Fine scale mapping of malaria infection clusters by using routinely collected health facility data in urban Dar es Salaam, Tanzania

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Abstract

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 visualise 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 neighbourhoods 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 optimise patient tracing success and eliminate biases by blinding personnel to test results.

Keywords: malaria, spatial heterogeneity, hot spots, mapping, GIS, Tanzania

Background

In many endemic countries of sub-Saharan Africa (D'Acremont et al. 2010, Gething et al. 2010b, Maharaj et al. 2012, Murray et al. 2012, O'Meara et al. 2010, World Health Organization 2013), including the United Republic of Tanzania (Bhattarai et al. 2007, Mtove et al. 2011, World Health Organization 2013), malaria incidence and morbidity rates have substantially decreased in recent years, following the successful scale-up of available front-line malaria intervention tools (Bhattarai et al. 2007, Ceesay et al. 2008, Steketee and Campbell 2010). These reductions of malaria transmission have encouraged a paradigm shift from the goal of burden control to pathogen elimination (Feachem et al. 2010, Kitua et al. 2011, Moonen et al. 2010a, Steketee and Campbell 2010).

Human malaria infection distributions are known to exhibit spatial heterogeneities on very fine scales. They may even vary between households within the same communities, particularly at low-transmission intensities (Bousema et al. 2012, Bousema et al. 2010b, Gaudart et al. 2006, Mirghani et al. 2010, Woolhouse et al. 1997). In areas where malaria transmission is low enough to enable implementation of the pre-elimination phase (World Health Organization 2007, 2012), information on the spatial distribution of remaining malaria infections is required to enable targeting of supplementary disease control interventions (Bejon et al. 2010, Bousema et al. 2012, Bousema et al. 2010b, Nourein et al. 2011, The malERA Consultative Group on Monitoring 2011, World Health Organization 2012). Spatially aggregated clusters of high infection rates often referred to as pockets of transmission (Tambo et al. 2014, Zhou et al. 2013) or hotspots, have been identified through a variety of survey methods (Bejon et al. 2010, Bejon et al. 2014, Bousema et al. 2010a, Bousema et al. 2010b, Clark et al. 2008, Hardy et al. 2015). A hotspot of malaria transmission may be defined as an area with a significantly higher proportion of positive malaria test results compared to its surrounding area (Bousema et al. 2010a).

Most of the standard measures for monitoring and mapping malaria transmission that have been used by research projects and by national monitoring and evaluation programmes have relied on surveys of well-defined demographic and spatial samples of relevant human populations (Bejon et al. 2010, Bousema et al. 2010a, Bousema et al. 2010b, Clark et al. 2008, Teuscher 1992). The greatest strength of population-weighted cross-sectional prevalence surveys is the representative nature of such probability sampling (Chanda et al. 2012, Moonen et al. 2010b, Roll Back Malaria , Rowe et al. 2009). However, national malaria indicator surveys and other household survey approaches are not designed or powered to determine local-level variation and are typically too costly and laborious to apply with sufficient sampling intensity to obtain spatial resolution finer than the district-level outside of research settings with limited geographic scope (Bousema et al. 2010b, World Health Organization 2007). The challenge remains to develop programmatically affordable and scalable approaches that deliver high-resolution maps of transmission risk for targeting supplementary control efforts, thus contributing to establishing effective surveillance-response systems (Tambo et al. 2014, Zhou et al. 2013), specifically in areas of low transmission where elimination may be feasible (Bejon et al. 2010, Bejon et al. 2014, Bousema et al. 2010a, Bousema et al. 2012, Mueller et al. 2011).

Passively collected routine health facility data are widely used to estimate the burden of malaria (Chanda et al. 2012, Gething et al. 2010a, Lippeveld et al. 2000, World Health Organization 2012) and for risk mapping in resource-limited settings. A common feature of those risk mapping approaches, however, is the considerable effort put into mapping the geographical coordinates of every participating household individually (Bejon et al. 2014, Bisanzio et al. 2015, Cohen et al. 2013, Cohen et al. 2010, Ernst et al. 2006, Kazembe et al. 2006, Sturrock et al. 2014, Yeshiwondim et al. 2009). Several studies have shown that passive case detection at health facilities could guide reactive case detection, whereby visits are made to the respective residence of each positive case reported at a health facility to screen household members and neighbours (Branch et al. 2005, Brooker et al. 2004, Cohen et al. 2013, Kreuels et al. 2008, Maharaj et al. 2012, Pinchoff et al. 2015, Zanzibar Malaria Control Programme 2010). Furthermore, data collection at health facilities during routine patient visits can allow the mapping of the spatial distribution of malaria infection burden (Alemu et al. 2013, de Oliveira et al. 2011, Kazembe 2007, Wimberly et al. 2012, Zacarias and Andersson 2011) as well as a variety of other diseases (Jennings et al. 2005, Lengeler et al. 1991, Mayala et al. 2004, Tornheim et al. 2010), across patient catchment areas (Oduro et al. 2011).

