AUTHOR CORRECTION



Correction to: SIGLECs and their contribution to tuberculosis

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Correction to: Nucleus

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Due to an oversight an error with respect to SNP number and associated polymorphism was crept in the abstract of the original version. The corrected version of the same should read as follows.

Abstract

Multiple host genes determine susceptibility or resistance to tuberculosis. In an exome-wide association study conducted among tuberculosis patients and their exposed but clinically asymptomatic household contacts, we found that the SNP rs61104666 located in the fifth exon of *SIGLEC15* gene is associated with the disease. No other variant in *SIGLEC15* has been reported previously to be associated with tuberculosis. The associated polymorphism results in a synonymous

change (E292E) and therefore is unlikely to be involved in disease pathogenesis. Bioinformatic analysis of epigenetic marks in the genomic region reveals an enhancer mark present in lung and blood, downstream to the *SIGLEC15* gene may harbor candidate causal SNPs which are in strong LD with the index SNP. This region overlaps with the 3'UTR region of the neighboring gene *EPG5*. *EPG5* has role in autophagy, a phenomenon relevant to clearing of the infection. The region also harbors DNAse I sensitive sites with SNPs of low RegulomeDB score indicative of potential transcription binding sites. All these evidences suggest further exploration of the enhancer region to understand its role in disease manifestation.

Keywords Tuberculosis · Genetic association · SIGLEC15

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