

**Invitation to M.Tech. Thesis Defense of Vikram Kumar: July 27, 2020 (Monday): 16.00-17.00 IST**

In Partial Fulfillment of the Requirements for the Degree of

**M.Tech. CB**

**Vikram Kumar (MT18250)**

Will defend his thesis

Title: **“Predicting Tuberculosis Progression from RNA Seq Data using Machine learning”**

IIIT-D Faculty and Students are invited

**Date: July 27, 2020 (Monday)**

**Time: 16.00-17.00 IST**

**Google meet link; <https://meet.google.com/bpn-hqwi-hyd>**

<b>Examiner:</b>	<b>Internal:</b>	<b>GPS Raghava</b>
	<b>External/Internal:</b>	<b>Gaurav Ahuja</b>
	<b>Advisor:</b>	<b>Tavpritesh Sethi</b>

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**Abstract**

"Mycobacterium tuberculosis (MTb), the causative agent of Tuberculosis (TB) is an apex killer of the human civilization since ages. Development of Multi-Drug Resistance (MDR) in Mycobacterium complex has resulted in the limited success of the Bacille Calmette-Guerin vaccine (BCG) across the globe. Finding an effective defence requires a deep understanding of the pathophysiology of the MTb. Our study exploits the mechanistic pathway of Mtb-induced HIF1A silencing by the antisense lncRNA-HIF1A-AS2 in T cells. Computational analysis of in-vitro T-cell stimulation assays in progressors (n=119) versus non-progressor (n=221) tuberculosis patients revealed the role of lncRNA mediated disruption of hypoxia adaptation pathways in progressors. We found 291 upregulated and 227 downregulated DE lncRNAs that were correlated at mRNA level with HIF1A and HILPDA which are major players in hypoxia response. We also report novel lncRNA-AC010655 (AC010655.4 and AC010655.2) in cis with HILPDA, both of which contain binding sites for the BARX2 transcription factor, thus indicating a mechanistic role. Detailed comparison of infection with antigenic stimulation showed a non-random enrichment of lncRNAs in the cytoplasmic fraction of the cell in TB progressors. SVM results showed the best precision and recall trade-offs along with the exponential rise in model performance curve, therefore they can be utilized efficiently for the classification of progressive TB samples along with the Decision Tree and Logistic Regression classifiers."