In Dar es Salaam, health facility data have been used for assessing the sensitivity and specificity of malaria diagnostic tools, as well as the quality of case management and health worker performance (Eriksen et al. 2007, Kahama-Maro et al. 2011, Nsimba et al. 2002). However, routinely collected health facility data have not yet been fully explored for mapping malaria infection burdens across the city, or for planning targeted delivery of appropriate control strategies, because patient records generally do not include accurate residential addresses. This exploratory study assesses the feasibility, cost, strengths and limitations of using 'anonymised' routine health facility data, supplemented with the names of patients' local government housing cluster leaders as geographic reference points, to map their home residence locations, and the usefulness of this approach for visualising the spatial distribution of malaria prevalence in two adjacent wards of urban Dar es Salaam.

Methods

Study area

Dar es Salaam is located on the Indian Ocean coast of Tanzania in East Africa (Figure 1) with a population of 4.4 million inhabitants in 2012 (The United Republic of Tanzania 2013). The city is characterised by highly heterogeneous land use, including industrial and commercial areas, planned residential areas and informal settlements, as well as areas with urban agriculture (Dongus et al. 2009). Dar es Salaam has a hot and humid tropical climate throughout the year, with two rainy seasons: the "long rains", which usually fall between March and May, and the "short rains", which occur less predictably anytime between October and January. Average annual rainfall is 1,042 mm (DCP 2004) and the average temperature 25.9°C. Malaria transmission in Dar es Salaam is perennial but relatively low following scale-up of insecticidal net coverage, house screening and larviciding, with a mean prevalence of detectable infection among residents in all age groups of approximately 10% (Msellemu et al. 2016) and an entomological inoculation rate of less than one infectious bite per person per year that both usually peak during and immediately after the main rainy season (Geissbühler et al. 2007, Maheu-Giroux and Castro 2013, Namango 2012).

Figure 1 about here

Study design

Dar es Salaam is divided into five administrative levels (city, municipality, ward, neighbourhood and Ten-Cell-Unit (TCU)) in order of declining geographic scale (de Castro et al. 2004, Dongus et al. 2007). The TCU normally comprises between 10 and 100 houses or compounds with an elected leader who represents the residents (Dongus et al. 2007). While the municipal and city councils of Dar es Salaam do implement a numbering system for houses in the region, this is only applied to formally planned settlements and very few people know the identification number of the house that they live in. In the absence of a widely used system of neighbourhood names and house numbers or postal codes, similar to those which are used in other parts of the world as a spatial reference system for residential locations, TCUs are attractive as a geographic frame of reference and have already proven useful as subdivisions for implementing and managing malaria surveillance and control in this city (Chaki et al. 2011, Chaki et al. 2012, Dongus et al. 2011, Dongus et al. 2007). However, patient registries of health facilities in Tanzania currently only record residential home location down to the neighbourhood level comprising an average of 70 TCUs each. Therefore, in order to be able to assign patient information to a residential location at much finer spatial resolution, the name of the patient's home TCU leader was added to the information recorded in the health facility registry in the context of this study.

In Tanzania, there are five levels of service in the public health care system, but only three are managed under the Dar es Salaam City Medical Office of Health (Mtasiwa et al. 2003): districts/municipalities (each with a municipal hospital), divisions (each with a health centre) and wards (with dispensaries and affiliated clinics). There is one public health facility per ward (called dispensary), which provides service at a lower cost than private facilities (Mamdani and Bangser 2004). This study was conducted at Buguruni Health Centre (BHC), a division-level facility located close to the boundary between the Buguruni and Vingunguti wards (Figure 2). BHC was selected because its malaria rapid diagnostic test (mRDT) procedures had been quality-controlled by previous research projects indicating adequate quality of the services provided according to the national guidelines for management of fever and malaria cases (United Republic of Tanzania 2006). Initial examination of the laboratory registry book revealed that the BHC served patients across all of Dar es Salaam. The majority of patients, however, came from Buguruni (29.8%) or Vingunguti wards (25.2%). For

demonstration purposes, this pilot study exclusively considered patients coming from these two wards. All individuals tested for malaria with a mRDT and treated according to the national guidelines for management of fever and malaria cases were eligible for inclusion in this study. The two study wards have a combined total area of 7.9km^2 and are subdivided into a total of eight neighbourhoods (Kisiwani, Mnyamani, Malapa, Madenge, Kombo, Mtambani, Mtakuja and Miembeni) (Figure 2), with a total of 177,531 inhabitants based on 2012 national census data (The United Republic of Tanzania 2013). Both wards are characterised by high housing density, largely unplanned settlements, low socio-economic background and relatively small TCU sizes (on average approximately 100 x 100 meters) (Dongus et al. 2007). They are bordered by industrial areas to the south, and one of the largest river valleys cutting through Dar es Salaam (Msimbazi River) to the north.

