apart, less related. The result is that measures of genetic relatedness can be used to assign an individual to their population of origin, and that measures of population structure can define the boundaries within which mating between two individuals is likely to occur. For filarial nematodes, two individuals can only mate if they are transmitted to the same host, so measures of genetic relatedness in filarial parasites are an indirect measure of the distances over which transmission occurs within a given population. Consequently, measures of population structure define the boundary of a parasite transmission zone and estimate the probability that an individual parasite is a "resident" of that transmission zone or is an immigrant. Similarly, measures of population structure can be used to estimate the risk of parasite transmission between two locations (for example, across a border between countries/states/districts with differing degrees of success in parasite elimination). We have used a variety of genotyping tools (whole genome sequencing, whole and partial mitochondrial and *Wolbachia* sequencing, and single locus genotyping) to characterise population structure and hence transmission zones for *Onchocerca volvulus* in West Africa and have shown that we can resolve population structure and transmission zones over several spatial and temporal scales. These measures may provide objective tools with which to determine the boundaries of implementation and evaluation units for mass drug administration and cessation of treatment. We have also coincidentally used genotyping data to estimate the number of females contributing to the microfilarial population in the skin of an individual patient, providing a novel measure of parasite infection intensity, and to track the rate at which a parasite population declines under MDA.

1190

DEVELOPING THE FIRST NATIONAL DATABASE AND MAP OF LYMPHATIC FILARIASIS CLINICAL CASES IN MALAWI

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The Lymphatic Filariasis (LF) Elimination Programme in Malawi is on track to meet the Global Programme to Eliminate Lymphatic Filariasis (GPELF) targets of 2020 by interrupting transmission with mass drug administration (MDA) and alleviating suffering by managing morbidity and preventing disability (MMDP). This study aimed to highlight the LF programme's approach to determining the number of people affected by lymphoedema and hydrocoele, and developing the first national database and morbidity map for targeted interventions across the 26 endemic districts. Such information is essential for certification of LF elimination as a public health problem. The first data on morbidity was collected during national MDA campaigns in 2009-2010 when community drug distributors (CDDs) reported the number of lymphoedema and hydrocoele cases at the health-centre-level. Once MDA was stopped in 2014, the three districts with the highest baseline prevalence and reported number of cases during MDA (Chikwawa, Nsanje and Karonga), were selected for intensive patient mapping using the mHealth tool *MeasureSMS-Morbidity* in which health surveillance assistants (HSAs) reported all cases in their communities by SMS. Each district reported approximately 350 lymphoedema and 800 hydrocoele cases, and provided specific village-level patient data on age, sex, condition and severity of condition (mild, moderate, severe) which could be used to further understand spatial-epidemiological patterns. Focal mapping is now planned for six to eight districts to help develop predictive maps in the remaining 23 districts. Each district will be strategically selected, considering its location, environment, baseline prevalence, and morbidity data reported by MDA. This will allow country-wide data and a map to be generated, highlighting and classifying areas of 'low', 'medium' and 'high' predicted prevalence/case numbers, which will then be verified. This information will allow the Malawi LF Programme to appropriately plan and deliver a basic package of care to those suffering from the disabling and debilitating clinical manifestations of LF across the country.

1191

FAMILIAL AGGREGATION AND HERITABILITY OF *LOA LOA* INFECTION

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Large scale treatment with ivermectin (IVM) against onchocerciasis needs to be expended to hypo-endemic areas to reach the elimination goal. In these areas, localities where community-directed treatment with IVM (CDTI) cannot be applied because of possible occurrence of *Loa*-related severe adverse events (SAE) have to be identified. At individual level, people at risk of SAE are those harboring >30,000 *Loa* microfilariae per mL of blood. For a given prevalence of microfilaremia, the proportion of people with such high densities varies significantly between communities. We hypothesized that the latter observation is related to the existence of familial clusters of hypermicrofilaremic individuals which would be the consequence of a genetic predisposition to present high *Loa* microfilarial densities. We tested this hypothesis in 10 villages in the Okola Health District of Cameroon. Intrafamilial correlation coefficients and heritability estimates were assessed for both *Loa* microfilaremia and individual microfilarial densities by controlling for age, sex, *Mansonella perstans* microfilaremia and household effects. Pedigree charts were constructed for 1,126 individuals. A significant familial susceptibility to be microfilaremic for *Loa* was found for first-degree relatives ($\rho = 0.08$, $P < 0.05$; heritability = 0.23). Regarding individual microfilarial densities, a significant familial aggregation was demonstrated ($\rho = 0.36$ for first- and 0.27 for second-degree relatives). For first-degree relatives, the highest coefficients were found between mothers and daughters ($\rho = 0.57$). Overall heritability estimate for intensity was 0.24. These results suggest that the *Loa* microfilaremic status is mainly driven by environmental factors and habits, while a genetic component governs the microfilarial density. These results support the hypothesis that a genetical predisposition to be hypermicrofilaremic exists, leading to the presence of familial clusters of individuals at risk for post-ivermectin SAE. This finding should be taken into account for developing sampling strategies to identify communities where CDTI cannot be applied.

1192

PREDICTIVE VALUE OF OV16 ANTIBODY PREVALENCE IN DIFFERENT AGE GROUPS FOR ELIMINATION OF AFRICAN ONCHOCERCIASIS

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Onchocerciasis is targeted for elimination in Africa by 2025 through mass drug administration (MDA) with ivermectin. Current WHO guidelines for stopping MDA and verifying elimination require that the Ov16 antibody prevalence in 0-9 year old children is brought below 0·1%, but the empirical evidence underlying the choice of age group and threshold is still limited. We assessed the predictive value of different Ov16 antibody prevalence thresholds for elimination of onchocerciasis, for various age groups, a variety of endemic settings and various MDA scenarios. We used the individual-based stochastic ONCHOSIM model to simulate trends in infection and Ov16 antibody prevalence levels during and after MDA. We