WOLBACHIA SUPERGROUPS A AND B IN NATURAL POPULATIONS OF MEDICALLY IMPORTANT FILTH FLIES (DIPTERA: MUSCIDAE, CALLIPHORIDAE, AND SARCOPHAGIDAE) IN THAILAND

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Abstract. Filth flies, belonging to suborder Brachycera (Family; Muscidae, Calliphoridae and Sarcophagidae), are a major cause of nuisance and able to transmit pathogens to humans and animals. These insects are distributed worldwide and their populations are increasing especially in sub-tropical and tropical areas. One strategy for controlling insects employs Wolbachia, which is a group of maternally inherited intracellular bacteria, found in many insect species. The bacteria can cause reproductive abnormalities in their hosts, such as cytoplasmic incompatibility, feminization, parthenogenesis, and male lethality. In this study we determined Wolbachia endosymbionts in natural population of medically important flies (42 females and 9 males) from several geographic regions of Thailand. Wolbachia supergroups A or B were detected in 7 of female flies using PCR specific for wsp. Sequence analysis of wsp showed variations between and within the Wolbachia supergroup. Phylogenetics demonstrated that wsp is able to diverge between Wolbachia supergroups A and B. These data should be useful in future Wolbachia-based programs of fly control.

Keywords: Wolbachia, fly control, medically important fly, wsp, Thailand

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