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Title: Morphological and Molecular Identification of Dengue Fever Vector Aedes aegypti (Diptera: Culicidae) in Jeddah Governorate-Saudi Arabia

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Abstract: Mosquito-borne diseases are still a major human and animal health problem in the world. Identification of mosquito vectors is important in many respects including development of vector control strategies. Adults and immature stages of Ae.aegypti were identified based on the morphological characters using light and electron microscope and appropriate illustration (pictorial) keys. It is common knowledge that morphological ID is not as accurate as molecular ID. Recently DNA-based identification methods using molecular markers such as nuclear ribosomal internal transcribed spacer (ITS), cytochrome b (Cyt-b) and cytochrome c oxidase subunit 1 and 2 COI, COII which become an important method to differentiate between siblings and closely related species of mosquitoes. Adults of Ae. aegypti were collected from five areas in Jeddah city. Molecular identification by isolating both of DNA and total protein of Ae. aegypti were conducted. The results showed that DNA was isolated from mature and immature stages of Ae.aegypti using PCR technique from either the lab strain or from older and/or field specimens. This assay consisted of different primers reaction, which could amplify the DNA of both mature and immature stages producing fragment of three distinct sizes, 1250 bp, 500 bp, similar to 400-600 bp and 300bp for CO1B, Cryb, ITS2 and ITS2-2 respectively Some of these loci were sequenced and submitted to the GenBank database NCBI Protein samples of (larva, pupa and adult) of the dengue fever vector, Ae. aegypti were isolated. The relative molecular weight of the detected bands was approximately in the range of 16.6 - 75.6 kDa.

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