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Abstract (poster session)

**Molecular epidemiology of *Orientia tsutsugamushi* in India: broad genetic variability and its implications**

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**Objectives:** *Orientia tsutsugamushi* causing scrub typhus, a re-merging multi-system infection in the Asia Pacific region, is known to have high antigenic variations and this information is crucial for the development of effective serodiagnostic tests and vaccines. The objective of this study was to analyse the genetic variability using sequence analysis of the 56kDa TSA gene, the standard genetic differentiation technique for *Orientia*, performed on patient samples from different regions of India. **Methodology:** A 396bp region of the 56kDa antigen genes was amplified and sequenced using eschar samples obtained from 111 patients from three regions of India – North, South and Northeast. BLAST analysis was carried out and the sequences obtained were aligned using CLUSTAL OMEGA. Phylogenetic analysis was performed with the MEGA version 5.05 software using Neighbor-Joining method with 500 bootstrap replications. Reference sequences for comparison were obtained from GenBank and dendrograms were constructed. **Results:** The study included 40 isolates from Vellore, 41 isolates from Shimla and 30 isolates from Shillong. The mean age of the patients was 39 years. Sixty-two percent of the isolates clustered into Kato like group and 31.5% were found to cluster into Karp like groups with 90 to 98% sequence similarity. Two isolates from Shillong and one from Tamil Nadu showed 99% sequence similarity to the Gilliam strain BA344\_1 from Thailand and 4 isolates from Shillong showed 96% sequence similarity to Neimeng 65 strains from Mongolia, China. Among the three geographic locations, the prevalence of Kato like group of isolates was highest in Tamil Nadu (80%), followed by Shillong (56%). Shimla was found to have an almost equal prevalence of Karp like and Kato like isolates (51.2% and 48.7%). The sequences from our study showed high sequence similarities to the Taiwanese strains Hualien3, Hualien 12 and Hualien 13. The mean distance was 2.728 between the two distinct larger clades of Kato like group and smaller clade of Karp like isolates. Each clade is further divided into sub-clusters of isolates from different geographic locations. **Conclusion:** This study demonstrated two distinct circulating clades of Kato like and Karp like strains with sequence similarities to that of Taiwanese isolates in majority of the cases. There genetic variability among these strains may have implications for future diagnostics and vaccines in India.

