Design, setting and methods

608 medical students in the Faculty of Medicine, Colombo were screened for colour blindness using Ishihara pseudoisochromatic charts (17 plates). Individuals found to be colour blind were given a self administered questionnaire and subjected for further examinations with Fransworth Munsell 100 Hue test, refraction errors and fundoscopy at the Eye Hospital, Colombo.

Results

The prevalence of colour blindness among medical students in Faculty of Medicine, Colombo was 1.89% (n=11) with a male predominance (3.67%, n=11) and 0% in females. Deutan (55.55%, n= 6) type was the commonest type of colour deficiency. X linked congenital colour vision deficiency was found to be the probable aeitiology. 45% - 54% of the colour blind individuals have experienced difficulties in day today, academic and clinical work due to defective colour vision. Among which identification of bacilli in Zeihl Neelson stain, end point of titer and different cannuli according to colour were reported. Majority has neglected their defective colour vision without seeking medical advice. 27% of the colour blind individuals use the opinion of another individual who is not colour blind, as a method to overcome their defect in colour vision

Conclusion and Recommendations

Prevalence of defective colour vision in Faculty of Medicine, Colombo is 1.89% with a male predominance (3.67%). Probable aeitiological factor is X linked recessive inheritance of congenital colour vision deficiency. Majority has neglected their defective colour vision. Self-awareness of defective colour vision will help them in choosing a field of specialization in the future, which has minimal requirement of proper colour vision.

PP1 Clinical profile of leishmaniasis in Polonnaruwa district Siriwardana HVYD¹, Leelarathne SH¹, Kahawita I², Karunaweera ND¹ ¹Department of Parasitology, Faculty of Medicine, University of Colombo ²General Hospital, Polonnaruwa

Introduction

Sri Lanka is a new focus of human leishmaniasis caused by *L. donovani*. Over 2200 cases have been referred to General Hospital, Polonnaruwa for diagnosis. *L.donovani* is a

species known to be transmitted anthroponotically without the involvement of an animal reservoir. Hence early case detection and management is accepted as the main control strategy. To facilitate early case detection and management, accurate case description is important. It is best done at local level due to the wide spectrum of clinical manifestations in cutaneous leishmaniasis patients. This information is also necessary to enable more effective awareness programs, field screening programs and drug trials which are all timely needs in this field.

Methodology

A descriptive study was carried out in a group of 117 clinically suspected cases of cutanoeus leishmaniasis presenting to the General Hospital, Polonnaruwa from the District of Polonnaruwa, over the period of 14 months (May 2009 to September 2010). Suspected cases, based on the lesion and a detailed history, presenting to the Dermatology unit of the Pollonnaruwa General Hospital were subjected to taking a slit skin smear and a lesion aspirate for definitive diagnosis.

Results

Parasites were demonstrated in 35.2% (n=45) of cases. The cases depicted a bimodal distribution being highest in early part of March (n=15, 12.3%) and the lowest in June (n=3, 4.9%).

Among these patients the disease was found to be more prevalent in males (in males n=69, 59% and n=48, 41% in females). Patients belonged to a wide age group ranging from 8 to 80 years. Majority of the patients were in 31 to 40 years age group.

The initial symptom of majority was painless non itchy papules, in 40.2% (n=49) of the cases. Other initial manifestations were ulcer or a nodule forms. Most of the lesions were of 2 or 3 months duration (n=14, 11.5%). During the examination of the patients, commonest feature found was erythema in the skin surrounding the lesion (n=54, 44.3%). Most lesions were single (n=76, 62.3%) and most had a maximum diameter of 1-2cm (n=24, 19.7%). Lesions were commonly found in the face and anterior neck (n=27, 22.1%). Most lesions had irregular edges (n=30, 24.6%) but a large number tended to be rounded in shape (n=28, 23%).

Conclusion

Cutaneous leishmaniasis is prevalent in Polonnaruwa and affects both sexes and a wide age range. Clinical appearance of lesions is non-specific, hence confirmation of diagnoses using laboratory methods is recommended. Seasonal variation in case numbers observed in the study might be due to the changing vector prevalence associated with environmental factors, which need further investigations.

PP2 Determining the geographical origin of *Plasmodium vivax* using five microsatellite markers, instead of twelve markers: a more cost effective tool

<u>De Silva C</u>, Karunaweera ND, Gunawardena S Department of Parasitology, Faculty of Medicine, University of Colombo, Sri Lanka

Introduction

Malaria transmission in Sri Lanka remains low and unstable with a plan in place for its elimination within the next 5 years. Recent epidemiology of malaria in Sri Lanka consists of infections imported from other endemic countries and locally acquired sporadic cases with focal spread among non-immune residents. Identifying the source of infection is vital for the implementation of vigorous and targeted control strategies enabling successful elimination. Twelve previously validated microsatellite markers have proved to be useful in revealing the geographic origin and population structure of *P. vivax* parasites, which is a costly method to adopt. Aim of this study was to determine the minimum number of markers required to achieve the same outcome.

Methods

Data from 425 field isolates genotyped using a previously validated panel of 12 microsatellite markers (MS1, MS2, MS3, MS4, MS5, MS7, MS8, MS10, MS12, MS15, MS16 and MS20) was used. These field isolates comprised samples collected from Sri Lanka (140), Myanmar (167) and Ethiopia (118). Different combinations of microsatellite haplotypes (varying from 3 to 5) were tested using 2/3rds of isolates as a model for predicting the ancestry by using the Bayesian algorithm software STRUCTURE. Isolates