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journal homepage: www.elsevier.com/locate/meegidChromosomal and environmental determinants of morphometric variation in natural populations of the malaria vector *Anopheles funestus* in CameroonDiego Ayala^{a,*}, Harling Caro-Riaño^a, Jean-Pierre Dujardin^a, Nil Rahola^a, Frederic Simard^{a,b}, Didier Fontenille^a^aIRD, UMR 224 MIVEGEC/BEES, 911 Av Agropolis, 34394 Montpellier, France^bIRSS-DRO, BP 545, Bobo-Dioulasso, Burkina Faso

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ABSTRACT

Anopheles funestus is one of the most proficient malaria vectors in the world, mainly because of its remarkable ability to populate a wide range of ecological settings across Africa. Its formidable environmental plasticity has been primarily associated to high amounts of genetic and inversion polymorphisms. However, very little is known about the morphological changes that this ecological adaptation entails. Here, we report on wing morphometric variations in karyotyped specimens of this species collected throughout a wide range of eco-geographical conditions in Cameroon (Central Africa). Our results revealed strong selection on mosquito wing traits. Variation of wing size was dependent on temperature and elevation ($p < 0.001$), while wing shape did not exhibit a specific environmental pattern. On the other hand, we observed a significant correlation of wing shape variation ($p < 0.001$), but not size ($p > 0.05$), with regard to karyotype. This pattern was maintained across different environmental conditions. In conclusion, our findings cast strong evidence that change in morphometric traits are under natural selection and contribute to local adaptation in *A. funestus* populations. Furthermore, the robust relation between chromosome polymorphisms and wing shape suggests new evolutionary hypotheses about the effect of chromosomal inversions on phenotypic variation in this malaria vector.

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1. Introduction

One of the major factors which establish the ability of an insect to become an important vector for human diseases is its “anthropophilic” behavior, e.g. its preference for feeding human blood and/or exploiting man-made resting or breeding habitats. Hence, medically important insects, such as malaria vector mosquitoes, are exposed to control pressures and habitat modifications due to their close contact with human populations, revealing frequent genotypic and phenotypic variations (Dujardin, 2008). In the field, these variations can be based either on genetic divergence, direct environmental effects, or both. Thus, studies on phenotypic variation can provide relevant insights into the evolution of vector systems and help detect local populations with potentially important characters, which might affect disease transmission (Dujardin, 2008; Pigliucci, 2005). However, despite their importance, little is known about phenotypic variation and

morphological plasticity in *Anopheles* species across the different habitats that they populate. This is an important limitation for studies aimed at exploring ecological adaptation in malaria vectors with direct consequences on disease epidemiology.

Morphometric traits have been employed to analyze adaptive variation in natural populations of animals and plants (Mayr, 1942). Patterns of morphological variation involving size or shape dimensions have been often interpreted with regard to their evolutionary importance (Pigliucci, 2005). In this sense, insect wings have been reported as an excellent model for studying morphological evolution in natural populations. Wing size is directly related to body size (Sokoloff, 1966) and there exists considerable evidence that size and shape are targets of natural selection (Soto et al., 2006). Moreover, they respond to environmental variation in complex ways, suggesting that the range of phenotypes produced by a particular genotype might be different depending on environmental conditions. As a result, morphological changes may be part of an adaptive response (Carreira et al., 2006; Weber, 1990). Consequently, investigations on morphological traits variation necessarily require to involve the simultaneous analysis of genetic and environmental factors, which somehow cause intra-specific variation and interspecific divergence (Mackay, 2004).

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