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Short communication: **Negative spatial association between lymphatic filariasis and malaria in West Africa**

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Summary

OBJECTIVE To determine the relationship between human lymphatic filariasis, caused by *Wuchereria bancrofti*, and falciparum malaria, which are co-endemic throughout West Africa.

METHODS We used geographical information systems and spatial statistics to examine the prevalence of lymphatic filariasis in relation to malaria prevalence, mosquito species distributions, vegetation and climate.

RESULTS A negative spatial association between *W. bancrofti* and falciparum malaria prevalence exists. Interspecies competition between parasites, seasonality, differences in the distribution and vector competence of *Anopheles* vectors, agricultural practices and insecticide resistance may be factors driving current (and potentially future) spatial distributions.

CONCLUSION Further investigating these factors will become crucial as large-scale lymphatic filariasis and malaria control programmes are implemented in West Africa that may influence the epidemiology of both diseases.

keywords *Anopheles*, lymphatic filariasis, malaria, West Africa, epidemiology, transmission, climate, environment, geographical information systems, statistical modelling

Lymphatic filariasis (LF), caused by *Wuchereria bancrofti*, and falciparum malaria are significant causes of morbidity and mortality worldwide, making them priorities for elimination and control programmes (Molyneux & Zagaria 2002; Zagaria & Savioli 2002; WHO 2005). Both diseases are endemic throughout sub-Saharan Africa, where they are transmitted by a number of common mosquito species (Lamontellerie 1972; Brengues 1975; Lindsay & Thomas 2000). Infection with *W. bancrofti* can be asymptomatic but frequently may produce severe, disfiguring and intractable lymphoedema and genital pathology that has a major social and economical impact for millions of people (Zagaria & Savioli 2002). *Plasmodium falciparum* remains one of the most important public health problems in sub-Saharan Africa where the parasite is responsible for approximately 300 million acute infectious episodes and 1 million deaths per annum (WHO/UNICEF 2003; WHO 2005). The two parasites exist in Africa in a complex and dynamic ecology; attempts to control one parasite may have inadvertent and unforeseen consequences on the other. In this regard, an important question, especially within the implementation of control or elimination programmes, is the nature of the interactions between these co-endemic parasites. To address this question, we used a comprehensive and recently acquired database for the seroprevalence of *W. bancrofti* in West Africa (Gyapong *et al.* 2002) to examine the spatial relationship between LF and malaria, and co-modelled a range of potentially important entomological and environmental variables.

LF seroprevalence data (with selective parasitological validations) obtained from Gyapong *et al.* (2002), were systematically collected between June and September 2000, from 401 villages throughout Benin, Burkina Faso, Ghana and Togo (see Figure 1a), using a validated grid system (Gyapong & Remme 2001). The prevalence of

