Largest-ever genome-wide study identifies genes for common childhood obesity

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Genetics researchers have identified at least two new gene variants that increase the risk of common childhood obesity.

"This is the largest-ever genome-wide study of common childhood obesity, in contrast to previous studies that have focused on more extreme forms of obesity primarily connected with rare disease syndromes," said lead investigator Struan F.A. Grant, Ph.D., associate director of the Center for Applied Genomics at The Children's Hospital of Philadelphia. "As a consequence, we have definitively identified and characterized a genetic predisposition to common childhood obesity."

The study, by an international collaborative group, the Early Growth Genetics (EGG) Consortium, appeared online today in Nature Genetics.

As one of the major health issues affecting modern societies, obesity has increasingly received public attention, especially given a rising prevalence of the condition among children. Research indicates that obese adolescents tend to have higher risk of mortality as adults. Although environmental factors, such as food choices and sedentary habits, contribute to the increasing rates of obesity in childhood, twin studies and other family-based evidence have suggested a genetic component to the disease as well.

Previous studies have identified gene variants contributing to obesity in adults and in children with extreme obesity, but relatively little is known about genes implicated in regular childhood obesity.

"The Center for Applied Genomics at the Children's Hospital of Philadelphia has recruited and genotyped the world's largest collection of DNA from children with common obesity," said Grant. "However, in order to have sufficient statistical power to detect novel genetic signals, we needed to form a large international consortium to combine results from similar datasets from around the world."

The National Institutes of Health partly funded this research, which analyzed previous studies supported by many other European, Australian and North American organizations.

The current meta-analysis included 14 previous studies encompassing 5,530 cases of childhood obesity and 8,300 control subjects, all of European ancestry. The study team identified two novel loci, one near the OLFM4 gene on chromosome 13, the other within the HOXB5 gene on chromosome 17. They also found a degree of evidence for two other gene variants. None of the genes were previously implicated in obesity. "The known biology of three of the genes," added Grant, "hints at a role of the intestine, although their precise functional role in obesity is currently unknown."

"This work opens up new avenues to explore the genetics of common childhood obesity," said Grant. "Much work remains to be done, but these findings may ultimately be useful in helping to design future preventive interventions and treatments for children, based on their individual genomes."

More information: "A genome-wide association meta-analysis identifies new childhood obesity loci," *Nature Genetics*, published online April 8, 2012, doi: 10.1038/ng.2247

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