Wolbachia and mtDNA diversity and distribution in palearctic *Drosophila melanogaster* populations

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Motivation and Aim: Wolbachia symbionts are found in *Drosophila melanogaster* populations all over the world [1, 2]. Genetic diversity of the symbiont in *D. melanogaster* is subdivided into several clades that have strong association with certain host mtDNA clades [3, 4]. Here we represent results of comprehensive surveys on cytoplasmic inheritance (*Wolbachia* and mtDNA) of fruit fly populations in a vast Palearctic territory. We address to the symbiont prevalence and symbiont genetic pattern as well as mtDNA pattern.

Methods and Algorithms: In total 1550 *D. melanogaster* samples were collected from different Palearctic localities. Samples were screened by PCR for *Wolbachia* infection and mitochondrial haplotypes.

Results: Wolbachia infection was found in every studied *D. melanogaster* populations from Western Europe to Far East. The average rate of infection was 0.56 (95 % confidence interval, 0.54–0.59). Infection rates are not dependent on longitude or latitude. Five mtDNA clades were found, where two of them (III and V clades) were predominant, that confirmed with previous data: the III clade is widely distributed in the world while the V clade is found only in Palearctic region.

Conclusion: We demonstrate wide *Wolbachia* distribution in Palearctic *D. melanogaster* populations. According to our data on symbiont diversity and distribution the fly populations of many regions in temperate zone renew after cold season. High frequency of the V clade of mtDNA in Palearctic populations may be explained by it having originated in this region.

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