

Molecular characterization of the African malaria vector *Anopheles funestus* using RFLPs

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Abstract : *Anopheles funestus* is one of the major malaria vectors in Africa, having a transmission potential that sometimes exceeds that of *An. gambiae s.s.* It is widespread throughout most of Sub-Saharan Africa. Until recently, remarkably little attention has been paid to the genetics of *An. funestus* and its close relatives, compared with the *An. gambiae* complex. Recent molecular studies on this important mosquito species has provided information on the genetic characterization of members of the *An. funestus* group and, in particular, of *An. funestus* itself from different geographic regions. Using restriction fragment length polymorphisms (RFLP), inter- and intra-specific variations were found. The PCR-RFLP of the D3 fragment digested by *MspI* was able to differentiate three clusters within *An. funestus* that differed by two D3 copies (M and W). Type M occurred in samples from Madagascar, Kenya and Uganda. Type W occurred in West-Central African samples from Senegal, Côte d'Ivoire and Cameroun. A third cluster was represented by specimens from Angola, Malawi, Mozambique and South Africa which exhibited both copies M and W.

The PCR-RFLP based on the digested-ITS2 fragment with the *BsiZI* endonuclease showed a high diagnostic power allowing the discrimination of all five members of the *An. funestus* group that were tested.