Validation of mathematically modeled serological data to compare malaria transmission intensities between two previous high malaria endemic districts in Sri Lanka under the prevention of re-establishment phase

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Sri Lanka has been co endemic to both *Plasmodium vivax* and *P. falciparum* for eons. Achieving malaria pre elimination status in 2008, in 2016 the country was certified malaria free by WHO. Sri Lanka's vulnerability and receptivity to malaria remain high with the persistence of vector mosquitos of the genus *Anopheles*, and a sporadic influx of imported malaria cases, rendering surveillance a critical requirement. Serology proved to rectify the lost precision of the existing malariometrics over declining numbers of cases, yet requires further validation. This study aimed to validate serology as a marker of malaria transmission intensity and to compare the levels of anti-malarial antibodies in two previously high malaria districts; Hambantota and Kilinochchi. Non-malarious Nuwaraeliya district served as the control site. Indirect ELISA measured seroprevalences against three recombinant marker antigens each from *P. vivax* and *P. falciparum* (CSP, MSP1, and AMA1). The control site showed zero seroprevalence against all markers. Based on respondents' seroprevalence and age, seroconversion rates for test districts were estimated using two reversible catalytic models and the loglikelihood ratio test determined the best data fitting model. Changes in transmission intensity were identified for the two previous malaria districts, concerning anti MSP1, AMA1, and CSP antibodies, in parallel to both *P. vivax* and *P. falciparum*. As per model-1, seroconversion rates of Hambantota and Kilinochchi were 0.0057 and 0.00121, 0.00023 and 0.00049, 0.00064 and 0.00138 and 0.00116 and 0.00127, 0.00004 and 0.00099, 0.00701 and 0.00625 for CSP, MSP1, AMA1 to *P. vivax* and *P. falciparum,* respectively. As per Model-2, Past and present seroconversion rates of Hambantota, Kilinochchi of *P.vivax* were –0.00049 and 0.00038, 1.11604 and 0.00064 for CSP, -0.00005 and 0.00009, 0.02243 and 0.00098 for MSP and 0.20494 and 0.00180, 0.00707 and 0.00050 for AMA1, while those of *P. falciparum* were 3.41184 and 0.00022, 0.34468 and 0.00127 for CSP, 3.41184 and 0.00022, -0.00123 and 0.00069 for MSP1, -0.00324 and 0.00487, -0.00099 and 0.00109 for AMA1.The likelihood ratio test determined thatModel-1 had the best-fit data (p=1). In conclusion, more recent infections of Kilinochchi in contrast to Hambantota, traced by seroconversion rates, showed the efficacy of serology in estimating malaria transmission intensities under malaria eliminated settings.

Keywords: Malaria, Prevention of re-establishment, serology