Figure 2 about here

Data collection

Personal and clinical data, mRDT (MAL-Pf®, ICT Diagnostics, Cape Town, South Africa) using histidine-rich protein II (HRP-II) results of individual patients attending the BHC, as well as the names of their local TCU leaders at their home residence were recorded routinely in the BHC laboratory registry books from June 2012 to January 2013.

Residential TCU locations were traced by comparing TCU leaders' names provided by patients to a list provided by the local government ward executive office where the details are recorded, regulated and regularly updated. Ward-level local government staff were consulted to solve unclear cases. Due to numerous, recent changes of TCU leaders resulting from routine electoral political processes, the previously described TCU maps and supporting databases (Dongus et al. 2011, Dongus et al. 2007) had to be updated. Validating the exact TCU boundaries and re-mapping them where changes had occurred would have been too labour-intensive. The much more affordable and practical approach taken, which nevertheless allowed for the same level of spatial precision as TCU boundary maps, was to geolocate the residences of all TCU leaders in Buguruni and Vingunguti that were successfully identified from patient records at BHC, using a hand-held Global Positioning System (GPS) receiver (Garmin, eTrex 10), at a positional precision of ≤5m.

Data analysis

Patient data were 'anonymised' during the process of data extraction from the registry books to specific data collection sheets. Data sheets were checked for consistency and accuracy and entered into a Microsoft Excel database. Data were cross-checked against BHC registry records, aggregated by TCU, and linked to GPS coordinates of the respective TCU leaders' residential locations with unique enumeration codes for each TCU. The resulting geo-database was then integrated into Geographic Information Systems (GIS) ArcGIS 10.1 software (ESRI, Redland, CA, USA). This enabled the visualisation of the spatial distribution of positive and negative test results of patients, and the diagnostic positivity rate, i.e. the number of patients in each TCU who tested positive for *Plasmodium falciparum* malaria divided by the total number of patients tested in this TCU.

Global Moran's *I* statistics in ArcGIS were used to test for spatial autocorrelation in the diagnostic positivity rates found in the different residential locations (Moran 1948). Spatial clustering was assessed on ward, neighbourhood and TCU levels.

For wards and neighbourhoods, generalised linear modelling analyses (binomial distribution) were performed with R software (Rx642.15.2) with prevalence (i.e. the proportion of patients tested for malaria that had a positive test result) as the dependent variable and neighbourhoods and wards as categorical independent variables. At the TCU level, spatial clustering of high prevalence rates were assessed by performing spatial scan statistics with FleXScan open source software (v3.1.2) (Takahashi et al. 2008, Takahashi et al. 2013, Tango and Takahashi 2005). FleXScan performs a flexibly shaped spatial scan statistic that can detect irregularly shaped clusters. The analysis parameters were set to purely spatial analysis, scanning for clusters with high prevalence rates using models with a binomial distribution and logit link function for this binary diagnostic status outcome and weighted according to the total number of patients tested and traced in a given TCU. The matrix definition file was created based on a spatial weights matrix generated in ArcGIS and the maximum spatial cluster size was set to 10 TCUs. Spatial relationships were set to Delaunay Triangulation with Euclidian distance. TCUs identified as being part of a spatial cluster were visualised with ArcGIS.

Results

Among 4,378 outpatients tested for the presence of *P. falciparum* malaria infections at BHC between June 2012 and January 2013, 9.1% (400/4,378) tested positive. Over half (55.0%; 2,407/4,378) of all patients tested for malaria reported that they were residents of Buguruni and Vingunguti wards, with 13.5% (325/2,407) out of these testing positive. The diagnostic positivity rate was much lower (3.8%; 75/1,971) among the tested patients that came from other wards of Dar es Salaam, including 17 patients who were residents of other regions of Tanzania. Among all tested patients living in Buguruni and Vingunguti wards, 80.6% (1,941/2,407) provided a local leader's name, and 46.6% (1,121/2,407) were successfully traced back to their residential TCU (Figure 3). Surprisingly, while the home residence TCU leader was unambiguously identified for 73.8% (240/325) of the patients from the study wards who tested positive for malaria, only 42.3% (881/2082) of those with a negative test result were successfully traced. Accordingly, the diagnostic positivity rate among the tested study ward residents who were successfully traced was considerably higher (21.4%; 240/1,121) than among untraced patients living in the same wards (6.6%; 85/1,286). The patients that could not be traced had provided none, unclear or inaccurate information regarding the names of their local leaders, wards, or neighbourhoods (Figure 3). Patients from a total of 411 TCUs were traced, corresponding to 57.3% of all TCUs in Buguruni and Vingunguti (717).

