forecasting of ACTs and, potentially, for other commodities procured using funding from the Global Fund. Further validation using data from other countries in different regions and environments will be necessary to confirm its generalizability.

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GENOTYPING OF PLASMODIUM VIVAX ISOLATES FROM ARMENIA

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Plasmodium vivax is the most widely distributed human parasite and the main cause of human malaria outside Africa. Recently, a research project funded by the European Commission (INCO Copernicus-2 project contract no. ICAZ-CT-2000-10046) on the molecular epidemiology of P. vivax malaria has been implemented in three countries belonging to the Community of the Newly Independent States (NIS-Countries), i.e. Armenia, Azerbaijan and Uzbekistan. To investigate the genetic makeup of the P. vivax population in Armenia, a study was carried out in the endemic regions of Ararat and Yerevan. A total of thirteen P. vivax isolates were collected from patients attending the local health centres from July to October 2004. Genotyping analysis was carried out combining different available molecular tools, namely polymerase chain reaction (PCR) amplification and sequencing of a polymorphic pvmsp-1 gene region as well as tandem repeat and microsatellite markers analysis. Plasmodial DNAs were extracted from infected blood samples spotted onto filter papers, using the QIAamp DNA blood Kit (QIAGEN), following the manufacturer's instructions. Pvmsp-1 fragment amplification was performed as previously described. All PCR products were sent to MWG Biotech (Germany) for sequencing; subsequently, pvmsp-1 sequences were compiled and analyzed at the ISS laboratory using the DSGene 1.5 computer program. Results from pvmsp-1 amplicons sequencing were used to identify the representative MSP-1 types described so far, i.e. Belem and Sal-1 and recombinant types. Among the thirteen Armenian isolates analyzed, eight have been ascribed to Belem type and five to Sal-1 type. We have also analyzed eight tandem repeats and fourteen microsatellite loci. The number of identified alleles varies from one to seven. One allele of a TR locus and two alleles of two microsatellite loci were detected which had never been found in our previous studies. Thus, the P. vivax Armenian population shows noticeable genetic diversity when compared to the low endemic situation for malaria in this region.

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THE TEMPORAL DYNAMICS OF PLASMODIUM DENSITY THROUGH THE SPOROGONIC CYCLE WITHIN ANOPHELES MOSQUITOES

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In order to develop mathematical models that describe the sporogonic cycle of Plasmodium within the mosquito vector using a parasite density framework and evaluate the impact of transmission blocking strategies, it is important to determine the temporal dynamics of the various developmental stages within the mosquito and the effect of parasite density on such dynamics. A series of three experiments, in which cages of Anopheles stephensi mosquitoes were fed on blood infected with a range of Plasmodium berghei oocinete densities (from 50 to 2,000 per µl), were conducted to determine patterns of oocyst and salivary gland sporozoite abundance over time after infection and throughout the course of the entire sporogonic cycle. Every 24-48 hours after membrane feeding, samples of 20 live mosquitoes were dissected and the number of established oocysts and salivary gland sporozoites counted. Both the average and the raw counts for each time-point were analyzed. The results from these experiments were used to parameterize a compartmental model (comprising differential equations for oocinets, oocysts, and sporozoites) and to quantify the rates of progression between the different Plasmodium developmental stages. Results indicate that the magnitude of these transition rates depends on parasite density with implications for our understanding of the impact of transmission blocking strategies on malaria transmission.

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ASSESSMENT OF SEXUAL STAGE SPECIFIC IMMUNITY IN CHILDREN (0-15 YEARS OF AGE) IN ZAMBIA

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Plasmodium falciparum transmission reducing immunity has been demonstrated to correlate with immune responses to sexual stage specific antigens Pfs48/45 and Pfs230, depending upon the specific locale and age group studied. The development of transmission blocking immunity in subjects with natural exposure to malaria has been studied previously almost exclusively in adult populations and by cross sectional analyses of subjects at one time point. Our study examined sexual stage specific immunity in children of various ages and over more than one transmission cycle. We conducted a prospective, longitudinal study of children [N=150 subjects] from age 0 to age 15 years in Zambia to determine the independent variables that may relate to the outcome of transmission reducing immunity as defined by the mosquito membrane feeding assay. Independent variables were age, sex, locale and history of maternal malaria infection in pregnancy. Malaria transmission is seasonal in Zambia and we documented a much lower rate of malaria infection by thick film during the dry season as compared to immediately following the rainy season. The relationship of specific immune responses to Pfs48/45 and Pfs230 as demonstrated by the subjects during the dry season as compared to immediately following the rainy season were analyzed to ascertain both the duration of transmission reducing immune responses as well as potential boosting of such responses by repeat exposure to malaria infection. Our analyses revealed a positive, statistically significant relationship between the age of the subjects and immune responses to Pfs48/45. In certain analyses, the locale or geographic location of the subject also emerged as a significant independent variable and further analysis of this finding is in progress. A more clear understanding of naturally induced transmission blocking immunity may be critical to the successful development of transmission blocking vaccines.

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USE OF LOT QUALITY ASSURANCE SAMPLING (LQAS) TO MONITOR BEDNET DISTRIBUTION

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The Equatorial Guinea Malaria Control Initiative, EGMCI, distributed bednets in 144 housing/ distribution areas. Volunteers carried out a rapid household census; inventoried sleeping areas; and supplied the households with one LLIN per sleeping area. EGMCI did a concurrent rapid household census; inventoried sleeping areas; and supplied the households with one LLIN per sleeping area. EGMCI did a concurrent rapid spot check using the LQAS methodology, in 19 households/census tract or lot. Indicators: A) Percent of households contacted and receiving at least one net. Threshold or decision rule: 15 homes. B) Percentage of households with one bed-net per sleeping surface, threshold equal to 13 homes. Data collection: Households were selected using paper bits with sequential numbers. Sample size was proportion to the hamlet's population. 8037 households were visited, and 41,498 nets were distributed. For LQAS monitoring, 896 households from 61 lots (census tracts) were visited, later aggregated into five municipalities. Two municipalities failed for indicator

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