GENE FLOW ANALYSIS OF *ANOPHELES ARABIENSIS* (DIPTERA: CULICIDAE) POPULATIONS IN SOUTHERN AFRICA USING MICROSATELLITE DNA MARKERS

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ABSTRACT

Anopheles arabiensis is considered an important vector of human malaria in the southern African region where the disease is the major cause of morbidity and mortality. Gene flow plays an important role in malaria control with the spread of insecticide resistance. The main objectives of this study were to (i) measure the genetic variability within and between five populations (Botswana, Namibia, South Africa, Swaziland and Zimbabwe) of wild *An. arabiensis* and (ii) estimate the level of gene flow between natural populations across the Southern-limits of *An. arabiensis.* A total of 1225 *An. arabiensis* specimens were identified out of 1300 mosquitoes collected from 2000-2003 with the sample sizes ranging from 180-292 per country. Variation at four microsatellite markers was investigated on non-denaturing polyacrylamide gels. The results showed fewer variations between populations (2.96%) than within populations (82.60%) suggesting considerable homogeneity. However, estimates of gene flow (Nm) calculated from mean F_{ST} and R_{ST} statistics were relatively low, 1.14 and 1.19 respectively, suggesting somewhat restricted gene flow between populations. The occurrence of gene flow within subpopulations of *An. arabiensis* in Zimbabwe but not in South Africa is interesting with regard to the spread of insecticide resistance in Zimbabwe.

The results presented here are obviously subject to the limitations inherent in manual, silver staining method of analysing microsatellite DNA markers. It is possible that a different set of results would be obtained if an Automated Sequencing Analyzer were used.