

ing for clustered, interlaced structures since interfering factors (obstructive/reflective structures, multi-story buildings, environmental diversity) may impact on the precision of GPS readings. Geospatial frames require constant updating, but could provide an approach for population-based investigations at probability samples of households in settings that are uncensused and lack longitudinal recording of socio-demographic and vital statistics.

<http://dx.doi.org/10.1016/j.ijid.2016.02.533>

#### Type: Poster Presentation

Final Abstract Number: 42.066

Session: Poster Session II

Date: Friday, March 4, 2016

Time: 12:45-14:15

Room: Hall 3 (Posters & Exhibition)

### Genetic variability of the G-L intergenic region sequences of Indian rabies virus strains circulating in animals



K. Pramina<sup>1,\*</sup>, B. Veeresh<sup>1</sup>, S.I. Isloor<sup>2</sup>, D. Rathnamma<sup>1</sup>, S. Yathiraj<sup>3</sup>, M. Narayanswamy<sup>3</sup>, R. Sharada<sup>4</sup>, Y. Chaitra<sup>3</sup>, N.R. Hegde<sup>5</sup>

<sup>1</sup> Veterinary College, Bangalore, India

<sup>2</sup> Veterinary college, Bangalore, Karnataka, India

<sup>3</sup> Veterinary college, Bangalore, India

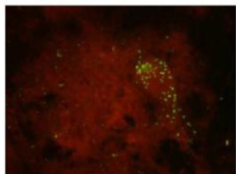
<sup>4</sup> Veterinary college, Hassan, India

<sup>5</sup> Ella Foundation, Hyderabad, Telangana, India

**Background:** The evolutionary studies of rabies virus (RABV) have targeted the N or G gene, or recently the G-L intergenic region sequences. Among these, G-L intergenic region is considered as the most variable since it is not subjected to immunological selective pressure. The present study was undertaken to understand the genetic variability of RABV in animals in India based on the G-L intergenic region

**Methods & Materials:** Twenty seven brain samples from suspected rabid animals (22 dogs and five cattle) resourced from Karnataka (n=9), Kerala (n=5), Rajasthan (n=3), Tamil Nadu (n=2), Manipur (n=4) and Uttar Pradesh, Gujarat, Puducherry and Jammu Kashmir (n=1 each) were confirmed by Direct Fluorescent Antibody (DFA) assay (Fig.1). The samples were further subjected to Reverse Transcription Polymerase Chain Reaction (RT-PCR) along with Dr. Larghi's strain (PV-3462) as reference to amplify the G-L intergenic region. The PCR products (1354 bp) were purified, sequenced and compared to the corresponding sequences of RABV from different countries, CVS and PV strains obtained from GenBank. Phylogenetic tree was constructed using the nucleotide sequences corresponding to 423 bp of the 1354 bp amplicon. The branching pattern of the trees was constructed by the Neighbor Joining method using Mega 5 software version 5.02.

Fig. 1. Rabid brain impression stained with the rabies virus anti nucleocapsid IgG-FITC conjugate (Rabies DFA III, Light Diagnostics, Cat # 8500) with counter stain



Group 2 restricted to two Southern states, Tamil Nadu and Kerala. Group 2 RABV showed high homology with the Sri Lankan isolates. Group 1 was further sub-grouped into four, designated as 1a, 1b, 1c and 1d. Group 1a included the majority of isolates from Karnataka and Puducherry, and one from Kerala. Group 1b included RABVs from Rajasthan, Gujarat, Uttar Pradesh and Karnataka, whereas Group 1c included an isolate from Jammu & Kashmir along with isolates from Pakistan. Group 1d included isolates from Manipur and Bangladesh.

Fig. 2. Neighbour-joining phylogenetic tree of 27 RABVs and Dr. Larghi (PV-3462) reference RABV nucleotide sequences based on G-L intergenic region rooted with the CVS strain.