Figure 3 about here

The numbers of traced patients were similar in Buguruni (n=576) and Vingunguti (n=546), and the highest number of patients came from the neighbourhood where the BHC is located (Table 1). No spatial patterns were obvious at the ward or neighbourhood levels, as no significant differences between diagnostic positivity rates were found when the data were aggregated at these coarser scales (Table 1). However, testing for spatial autocorrelation of diagnostic positivity rates in the different residential locations indicated a clustered pattern at the TCU level (z-score=2.23, p=0.026).

Table 1 about here

Cluster analysis with spatial scan statistics based on the spatial distribution of malaria diagnostic positivity rate identified one small cluster (p=0.047) of high-infection rates (Figure 2) consisting of only four TCUs within 100m of each other, where 100% of tested patients (seven out of seven) had positive test results.

The total cost for eligible patients to be traced back to their area of residence over a period of eight months was US$10.2 per individual, comprising all personnel and transport costs for conducting this study. The additional workload for laboratory technicians resulting from this study was observed to be readily manageable and did not appreciably affect the routine daily activities of the laboratory staff who filled out >90% of the forms correctly.

Discussion

Despite the known limitations of routine health facility data in terms of representativeness and completeness (Rowe et al. 2009, Tornheim et al. 2010), this exploratory study indicates that routine patient records allow mapping the spatial distribution and heterogeneities of malaria infection rates at high levels of spatial detail (Figure 2) for every second patient tested for malaria at a health facility. This can be achieved at an affordable cost by adding simple geographic or administrative points of reference that are widely used within a community - in this case we added only the name of the patient's local leader that is generally well known in the community, a variable describing a widely-used, fine-scale geographic or administrative reference point to the health facility patient register. In contrast to previous studies that predicted fine-scale risk by fitting statistical models to aggregated health facility catchment data (Sturrock et al. 2014) or by actively tracing all patients to their homes (Bejon et al. 2014, Ernst et al. 2006), our approach demonstrates that comparably fine spatial resolutions can be derived from passively collected routine case data. Indeed, cluster analysis with spatial scan statistics identified one cluster of high diagnostic positivity that had a diameter of only 100m.

This small-scale pilot study, and indeed the overall approach taken, has considerable limitations and caveats that merit careful consideration. The most obvious limitation was that 53.4% of all tested patients could not be traced back to their residential areas. This might be due to potential selection bias for locations with more readily identifiable TCU leaders, which could possibly lead to an overestimation or underestimation of the actual malaria infection burden. The largest potential opportunity for optimising this approach therefore probably lies in improving rates of successful patient tracing. Note, however, that patient tracing may be more difficult in rural areas with more scattered populations. Indeed, only 27% of patients were successfully traced by a very similar study conducted in rural Kenya (Stresman et al. 2014). A very successful example with household traceability of up to 100% is work performed in Solomon Islands and Vanuatu, where a comparable spatial resolution was also achieved based on routinely collected data, including successful integration in an automated GIS platform for identifying areas for targeted response (Kelly et al. 2013). However, the high traceability was only possible by geo-referencing all households (>10,000) in the study area beforehand, which might be more a suitable approach in the elimination context of these Pacific Islands compared to fast growing megacities such as Dar es Salaam.

However, perhaps the most important caveat to this pilot study is the clear bias towards successful tracing of malaria-positive cases, compared to malaria-negative cases. This discrepancy is surprising, considering that residential information of the patients was recorded before the patients were tested, but it seems likely that it may have arisen from the understandably greater enthusiasm, priority and effort investment for identifying TCU leaders

of patients known to be malaria-infected. The larger number of malaria-negative patients may well have been mistakenly perceived as less interesting to those tasked with mapping the malaria risk, who may not have fully appreciated the statistical necessity to treat malaria-positive and malaria-negative patients identically. It will thus be crucial for future studies to minimize the risk of bias in the recording procedure and to blind personnel responsible for patient tracing to the diagnostic outcome of the patients. Furthermore, in order to maximize cost-effectiveness and minimize disease-specific biases, future studies should ideally map several spatially heterogeneous diseases in an integrated manner. It would be essential for further applications of this approach to also record, assess and account for the effect of patient age and the associated immunity level (Bejon et al. 2014, Bisanzio et al. 2015, Yeshiwondim et al. 2009). In the case of Dar es Salaam though, the risk of detectable malaria infection appears to be essentially equivalent across all age groups, following the strongly reduced transmission over the last several years that resulted in loss of exposure-acquired immunity (Msellemu et al. 2016).

