

Are microRNAs steering the development of the honeybee hypopharyngeal gland?

Monika Krahnstöver¹, Pooja Gupta², Benedikt Polaczek¹, Stefan Börno³, Ralf Einspanier¹

¹ Free University of Berlin, Institute of Veterinary Biochemistry, Berlin

² Free University of Berlin, Institute of Mathematics, Berlin

³ Max Planck Institute for Molecular Genetics, Berlin

E-mail of corresponding author: monika.krahnstoever@fu-berlin.de

Honeybee's maintenance and survival relies on the success of reproduction, a function typically associated with the reproductive tract of the queen. Likewise, the workerbee's hypopharyngeal glands represent another important organ for the sustenance of offsprings. Since secretions of these glands (royal jelly) are essential feed components for the bee larvae, amount and composition of the royal jelly is important for the breeding success of the bee colony. Furthermore, some factors are described that may directly influence the performance of these glands, like colony conditions or pesticides.

However, the presence and role of microRNAs, known as superior regulators of

the cellular expression, have not been elucidated within the hypopharyngeal gland. The aim of our study is to profile the microRNA pattern and to better understand the effects of microRNAs on the development of the hypopharyngeal glands and its secretion.

Hypopharyngeal glands were isolated in different physiological stages: inactive and active. RNA was extracted and Next Generation Sequencing was used to identify differences in the two sampling groups. First results indicate regulated microRNA candidates and a quantitative validation of these interesting results are on the route.