

ABSTRACT

Vector borne diseases such as dengue, malaria, chikungunya, yellow fever etc. are a major medical concern for developing countries like India. Several strategies have been developed to control the spread of these mosquito vectors, however, none of the method imparts a sustainable promise. *Wolbachia*, an endosymbiotic bacterium resides inside the host, manipulates their reproductive fitness and is transmitted through maternal cytoplasm. *Wolbachia* ensures its spread in the host population by causing cytoplasmic incompatibility, male-killing, parthenogenesis or feminisation. It is found to be present in a wide range of host, mainly infecting the arthropod and nematodes. Studies have shown that *Wolbachia* strains of *Drosophila* host i.e. *wMel*, *wMelPop*, *wRi* cause viral resistance, reduces adult longevity and cytoplasmic incompatibility respectively, and these effects are strain and host-specific. The phenotypic effects of *Wolbachia* strains make it an ideal biocontrol agent targeting the vector population or their ability to spread diseases. Much literature on the distribution, characterisation and effect of *Wolbachia* strain in Indian *Drosophila* is not available. The present study was thus designed in an attempt to bridge the gaps in the existing literature. The objective of the present work was to explore diversity of *Wolbachia* in *Drosophila* host species collected from different eco-climatic regions of India. We further aim to study gene-genome organisation, identify significant genes involved in host-symbiont interactions and perform comparative analysis to study strain-specific association of *Wolbachia* with its host by obtaining the whole genome sequences of Indian *Wolbachia* strains based on NGS approach. Finally, we also studied *Wolbachia-Drosophila* interactions and functional implications of *Wolbachia* infection in its host by generating *Wolbachia* infected and uninfected lines.

In the present study, we observed that infection of *Wolbachia* was limited to three *Drosophila* host species in a total of 10 species collected from different eco-geographic regions of India. Further, the *Wolbachia* whole genomes of two different strains generated for the first time from India clearly highlight the strain-specific variations throughout the significant functional genes, highlighting the different evolutionary history of these strains. We also observed events of reductive evolution in the endosymbiont genome in several genes. Finally, through the phenotype studies we observed that the presence of *Wolbachia* infers a fitness benefit to *Drosophila melanogaster*. The present work on these host-symbiont interactions through comparative genomics and phenotypic studies can become useful in establishing *Wolbachia* as a disease control model for different vector borne diseases.