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The impact of rapid decrease of *Aporia crataegi* (Lepidoptera: Pieridae) population size on *Wolbachia* infection rate

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Motivation and Aim: *Wolbachia* endosymbionts are widely distributed among insects. The high level of infection was observed in populations of black-veined white (*Aporia crataegi*) of Novosibirsk province in 2006. Rapid population decrease had occurred in 2007 due to late mid-May frosts. Here we examined *Wolbachia* infection rate in Novosibirsk *A. crataegi* population that restored its abundance in 2015–2016 seasons. Also we try to compare data of infection rates, *Wolbachia* and mtDNA diversity derived from different populations of black-veined white.
Methods and Algorithms: The collection includes 246 *A. crataegi* specimens from Novosibirsk and Kemerovo provinces, Altai Republic, and Yakutia. *Wolbachia* infection status was determined by PCR with primers to *coxA* and *16SrRNA Wolbachia* loci. The barcoding region of *COI* gene of both infected and uninfected specimens was sequenced. The phylogenetic tree *COI* gene was reconstructed in Mega7 using all available sequences from BOLD database and our data.
Results: *Wolbachia* symbionts were not found in *A. crataegi* from Altai Republic, Novosibirsk and Kemerovo provinces, while several infected specimens were found in Yakutia. Their *Wolbachia* symbionts had *coxA-6* allele. New alleles of *A. crataegi* mitochondrial gene ... were found.
Conclusion: *Wolbachia* infection rate in black-veined white of Novosibirsk province dramatically decreased after a severe drop of host population in 2007. No *Wolbachia* infection was detected at neighboring provinces as well. Also we found association of *Wolbachia* infection with a certain mtDNA allele of *A. crataegi.*
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