

Genetic diversity, molecular markers and population genetics of human lymphatic filarial parasites

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Lymphatic filariasis (LF) is one of the most disfiguring diseases and a major public health problem in tropical world. The disease is caused majorly by *Wuchereria bancrofti*, and to smaller extent by *Brugia malayi* and *B. timori*. It transmitted by mosquito vectors belonging to genera *Culex*, *Anopheles*, *Aedes* and/or *Mansonia*. Currently, LF is targeted for elimination with Mass Drug Administration of a combination of Diethyl carbamazine/Ivermectine and Albendazole as a tool. Several rounds of MDA have already been administered in several LF endemic countries. However, there is a continuance of parasite prevalence in some areas despite repeated rounds of MDA. This could be due to genetic variations in the parasite strains that may not be responding to the antifilarial drug administered. These variations could be the result of various factors such as geographic isolation, infra-population or refugia, environmental factors and drug pressure. The long term administration of drug in

the elimination programme itself might have lead to this phenomenon or wide geographic distribution spanning continents might have effected variation. Investigating genetic variations among these variants may reveal the differential response to the antifilarial drugs and such studies are important for devising the drug administration strategies. In summary, there is a need to understand the genetic variation among the parasite populations in different LF endemic areas for which there is a need to develop appropriate markers. This review discusses the biological, physiological and genetic variations among LF parasites.

Speaker Biography

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