

Modeling the spatio-temporal distribution of M and S molecular forms of *Anopheles gambiae* and *Anopheles funestus* in south Benin

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Species and ecotypes of malaria vectors adopt different strategies to avoid vector control intervention based on residual insecticides. Mapping their distributions would be useful to improve vector control and to reach objectives of malaria elimination. Here, we analyzed the spatio-temporal distribution of *An. funestus* (AF) and both M and S molecular forms of *An. gambiae* s.s. (AGM and AGS) that are sympatric in south Benin.

Presence-absence data of AGM, AGS and AF from 1-year human-landing collections in 28 villages were assessed using binomial mixed-effects (BME) models with a set of environmental covariates. Temperatures, rainfall and NDVI were derived from satellite images. Landscape metrics based on an object-oriented classification of land-use were computed in a buffer area around each village. A breeding sites inventory was performed in the perimeter of each village. The vector control interventions implemented in the villages were also introduced in the models. After 8-fold cross-validations of the models, predictive maps of presence of AGM, AGS and AF were computed.

BME models showed that presence of AGM and AGS were positively associated with the presence of domestic breeding sites positive for *Anopheles* larvae, market gardening, hydromorphic soils and the cumulated rainfall during the 15 days preceding the caught. Nocturnal temperatures were positively correlated with the presence of AGS and negatively with AGM. The opposite was found with NDVI. Presence of AF was highly correlated with the land-cover evenness, nocturnal temperatures, cumulated rainfalls and the presence of surface freshwater. Model validations showed the AF, AGM and AGS models provided respectively an excellent (AUC>0.9), a good (AUC>0.8) and an acceptable (AUC>0.7) level of prediction.

These results showed that available remote sensing data could help to predict the presence of several species of malaria vectors at a village level. These models could be used to map species-dependant parameters like biting behaviour or mechanisms of resistance to vector control.