obtained for genome-scale protein microarray analysis using a combined Pf500/Pv500 chip containing a down-selected list of the 500 most sero-reactive antigens. Considering qPCR as gold standard, microscopy was able to detect 40.2% and 22% of any Pv and Pf infection, respectively. Considering passive surveillance, microscopy detected 48.1% and 54.5% of the Pv and Pf cases, respectively; while considering active surveillance, microscopy was detected 38.3% and 19.6% of the Pv and Pf cases, respectively. This study was able to detect *Plasmodium* infections through very active surveillance and qPCR that otherwise would go undetected under current surveillance and diagnostic tools. Protein microarray analysis was performed during highand low (September) malaria seasons: 324 samples for protein microarray analysis. The top 200 most seroreactive antigens were selected for comparison. Seroreactivity increased with age, and in response to documented malaria infection, but was lower in September than in March for all age groups. While there was a gradual increase in seroreactivity associated with age, the differential seroreactivity between high and low transmission season was greatest in youngest and this difference decreased with age. Monitoring changes in transmission intensity and identification of malaria *foci* is mandatory for best intervention efforts. Without better strategies accounting for remote underserved villages, asymptomatic, and submicroscopic infections, and better diagnostic and surveillance tools, it will not be sufficient to decrease the continued malaria transmission due to a high reservoir of infection impeding progress towards attaining a sustainable control and even to progress into elimination of malaria transmission. Elimination efforts will most likely need a more sensitive assay such as a q-PCR or other field deployable molecular based assay.

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FINE SCALE MAPPING OF MALARIA INFECTION CLUSTERS BY USING ROUTINELY COLLECTED HEALTH FACILITY DATA IN URBAN DAR ES SALAAM, TANZANIA

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This study investigated whether passively collected routine health facility data can be used for mapping spatial heterogeneities in malaria transmission at the level of local government housing cluster administrative units in Dar es Salaam, Tanzania. From June 2012 to Jan 2013, residential locations of patients tested for malaria at a public health facility were traced based on their local leaders' names and geo-referencing the point locations of these leaders' houses. Geographic information systems (GIS) were used to visualize the spatial distribution of malaria infection rates. Spatial scan statistics were deployed to detect spatial clustering of high infection rates. Among 2,407 patients tested for malaria, 46.6% (1,121) could be traced to their 411 different residential housing clusters. One small spatially aggregated cluster of neighborhoods with high prevalence was identified. While the home residence housing cluster leader was unambiguously identified for 73.8% (240/325) of malaria-positive patients, only 42.3% (881/2,082) of those with negative test results were successfully traced. It was concluded that recording simple points of reference during routine health facility visits can be used for mapping malaria infection burden on very fine geographic scales, potentially offering a feasible approach to rational geographic targeting of malaria control interventions. However, in order to tap the full potential of this approach, it would be necessary to optimize patient tracing success and eliminate biases by blinding personnel to test results.

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EVALUATION OF MALARIA URBAN RISK BY USING AN IMMUNO EPIDEMIOLOGICAL BIOMARKER OF HUMAN EXPOSURE TO *ANOPHELES* BITES

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Urban malaria represents an underestimated serious health concern in African countries. This study aims to evaluate the risk of malaria transmission in urban area by evaluating the level of human exposure to *Anopheles* bites using an *Anopheles* salivary biomarker (gSG6-P1 peptide). Two multidisciplinary cross-sectional studies were undertaken in five sites of Bouaké city (three urban districts and two surrounding villages, used as control; Côte d'Ivoire) during the rainy season and the dry season. Blood samples were obtained from children aged 6 months to 14 years-old for immunological tests. The level of anti-gSG6-P1 IgG antibodies was significantly higher in rainy season compared to dry season ($p < 0.0001$) in the urban sites. Interestingly, children with the highest anti-gSG6-P1 IgG responses in rainy season were infected by *P. falciparum*. Surprisingly, no difference of anti-gSG6-P1 IgG level was observed between urban and rural areas, whatever the season. The *Anopheles* salivary biomarker is a suitable tool for accurately assessing the risk of malaria transmission in urban areas. It shows that urban population could be as highly exposed to *Anopheles* bites as children living in rural area. This study highlights, highlighting the high risk of malaria transmission in African urban settings.

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PREVALENCE OF MIXED-SPECIES MALARIA INFECTIONS IN UGANDA

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In sub-Saharan Africa malaria is principally caused by *Plasmodium falciparum*, and contributions of other plasmodial species are uncertain. As part of a drug resistance surveillance program, we collected blood samples from 50 children aged 6 months - 10 years presenting with malaria at each of 10 diverse sites around Uganda in 2016. Children presenting with fever were diagnosed by clinic personnel by either Giemsa-stained blood smear (176 subjects) or HRP-2-based rapid diagnostic test (RDT; 323 subjects). To assess infecting species, DNA was extracted from blood spots with Chelex, species-specific primers were used to amplify 18S ribosomal RNA genes, and species were discriminated based on amplicon size using electrophoresis. Of 499 studied samples, 474 (95.0%) demonstrated plasmodial infection. *P. falciparum* was identified in 472 samples, *P. malariae* in 22, *P. ovale* in 15, and *P. vivax* in 4. 435 were pure *P. falciparum*, 2 did not contain *P. falciparum* (one pure *P. malariae*, one *P. malariae/P. vivax*), and the remainder were mixed infections including *P. falciparum*. Non-falciparum species varied geographically, with 0-13 samples demonstrating *P. malariae*, 0-9 demonstrating *P. ovale*, and 0-2 demonstrating *P. vivax* at different sites. No pure non-falciparum infections were identified in RDT-positive samples. Results were complicated by use of two different diagnostic tests, but 41/474 (8.7%) samples with molecular identification of plasmodial infection included non-falciparum infections. Five of 10 study sites underwent regular indoor residual spraying of insecticide (IRS) programs either from 2010-14 or from 2014 to