

Genetic diversity and phylogeny of *Wolbachia* in lepidopteran hosts

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Motivation and Aim: *Wolbachia* are maternally inherited intracellular symbionts of arthropods and some nematodes. The genetic diversity of *Wolbachia* is subdivided into 16 supergroups (phyletic lines). Significant number of insect families appears to be unexplored for *Wolbachia* symbionts. Seventeen families of Lepidoptera are known to be infected with *Wolbachia*, while this order includes up to 200 families. Here we try to find *Wolbachia* infection in hosts of poorly investigated lepidopteran families and further analyse genetic data of *Wolbachia* isolates.

Methods and Algorithms: The insect collection consisted of 519 samples and included 255 species of 23 lepidopteran families. Some of these species are dangerous forest pests. The DNA extraction was individually performed from each specimen. Infection status was determined by PCR with *Wolbachia* specific primers targeted to the *wsp* and *16SrRNA* loci. Genetic diversity of *Wolbachia* was determined by the multilocus sequence typing (MLST) protocol [1], which included five loci. Phylogenetic analysis was conducted using MEGA 6 [2].

Results: *Wolbachia* symbionts were found in 36 species of 12 lepidopteran families. Some of these species were forest pests. We found both new haplotypes and previously described *Wolbachia* variants. Most of symbiont haplotypes belonged to supergroup B, and remaining haplotypes belonged to supergroup A.

Conclusion: We present comprehensive results of *Wolbachia* incidence and *Wolbachia* genetic diversity in Lepidoptera. The results of this study are necessary to develop *Wolbachia*-based biotechnological methods of pest control.

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References

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