

Abstract

Peptides with an antimicrobial activity are a well-known component of an innate immunity of insects. A major part of them has been found in haemolymph, but they occur at the body surface and various glands of insects as well. Some of them have been found in venom glands of Hymenoptera. Whereas their immunity function in haemolymph seems to be obvious, the purpose of their frequent presence in venom glands is still more or less a matter of speculation. A hypothesis of their function in a collective immunity comes into consideration in social Hymenoptera. But this hypothesis doesn't explain, why does this sort of peptides occur also at solitary bees (and even in such diversity). There is not only little explanation of their function, but there is not even not much information about their origin and diversity.

This thesis brings a detailed description of the evolution of peptides in venom glands of cuckoo-bees from the genus *Nomada*. A possible homology of two peptides from *Nomada* bees with previously known peptides melittin and MCD-peptide of *Apis mellifera* is revealed. The evolution of a main peptide with antimicrobial activity in *Nomada* genus is traced with a method of ancestral reconstruction. Except for species *N. fuscicornis* the differences among species are based on changes that do not alter the antimicrobial activity of the peptide. We cannot rule out, that the selective pressure, which maintains the antimicrobial function, is really caused by microorganisms.

Furthermore, the rate of substitution a deletion changes in *Nomada* genus is compared to the rates of other, less related species. Based on the information acquired, a hypothesis on the function of antimicrobial peptides in solitary bees is proposed.

Keywords:

venom gland, venom, peptides, antimicrobial activity, bees