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New T_{REG} gene signature for T1DM

Dysfunctional regulatory T cells (T_{REG} cells) are thought to be a hallmark of type 1 diabetes mellitus (T1DM). Now, new research has revealed that a signature of six genes specific to T_{REG} cells might be sufficient to identify patients with new-onset T1DM.

The investigators first identified 31 genes that could be used to distinguish T_{REG} cells from other conventional T cells in healthy adults by sorting these cells into different activation states and analysing their gene expression. The expression levels of these genes could be used to distinguish between the two types of T cell, regardless of the activation state of the cells. Of the genes identified, some are known to be involved in T_{REG} cell function, including *FOXP3*, which is also

associated with the development of T1DM. The investigators then compared the expression of these 31 genes in individuals with new-onset T1DM (n = 29), established T1DM (n = 27) and paediatric controls without T1DM (n = 24). As in healthy adults, this gene signature could be used to discriminate between T_{REG} cells and conventional T cells, regardless of whether the patient had new onset or established T1DM. Finally, using a biomarker discovery approach with principle component analysis, the team refined the 31 genes to six (TNFRSF1B, TMEM23, FOXP3, ANK3, ZNF532 and LRRC32) that were significantly different in T_{REG} cells from patients with new-onset T1DM compared with controls.

"Our findings suggest that measuring gene expression in T_{REG} cells might be a good way to detect disease-associated changes in these cells," says Megan Levings, who led the study. "The hope is that this biomarker test will help identify patients who might be the most responsive to therapies designed to improve T_{REG} cell function, and be useful for tracking the response to these therapies," clarifies Levings. "Of course we also want to test if measuring T_{REG} cell gene signatures might also be useful in other autoimmune diseases."

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