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## 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.