

## **Size matters: Changing population structure means changing sampling requirements for schistosome populations**

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Eradication of schistosomiasis is a goal for nearly all control programs today. We demonstrated how genetic markers can be used to evaluate control programs, indicate incipient resistance and perhaps predict the extinction of a local population. Our studies have been conducted by collecting parasites from all identified infections in a population to calculate individual host differentiation indices ( $D_i$ ) and community effective population size ( $N_e$ ). Collecting all individuals and genotyping their parasites would be impractical on a large-scale, thus we sought to determine the relative error associated with different sample sizes. Using data collected in 2009 and 2012 from two villages in Bahia, Brazil, we calculated  $D_i$  based on samples of different sizes. We used the R to produce 30 samples of those infected selected at random ranging from 5-50% of the total.  $D_i$  was then calculated for each of these groups using SPADE. Error rates of  $\pm 5\%$ -10% of the true value of  $D_i$  were taken as acceptable limits. Between 2009-2012 there was no difference in  $D_i$  for JEN, but the increase was significant for VDR.  $N_e$  fell by 15 fold for each site. When the  $D_i$  is moderate and  $N_e$  large, taking samples of 30-40% of the population was within the 10% limit 60% of the time. When the  $D_i$  increased and  $N_e$  reduced, the curves were less steep, but shifted upward so that samples from JEN composed of 30% of the infected had only a 50% chance of being with 10% of the true value and in VDR, where the  $D_i$  was significantly higher, only a 40% chance of being in this range. The chance of obtaining differentiation indices outside of the acceptable error range with smaller sample sizes increases when the population has undergone a bottleneck. In order to acquire the most representative results regarding population genetics of *S. mansoni* some characteristics such as population size, prevalence of the parasite, history of treatment in the community has be taken into account.

Palavra-Chave: population genetics; eradication; sample size