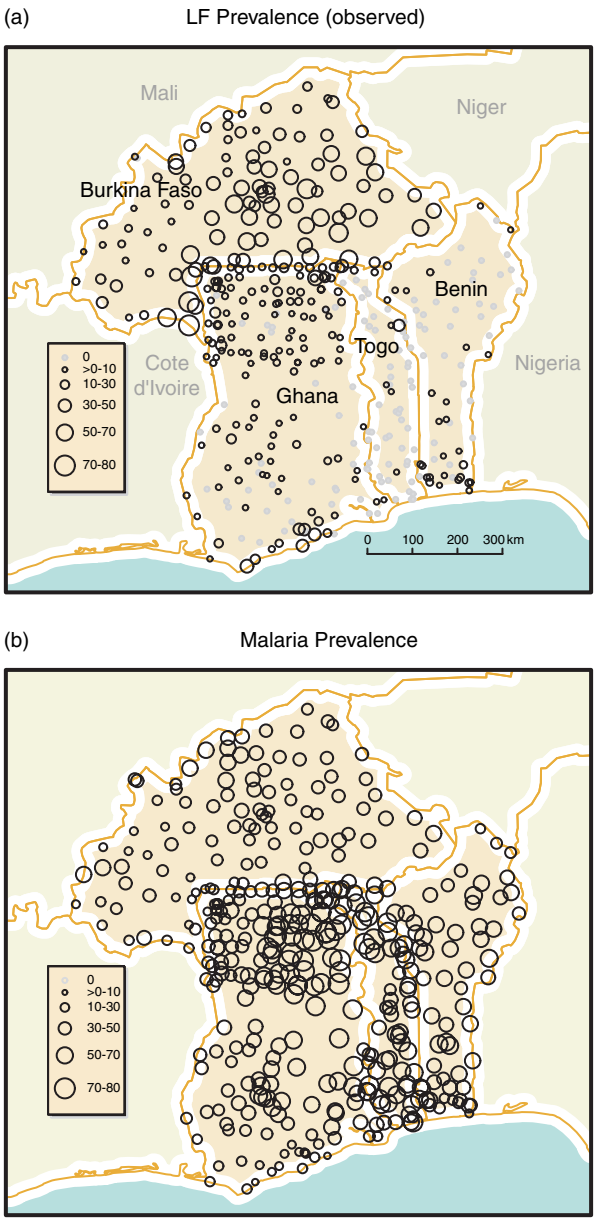

Figure 1 Distribution of *Wuchereria bancrofti* and *Plasmodium falciparum* malaria in Benin, Burkina Faso, Ghana and Togo.

W. bancrofti antigenaemia at each sampling site was determined by studying 50–100 individuals of at least 15 years of age, using commercial immunochromatographic card tests for filarial antigen (ICT Diagnostics, Sydney, Australia; Weil *et al.* 1997). The seroprevalence was validated by night blood film parasitology in some randomly selected sites to check the validity of the antigenaemia prevalence values. As direct measurements of malaria prevalence at each of the LF study sites were not available, estimates of *P. falciparum* parasitaemia were derived at each of these sites (Figure 1b), by using a prevalence map for West Africa that had been constructed from extensive data obtained from children aged 2–10 years in non-epidemic periods (Kleinschmidt *et al.* 2001). The prevalence map had been produced using a generalized linear mixed model, with spatial correlation structure estimated from the deviance residuals. Predictive accuracy was assessed by assigning predicted and observed prevalences at each surveyed location to categories corresponding to prevalences <10%, 10–30%, 30–70% and over 70%. This resulted in a 78% agreement between predicted and observed prevalence categories, with only three survey locations misclassified by more than one category (MARA/ARMA: http://www.mara.org.za/).

In addition, we examined the distribution of a number of mosquito species, vegetation cover, average annual temperature, average annual precipitation and maximum absolute humidity to assess their possible influence on parasite distribution. Mosquito species data were derived from modelled probability maps of *Anopheles arabiensis* (Lindsay *et al.* 1998) and the *Anopheles gambiae sensu stricto* chromosomal forms of Bissau, Forest, Mopti and Savanna (Bayoh *et al.* 2001), which had been produced using non-linear and binary regression models. Vegetation data were based on the Normalized Difference Vegetation Index and obtained from SPOT Satellite Image Processing and Archiving Centre (Vito, Belgium) (http://www.vgt.vito.be). Land surface temperature data were obtained from GAC-Africa monthly composites databases from the Joint Research Centre, Ispra, Italy. Precipitation and humidity data were obtained from the Climate Research Unit, University of East Anglia (http://ipcc-ddc.cru.uea.ac.uk).

