
Epilogue

The presented work in this thesis clarifies the genetic contribution in susceptibility to tuberculosis in north Indians. This study has also tried to work out the “cause” and “effect” by correlating the serum cytokine levels with the SNPs detected in relevant genes. Many successful associations explored for the first time in tuberculosis were identified here that define the genetic profile of north Indians and their proneness to develop or resist tuberculosis. The quest that was started in by framing the aims and objectives of this thesis is complete but the understanding and information that has emerged needs to be validated in large and different cohorts. A GWAS on tuberculosis from India is highly warranted and the regions of most association obtained in the study could serve as hotspots to proceed.

Also, the identified variants and their contribution can be mapped to provide us mechanistic insights to the complex nature of biological interactions in tuberculosis. Also, the biomarkers identified for LNTB, could be validated in prospective studies and can serve as an important aid in diagnosis of LNTB.

The differential immune response in pulmonary and lymph node TB identified in this study could be probed to understand the different clinical manifestations of tuberculosis. The questions answered in this thesis have come a long way but still has a longer path to traverse. Further, systematic efforts would facilitate better understanding of the genetic basis of resistance or susceptibility to TB which could be translated into targeted immunotherapy as a preventive measure as well as an effective adjunct to multidrug therapy for TB.