

year of diagnosis were associated with mortality in the multivariate regression model.

Conclusion This large population level TB study identifies an alarming trend of patients dying within months of starting treatment. These early deaths could be due to late diagnosis and multidrug-resistance. The study warrants further investigation to go beyond already established indicators which remained constant (including HIV co-infection), to explore host, disease or health system related factors that may explain the observed trend.

PO 8418 NEW MALARIA EPIDEMIOLOGY IN COASTAL LAGOON OF BENIN: *PLASMODIUM* INFECTION IN *ANOPHELES MELAS*

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10.1136/bmjgh-2019-EDC.90

Introduction Malaria is a worldwide disease affecting many people particularly in the tropical and sub-tropical areas. It is caused by *Plasmodium* parasites and essentially transmitted by female mosquitoes belonging to the *Anopheles* genus. Our understanding of the infectivity of these vectors to *Plasmodium* is necessary to design sustainable strategies for their control. This aspect remains unknown in the coastal and lagoon area of Benin where *Anopheles melas* and *Anopheles coluzzii* are sympatric. This study aims to investigate the infectivity of these two vectors to *Plasmodium* to understand their role in malaria transmission in southern Benin.

Methods Insecticide spray catch technique was used to collect females in 80 houses randomly selected in our study site. Three hundred and twenty (320) females were identified using PCR-species technique, *Plasmodium* infection was determined by the TaqMan method during the dry season. This assay detects all four malaria-causing species and discriminates *Plasmodium falciparum* from *Plasmodium ovale*, *Plasmodium vivax* and *Plasmodium malariae* (OVM).

Results During the dry season, the sporozoite rates were 0.2% and 0.3% for *Anopheles melas* and *Anopheles coluzzii*, respectively. However, we observed that positivity to the OVM (one of *Plasmodium ovale*, *Plasmodium vivax* and *Plasmodium malariae* species) was significantly higher in *Anopheles melas* (95%) than in *Anopheles coluzzii* (33.33%) (Chi-sq=15 857, df=1, p<0.001). These results indicated that *Anopheles melas* is more infected by one of the species *Plasmodium ovale*, *Plasmodium vivax* and *Plasmodium malariae* than by *Plasmodium falciparum*, contrarily to *Anopheles coluzzii*.

Conclusion These findings reinforce the debate on the role of *Anopheles melas* in malaria transmission in coastal lagoon areas of Benin.

PO 8419 SPATIO-TEMPORAL MAPPING OF ASYMPTOMATIC AND CLINICAL MALARIA INFECTIONS REVEALS FOCI OF MALARIA TRANSMISSION FOR TARGETED CONTROL INTERVENTIONS

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10.1136/bmjgh-2019-EDC.91

Background The global decline of malaria incidence over the past decade has led to the thought that elimination could be achieved. This has resulted in an increased interest to design strategies to target the hidden reservoir of asymptomatic infections among populations and interrupt on-going residual local malaria transmission. This study explored the reservoir of asymptomatic *Plasmodium* infections and its relationship with subsequent clinical malaria infections in low-transmission areas in Senegal.

Methods Cross-sectional surveys were carried out in 2013, 2014, 2015, and 2016 and combined with longitudinal follow-up to determine and geolocalise both asymptomatic and clinical malaria episodes in Dielmo and Ndiop, Senegal. The prevalence of asymptomatic *Plasmodium* carriage in the community was investigated by real-time PCR while clinical malaria attacks were identified at health facilities during the transmission season. All households were georeferenced to spatially map asymptomatic and clinical infections.

Results The study revealed substantial asymptomatic infections with average parasite carriage of 8.11% and 7% in Dielmo and Ndiop, respectively. *P. falciparum* accounted for most asymptomatic infections (more than 90%). In Dielmo, 95% of asymptomatic infections clustered within the same geographical areas while infections were disparate in Ndiop. Preliminary fine-scale mapping of asymptomatic and clinical malaria infections identified clusters of higher malaria incidence interpreted as foci of transmission across the four-year study period with 95%–98% of clinical infections occurring in households where an asymptomatic malaria infection existed.

Conclusion This study revealed substantial asymptomatic *Plasmodium* infections in both settings throughout the four-year study period and spatial clusters of malaria infections at the microepidemiological level. Together, these findings could offer a feasible approach for a rational targeting of malaria control interventions to achieve elimination.

PO 8421 LITERATURE REVIEW OF BIOMARKERS FOR HUMAN AFRICAN TRYPANOSOMIASIS POST-TREATMENT FOLLOW-UP

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10.1136/bmjgh-2019-EDC.92

Introduction Human African trypanosomiasis (HAT) is caused by *Trypanosoma brucei gambiense* and *rhodesiense* and is transmitted to humans by tsetse flies in sub-Saharan Africa. To detect cure or treatment failure, patients are followed up after treatment integrating the use of biomarkers in blood or cerebrospinal fluid (CSF).

Methods A systematic review of the literature according to the PRISMA Statement for Reporting Systematic Reviews was done, focusing on biological markers for HAT post-treatment follow-up. Articles were retrieved from PubMed (<https://www.ncbi.nlm.nih.gov/pubmed/>) by using keywords: Human African Trypanosomiasis, Biomarkers, Follow up, Post treatment.

Results A panel of biomarkers is used to detect relapses or to confirm recovery. For post-treatment follow-up, an examination of the CSF is performed. White blood cell counts in CSF with a defined cut-off value have been proven to be the most accurate to assess the treatment outcome. The intrathecal immunoglobulin M synthesis is a specific and sensitive parameter for