

Title: Multi-Omics Integration to Identify Biomarkers Related to T1D Risk in Children

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Abstract

Type 1 diabetes (T1D) is a chronic autoimmune disease where pancreatic β -cells are destroyed by the immune system. The incidence is particularly high in Finland, but the environmental and molecular factors potentially affecting disease development remain still unknown. Typically, T1D-associated islet autoantibodies appear years before clinical onset, which provides an early window to study disease-related processes. Increasing evidence points to the gut microbiome and its metabolic products as key modulators of immune regulation. Identifying early microbial and metabolic signatures is therefore essential to improve our understanding of T1D pathogenesis and to support the search for biomarkers for prevention.

The aim of this study was to investigate whether integration of stool-derived multi-omics data can reveal microbial and metabolic features linked to diabetes-related autoimmunity and seasonal variation.

We combined microbiome (16S rRNA and shotgun metagenomics), metabolome (NMR and LC-MS), and volatilome (DMS and GCxGC/TOF-MS) data from Finnish children collected during both summer and winter. Statistical and machine learning approaches were applied to identify signatures differentiating autoantibody-positive children from healthy controls, followed by cross-omics integration.

Cross-omics correlations were observed between microbiome, metabolome, and volatilome datasets, suggesting potential interactions between microbial taxa and metabolic compounds. Autoantibody-positive children showed shifts in microbial composition and reduced short-chain fatty acids, together with altered glucose profiles. Machine learning further highlighted microbial features such as *Eggerthellaceae* and *Veillonella*, also reported in previous T1D cohorts.

These early findings indicate that multi-omics integration can reveal candidate microbial and metabolic signatures linked with diabetes-related autoimmunity and pathways. However, further validation is required.