ABSTRACT

Wolbachia based diseased vector control approaches have been purposed as a mean to augment the prevailing Dengue vector control strategies. Therefore, it is essential to have thorough knowledge about the prevalence and Wolbachia-host (vector) interaction. This study was performed for the detection and characterization of the local Wolbachia strain in 2 mosquito species (Culex quinquefasciatus, Aedes albopictus) and one species of fruit flies (Drosophila simulans) collected from different indoor and outdoor sites of Lahore, Pakistan. For this purpose, twenty insect pools from each sample containing 20 pairs of ovaries were examined for the presence of Wolbachia gDNA was isolated using standard procedure described in 3.6. DNA was amplified by PCR using gene specific primers (wsp and ftsZ). Ten pools of Cx. quinquefasciatus (50%) were found to be positive for Wolbachia. NCBI Blast of Wolbachia wsp sequence found from Cx. quinquefasciatus showed 99% homology to the wPip isolate reported from U.K. belonging to super group B. Wolbachia ftsZ sequence showed 100% homology to the wPip isolates from Cx. quinquefasciatus and other related species belonging to Wolbachia super group B reported in USA, U.K and Argentina. In Ae. albopictus, all the twenty pools (100%) were found to be positive with wAlbA and wAlbB. NCBI blast of the wsp-A and wsp-B isolates showed 99% and 100% homology to the Wolbachia isolate of Ae. albopictus from USA and Malaysia respectively. FtsZ isolate of wAlbB showed 100% homology to the wAlbB from USA. Phylogenetic analysis showed that A and B Wolbachia isolates in current study were clustered in A and B subgroups already reported from different countries. All pools of D. simulans (100%) were found to be positive for Wolbachia wsp sequence. NCBI Blast showed 99% homology to the wRi isolate from different Drosophila species reported from USA, China, Austria and Sweden. FtsZ isolate of wRi showed 99% homology to the Wolbachia isolate of D. simulans reported from Sweden. Phylogenetic analysis showed that it was closely related to wRi and the super group A.