

Sri Lanka Molecular Xenomonitoring (MX) Study: Gates RCC data

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Molecular xenomonitoring (MX) provides a measure of the prevalence of active infection or microfilaremia in the community. This xenodiagnostic measure might be used at the end of a mass drug administration effort for surveillance purposes to detect changes in the parasite load in the community over time. However, in order to have confidence that a PoolScreen point estimate of infection can be used as a baseline measure for surveillance, we must first show that the point estimate is replicable. As yet there has been no clearly defined sampling strategy for the collection of mosquito vectors for the purposes of MX of lymphatic filariasis infection in human populations. A defined vector sampling strategy was tested in an evaluation unit with *Culex* transmission in Sri Lanka.

The sampling design was based on the household (HH) sampling design used for the human blood collection monitoring. Two independent surveys were conducted to determine the consistency of the point estimate results using this HH sampling, as well as assessing the sample size and number of mosquitoes needed from each trap location. The vector collections and human sampling were done in the same post-MDA evaluation unit in Sri Lanka to enable a comparison between the infection surveillance determined by human blood sampling and that of the mosquito population survey. Pools of mosquitoes were tested by qPCR and the results were entered into the PoolScreen statistical software program designed to determine a point estimate of infection prevalence in the community.

Two independently selected samples with one pool of 25 recently fed vector mosquitoes collected from each of approximately 200 traps locations, yielded the same point estimate of infection at 0.321% and 0.263% respectively (Figure 1). A one-way analysis of variance indicates that there is no significant difference ($p=0.563$) between these two samples¹. This study also compares this to a sample collected from half as many trap locations (~100) with two pools of 25 mosquitoes collected from each, resulting in a point estimate of 0.314%. A one-way analysis of variance again shows that there is no significant difference between these two samples ($p=0.64114$)¹.

The results of this study show that the HH sampling strategy used to collect mosquitoes for molecular xenomonitoring yields a consistent and replicable point estimate of infection for lymphatic filariasis. This measure can be used with confidence as a baseline for comparison in future surveillance studies to determine if there has been a significant change in the level of microfilaremia in the community to which the mosquito population has been exposed. Furthermore, the second study set of collecting two pools at half the number of locations also showed no difference in the point estimate of infection, and therefore, could be used as an alternative sampling strategy to reduce the labor intensiveness of the HH sampling strategy.

Finally, the evaluation of human infection status from the same evaluation unit indicated 14 individuals of 1179 tested positive by ICT (1.19%) and two of those ICT positive cases tested positive for Mf by blood smear (0.17%).

¹Calculated by Charles Katholi using his new program to complement PoolScreen (unpublished)