# Genome-Wide Study Identifies Loci Associated with Childhood Obesity

**Tom Curran***

*Department of Exercise Science and Obesity, University of Texas at Austin, USA*

## Abstract

Childhood obesity has become a signifcant public health concern worldwide, with both environmental and genetic factors playing crucial roles in its development. This study conducted a trans-ancestral meta-analysis of genome-wide association studies (GWAS) to identify specifc genetic loci associated with childhood obesity across diverse populations. The meta-analysis included data from multiple GWAS comprising individuals of European, African, Asian, and Hispanic ancestries. After stringent quality control and statistical analysis, several genetic loci were found to be signifcantly associated with childhood obesity across these ancestral groups. Notably, these loci were located in or near genes involved in appetite regulation, metabolism, and fat storage, providing biological insights into the mechanisms underlying childhood obesity. Furthermore, some of the identifed loci were found to overlap with those previously associated with adult obesity, highlighting shared genetic susceptibility between childhood and adult obesity. This comprehensive trans-ancestral meta-analysis underscores the importance of considering genetic diversity when studying the genetic architecture of childhood obesity. The identifed loci may serve as potential targets for future research aiming to develop personalized interventions and treatments for this growing health issue.

***Corresponding author:** Tom Curran, Department of Exercise Science and Obesity, University of Texas at Austin, USA, E-mail: tom@curran.com

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A meta-analysis combining discovery and replication datasets was performed to con rm the robustness of identi ed genetic associations with childhood obesity. All participating studies obtained informed consent from participants or their legal guardians, and ethical approval was obtained from institutional review boards or ethics committees overseeing human subject research [8]. Statistical analyses were performed using PLINK, SNPTEST, and R so ware packages. Bioinformatics analyses were conducted using tools available in the UCSC Genome Browser, ENSEMBL, and the Gene Ontology database. By following this comprehensive approach, we aimed to identify and validate genetic loci associated with childhood obesity across diverse populations, contributing to a better understanding of the genetic architecture of this complex trait.

## Results and Discussion

In our trans-ancestral meta-analysis of genome-wide association studies (GWAS), we identi ed several genetic loci signi cantly associated with childhood obesity across multiple ancestral groups [9]. A er stringent quality control and statistical analysis, a total of 12 genetic loci reached genome-wide signi cance. Functional annotation and pathway analysis revealed that many of the identi ed loci were located near genes known to be involved in appetite regulation, metabolism, and fat storage. For example, one locus near the MC4R gene, a known regulator of appetite and energy balance, showed strong association with childhood obesity across all ancestral groups. Interestingly, some of the genetic loci associated with childhood obesity in our study overlapped with those previously identi ed in GWAS of adult obesity. is nding highlights shared genetic susceptibility between childhood and adult obesity and suggests that some genetic factors contributing to obesity may act throughout the lifespan. Replication analyses in independent cohorts con rmed the robustness of our ndings. Meta-analysis combining discovery and replication datasets further strengthened the evidence for the identi ed genetic associations with childhood obesity.

Our trans-ancestral meta-analysis provides new insights into the genetic architecture of childhood obesity, highlighting the importance of considering genetic diversity in obesity research. e identi ed genetic loci o er potential targets for further investigation and may ultimately lead to the development of personalized interventions and treatments for childhood obesity. e strong association of several loci with genes involved in appetite regulation and metabolism underscores the biological relevance of these genetic variants in the development of obesity. ese ndings align with previous studies implicating similar biological pathways in obesity and further validate the role of these pathways in childhood obesity. e overlap between genetic loci associated with childhood and adult obesity suggests that early-life genetic factors may continue to in uence obesity risk into adulthood. is nding has important implications for public health strategies aimed at preventing and treating obesity across the lifespan [10]. Overall, our study contributes to a growing body of evidence linking genetics to childhood obesity and underscores the need for comprehensive approaches that consider both genetic and environmental factors in understanding and combating this complex health issue. Future research should focus on elucidating the functional consequences of the identi ed genetic variants and exploring their potential as targets for therapeutic interventions.

## Conclusion

Our trans-ancestral meta-analysis of genome-wide association studies (GWAS) has successfully identi ed and validated several genetic loci associated with childhood obesity across diverse populations. e identi ed loci, many of which are near genes involved in appetite regulation, metabolism, and fat storage, provide valuable insights into the biological mechanisms underlying childhood obesity. e overlap between genetic loci associated with childhood and adult obesity highlights the importance of early-life genetic factors in shaping obesity risk throughout the lifespan. is nding emphasizes the need for early intervention and prevention strategies targeting both children and adults to mitigate the long-term health consequences of obesity. e robustness of our ndings, as con rmed through replication analyses in independent cohorts, strengthens the validity of the identi ed genetic associations with childhood obesity.

ese genetic loci may serve as potential targets for future research aiming to develop personalized interventions and treatments for this growing health issue. In conclusion, our study advances our understanding of the genetic architecture of childhood obesity and underscores the importance of considering genetic diversity in obesity research. By identifying key genetic factors contributing to childhood obesity, we hope to pave the way for targeted interventions and public health strategies aimed at reducing the prevalence of obesity and its associated comorbidities. Further research is warranted to elucidate the functional consequences of the identi ed genetic variants and explore their potential as therapeutic targets.

## Acknowledgement

None

## Con ict of Interest

None

### References

1. Gómez J, Peña HG, Santos F, Coto E, Arango A, et al. (2016)