Study offers first genetic analysis of people with extremely high intelligence

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The first ever genetic analysis of people with extremely high intelligence has revealed small but important genetic differences between some of the brightest people in the United States and the general population.

Published today in *Molecular Psychiatry*, the King's College London study selected 1,400 high-intelligence individuals from the Duke University Talent Identification Program. Representing the top 0.03 per cent of the 'intelligence distribution', these individuals have an IQ of 170 or more - substantially higher than that of Nobel Prize winners, who have an average IQ of around 145.

Genetic research on intelligence consistently indicates that around half of the differences between people can be explained by genetic factors. This study's unique design, which focused on the positive end of the

intelligence distribution and compared genotyping data against more than 3,000 people from the general population, greatly enhanced the study's power to detect genes responsible for the heritability of intelligence.

Researchers analysed single nucleotide polymorphisms (SNPs), which are DNA differences (polymorphisms) between individuals in the 3 billion nucleotide base pairs of DNA - steps in the spiral staircase of the double helix of DNA that make up the human genome. Each SNP represents a difference in a single nucleotide base pair, and these SNPs account for inherited differences between people, including intelligence. The study focused, for the first time, on rare, functional SNPs – rare because previous research had only considered common SNPs and functional because these are SNPs that are likely to cause differences in the creation of proteins.

The researchers did not find any individual protein-altering SNPs that met strict criteria for differences between the high-intelligence group and the control group. However, for SNPs that showed some difference between the groups, the rare allele was less frequently observed in the high intelligence group. This observation is consistent with research indicating that rare functional alleles are more often detrimental than beneficial to intelligence.

Professor Robert Plomin from the Institute of Psychiatry, Psychology & Neuroscience (IoPPN) at King's College London, said: 'Rare functional alleles do not account for much on their own but in combination, their impact is significant.

'Our research shows that there are not genes for genius. However, to have super-high intelligence you need to have many of the positive alleles and importantly few of the negative rare effects, such as the rare functional alleles identified in our study.'

The researchers also analysed genome-wide similarity to explore the genetic architecture of intelligence.

Professor Plomin added: 'Previous research suggests that common SNPs in total account for around 25 per cent of the variance in intelligence. The question we asked, for the first time, was - how much will these functional variants account for? We found that the functional SNPs in our study explain around 17 per cent of the differences between people in intelligence.'

The authors acknowledge that environmental influences also have an impact, often interacting with genetic factors. Professor Plomin said: 'Clearly super-bright people such as those in our study are more likely to select environments conducive to their genetic propensity, so they might have grown up reading books that present intellectual problems or be more likely to attend a university.'

Professor Michael Simpson from the Division of Genetic and Molecular Medicine at King's College London, said: 'Our study demonstrates the challenges in identifying specific genetic variants that contribute to this complex trait, but provides potential insight into its genetic architecture that will inform future studies.'

More information: "A genome-wide analysis of putative functional and exonic variation associated with extremely high intelligence." *Molecular Psychiatry* advance online publication 4 August 2015; DOI: 10.1038/mp.2015.108

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