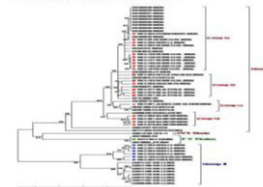
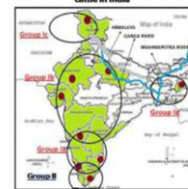


Fig 3: G-L intergenic region based clustering of RABV from dogs and cattle in India



**Conclusion:** Rabies viruses circulating in animals in India belong to Genotype 1, and are genetically diverse. In the present study, the sub grouping of RABVs could be due to major geographical barriers such as Himalayan range, Western ghats and major rivers including Ganga and Brahmaputra.

<http://dx.doi.org/10.1016/j.ijid.2016.02.534>

#### Type: Poster Presentation

Final Abstract Number: 42.067

Session: Poster Session II

Date: Friday, March 4, 2016

Time: 12:45-14:15

Room: Hall 3 (Posters & Exhibition)

### Prevalence of rickettsial infections in acute coronary syndromes in Sri Lanka: A case control study



C.D. Mettananda<sup>1</sup>, R. Premaratna<sup>2,\*</sup>, D. Danansuriya<sup>3</sup>, N.B. Bandara<sup>3</sup>

<sup>1</sup> University of Kelaniya, Sri Lanka, Ragama, Sri Lanka

<sup>2</sup> Faculty of Medicine University of Kelaniya, Ragama, Sri Lanka

<sup>3</sup> University of Kelaniya, Ragama, Sri Lanka

**Background:** Interest in the relationship between infection and atherosclerosis induced coronary heart disease has recently increased. Rickettsiae are a group of obligate intracellular pathogens who invade endothelial cells and cause vasculopathy. In a longitudinal nation wide study conducted in Thailand, the incidence of acute coronary syndromes (ACS) in patients with scrub typhus was found to be higher than a comparison cohort (3.10 vs 1.92 per 1000 person-years). A 37% increased risk in subse-

quesnt development of ACS has been demonstrated compared to general population after adjusting for age, sex and other independent risk factors; hypertension, diabetes, hyperlipidaemia, chronic obstructive pulmonary disease and coronary artery disease. The prominent effect of scrub typhus on subsequent ACS development has appeared within 1 year after infection.

**Aims:** To assess the prevalence of Rickettsial infections in patients with ACS who live in the Western province, Sri Lanka.

**Methods & Materials:** Patients admitted with ACS to the Professorial Medical Unit, Colombo North Hospital, Ragama, Sri Lanka from April to December 2011 were studied for the serological prevalence of rickettsial infections and were compared with a matched control group; who had no fever or ACS and admitted during the same period. 2 ml serum samples were obtained at enrolment and 2 weeks after, to assess exposure to rickettsial infections by IFA-IgG antibody titres against *Orientia Tsutsugamushi* (OT) and Spotted fever group (SFG) rickettsioses. An IgG titre >1:128 or a rising/declining titre were considered positive for acute rickettsioses. A static titre was considered previous exposure to Rickettsioses.

**Results:** 46 ACS [males n(23.9%), mean age (SD) 61.1(13.1) y] and 52 controls (males n (50%), mean age(SD) 56.0(13.6) y] were studied. None had evidence of acute rickettsial infection. Seroprevalence of IgG (OT) was 6.4% and IgG-SFG was 15.2% among ACS patients while that of control group were 3.8% and 11.5% respectively. There was no significant difference in sero-prevalence of OT [OR=0.74 (CI, 0.28-10.93), p=0.66] or SFG [OR=1.376 (CI, 0.43-4.44), p=0.59] in patients with ACS compared to controls.

**Conclusion:** We observed no significant difference in seroprevalence of rickettsioses in patients with acute coronary syndromes compared to controls in this study.

<http://dx.doi.org/10.1016/j.ijid.2016.02.535>

#### Type: Poster Presentation

Final Abstract Number: 42.068

Session: Poster Session II

Date: Friday, March 4, 2016

Time: 12:45-14:15

Room: Hall 3 (Posters & Exhibition)

#### Influence of $\alpha$ thalassemia on the protective effect of sickle cell gene on severity of *P. falciparum* malaria

P. Purohit\*, S. Patel, P.K. Mohanty

VSS Institute of Medical Sciences and Research,  
Burla, India

**Background:** *P. falciparum* malaria and sickle-cell-anemia are two major public health problems in western Odisha. It has been hypothesized that sickle-cell-gene protects against severe *P. falciparum* malaria. Again, African studies described the negative epistatic interaction for protection against malaria between sickle-cell-gene and  $\alpha$ -thalassemia when co-inherited together. This study was undertaken to assess the role of  $\alpha$ -thalassemia on the protective effect of sickle-cell-gene on severe *P. falciparum* malaria.

