Results

Total of 2991(634 female and 2357 males) sandflies were collected. The majority (99%) was identified as *Phlebotomus argentipes*. Rest of the sandflies (1%) were *Sergentomyia zeylanica* a non human vector of leishmaniasis. Presence of *Leishmania donovani* DNA was confirmed in 2/634 of female sand flies using PCR. Both sandflies positive for DNA were identified as *P.argentipes*. Further analysis of isolated parasite DNA revealed almost 100% sequence similarity with regional *L. donovani* from Bangladesh and India.

Conclusions and recommendations

Phlebotomus argentipes is the major sandfly species distributed in the study area. Two female sandflies that were positive for *Leishmania* DNA were also *P,argentipes.* Therefore this study provides the first evidence to establish *P. argentipes* as the disease transmitting agent of leishmaniasis in Sri Lanka. Further studies are needed to confirm its true vectorial capacity using laboratory and experimental models.

Acknowledgement

Authors would like to acknowledge W.D.A. Mahakumara from Malaria Field Research Station, Kataragama and K H Weerasena from Dept of Parasitology, Faculty of Medicine, and Colombo for their assistance in the field work.

OP2 Geographic structure of *Plasmodium vivax*: microsatellite analysis of parasite populations from Sri Lanka, Myanmar and Ethiopia

Gunawardena S[1], Karunaweera ND[1], Ferreira MU[2], Phone-Kyaw M[3], Pollack RJ[4], Alifrangis M[5], Rajakaruna RS[6], Konradsen F[5], Amerasinghe PH[7], Schousboe ML[5], Galappaththy GNL[8], Abeyasinghe RR[8], Hartl DL[9], Wirth DF[4]

[1]Department of Parasitology, Faculty of Medicine, University of Colombo, Sri Lanka, [2]Department of Parasitology, Institute of Biomedical Sciences, University of São Paulo, Brazil, [3]Parasitology Research Division, Department of Medical Research (Lower Myanmar), Myanmar, [4]Department of Immunology and Infectious Diseases, Harvard School of Public Health, USA, [5]Centre for Medical Parasitology, Department of International Health, Immunology & Microbiology, University of Copenhagen, and Department of Infectious Diseases and Department of Clinical Microbiology, Copenhagen University Hospital (Rigshospitalet), Copenhagen, Denmark, [6]Department of Zoology, University of Peradeniya, Sri Lanka, [7]International Water Management Institute, India,[8]Anti-Malaria Campaign, Ministry of Health, Sri Lanka, [9]Department of Organismic and Evolutionary Biology, Harvard University, USA.

Introduction and rationale

Genetic diversity and population structure of *P. vivax* parasites can predict the origin and spread of novel variants within a population enabling population specific malaria control measures. The aim of our study was to determine the genetic diversity and population structure of *P. vivax* patient isolates collected from Sri Lanka, Myanmar and Ethiopia.

Methodology

425 *P. vivax* isolates collected from Sri Lanka (between 2003 and 2008), Myanmar (2007) and Ethiopia (between 2006 and 2008) were genotyped using 12 highly polymorphic microsatellite markers. The 12 markers were PCR-amplified using oligonucleotide primers with the forward primer labeled with fluorescent dyes. The PCR products were size fractionated by capillary gel electrophoresis. The single or predominant allele at each locus was considered for computing allele frequencies. The presence of more than one allele at a particular locus was interpreted as a multiple-clone infection. Genetic diversity was determined by calculating heterozygosity (H_E) and standardized index of association (I^S_A) used to test for multilocus linkage disequilibrium. STRUCTURE software was used to test for clustering of haplotypes according to geographic origins and ancestry of the isolates.

Results

All three parasite populations were highly polymorphic with 3-44 alleles per locus. Almost 65% were multiple-clone infections. Mean genetic diversity (H_E) was: 0.7517 (Ethiopia), 0.8450 (Myanmar) and 0.8610 (Sri Lanka). Significant linkage disequilibrium was maintained. Population structure revealed two clusters (Asian and African) according to geography and ancestry. Strong clustering of outbreak isolates from Sri Lanka and Ethiopia was observed. Predictive power of ancestry using 2/3rds of isolates as a model identified 78.2% of isolates accurately as being African or Asian.

Conclusion

Microsatellite analysis appears to be a useful tool for mapping short-term outbreaks of malaria and for predicting ancestry.

Acknowledgements
We gratefully acknowledge the financial support provided by the National Institutes of Health (5R03TW007966-02), USA and technical assistance by Mr. GMG Kapilananda of the Department of Parasitology, Faculty of Medicine, University of Colombo.

OP3 Factors affecting non-adherence with home exercises prescribed by rehabilitation therapists for stroke patients discharged from the National Hospital of Sri Lanka

Weerasinghe E[1], Jayawardana S[1], Dissanayake D[2]
Allied Health Sciences Unit[1], Department of Physiology[2], Faculty of Medicine, University of Colombo

Back ground and justification

Exercise adherence is defined as "the degree to which patient behaviours coincide with the clinical recommendations of health care providers''. Promoting exercise adherence is important to maximize the therapeutic out comes of stroke rehabilitation programmes. The aim of the study was to identify the factors which affect non-adherence with home exercise programmes prescribed by rehabilitation therapists for stroke patients discharged from National Hospital of Sri Lanka.

Methodology

The study was cross-sectional in its design using 100 stroke diagnosed patients who attended the monthly clinic of stroke unit of National Hospital of Sri Lanka (NHSL), Colombo and Physiotherapy Department of Neurology Unit, NHSL. The study population consisted of two groups 'non compliant' (n =50) and 'compliant' (n = 50) who met the inclusion criteria. The responses given for the specific questions "In a typical week how often do you do the exercises" and "how long do you exercises in a one session" were compared with the recommended exercise regime to assess the degree of adherence to home exercises. Based on that compliant and non-compliant groups were selected. The data was collected using an interviewer administered questionnaire designed to assess the level of adherence with home exercises, socioeconomic level, patients' perception on following exercises, participants' ability in performing activities of daily living and the encountered barriers which affect non compliance to home exercises in the population. The results were analyzed using appropriate descriptive statistics and chi square test using SPSS statistical software to identify the relationship between tested variables and non- compliance. The