rainfall. The forecasting accuracy improved with the series stratified by age group and the environmental predictors were significant for malaria prevalence for ages 0–5 and 5–15 but less often significant for ages 15 and over. The forecasting accuracy deteriorated with increased forecasting intervals and the short-term forecast accuracy ranged from 5% to 29% across the sites (mean absolute percent error).
CONCLUSIONS Our work demonstrated the utility of using environmental covariates in the prediction of malaria, when used in conjunction with historical counts of malaria. Future work includes examining the predictive influence of treatment and malaria screening practices which we anticipate will improve the forecast accuracy of our models.

O.1.5.8.004

Evaluating changing malaria transmission in a rural village, in coastal Tanzania, by assessment of IgG antibodies against *Plasmodium falciparum* and *Anopheles gambiae* antigens

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INTRODUCTION The changing epidemiology of malaria in Sub-Saharan Africa over the last decade needs further understanding. A longitudinal project on the epidemiology of malaria was set up in the Nyamisati village, Rufiji District, Tanzania in 1985. Cross-sectional surveys have revealed a gradual decrease in parasite prevalence over the last 25 years, from >90% to 13% (by PCR), despite the absence of large scale control interventions. Although PCR provides good detection of low-level parasitemia, assessment of parasite prevalence alone may not fully reflect the level of exposure in a population. In order to further understand the long-term dynamics of malaria transmission in this setting, we combined an assessment of parasite prevalence with analyses of IgG antibodies against antigens of the *P. falciparum* parasite and a salivary antigen of the Anopheles vector.
MATERIAL AND METHODS The study included children 1–16 years old participating in cross-sectional surveys in Nyamisati village in 1995, 1999 and 2010. Parasite prevalence was established by PCR. Detection and quantification of IgG antibodies against *P. falciparum* crude schizont extract (PfSE) and Anopheles gambiae salivary gland protein 6 (gSG6) were performed with enzyme-linked immunosorbent assay (ELISA). Levels of IgG antibodies against merozoite surface protein 1–19 (MSP-119) and merozoite surface protein 2 (MSP-2) were assessed using a multiplexed bead-based immunoassay.
RESULTS AND CONCLUSIONS Parasite prevalence and the prevalence and levels of IgG antibodies against PfSE, MSP-119 and MSP-2 decreased between 1999 and 2010, with the most marked reduction among the youngest children (1–4 years of age). The prevalence and levels of anti-gSG6 IgG antibodies showed a similar pattern. These findings suggest a substantially decreased intensity of malaria transmission in the Nyamisati area over the past 10 years, together with an evident decrease in the population level of exposure to the malaria vector.

O.1.5.8.005

Spatio-temporal clustering of clonal parasites in recurrent vivax malaria infections after radical cure treatment in the Peruvian Amazon

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INTRODUCTION Despite the large burden of *Plasmodium vivax*, little is known about its transmission dynamics. The study of the parasite population structure and dynamics give insights on particular epidemiological features of malaria in endemic areas. We explored the population structure and spatio-temporal dynamics of *P. vivax* infections in a 2-year cohort study carried out in a rural community of the Peruvian Amazon.
MATERIALS AND METHODS Between March and December 2008, 37 *P. vivax* patients were treated with chloroquine and primaquine and followed up monthly for 2 years with systematic blood sampling. All samples were screened by microscopy and species-specific PCR for malaria parasites and subsequently all *P. vivax* infections genotyped using 15 microsatellites. Parasite population structure and dynamics were determined by computing different genetic indices and using spatio-temporal statistics.
RESULTS Seventy-six percent of the study participants experienced one or more recurrent *P. vivax* infections during their follow-up. Fifty-five percent of the recurrences were sub-patent and asymptomatic. The *P. vivax* population displayed limited overall genetic diversity (He = 0.49), high frequency of monoclonal infections (84%), presence of linkage disequilibrium (LD) and low probability of outbreeding (Psex<0.0001). Up to 20 unique haplotypes unequally distributed in four haplogroups were found. Haplotype replacement was reflected by spatio-temporal clustering and changes on the degree of LD and the genetic diversity after the first year of follow up ($P < 0.001$).
CONCLUSIONS The parasite population and dynamics found in this study may explain some epidemiologic features of the study area: (i) the clonal parasite population and haplotype clustering could be favored by the geographical isolation of the study area; (ii) continuous infections with the same clones may facilitate the development of clinical immunity, reflected on high recurrence of asymptomatic infections; (iii) the high rate of recurrent infections after treatment could be associated to the increased risk of spread of drug resistance traits in clonal populations.

1.5.9 Malaria diagnosis

O.1.5.9.001

Development and evaluation of a sensitive direct-on-blood PCR – lateral flow assay for the near point of care diagnosis of malaria

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Molecular tools allow for specific/sensitive malaria diagnosis, but current formats, like PCR with gel-electrophoresis, are difficult

