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Abstract (poster session)

Distribution of Plasmodium falciparum drug-resistant pfmdr1 86Y allele in two different zones of Uganda

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Objectives Increasing resistance to antimalarial drugs is a leading problem in fighting against malaria. Nowadays, since in most malaria endemic countries the antimalarial regimens are based on artemisin combination therapies (ACT), monitoring Plasmodium falciparum resistance to the combination is the most important issue and an emerging global problem in public health. There are now many evidences that link artemisinin resistance to parasite pfcrt, pfmdr1, pfmrp1, pfatp6 polymorphisms. Here we test and discuss the spread of the resistant pfmdr1 86Y allele in Kampala and Karamoja regions, two zones of Uganda, with different transmission intensity and drug usage. Methods Blood collection was performed in two different zones of Uganda: in the Kampala suburbs (Central-Southern Uganda) and in rural sites of Karamoja region (North-Eastern Uganda) during two distinct malaria cross-sectional surveys done at the end of 2007 transmission season. At the time of the study the available antimalarial therapy was mainly a combination of artemether and lumefantrine (AL) and, as an alternative, artesunate (AS) plus and amodiaquine (AQ). We analysed 261 DNA specimens from young asymptomatic subjects. P. falciparum DNA was amplified by nested PCR-RFLP technique to identify N86Y polymorphism in pfmdr1 gene. Results The parasite rate in the two different contexts was 25.6% in urban zone and 54.5% in rural zone ($P << 0.001$). Moreover, the rate of drug resistant genotypes was higher in the urban than in the rural zone, being 87.8% and 74.5%, respectively ($P = 0.0002$, when stratifying for all the three different parasite genotypes: pure resistant infection, wild-type sensitive infection, mixed infection). Conclusion The results are in line with the evidence that selection and exposure to drug resistant malaria parasites is higher in a urban context than in the rural one.