PhD defence Irina Matetovici

The dynamic interplay between Trypanosoma brucei and the tsetse fly vector revealed by transcriptome analysis

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Booking recommended

Dit is de omschrijving

Supervisors:

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Summary:

A group of devastating vector-borne parasitic diseases, African trypanosomiasis in sub-Saharan Africa, is caused by protozoan parasites of the genus *Trypanosoma*, including two human-pathogenic species of the *T. brucei* complex. For their development and transmission, African trypanosomes rely on their blood feeding vector, the tsetse fly (*Glossina* sp.). Here, the *T. brucei* parasites must overcome a series of barriers to colonize the midgut and subsequently achieve maturation and infectivity in the salivary glands. Understanding the interactions between trypanosomes and the tsetse fly is of great interest, and could possibly lead to the development of efficient ways to minimize or block the parasite transmission by its vector.

The main goal of this project was to understand the trypanosome-associated changes of immune-related processes in the tsetse fly salivary gland. This was achieved by an extensive comparative transcriptome analysis of *T. brucei*-infected salivary glands versus non-infected glands. This transcriptome analysis allowed us to gain novel insights into key immune-related genes affected upon infection and on the negative impact the parasite has on the integrity and functioning of the gland epithelium. Through this approach we identified the thioester-containing proteins family as possible immunity-associated molecules involved in controlling the trypanosome parasite. This interesting lead was then further explored more in-depth by revealing detailed information about their structure, evolutionary relationships and expression profiles in response to different trypanosome species – *T. brucei* and *T. congolense*.

Additionally, the generated *T. brucei* “salivary gland population” transcriptome was compared with that of trypanosome population in other infected tsetse tissues (proventriculus and midgut) to identify genes differentially expressed genes that could be related to the parasite sensing of/adaption to these micro-environments. This gene profiling showed evidence of profound differences between *T. brucei* life stages.

Overall, these findings contribute to a better understanding of the biological impact of the sleeping sickness parasite on the tsetse fly and how the insect vector keeps this impact under control. Moreover, these results offer a foundation for further studies on host-parasite interactions where the simultaneous gene expression analysis of the two organisms is essential.