Bacterial associates of the planthopper *Ommatidiotus dissimilis* (Fallén, 1806) (Hemiptera: Caliscelidae)

A. Michalik & T. Szklarzewicz. Department of Developmental Biology and Morphology of Invertebrates, Institute of Zoology and Biomedical Research, Jagiellonian University, 9, Gronostajowa St., PL30-387 Kraków, Poland
J. Szwedo. Department of Invertebrate Zoology and Parasitology, University of Gdańsk, 59, Wita Stwosza St., PL80-309 Gdańsk, Poland
A. Stroiński. Museum and Institute of Zoology, Polish Academy of Sciences, 64, Wilcza St., PL00-679 Warszawa, Poland
D. Świerczewski. Department of Zoology and Animal Ecology, Jan Długosz University, 13/14, Al. Armii Krajowej, PL42-201 Częstochowa, Poland

Nutritional symbiosis between insects and microorganisms (bacteria and/or yeast) is widespread in nature (Buchner 1965). Numerous studies (Wilkinson and Ishikawa 2001; Douglas 2009; McCutcheon & Moran 2010) indicate that the occurrence of symbiotic microorganisms in hemipterans which feed on phloem or xylem sap is related to their restricted diet which is deficient in essential amino acids and vitamins. It is known that the major function of these symbiotic microorganisms is to provide amino acids and vitamins lacking in phloem or xylem sap to their host insect. Among insects, symbiotic systems (the localization of symbionts in the host insect body, their systematic affinity and mode of transmission between generations) of Fulgoromorpha are poorly known. Fragmentary data concerning symbionts of planthoppers reveal that their ancestral, obligatory symbionts are bacteria *Sulcia muellerii* and *Vidania fulgoroidea* (Urban and Cryan 2012). The aim of this research was to study the systematic affinity, distribution and the mode of inheritance of microorganisms associated with the planthopper *Ommatidiotus dissimilis* (Caliscelidae), strictly monophagous on *Eriophorum vaginatum* (Cyperaceae). Our histological and ultrastructural observations have shown that *O. dissimilis* is host to five distinct types of bacteria. Molecular analysis based on 16S rDNA sequences of bacteria has indicated that they belong to the following genera: *Sulcia*, *Vidania*, *Sodalis*, *Wolbachia* and *Rickettsia*. Bacteria *Sulcia*, *Vidania* and *Sodalis* are localized in separate bacteriocytes, whereas small, rod-shaped bacteria *Wolbachia* and *Rickettsia* are dispersed in various insect tissue types. All symbionts are transovarially transmitted from one generation to the next. Individual bacteria leave the bacteriocytes and migrate towards the ovaries. The infection of ovarioles takes place during late vitellogenesis. The bacteria invade the posterior pole of the oocyte. They pass through spaces between the neighboring follicular cells or through their cytoplasm and then gather in the perivitelline space.

References

Buchner, P. (1965) *Endosymbiosis of Animals with Plant Microorganisms*. Interscience Publishers, New York, 909 pp.

Douglas, A.E. (2009) The microbial dimension in insect nutritional ecology. *Functional Ecology*, 23, 38–47.

McCutcheon, J.P. & Moran, N.A. (2010) Functional convergence in reduced genomes of bacterial symbionts spanning 200 My of evolution. *Genome Biology and Evolution*, 2, 708–718.

Urban, J.M. & Cryan, J.R. (2012) Two ancient bacterial endosymbionts have coevolved with the planthoppers (Insecta: Hemiptara: Fulgoroidea). *BMC Evolutionary Biology*, 12, 87–106.

Wilkinson, T.L. & Ishikawa, H. (2001) On the functional significance of symbiotic microorganisms in the Homoptera: a comparative study of *Acyrthosiphum pisum* and *Nilapavata lugens*. *Physiologial Entomology*, 26, 86–93.