Comparison Between Transcriptome And Proteome Response In Human T-Cells During Activation

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Transcriptomic studies are the commonly used approach in characterizing molecular events following T-cell receptor mediated activation of T-cells; the key event in adaptive immunity. However, large discordance between transcriptomic and proteomic profiles has been identified in relation to different physiological and pathological conditions. Aim of this study was to identify the relationship between transcriptomic and proteomic expression profiles during T-cell activation where biology of the cells is rapidly changing.Next generation RNA-sequencing and label free shotgun proteomics were performed on in vitro activated human T-cells at five different time points (0h, 6h, 12h, 24h, 3d and 7d) over 7 days. These transcriptomic and proteomic data were compared to identify their correlation at expression, pathway and network levels.Principal component analysis showed clustering of RNA-sequencing and proteomics data according to the time points indicating donor independent in vitro T-cell activation process. Expression profiles of majority of genes at transcriptomic level were poorly correlated with that of the proteomic profiles. At 6 hours, only 10% of differentially expressed genes were concordant with differentially expressed proteins. However, a strong correlation was observed in 50% of genes at later time points, indicative of a time-delay for transcriptome changes to be reflected at proteome level. Pathway and network analysis also showed a poor relationship between temporal proteomic and transcriptomic expression profiles.This integrative multi-omic evaluation of T-cell activation showed a poor relationship between transcriptomic and proteomic data with rapid molecular changes in cells. Hence, the dynamic functional changes of these cells cannot be characterized using transcriptomic data only.

Keywords: Proteomics, Transcriptomics, human T-cells