All data were imported into ArcGis 8.2 (ESRI, Redlands, CA, USA) and geo-referenced using the Africa boundary file map from the Africa Data Sampler (http://www.wristore.com/afdatsamgeor.html). The relationship between the prevalence of *W. bancrofti* antigenaemia at the 401 study sites and each of the study variables used in the spatial model are depicted in Figure 2. Subsequently, all the data corresponding to the longitude and latitude of each of these 401 sampling sites were extracted and examined using model-based geostatistics (Diggle *et al.* 1998). We analysed the effect of malaria prevalence on the spatial distribution of *W. bancrofti*, adjusting for the possible effects of mosquito species compositions, environmental variables and an overall spatial trend. The response variable (i.e. prevalence of *W. bancrofti*), *Y*, at each location was defined as the empirical logit of observed prevalence, assuming a sample size of 50; hence,

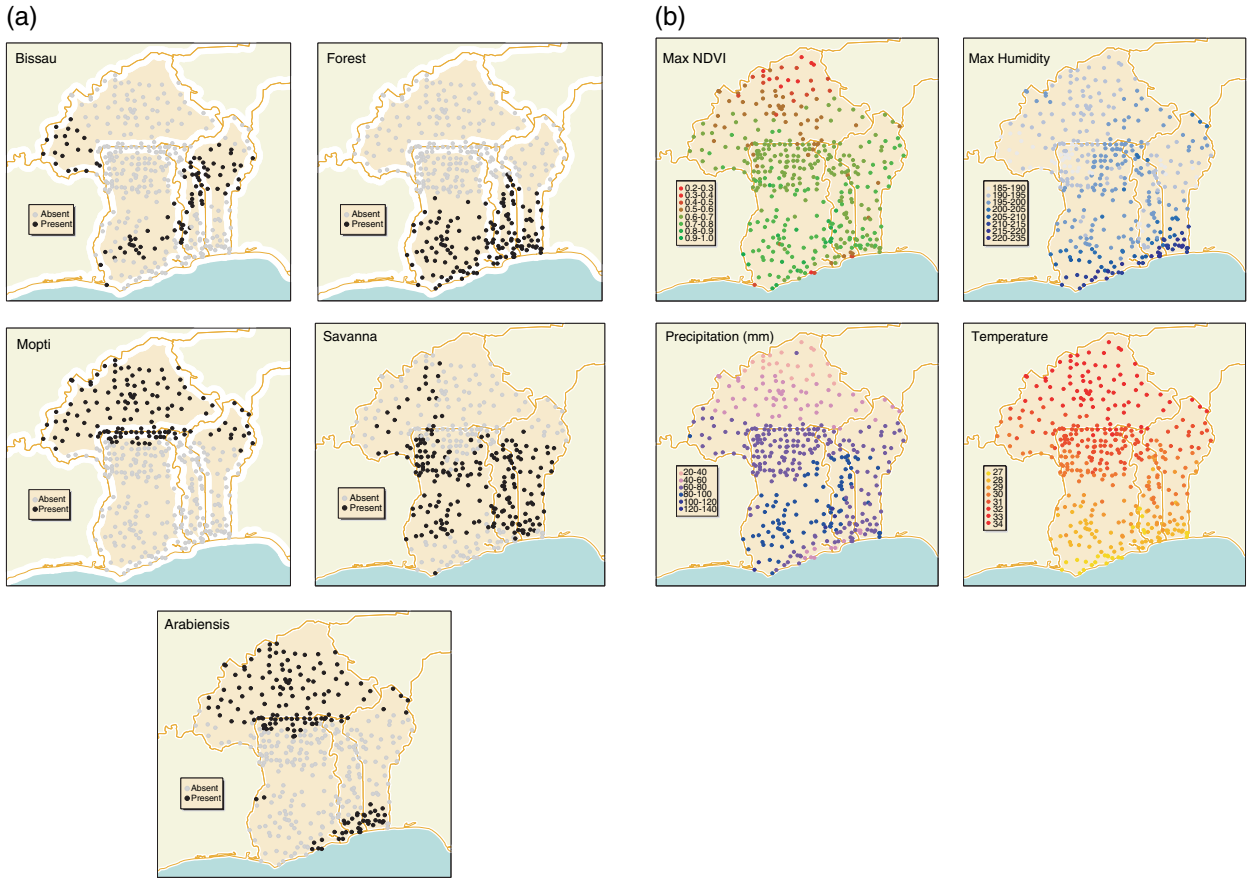

Figure 2 The spatial distributions of the explanatory variables at each LF sampled location. (a) Presence/absence of different mosquito forms (*Anopheles arabiensis*, *Anopheles gambiae* Bissau, Forest, Mopti and Savanna) and estimated malaria prevalence. (b) Vegetation and climate variables.

