**Supporting Text**

**Description of Data Sets.** In all surveys, a Holth-type corneoscleral punch was used for skin-snipping (at least two biopsies were taken from each patient). Snips were incubated during 8-24 h and weighed to obtain the arithmetic mean number of microfilariae (mf) per mg of skin. For the Cameroonian data, a mean weight of 2.84 mg per snip was assumed (1).

One of the criteria for including villages in each study (mf prevalence >20%), is based on the definition of endemicity levels adopted by the Onchocerciasis Elimination Program for the Americas (2).

Although in Guatemala there had been control interventions based on nodulectomy (3, 4), these are thought to have had negligible impact (5), so we consider that the parasite population was at equilibrium.

The age profiles of the populations studied in each country are characterized to good approximation by an exponential distribution of survival times (Fig. 3)

**Derivation of the Model for Mean Parasite Loads.** The dynamics of the mean loads of parasite stages in humans and vectors are described by the following system of integral partial-differential equations,

$$\begin{aligned} \frac{\partial W_s(a)}{\partial t} + \frac{\partial W_s(a)}{\partial a} &= m\beta\, \Omega_s(a-p)\, \Pi_H[L, W_s(a), a]\, L - \sigma_W\, W_s(a) \\ \frac{\partial M_s(a)}{\partial t} + \frac{\partial M_s(a)}{\partial a} &= \Delta\, W_s(a) - \sigma_M\, M_s(a) \end{aligned} \qquad [5]$$

$$\frac{\partial L_s(a)}{\partial t} + \frac{\partial L_s(a)}{\partial a} = \beta\, \Omega_s(a)\, \Pi_V[M_s(a)]\, M_s(a) - \sigma_L[M_s(a)]\, L_s(a) \qquad [6]$$

where explicit time dependency in $W_s, M_s, L_s$ and $L$ is omitted, and parasite loads are zero for $a < p$. We define here quantities not defined in the main text:

$\Pi_H[L, W_s(a), a] = S_s(a)\, \delta_H[L, W_s(a)]\, e^{-\mu_H p}$, the probability of establishment of incoming L3 larvae, with $S_s(a)$ the host's susceptibility, $\delta_H[L, W_s(a)]$ the probability of an infective larva developing into an adult worm as a function of incoming larvae and/or established worms, and $e^{-\mu_H p}$ the host's probability of survival during $p$; $\Delta = \phi F / 2$, with $\phi$ the mating probability, $F$ the fecundity rate of a female adult worm scaled per mg of skin (6), and 1/2 the proportion of female worms (we assume that every female is fertilized, i.e., $\phi = 1$, in a precontrol, highly overdispersed and polygamous parasite population (6, 7)); and $\sigma_L[M_s(a)] = \sigma_{L_0} + (a_H / g) + \mu_V + \alpha_V M_s(a)$, with $a_H$ the probability that an L3 larva is shed per vector bite, $\sigma_{L_0}$ and $\mu_V$ the per capita background mortality rates of L3 larvae and vectors, and $\alpha_V$ the rate of vector mortality induced per mf (4, 6). The normalization factors $\gamma_s$ in the exposure function $\Omega_s(a)$ (Eq. **1**) are determined by the condition $1 = \int \rho(a)[\Omega_s(a) / E_s]\, da$. There is density dependence in parasite development within humans and vectors, and in vector mortality. Note that this formulation allows for a clear distinction between age- and sex-specific exposure and susceptibility. Here, we consider that all hosts have identical susceptibility ($S_s(a) = 1$), and the probability that an L3 larva develops into an adult worm has the form (4, 6),

$$\delta_H(L) = \frac{\delta_{H_0} + \delta_{H_\infty} c_H m \beta L}{1 + c_H m \beta L}. \qquad [7]$$

with parameters described in Table 4.

To determine the mean infective larval load in vectors, $L(t)$, in Eq. **5**, we use definition Eq. **2**, extended to allow for time dependency, where $L_s(t) = \int \rho(a)\Omega_s(a)L_s(a,t)\,da$ is the mean L3 load per fly transmitted from humans of sex $s$. An equation for $L_s(t)$ is derived by multiplying Eq. **6** by $\rho(a)\Omega_s(a)$ and integrating over host age. Because the dynamics of L3 larvae in flies are much faster than those of the other parasite stages (Tables 1 and 4), we assume that vector larval load is at equilibrium with respect to changes in loads of other parasite stages, giving

$$L_s(t) = \frac{\beta \int_p^{a_m} \rho(a)\Omega_s(a)^2 \delta_V[M_s(a,t)]M_s(a,t)\,da}{\sigma_L[M_{V,s}(t)] + \alpha_s + \mu_H}, \qquad [8]$$

where we set $L_s(0) = 0$, omit negligible terms (evaluated at $a = a_m$), and, for simplicity, replace $M_s(a,t)$ with $M_{V,s}(t)$ in the density-dependent vector mortality rate, where $M_{V,s}(t) = \int \rho(a)\Omega_s(a)M_s(a,t)\,da$ is the average density of mf in the population of vectors feeding on blood from humans of given sex.

