



Category: Miscellaneous

Ecology and host-symbiont interactions drives the strain-specific association of *Wolbachia* with Indian *Drosophila* host

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Abstract

The discovery of *Wolbachia*, a gender bender of insect population revolutionized the field of medical biology with the possibility of using *Wolbachia* infected host to control the spread of major vector borne diseases. *Drosophila* has long been known as an invertebrate experimental model and the presence of *Wolbachia* strains in this species makes it unique for the entomologist to explore the different *Wolbachia* strains present in the *Drosophila* host and understand host-symbiont interactions. In the light of these developments we obtained whole genome sequences of four different *Wolbachia* strains using NGS technology based on Illumina platform isolated from two human commensal Indian *Drosophila* species i.e. *Drosophila melanogaster* and *Drosophila ananassae* from Kochi (Southern India) and Ahmedabad (Western India). The strains were identified as wMel to be present in *D. Melanogaster* and wRi in *D. Ananassae* based on BLAST analysis. This was the first attempt at obtaining the whole genomes of Indian *Wolbachia* strains. Further we compared these novel genome assemblies and observed strain-specific sequence similarity in certain gene sequences known for their significant role in strain identification or host symbiont interaction. Upon comparison of the Indian *Wolbachia* genomes with the earlier sequences one, we also observed India specific sequence similarity in some of the genes. In order to understand better the *Wolbachia*-host association we also studied the associated bacterial diversity in these two *Drosophila* species. The distribution of the associated bacterial species was found to be both species as well region dependent. The findings of the current study support that ecology also plays a major role in gene-genome evolution and host preferences. The results of the above study provide us an overview of *Wolbachia*-host interaction and strain specific nature of this endosymbiont. However, in order to further understand the exact forces at play that makes such an association, deeper study needs to be carried out.

References

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