Furthermore, the modest scale of this pilot study also represents a clear limitation that needs to be addressed with much more geographically and temporally extensive evaluations. Using only a single public facility clearly limited the coverage and completeness, so much larger scale and evaluation over longer terms will be required to fully assess both the full power and fundamental limitations of this strategy. Using this approach over longer periods of time could also enable more robust assessment of spatial clustering as well as capturing seasonality and other short- and long-term temporal trends.

Future applications of this approach will need to cope with the highly dynamic nature of local government political processes on such fine scales. The identities of local government leaders, especially those of the TCUs, change frequently due to normal electoral, political and demographic processes, so it is essential to regularly and routinely update TCU locations and leadership information by frequently consulting with local authorities at ward and neighbourhood levels or their equivalents in other settings. In this pilot study, 42.8% (820/1,941) of patients that provided a TCU leader's name could not be matched to a location because the name they provided was either wrong or misspelt in such a way that neither automated nor manual matching was possible. A possible solution for this might be to provide health facilities with up-to-date lists of all municipalities, wards, neighbourhoods and TCU leaders, from which patients can choose their respective residential location. Using electronic devices such as tablets or mobile phones for data collection might be very beneficial in this respect, and also in terms of facilitating timely reporting and responses.

The techniques presented here can be extended to include public and private health facilities at any given scale of catchment area, and can be scaled up to other comparable low-income settings with limited resources and no physical address system, wherever a similar local government system exists. In Tanzania, TCUs and their leaders have been established across the mainland and similar fine-scale local government subdivisions, known as *sheha*, also exist in the Zanzibar archipelago. In malaria-affected regions elsewhere, where the existing administrative structures do not allow for simple replication of this approach, potential alternatives to using the names of local leaders might be self-reported landmarks such as nearby schools, health facilities, churches or mosques (Stresman et al. 2014) . Alternatively, a "map-book approach", based on printouts of aerial imagery, could be applied but this may well increase cost and burden upon health facilities that are already overstretched, because it requires some time investment in explanation by health facility staff (MacPherson et al.

2013). While the clear shortcoming of both these alternatives is their much coarser spatial resolution, their potential lies in the relatively large patients numbers that can be traced (MacPherson et al. 2013, Stresman et al. 2014).

In addition to the demonstrated functionality of this fine-scale mapping procedure, a clear strength of this approach is that it is affordable and practical because it does not require any active data gathering other than maintaining up-to-date information about the residential location and identities of elected local leaders. Other than that, it relies entirely on routine health facility data which is widely available across many countries with even the most basic health services (Cohen et al. 2013). With regard to malaria control interventions, the approach might have its largest potential when integrated with a GIS-based surveillance system at the local, provincial or national level to generate dynamic risk maps for guiding targeted interventions in real time, thus contributing to effective surveillance-response systems (Tambo et al. 2014, Zhou et al. 2013).

Conclusions

Recording simple points of reference that community members can readily relate to during routine health facility visits, in this case the names of their local leaders, can be used for mapping spatial heterogeneity in confirmed clinical malaria rates at remarkably fine geographic scales. Such passively collected routine clinical data can be used to identify hotspots of elevated risk, offering a feasible approach to targeting malaria control interventions under programmatic conditions. In contrast to traditional active surveillance approaches, such as cross-sectional or incidence cohort surveys, mapping the spatial distribution of malaria infection rates using passively collected routine health facility data offers high spatial resolution at an affordable cost. However, in order to tap the full potential of this approach, optimising the success rate in tracing patients and eliminating biases associated with diagnostic test results will be necessary. Closing these methodological gaps could result in a refined surveillance tool that has the potential to become a scalable, integral, sustainable component of control programmes, which can then target supplementary interventions to foci of elevated risk.

Ethical considerations

Ethical approval was obtained from the Institutional Review Board of the Ifakara Health Institute (Approval A.50), the National Institute of Medical Research in Tanzania (Approval NIMR/HQ.R.8a/Vol IX/801) and the Masters Review Panel and Research Ethics Committee of the Liverpool School of Tropical Medicine (Approval 09.60).

