

## Accepted Manuscript

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PII: S1055-7903(16)30471-7

DOI: <http://dx.doi.org/10.1016/j.ympev.2016.12.034>

Reference: YMPEV 5713

To appear in: *Molecular Phylogenetics and Evolution*

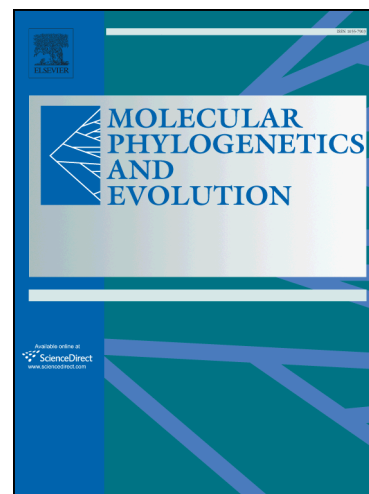
Received Date: 11 September 2016

Revised Date: 7 December 2016

Accepted Date: 28 December 2016

Please cite this article as: Ilinsky, Y., Kosterin, O., Molecular Diversity of *Wolbachia* in Lepidoptera: Prevalent Allelic Content and High Recombination of MLST Genes, *Molecular Phylogenetics and Evolution* (2016), doi: <http://dx.doi.org/10.1016/j.ympev.2016.12.034>

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## Molecular Diversity of *Wolbachia* in Lepidoptera: Prevalent Allelic Content and High Recombination of MLST Genes

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**Running title:** *Wolbachia* MLST Diversity in Lepidoptera.

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**Keywords:** *Wolbachia*, recombination, MLST, Lepidoptera, symbiosis, evolution

**Highlights:**

*Wolbachia* incidence in butterflies of temperate latitudes is greater than 50 %.

The core of *Wolbachia* MLST diversity in Lepidoptera hosts is the allele content of ST-41.

Recombination often occurs between strains within the *Wolbachia* supergroup.

**Abstract**

*Wolbachia* are common endosymbiotic bacteria of Arthropoda and Nematoda that are ordinarily transmitted vertically in host lineages through the egg cytoplasm. Despite the great interest in the *Wolbachia* symbiont, many issues of its biology remain unclear, including its evolutionary history, routes of transfer among species, and the molecular mechanisms underlying the symbiont's effect on its host. In this report, we present data relating to *Wolbachia* infection in 120 species of 13 Lepidoptera families, mostly butterflies, from West Siberian localities based on Multilocus sequence typing (MLST) and the *wsp* locus and perform a comprehensive survey of the distribution of *Wolbachia* and its genetic diversity in Lepidoptera worldwide. We observed a high infection incidence in the studied region; this finding is probably also true for other temperature and latitude regions because many studied species have broad Palearctic and even Holarctic distribution. Although 40 new MLST alleles and 31 new STs were described, there was no

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