Predicting personal activation potential of CD4 T cells

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Human individuals show great variance in both innate and adaptive immune responses following immune stimuli. However, little is known about which and how molecular subnetworks quantitatively control the immune response potential. Such knowledge would generate a huge impact and have far-reaching consequences for shaping individual immune responses to vaccinations, antigen-specific immunotherapies (IT), anti-cancer immunotherapies and others. Here we used machine learning approaches to infer gene subnetworks that could quantitatively predict activation potential of different individuals using transcriptome of baseline CD4+CD25- effector T cells (Teffs) sorted from peripheral blood mononuclear cells (PBMC) of distinct donors. The top-ranked candidate genes were further tested using siRNA knockdown methods and indeed showed a significant effect on the activation potential of human Teffs. The in-vitro results will be further validated in a clinical trial using multi-layer 'Omics' analysis on various subsets of CD4 T cells sorted from time-series blood samples of allergy patients following antigen-specific IT. The resulted subnetworks before the commencement of IT could be used as valuable predictive biomarkers to support clinical decisions on tailored immunotherapies of different patients.