Acknowledgements

We thank the staff of the Buguruni Health Centre, the Ilala Municipal Medical Office of Health and the Dar es Salaam City Medical Office of Health, as well as the neighbourhood chairmen and executive officers for their cooperation and assistance. We are grateful to M Hamel, J Stevenson, J Cox and CJ Drakeley for stimulating discussions that informed the design and interpretation of this study. Funding was kindly provided by the Wellcome Trust (www.wellcome.ac.uk) through a Masters fellowship awarded to YPM (096358/Z/11/Z), the Bill & Melinda Gates Foundation (www.gatesfoundation.org) through the Malaria Transmission Consortium (Award 41151), and the Swiss National Centre of Competence in Research North-South (www.north-south.unibe.ch) through a PhD stipend awarded to SD. VMM was supported through a PhD fellowship from the Consortium for Advanced Research Training in Africa (www.cartafrica.org), jointly led by the African Population and Health

Research Center (aphrc.org) and the University of the Witwatersrand (www.wits.ac.za). VMM was also supported by a Hassan Mshinda Career Development Fellowship, which was collaboratively funded by the Liverpool School of Tropical Medicine (www.lstmed.ac.uk) and the Ifakara Health Institute (www.ihi.or.tz). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Authors' contributions

YPM, SD, GFK, and DJT designed the study with support from PPC and NJG. YPM implemented the study. YPM and SD analysed the data and drafted the manuscript with support from GFK and DJT. VMM, ADM, AJL, JMP, DFM, and ZDM supported the study implementation and data analysis. SD prepared the maps.

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Table 1: Malaria test results per ward and neighbourhood, and results of logistic generalised linear models for comparing diagnostic positivity rates of different wards and neighbourhoods

Ward	**Neighbourhood**	**No. of tested patients**	**No. of positive cases**	**Diagnostic Positivity**	**Coefficient**	**Z-value**	**P-value**
Buguruni	Kisiwani	137	31	0.23	1	NA	NA
	Mnyamani	302	71	0.24	1.046436	0.185	0.853
	Malapa	48	13	0.27	1.270042	0.623	0.533
	Madenge	88	17	0.19	0.830415	-0.548	0.583
Vingunguti	Mtambani	166	33	0.20	0.848411	-0.583	0.560
	Mtakuja	87	23	0.26	1.228827	0.649	0.516
	Miembeni	54	8	0.15	0.594669	-1.197	0.231
	Kombo	239	44	0.18	0.771545	-0.983	0.325
Buguruni	all	575	132	0.23	1	NA	NA
Vingunguti	all	546	108	0.20	0.827522	-1.295	0.195
Total		1121	240	0.21			