**Methods & Materials:** Adults patients with severe *P. falciparum* malaria were included. Age, sex and ethnic matched control (no malarial infection since 5 years) were taken. Sickle-cell-gene and  $\alpha$ -thalassemia was confirmed by ARMS-PCR and GAP-PCR respectively. Clinical and haematological data were analyzed.

**Results:** 396 patients were registered, including 284, 66 and 46 patients with HbAA, HbAS and HbSS respectively. In control (total

391 cases), 301 cases had HbAA and 90 cases had HbAS. In HbAA with severe *falciparum* malaria, the incidence of  $\alpha$ -thalassemia was 36.6% (104/284) in patients compared to 47.2% (142/301) in control ( $\chi^2, 6.25$ ;  $p=0.012$ ). In HbAS, the incidence of  $\alpha$ -thalassemia was 81.8% (54/66) in patients compared to 52.2% (47/90) in control ( $\chi^2, 13.3$ ;  $p=0.0003$ ). In HbSS, the incidence of  $\alpha$ -thalassemia was 63.0% (29/46). In HbAA, patients with  $\alpha$ -thalassemia had increased Hb and RBC levels with lowered MCV and MCH compared to normal  $\alpha$ -genotype. In HbAA, the incidence of ARF, Jaundice, cerebral malaria and death were significantly low in patients with  $\alpha$ -thalassemia. The number of complications has increased with decreased  $\alpha$ -globin gene number in both patients with HbAS and HbSS. In HbAS, patients with  $\alpha$ -thalassemia had a greater HbA/HbS ratio compared to patients with normal  $\alpha$ -genotype ( $p<0.01$ ).

**Conclusion:** Patients with  $\alpha$ -thalassemia had better haematological and clinical parameters compared to normal  $\alpha$ -genotype in HbAA. The high incidence of  $\alpha$ -thalassemia in patients with HbAS, suggest the negative epistatic interaction of  $\alpha$ -thalassemia on the protective effect of HbAS against severe malaria. This hypothesis again supported by high HbA/HbS ratio in our patients with HbAS and  $\alpha$ -thalassemia. Longitudinal cohort study is essential to understand the pathophysiology of malaria and haemoglobin disorders in India.

<http://dx.doi.org/10.1016/j.ijid.2016.02.536>

#### Type: Poster Presentation

Final Abstract Number: 42.069

Session: Poster Session II

Date: Friday, March 4, 2016

Time: 12:45-14:15

Room: Hall 3 (Posters & Exhibition)

#### Role of medical colleges in TB control under RNTCP - Five years experience in Puducherry, S. India (2010 -2014)



A. Purty\*, Z. Singh, M. Natesan, R. Chauhan, D. Ramachandran

Pondicherry Institute of Medical Sciences,  
Pondicherry, India

**Background:** A substantial proportion of patients with TB are managed at medical colleges across India. The RNTCP of Govt. of India conceived and implemented the unique experiment over a decade ago of involving the academicians who constitute the faculty in the public health programme for TB control by a mechanism of National, Zonal and State level Task Forces. A periodic review of role of Medical college in TB control is important to monitor the progress.

**Methods & Materials:** Puducherry at U.T. in Southern India with a population of 1.2 million has nine medical colleges, two are government and seven are private institutions involved in implementing the RNTCP and report their progress in a structured format every quarter to the State Task Force (Puducherry) which is reviewed and feedback provided to all concerned. A consolidated report submitted to the Zonal and National Task Forces of RNTCP.

A record based study of the RNTCP STF Quarterly reports from 2010 to 2014 was conducted to find the proportion of TB patients screened, the proportion of sputum smear positive, negative and extra pulmonary TB patients diagnosed, the proportion of patients referred for treatment and proportion of pre-treatment loss to follow up among them.

