How parasitoid wasps vary in virulence: what venom tell us

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Sixth International Symposium on Molecular Insect Science; 2-5 October 2011; NH Grand Krasnaplosky, Amsterdam, The Netherlands

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Endoparasitoid wasps lay their eggs in arthropods, eventually killing them as the result of their development. To ensure successful parasitism, they inject various components, including venom factors that affect host immunity and/or manipulate its physiology. Until now, a limited number of venom proteins have been characterized from parasitoids, and very few have been demonstrated to be involved in parasitoid virulence (Colinet et al., 2009; Colinet et al., 2010). Even less is known of the degree of inter-specific and intra-specific variation of parasitoid venom factors, and the selective parameters driving their evolution. Estimation of the potential for evolution of virulence molecules in a parasitoid species is nevertheless essential information to understand and improve the success of biological control assays.

We have addressed these questions using different parasitoid species. We report here results obtained using the figitid parasitoids of Drosophila, *Leptopilina heterotoma*, a generalist species, and *L. boulardi*, more specialists, as well as on the aphid braconid species *Aphidius ervi*. Virulence variation has been reported in *L. boulardi* with two different, well-characterized strains. Studies were based on transcriptomic and proteomic analyses, combined with specific studies on virulence factors we previously characterized.

Results reveal extensive inter-specific differences in venom proteins, with most of the abundant proteins in the venom of one species absent or rare in the venom of the other species, even from the same genus i) important intra-specific variations in *L. boulardi*, which is explained for the major virulence factor by differences in regulation of transcription ii) inter-individual variations for the major virulence factor of *L. boulardi* and its response to selection.

In conclusion, venom virulence factors of parasitoid wasps can show extensive variations even in the same genus or the same species suggesting a large potential for short-term evolution in response to selective parameters such as host substition or temperature variation.

Key-words : venom, virulence factors, variability, proteomics, selective parameters

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