

Publication

A large repertoire of parasite epitopes matched by a large repertoire of host immune receptors in an invertebrate host/parasite model

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**ID** 462204**Author(s)** Mone, Yves; Gourbal, Benjamin; Duval, David; Du Pasquier, Louis; Kieffer-Jaquinod, Sylvie; Mitta, Guillaume**Author(s) at UniBasel** [Du Pasquier, Louis](#) ;**Year** 2010**Title** A large repertoire of parasite epitopes matched by a large repertoire of host immune receptors in an invertebrate host/parasite model**Journal** PLoS neglected tropical diseases**Volume** 4**Number** 9**Pages / Article-Number** e813

For many decades, invertebrate immunity was believed to be non-adaptive, poorly specific, relying exclusively on sometimes multiple but germ-line encoded innate receptors and effectors. But recent studies performed in different invertebrate species have shaken this paradigm by providing evidence for various types of somatic adaptations at the level of putative immune receptors leading to an enlarged repertoire of recognition molecules. Fibrinogen Related Proteins (FREPs) from the mollusc *Biomphalaria glabrata* are an example of these putative immune receptors. They are known to be involved in reactions against trematode parasites. Following not yet well understood somatic mechanisms, the FREP repertoire varies considerably from one snail to another, showing a trend towards an individualization of the putative immune repertoire almost comparable to that described from vertebrate adaptive immune system. Nevertheless, their antigenic targets remain unknown. In this study, we show that a specific set of these highly variable FREPs from *B. glabrata* forms complexes with similarly highly polymorphic and individually variable mucin molecules from its specific trematode parasite *S. mansoni* (*Schistosoma mansoni* Polymorphic Mucins: SmPoMucs). This is the first evidence of the interaction between diversified immune receptors and antigenic variant in an invertebrate host/pathogen model. The same order of magnitude in the diversity of the parasite epitopes and the one of the FREP suggests co-evolutionary dynamics between host and parasite regarding this set of determinants that could explain population features like the compatibility polymorphism observed in *B. glabrata*/*S. mansoni* interaction. In addition, we identified a third partner associated with the FREPs/SmPoMucs in the immune complex: a Thioester containing Protein (TEP) belonging to a molecular category that plays a role in phagocytosis or encapsulation following recognition. The presence of this last partner in this immune complex argues in favor of the involvement of the formed complex in parasite recognition and elimination from the host.

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