

EPIGENOME-WIDE ASSOCIATION STUDY IN PAEDIATRIC COELIAC DISEASE IDENTIFIES SIGNIFICANT METHYLATION ALTERATIONS IN WHOLE BLOOD

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Poster

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A study of 36 paediatric coeliac disease patients and 35 controls identified 53 significant DNA methylation changes in whole blood, with top differentially methylated genes including PTPN6, CDC42, and COL4A1, but found no HLA region methylation differences or epigenetic age acceleration.

KEY POINTS

- Fifty-three CpGs showed genome-wide significant methylation differences (FDR <0.05) between paediatric coeliac disease patients and healthy controls, with 23 hypermethylated and 30 hypomethylated.
- Top differentially methylated loci included PTPN6 ($p=4.79 \times 10^{-9}$), CDC42 ($p=1.28 \times 10^{-9}$) involved in cell migration and phagocytosis, and collagen gene COL4A1 ($p=9.95 \times 10^{-8}$).
- Significant probes were associated with cytidine metabolism ($p=6.68 \times 10^{-5}$), collagen metabolism ($p=1.0 \times 10^{-3}$), and filopodium assembly ($p=8.6 \times 10^{-4}$).
- No significant CpGs were found in the HLA region, contrasting with some reports in adult coeliac disease, and no epigenetic age acceleration was observed in paediatric patients.
- Differentially methylated regions were identified in APOBEC3B, ASGR1, and CCNG1 genes, with NOP10 showing the strongest evidence of genetic regulation of methylation.

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