$$Y = \log\left\{\frac{\mathrm{PREV}+1}{101-\mathrm{PREV}}\right\},$$

where PREV is the prevalence expressed in percentage. The model assumes that responses Y_i at locations x_i are conditionally independent given an unobserved spatial stochastic process $S(x)$, and that the conditional mean response μ_i at location x_i depends linearly on explanatory variables and on $S(x_i)$, hence $\mu_i = d_i\beta + S(x_i)$, where d_i is a vector of explanatory variables associated with the location x_i, β is a vector of regression parameters and $S(x)$ is a Gaussian process with mean zero, variance σ^2 and correlation function $\rho(u) = \exp(-u/\varphi)$ where u denotes distance. Conditional on the μ_i and the Y_i are mutually independent Gaussian with mean values μ_i and variances $T^2\sigma^2$. The parameter $T^2\sigma^2$ represents the ratio between the sampling variance at each location and the spatial variance, σ^2 of the process $S(x)$. We used Bayesian inference, in conjunction with direct Monte Carlo as implemented in the R package geoR (http://www.est.ufpr.br/geoR/). Prior specification was as follows: improper uniform for all regression parameters; reciprocal for σ^2; discrete uniform for φ over the range 0.2–9.0; discrete uniform for $T^2\sigma^2$ over the range 0.05–2.0. Posterior distributions were estimated from a Monte Carlo sample of size 10 000, which was sufficiently large to make the Monte Carlo variation negligible by comparison with the inherent statistical variation in the posterior distributions. The importance of each parameter was assessed graphically by inspection of its posterior distribution, and summarized in tabular form by its posterior mean and 95% Bayesian credible interval. A credible interval excluding zero is the Bayesian counterpart of rejecting, at the conventional 5% level of significance, the hypothesis that the corresponding parameter is zero.

Table 1 Summaries of posterior distributions for parameters in the model for empirical logit of LF prevalence

	Parameter	Posterior mean	Odds ratio	Bayesian 95% credible interval
Regression parameters				
Malaria prevalence	−0.009	0.991	0.982	1.000
Precipitation	−0.001	0.999	0.980	1.017
Normalized Difference Vegetation Index	0.693	1.999	0.346	11.491
Humidity	0.016	1.016	0.981	1.052
Temperature	−0.165	0.848	0.670	1.062
Anopheles arabiensis	0.268	1.307	0.856	1.979
Anopheles gambiae Bissau	−0.074	0.929	0.612	1.392
Forest	−0.039	0.962	0.432	2.122
Mopti	0.264	1.302	0.719	2.336
Savanna	−0.098	0.906	0.680	1.209
Trend surface parameters				
Intercept	−0.321		−10.597	10.044
Latitude	0.145		−0.413	0.636
Longitude	−0.145		−0.621	0.338
Latitude squared	0.025		−0.092	0.146
Longitude squared	−0.081		−0.203	0.041
Latitude times longitude	0.024		−0.111	0.161
Spatial covariance parameters				
σ^2	3.772		1.079	8.460
φ	4.479		1.300	9.000
$T^2\sigma^2$	0.165		0.050	0.450

In rows one to 10 the parameters are the regression coefficients associated with the named explanatory variables. Columns two and three give point estimates (posterior mean values) of the regression coefficient and its exponential, the latter being interpretable as an odds ratio. Columns four and five give the 95% Bayesian credible intervals on the odds ratio scale. In rows 11–16 the parameters are the coefficients, which collectively define the fitted trend surface. Column two again gives point estimates whilst columns three and four give the 95% Bayesian credible intervals on the untransformed scale; an odds ratio interpretation is inappropriate here, because there is no meaning to a unit change in one of the explanatory variables whilst holding the other explanatory variables constant. In rows 17–19 the parameters define the spatial covariance structure of the model. Columns two to four give point estimates and 95% Bayesian credible intervals.