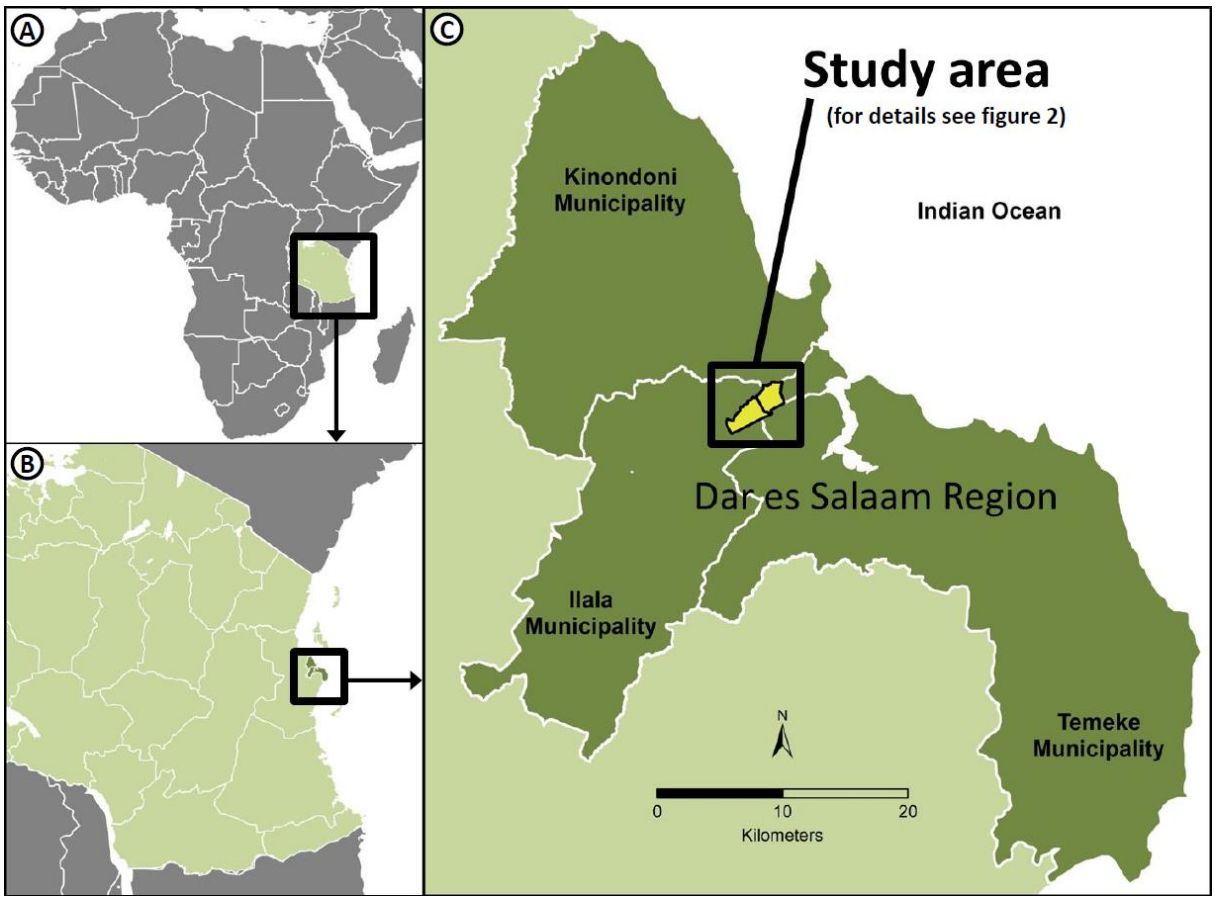

Figure 1: Location of study area in Dar es Salaam, Tanzania. A – overview map of Africa; B – overview map of Tanzania; C – overview map of Dar es Salaam Region, indicating the location of the study area (Buguruni and Vingunguti wards, see figure 2).

