

# Genome-wide complex trait analysis - a new method to investigate the molecular ge...

[Science](#), [Biology](#)



The paper "Genome-Wide Complex Trait Analysis to Learn the Molecular Genetic Heritability of Body Weight" is an outstanding example of a term paper on health sciences & medicine. In this study, researchers used a new method known as Genome-wide Complex Trait Analysis (GCTA) to investigate the molecular genetic heritability of body weight in children. The study underlines the importance of genetic effects on childhood obesity. They support the current thinking that children of obese parents are most at risk of becoming obese. Single-nucleotide polymorphisms (SNPs) show that less than 2 percent of the variation in Body Mass Index (BMI) in spite of evidence showing a greater than 50 percent of heritability from twin and family phenomena called Missing heritability. The result of the study depicts the significance of additive genetic effects on the development of adiposity in childhood. It is the first pediatric study to carry out this research using the new method. It estimates the genetic influence on the adiposity attributable to additive genetic effects from common SNPs. GCTA method takes the advantage that there is genetic resemblance for common SNPs distributed among individuals who are not related at all. The study is based on data from a population-based cohort of monozygotic and dizygotic known as Twins Early Development Study. The number of children was 2, 269 whose age varied from eight to eleven years old. The researchers found out, that based on the research they had taken, additive effects of multiples genes across the whole genome accounted for 30 percent of individual body weight. The finding also suggests that there are hundreds of other genetic variants influencing body weight that are yet to be discovered (International

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Journal of Obesity, 2).

### Critique

The study may have brought some insights that are useful but also it does not answer everything. One of the issues is that this is the first pediatric to use the Genome-wide Complex Trait Analysis to estimate the genetic influence on the adiposity in childhood (International Journal of Obesity, 2). There need to be more studies to be carried out to paint a clear picture of the findings. There need to be subsequent pediatric studies so that the assumptions that have been there may be eliminated. There is also the issue of carrying out analysis on the subgroup. The sample size dictates that it is not possible to analyze different subgroups. This limits this novel scientific method giving a more conclusive and convincing finding. It lacks a well-defined case, control groups, an insufficient sample size. The study needs to take care of this issue to be able to give correct and more conclusive findings that will leave no doubts in people. GCTA also does not identify the specific Single-nucleotide polymorphisms related to the target phenotype, but rather estimate the total additive genetic effect of the common SNPs used on currently available DNA (International Journal of Obesity, 2). The identification of various Single-nucleotide polymorphisms involved could have paved the way for more research on them and determine their effects. Assumptions will be eliminated because more research could give better findings. The findings could also not be reliable because the height and weight data were parents reported (International Journal of Obesity, 2). This

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may give room for errors because parents may make assumptions. This may prove less reliable than researcher-measured values because they are trained on how to approximate. The researcher-measured anthropometrics may be more reliable compared to parent data. This could have resulted in errors in the final findings and hence not give a clear picture at the end.