

## Conclusion

Insect immune response is a complicated process. Antimicrobial peptides frequently act synergistically, some proteins have transporter functions, peptide inhibitors can block processing enzymes involved in activating cascades or different enzymes can activate antimicrobially active proteins or peptides. In this study we presented two different isolation protocols, which resulted in the identification of several already known and two novel antimicrobial proteins or peptides from the hemolymph of the larvae of fleshfly *Sarcophaga bullata*.

We are the first group to monitor the time-course of tissue-specific expression patterns of eight genes in *Sarcophaga bullata* larvae after different immune challenges using qPCR. We show similarities, as well as differences in insect immune responses. We are also the first group to analyze the expression patterns of the genes that encode SBP and sarcocystatin, proteins that are mainly connected with larval development and metamorphosis. Using 2D-electrophoresis we analyzed the time-dependent immune response in larval fat bodies and hemocytes. We detected 9 up-regulated proteins in hemocytes and 15 differentially expressed proteins in fat body cells.

We hope that our study will shed more light into the complex processes of immune responses in *Sarcophaga bullata* larvae.