The statistical relationship between each variable and the prevalence of *W. bancrofti* circulating antigen is summarized in Table 1. There was a positive association between the prevalence of *W. bancrofti* antigen levels and *An. arabiensis*, *An. gambiae* Mopti and vegetation although the 95% Bayesian credible intervals in each of these cases crossed zero. Importantly, there was a small but just conventionally significant negative association between the prevalence of malaria and LF (mean −0.009, odds ratio 0.991, 95% Bayesian credible interval 0.982–1.000). This association is robust in the sense that it holds after adjustment for environmental variables, mosquito species composition and both large-scale and small-scale residual spatial variation represented, respectively, by the fitted quadratic trend surface and the Gaussian process $S(x)$. As the values available for the prevalence of *P. falciparum* are model predictions rather than direct measurements, it is likely that the estimate of the magnitude of the negative association between LF and malaria is in fact conservative because of a degree of mis-specification for the malaria prevalence rates (Amexo *et al.* 2004).

This is the first time that the distributions of *W. bancrofti* and *P. falciparum* have been examined on such a scale. The study suggests that an intriguing relationship exists between the two parasites, whereby one parasite tends to dominate the other, despite sharing similar *Anopheles* vectors and environmental factors which support both replication and endemicity in this region. However, these findings can only provide a relatively limited view of a highly complex and dynamic system and we have had to use relatively crude measures of both the human infection burden and the associated environmental and entomological variables; consequently, the nature and magnitude of the interaction between *W. bancrofti* and *P. falciparum* may well vary with time and location, and different variables may assume importance at one time or another.

The reasons for the contrasting spatial distributions found in this study remain a matter for conjecture and could be influenced by additional factors that were not included in

this study. It is possible a degree of interspecies competition may exist between microfilaria and *Plasmodium* within *Anopheles* mosquitoes or the human host. Interactions between parasites can occur in vertebrate and invertebrate hosts, and a wide variety of environmental and host-dependent factors influence the structure, dynamics, seasonality and transmission success of parasite communities (Burkot *et al.* 1990; Albuquerque & Ham 1995; Petney & Andrews 1998; Petney 2001; Spiegel *et al.* 2003; Graham *et al.* 2005). In Tanzania, Muirhead-Thomson (1953) found mixed filarial-malarial infections rare in *An. gambiae*. The duration of transmission may also be important as evidenced by the high prevalence of *W. bancrofti* in Burkina Faso that coincides with a shorter, rather than longer malaria season (MARA/ARMA: http://www.mara.org.za/), suggesting that seasonal malaria may somehow effect the dominance of *W. bancrofti*, or conversely, perennial malaria may inhibit filarial development (Schmidt & Esslinger 1981). Another possible explanation for the distinct epidemiological patterns may be related to the differential distribution and vector competence of mosquitoes within the *An. gambiae* and *An. funestus* complexes, as these vary between species (Coluzzi *et al.* 1985; Appawu *et al.* 1994; Powell *et al.* 1999; della Torre *et al.* 2001; Coetzee & Fontenille 2004). Initial studies suggest that *An. funestus*, *An. arabiensis* and *An. gambiae* Mopti are potentially important for transmission of *W. bancrofti* (Dzodzomenyo *et al.* 1999; Appawu *et al.* 2001), with the latter species' success intrinsically linked to irrigated agriculture; a risk factor more associated with *W. bancrofti* (Lamontellerie 1972; Hunter 1992), than with increased malaria transmission in the region (Ijumba & Lindsay 2001). It may also be because *An. gambiae* Mopti frequently dominates irrigated areas, and is a relatively poor vector of malaria compared with other species such as *An. gambiae* Savanna (Coluzzi 1993; Carnevale *et al.* 1999). A further consideration is the impact of insecticide resistance on filarial worm development. Highly elevated esterases involved in insecticide-resistance inhibit development of microfilariae in *Culex* (McCarroll *et al.* 2000). A similar effect could occur in insecticide resistant *Anopheles* (Hemingway & Ranson 2000).

