Joseph Pryce Abstract: BSP Parasites Online

Background

Molecular xenomonitoring (MX) is the detection of parasite DNA in vector populations. In lymphatic filariasis (LF) and onchocerciasis elimination settings, MX is a recommended surveillance tool for verifying interruption of transmission and monitoring for disease resurgence. However, the sensitivity of MX for detecting communities positive for either disease has not been evaluated. Due to the limitations of other surveillance tools, MX may have utility for a range of additional programmatic goals, but its use is currently restricted by a limited understanding of the relationship between MX results and human prevalence.

Methods

We conducted a systematic review of studies reporting the prevalence of filarial worm DNA in wild-caught mosquitoes or black fly vectors (MX rate) and the corresponding prevalence of microfilaria (mf) in humans. We estimated the sensitivity of MX for detecting positive communities at a range of mf prevalence values and vector sample sizes. We evaluated the relationship between mf prevalence and MX rates using linear regression models.

Results

LF: We identified 24 studies comprising 144 study communities. MX had an overall sensitivity of 98.3% (95% CI 41.5, 99.9%) and identified 28 positive communities that were negative in the mf survey. Low sensitivity in some studies was attributed to small mosquito sample sizes (<1,000) and very low mf prevalence (<0.25%). Human mf prevalence and mass drug administration status were significantly associated with MX rate measurements, accounting for approximately half of the variation in MX rate ($R^2 = 0.49$, $p<0.001$). Data from longitudinal studies showed that, within a given study area, there is a strong linear relationship between MX rate and mf prevalence ($R^2 = 0.78$, $p < 0.001$).

Onchocerciasis: We identified 15 studies comprising 34 study communities that were included in the quantitative analyses. Most communities were at advanced stages towards elimination and had no or extremely low human prevalence. MX detected positive flies in every study area with >1% mf prevalence, with the exception of one study where comparisons between entomological and epidemiological surveys were complicated. We identified a significant relationship between the two measurements, with mf prevalence accounting for half of the variation in MX rate (R^2 0.50, $p<0.001$).

Conclusion

MX shows clear potential as a sensitive tool for detecting LF and onchocerciasis-positive communities, and as a predictor of human mf prevalence. Further data is required to understand how this relationship can be used to support the evaluation of programmatic goals.