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## Characterization of genomic variations in SNPs of PE\_PGRS genes reveals deletions and insertions in extensively drug resistant (XDR) *M. tuberculosis* strains from Pakistan

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### ARTICLE INFO

#### Article history:

Received 21 October 2014

Accepted 26 October 2014

Available online 24 December 2014

#### Keywords:

Tuberculosis

Pakistan

### ABSTRACT

**Background:** *Mycobacterium tuberculosis* (MTB) PE\_PGRS genes belong to the PE multi-gene family. Although the function of the members of the PE\_PGRS multi-gene family is not yet known, it is hypothesized that the PE\_PGRS genes may be associated with genetic variability.

**Material and methods:** Whole genome sequencing analysis was performed on ( $n = 37$ ) extensively drug resistant (XDR) MTB strains from Pakistan which included Central Asian ( $n = 23$ ), East African Indian ( $n = 2$ ), X3 ( $n = 1$ ), T group ( $n = 3$ ) and Orphan ( $n = 8$ ) MTB strains. **Results:** By analyzing 42 PE\_PGRS genes, 111 SNPs were identified, of which 13 were non-synonymous SNPs (nsSNPs). The nsSNPs identified in the PE\_PGRS genes were as follows: 6, 9, 10 and 55 present in each of the CAS, EAI, Orphan, T1 and X3 XDR MTB strains studied. Deletions in PE\_PGRS genes: 19, 21 and 23 were observed in 7 (35.0%) CAS1 and 3 (37.5%) in Orphan XDR MTB strains, while deletions in the PE\_PGRS genes: 49 and 50 were observed in 36 (95.0%) CAS1 and all CAS, CAS2 and Orphan XDR MTB strains. An insertion in PE\_PGRS6 gene was observed in all CAS, EAI3 and Orphan, while insertions in the PE\_PGRS genes 19 and 33 were observed in 19 (95%) CAS1 and all CAS, CAS2, EAI3 and Orphan XDR MTB strains.

**Conclusion:** Genetic diversity in PE\_PGRS genes contributes to antigenic variability and may result in increased immunogenicity of strains. This is the first study identifying variations in nsSNPs, Insertions and Deletions in the PE\_PGRS genes of XDR-TB strains from Pakistan. It highlights common genetic variations which may contribute to persistence.

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<http://dx.doi.org/10.1016/j.ijmyco.2014.10.051>

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