyses revealed protein sets exclusive to sand flies as well as orthologs shared among hematophagous insects. Blood-induced gut proteins exclusive to sand flies emerged as promising markers of the digestive process.

Keywords

Lutzomyia, proteome, digestion, blood feeding, sugar feeding

Registration ID

OHS26-31

Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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Vortragende(r): WELBERT, Juliana (Fiocruz)

Track Klassifizierung: Vectors

Typ des Beitrags: Poster presentation

Eingereicht von **WELBERT, Juliana** <juliana.welbert@hotmail.com> am **Donnerstag, 18. Juni 2026**