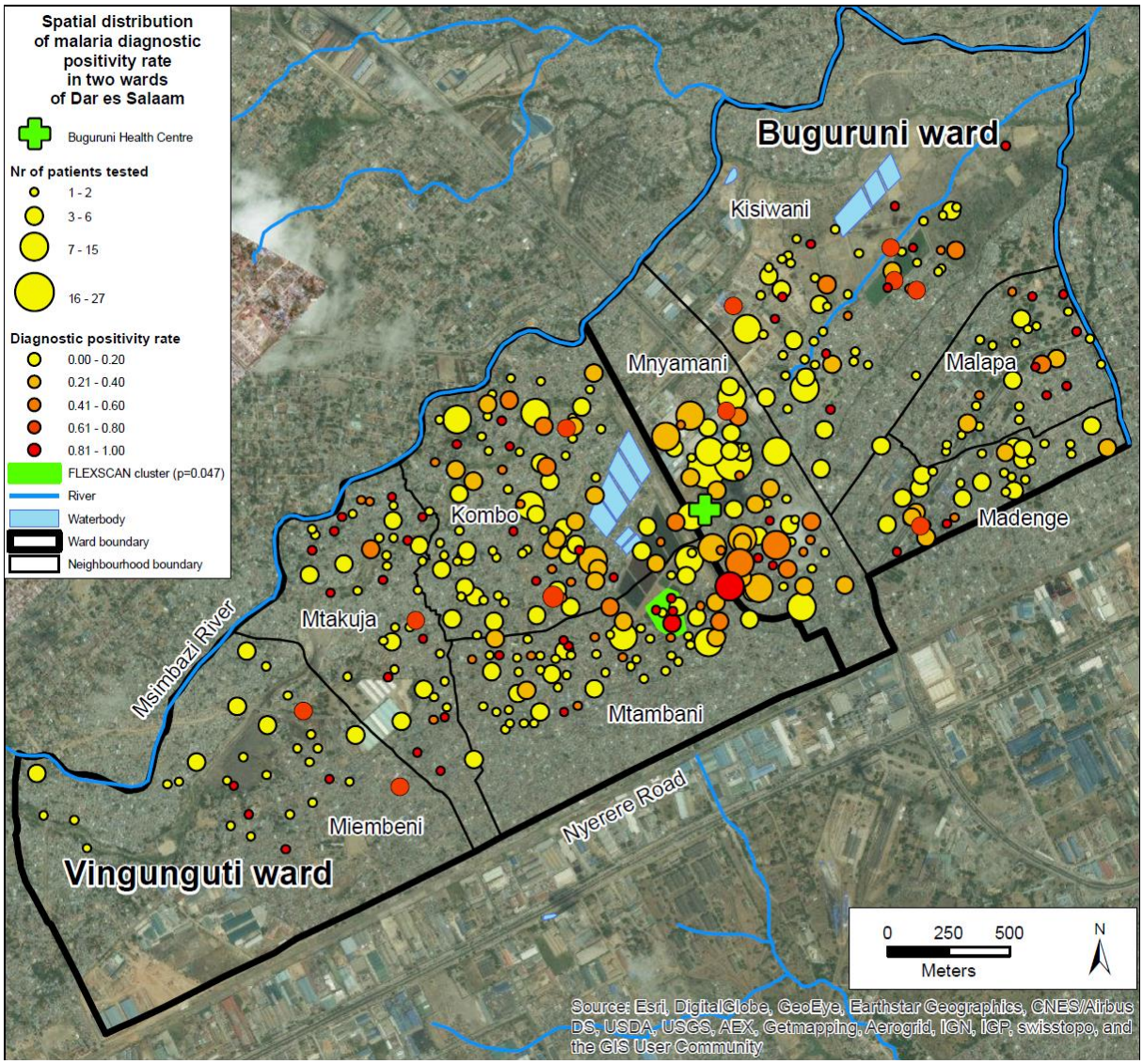

Figure 2: Spatial distribution of malaria diagnostic positivity rate (i.e. the proportion of patients tested for malaria that had a positive test result) in two wards of Dar es Salaam (Buguruni and Vingunguti). The size of the dots is proportional to the number of tested patients. The locations of the dots refer to residential housing cluster (TCU) locations, represented by the location of the TCU leader's house. The spatial cluster (p=0.047) of high malaria diagnostic positivity rate (based on FleXScan analysis) is marked in green. All results based on data from patients tested for malaria at Buguruni Health Centre (BHC) from June 2012 to January 2013. Base Map: aerial imagery (www.bing.com/maps).

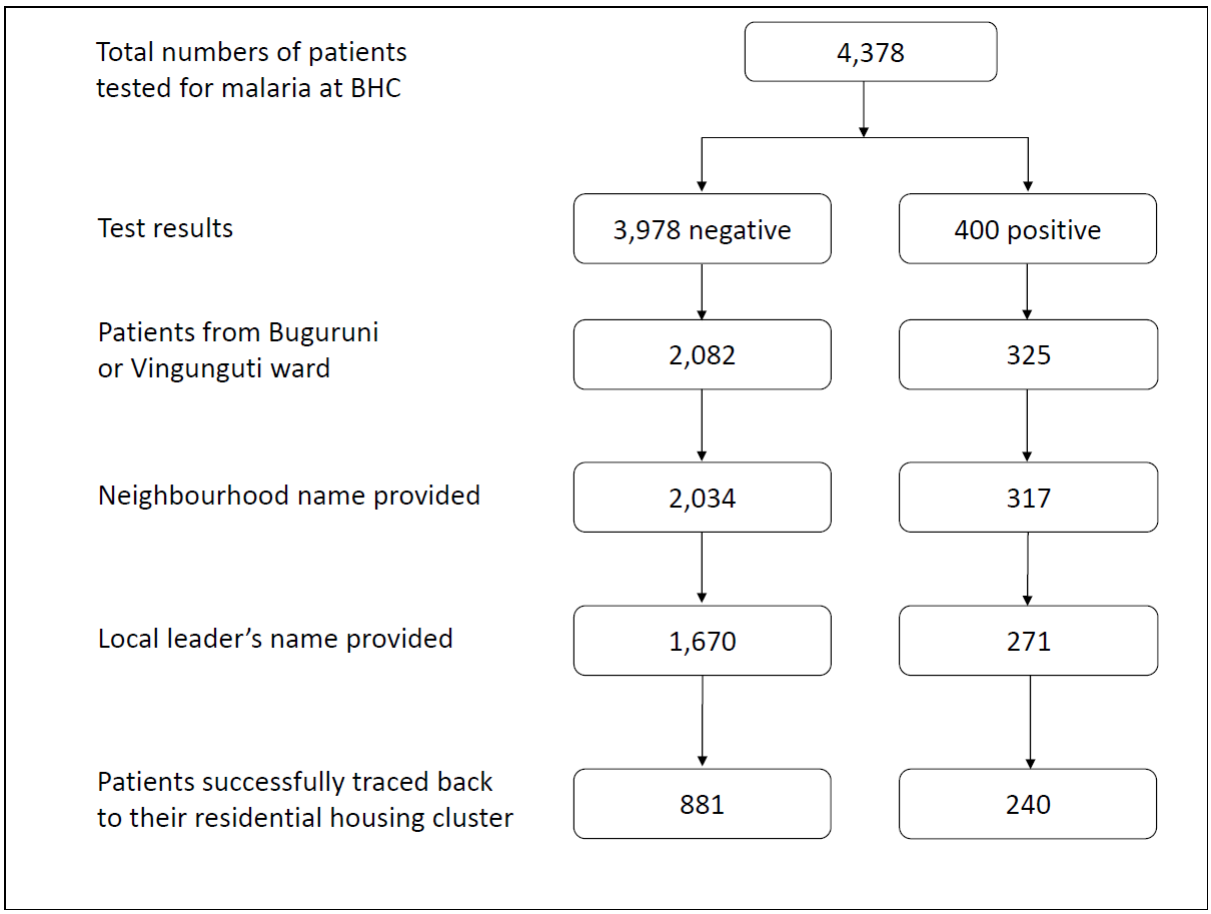

Figure 3: Number of patients sampled at Buguruni Health Centre (BHC), and patient flow with regard to number of patients who were successfully traced back to their residential location (TCU)