

Publication

Bayesian geostatistical modelling of malaria and lymphatic filariasis infections in Uganda : predictors of risk and geographical patterns of co-endemicity

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ABSTRACT: BACKGROUND: In Uganda, malaria and lymphatic filariasis (causative agent *Wuchereria bancrofti*) are transmitted by the same vector species of *Anopheles* mosquitoes, and thus are likely to share common environmental risk factors and overlap in geographical space. In a comprehensive nationwide survey in 2000-2003 the geographical distribution of *W. bancrofti* was assessed by screening school-aged children for circulating filarial antigens (CFA). Concurrently, blood smears were examined for malaria parasites. In this study, the resultant malariological data are analysed for the first time and the CFA data re-analysed in order to identify risk factors, produce age-stratified prevalence maps for each infection, and to define the geographical patterns of *Plasmodium* sp. and *W. bancrofti* co-endemicity. **METHODS:** Logistic regression models were fitted separately for *Plasmodium* sp. and *W. bancrofti* within a Bayesian framework. Models contained covariates representing individual-level demographic effects, school-level environmental effects and location-based random effects. Several models were fitted assuming different random effects to allow for spatial structuring and to capture potential non-linearity in the malaria- and filariasis-environment relation. Model-based risk predictions at unobserved locations were obtained via Bayesian predictive distributions for the best fitting models. Maps of predicted hyper-endemic malaria and filariasis were furthermore overlaid in order to define areas of co-endemicity. **RESULTS:** *Plasmodium* sp. parasitaemia was found to be highly endemic in most of Uganda, with an overall population adjusted parasitaemia risk of 47.2% in the highest risk age-sex group (boys 5-9 years). High *W. bancrofti* prevalence was predicted for a much more confined area in northern Uganda, with an overall population adjusted infection risk of 7.2% in the highest risk age-group (14-19 year olds). Observed overall prevalence of individual co-infection was 1.1%, and the two infections overlap geographically with an estimated number of 212,975 children aged 5 - 9 years living in hyper-co-endemic transmission areas. **CONCLUSIONS:** The empirical map of malaria parasitaemia risk for Uganda presented in this paper is the first based on coherent, national survey data, and can serve as a baseline to guide and evaluate the continuous implementation of control activities. Furthermore, geographical areas of overlap with hyper-endemic *W. bancrofti* transmission have been identified to help provide a better informed platform for integrated control

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