Analysis of thoracic proteins of female *Aedes togoi, Anopheles lesteri* and *Anopheles paraliae*, responsible for nocturnally subperiodic *Brugia malayi* infection

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Brugia malayi is a mosquito-borne filarial nematodes causing human filariasis lymphatic (LF). Understanding the host responding to *B. malayi* would be useful to prevent the transmission of the disease. The ability of pathogen transmission is depend on the relationship between host and parasite that occurring in the thoracic muscles. However, little is known about mosquito proteins responding during developing processes. We aim to characterize and compare the proteomic profiles of the thoracic proteins of the three mosquito species responsible for nocturnally subperiodic *B. malayi* infections. Highly susceptible (*Aedes togoi, Anopheles lesteri*) as well as low susceptible (*Anopheles paraliae*) filariasis vectors were used in this study. The thoraces of *B. malayi*-infected mosquitoes (test group) and uninfected blood meals (control group) of each mosquito species were collected at 96 hours post blood meal. The SDS-PAGE-separated-protein profiles of *B. malayi*-infected *Ae. togoi, An. lesteri* and *An. paraliae* showed at least 10, 9 and 8 major protein bands, respectively, whereas 6 major protein bands were found in the control groups. Nano-liquid chromatography mass spectrometry (nanoLC-MS/MS) revealed 22, 9 and 12 previously known proteins in *B. malayi*-infected *Ae. togoi, An. lesteri* and *An. paraliae*, respectively. Of interest, peroxiredoxin 5, thioredoxin and superoxide dismutase, were expressed only in *B. malayi*-highly susceptible *Ae. togoi* and *An. lesteri*. This is the first study provides the data on thoracic protein profile responding during *B. malayi* development and demonstrates that antioxidant and detoxifying proteins might play important role and/or provide favorable environment in facilitating further development of the *B. malayi* microfilariae to the human infective stage in the vectors.

Speaker Biography

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