Differentiating between the various hypotheses will become crucial as large-scale LF and malaria control programmes are implemented in West Africa that may impact on the epidemiology of both diseases. Among the many testable hypotheses we feel the following deserve special emphasis: first, a further understanding of the vector competence of mosquitoes infected with one or both parasites would be of particular interest and could be addressed using a range of *in vitro* and *in vivo* models. Second, the relative exclusivity of one parasite in preference to the other may provide an insight into the immunobiology of the host–parasite interaction, whereby a particular host response to one parasite may facilitate or protect against the other. Third, and perhaps most importantly is the possibility that attempts to control one parasite may inadvertently lead to a change in prevalence of the other. This is a vital question given the efforts of elimination programmes and is directly testable using serial point prevalence studies.

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Association spatiale négative entre la filariose lymphatique et la malaria en Afrique de l'ouest

OBJECTIF Déterminer la relation entre la filariose lymphatique causée par *Wuchereria bancrofti* et la malaria falciparum, toutes deux endémiques en Afrique de l'ouest.
MÉTHODES Nous avons utilisé les systèmes d'information géographique et des statistiques spatiales pour examiner la prévalence de la filariose lymphatique en relation avec la prévalence de la malaria, la distribution des espèces de moustiques, la végétation et le climat.
RÉSULTATS Une association spatiale négative existe entre *W. bancrofti* et la prévalence de la malaria falciparum. La compétition inter-espèce des parasites, la saisonnalité, les différences dans la distribution et la compétence des vecteurs *Anopheles*, les pratiques agriculturales et la résistance aux insecticides peuvent être des facteurs responsables des distributions spatiales actuelles et probablement futures.
CONCLUSION Une investigation plus poussée de ces facteurs s'avérera cruciale avec l'introduction de programmes de contrôle à grande échelle de la filariose lymphatique et de la malaria en Afrique de l'ouest, qui peuvent influencer l'épidèmiologie de ces deux maladies.

mots clés *Anopheles*, filariose lymphatique, malaria, Afrique de l'ouest, épidémiologie, transmission, climat, environnement, systèmes d'information géographique, modélisation statistique.

Asociación espacial negativa entre filariasis linfática y malaria en Africa del Oeste

OBJETIVO Determinar la relación entre la filariasis linfática humana, causada por *Wuchereria bancrofti*, y malaria por *Plasmodium falciparum* malaria, las cuales son co-endémicas en todo África del oeste.
MÉTODO Utilizamos sistemas de información geográfica (SIG) y estadística espacial para examinar la prevalencia de filariasis linfática en relación a la prevalencia de malaria, la distribución espacial de los mosquitos, la vegetación y el clima.
RESULTADOS Existe una asociación espacial negativa entre *W. bancrofti* y malaria por *P.falciparum*. Los factores que podrían estar influenciando las distribuciones espaciales actuales (y potencialmente las futuras) son la competencia entre especies de parásitos, la estacionalidad, diferencias en la distribución y competencia de los vectores *Anopheles*, prácticas agrícolas y resistencia a insecticidas.
CONCLUSIONES Investigar más a fondo estos factores será crucial a medida que se implementen en África del Oeste, programas de control a gran escala para la malaria y la filariasis linfática, que puedan influenciar la epidemiología de ambas enfermedades.

Palabras claves *Anopheles*, filariasis linfática, malaria, África del oeste, epidemiología, transmisión, clima, medio ambiente, sistemas de información geográfica, modelaje estadístico