

Molecular identification and composition of cyclorrhaphan flies associated with cafeterias

ABSTRACT

Cafeterias are routinely visited by people to fulfil their daily feeding and drinking requirements. Unnoticed visitors, such as cyclorrhaphan flies, are also present in these places which can be a source of food poisoning and disease spread. These flies were collected from garbage piles, kitchen and vacant sites of two cafeterias (Cafeteria Serumpun and Cafeteria Agro-bio) within Universiti Putra Malaysia and one cafeteria (Cafeteria Old-flat) outside the university. A total of 1,037 fly specimens were collected and identified belonging to Calliphoridae, Muscidae and Sarcophagadae. The COI and COII gene sequences and phylogenetic results revealed five species of cyclorrhaphan flies, namely *Chrysomya megacephala*, *Lucilia cuprina*, *Musca domestica*, *Ophyra spinigera* and *Sarcophaga dux*. The highest number of flies was found at Cafeteria Serumpun (44%), followed by Cafeteria Old-flat (36%) and Cafeteria Agro-bio (20%). The most populated sampling site was kitchen and the abundant species was *C. megacephala* (92.66%). Analysis of data showed significant difference between individuals of different species at different cafeterias and sampling sites.

Keyword: Cyclorrhaphan flies; COI gene; COII gene; Phylogenetic study; Cafeteria