An expression for the effective reproductive ratio, $R_e$, defined as the average number of adult female worms produced by an adult female worm during its reproductive lifetime in the presence of density dependence, can be derived,

$$R_e(t) = \sum_s \int_p^{a_m} \rho_s(a)\frac{\Delta}{\sigma_W}\frac{m\beta\Omega_s(a)}{\sigma_M}\frac{\delta_V[M_s(a,t)]}{\sigma_L[M_s(a,t)]}da \times \sum_{s'} \int_0^{a_m - p} \rho_{s'}(a')\beta\Omega_{s'}(a')\delta_H[L(t)]e^{-\mu_H p}\,da' \qquad [9]$$

The basic reproductive ratio, $R_0$, is the density-independent version of Eq. **9**. Note that this expression is not obtained directly from Eqs. **5** and **6**, and that the equilibrium Eq. **3**

is derived from Eqs. **5** and **6** by removing time derivatives, not by imposing $R_e = 1$. Hence, an estimate $R_e \approx 1$ would support the adequacy of expression Eq. **9**.

Eqs. **5**, **6**, and **8** form a closed system of nonlinear integrodifferential equations. Assuming parasite and human populations are at endemic equilibrium, Eqs. **5** and **8** become Eqs. **3** and **4**, respectively (using $L = \sum \rho_s L_s$ ). In deriving the latter equations, we replace $M_{V,s}$ with $M_V$ and $\alpha_s$ with $\bar{\alpha}$, and consider that the probability of larval development within the vector (5) is density-independent, $\Pi_V[M_s(a)] = \delta_{V_0}$, i.e., regulation within the vector occurs only through parasite-induced mortality (8). These simplifications allow for an explicit solution of the model, which is used to reduce numeric computation and increase efficiency of parameter estimation. Values used for parameters introduced above are given in Table 4.

**Parameter Estimation.** Skin snip counts of mf ( $x_i$ ) in individual humans ( $i$ ) in either of the study areas are assumed to follow a negative binomial (NB) distribution, with mean $M_s(a)$, aggregation index $k_s(a) = M_s(a)^2 / [\sigma_s^2(a) - M_s(a)]$, and variance $\sigma_s^2(a)$, specific to the country, age and sex of the individual. The likelihood of the parameters ( $\theta = \{m, q, E_s, \alpha_s, b_0, b_1, b_2\}$ ), given the data ( $\mathbf{x} = \{x_i\}$ ), is

$$L(\theta \mid \mathbf{x}) = \prod_i \left[ \frac{\Gamma(x_i + k_i)}{\Gamma(k_i) x_i!} p_i^{x_i} (1 - p_i)^{k_i} \right] \qquad [\mathbf{10}]$$

where $\Gamma$ is the Gamma function; the product runs over every individual $i$, and the index in $M_i$, $k_i$, and $p_i = \frac{M_i}{M_i + k_i}$ refers to the individual's country, age and sex. To get insight, we first evaluated $k_s(a)$ empirically for groups of individuals of the same country, age and sex, using a sample-moment estimator corrected for group size ( $n$ ), $\hat{k} = [\hat{M}^2 - s^2 / n] / [s^2 - \hat{M}]$ (9, 10). The results (Fig. 1) suggest that $k_s(a)$ can be

approximated by a 3-parameter function of age, with parameters common to both sexes. We adopt lognormal ( $k(a) = b_0 \exp(-b_1[\log(a/b_2)]^2)$ ) or logistic ( $k(a) = b_0/[1+\exp(-[a - b_1]/b_2)]$ ) functions, depending on country. Parameters are estimated by maximizing the log-likelihood, with $M_i$ being the solution of [3] and [4], and $k_i$ as described, using a simplex optimization algorithm (NAG routine E04CC). Fitting the data with sex-specific $k$ parameters did not yield significant improvement (results not shown).

**Zero-Inflated Distribution.** We allow for the number of zero mf counts to differ from that of the NB distribution. For an individual $i$, we set the probability of a zero count proportional to $(1-p_i)^{k_i\Psi}$. To ensure normalization, the original probability of each count is divided by $1+(1-p_i)^{k_i\Psi}-(1-p_i)^{k_i}$. The value $\Psi = 0.7$ is used for the three countries, as it generally provides superior model fits to the data and maximum-likelihood estimates of $k(a)$ close to empirical estimates (Fig. 1). This extension of the NB relates to previous approaches (11, 12) and can be interpreted as allowing for false-negative mf counts, nonsusceptible hosts [putative immune (13)], or simply a more flexible distribution.

**Calculation of Prevalence.** Within a group of individuals of given country, age and sex, denoted $j$, the predicted prevalence of mf infection, $P_j$, is 1 minus the probability of zero counts,

$$P_j = 1 - \frac{(1-p_j)^{k_j\Psi}}{1+(1-p_j)^{k_j\Psi}-(1-p_j)^{k_j}} = \frac{1-(1+M_j/k_j)^{k_j}}{1+(1+M_j/k_j)^{-k_j\Psi}-(1+M_j/k_j)^{-k_j}}.$$

The predicted overall prevalence of infection is the average over the human population of the age- and sex-specific prevalence, $P = \sum \rho_s \int \rho(a) P_s(a)\, da$ .

**Goodness of Fit.** The goodness of model fit can be assessed qualitatively from Fig. 2. In addition, a quadratic augmentation of the model for age- and sex-specific mean mf load yields a likelihood-ratio statistic that is non-significant for either country ($P$ = 0.18, 0.09, and 0.07 for Cameroon, Guatemala, and Venezuela, respectively). Analyses of residuals (quadratic fits) suggest the fit is best for the Cameroonian dataset (the largest) and least good for the Venezuelan dataset [smaller and collated over a longer time-span (14, 15, 16)]. In addition, difficulties in estimating host age may have a greater effect in smaller studies.

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