Neglected major malaria vectors in Africa : recent data and new ways of research

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This document shows some of the ideas submitted to the Gates GCGH

Vector control is a major component of malaria control. For historical and practical reasons, most studies have so far focused on *Anopheles gambiae*, the most notorious vector of human malaria, and almost all ongoing work targets this species complex, particularly since genome sequence was published. For example new vector control strategies are being developed mainly based on recent acquired knowledge on *An. gambiae* genomics.

However, malaria is a complex vector system and transmission is much more complicated than expected (and generally believed). *An. gambiae* is not the only one vector.

In many locations of Africa species from *An. funestus*, *An. nili* and *An. moucheti* groups are also major, but neglected, malaria vectors, and targeting only *An. gambiae*, whatever the method of control, is nonsense. There is a tremendous lack of knowledge on bionomics, vectorial role, systematics, population genetics, genomics and functional genomics on these vectors. Members of these species complexes widely differ in their biology and vectorial competence. Some of them, morphologically indistinguishable from others, are even non-vectors. Thinking about an African-wide vector control needs to fill the gap in these species. New data on these vectors will confront and enrich results obtained for *An. gambiae*, particularly in the field of population structure and genetic bases of transmission (genes and expression of genes involved in mating, in selection of breeding sites and hosts, in immunity, in *Plasmodium*-mosquito relationships, related to insecticides)..

Some preliminary data have been obtained within the sixties, and more recently thanks to NIH, WHO and French Ministry of Research (Pal+) funding. Here data obtained by the "Anopheles d'Afrique" research network involving teams from Senegal, Burkina Faso, Cote d'Ivoire, Benin, Cameroon, Madagascar, South Africa, France and Italia, will be presented.

An. funestus

Species from *An. funestus* group can only be differentiated by minor morphological characteristics, and by recently developed PCR assays. Bionomic and genetic studies, based on paracentric inversions and microsatellite markers, highlight the high polymorphism of *An. funestus*. In West Africa, huge Hardy-Weinberg and linkage disequilibria between chromosomal inversions allow the description of two chromosomal forms (Kiribina and Folonzo) and suggest an incipient speciation within *An. funestus* s.s. These two chromosomal forms seem to have different vectorial capacity and competence. However, comparisons of genetic structures based on microsatellite markers are giving conflicting results showing gene flow between chromosomal forms, and suggest that inversions are adaptive to local environment.

An. nili

An. nili s.l. has a wide distribution in tropical Africa and is the main vector along some rivers. Four species have been recently described within the *An. nili* complex depending on variations in morphology, biology and genetics: *An. nili, An. carnevalei, An. ovengensis* n.sp.

and *An. somalicus*, the first three being malaria vectors. These four species can be identified by a new PCR test.

An. moucheti

Mosquitoes belonging to the *An. moucheti* group are forest mosquitoes. Three "sub-species" have been described based on morphological characters: *An. moucheti moucheti*, *An. m. nigeriensis* and *An. m. bervoetsi*. Preliminary data on morphology, crossing and comparison of genetic sequences suggested that at least 2 different true species exist: *An. moucheti* in forested areas and *An. bervoetsi*, located in forest galleries.

Despite the fact that species from Nili and Moucheti complexes are major vectors, with inoculation rates reaching 100 infective bites per person per year, there are few data on their distribution and bionomics throughout Africa, and almost nothing is know on their genetics and their relationships with *Plasmodia*.

New ways of research

Thanks to experience and knowledge obtained on *An. gambiae* s.l., and to a lesser extent on *An. funestus*, thanks to recent advances in molecular biology and genetics, it is possible compete our knowledge on these neglected vectors. Research should be undertaken in the following areas:

- Field researches on new methods for sampling (ie, targeting less anthropophilic or exophilic mosquitoes), systematics, distribution, larval and adult ecology, vectorial capacity, vectorial competence to *Plasmodium*, sensitivity to insecticides, population genetics, etc…
- Laboratory researches on rearing, experimental transmission, development of population genetic markers (cytogenetics, microsatellite, SNPs), phylogeny, identification and analysis of the expression of genes of interest involved in malaria transmission (based on *An. gambiae* experience and available microarrays, and following development of new chips from *An. gambiae* and neglected vectors). Such genes can be related to immunity, metabolism, behaviour (mating, feeding...), insecticide resistance, etc...

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