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A tall story: New research adds to growing body of knowledge of genetics of height

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Scientists are beginning to develop a clearer picture of what makes some people stand head and shoulders above the rest. A team of researchers who last year identified the first common version of a gene influencing height has now identified a further twenty regions of the genome which together can make a height difference of up to 6cm.

The results, published together with two independent studies online today in the journal *Nature Genetics*, mean that scientists now know of dozens of genes and genetic regions that influence our height. This provides scientists with a fascinating insight into how the body grows and develops normally and may shed light on diseases such as osteoarthritis and cancer.

Unlike a number of other body size characteristics such as obesity, which is caused by a mix of genetic and environmental factors (so called "nature and nurture"), 90 per cent of normal variation in human height is due to genetic factors rather than, for example, diet. Last year, a team of researchers including Dr Tim Frayling from the Peninsula Medical School, Exeter, and Professor Mark McCarthy from the University of Oxford identified the first common gene variant to affect height, though it made a difference of only 0.5cm.

Now, using DNA samples from over 30,000 people, many taken from the Wellcome Trust Case Control Consortium – the largest study ever undertaken into the genetics underlying common diseases – and from the Cambridge Genetics of Energy Metabolism (GEM) consortium and the

CoLaus Study in Switzerland, the researchers have identified 20 loci (regions of genetic code), common variations of which influence adult height.

"The number and variety of genetic regions that we have found show that height is not just caused by a few genes operating in the long bones" says Dr Frayling. "Instead, our research implicates genes that could shed light on a whole range of important biological processes.

"By identifying which genes affect normal growth, we can begin to understand the processes that lead to abnormal growth – not just height disorders but also tumour growth, for example."

Half of the new loci identified by Dr Frayling and colleagues contain genes whose functions are well documented. Some help regulate basic cell division, which may have implications for cancer research: unregulated cell division can lead to the growth of tumours. Other genes are implicated in cell-to-cell signalling, an important process in the early development of embryos in the womb. Yet others are so-called "master regulators", acting as switches to turn genes elsewhere in the genome on or off.

One locus in particular is also implicated in osteoarthritis, the most common form of arthritis involving the effects of wear and tear on the body's structures. This locus reinforces a similar link identified by a previous study, and may be involved in the growth of cartilage.

However, of the twenty loci identified by Dr Frayling and colleagues, half contain genes about which little or nothing is known. The researchers compare these findings to their work last year which identified the first common gene for obesity, the FTO gene. Even though the gene has been shown without a doubt to be influence body size, its role is still unclear.

"There may be more than a hundred genes which affect our height, many of which will work in surprising or unpredictable ways," says Dr Mike Weedon, lead author on the paper. "The challenge now for us is to understand how they influence growth in the body. This could open up new avenues for treating a range of diseases."

Source: Wellcome Trust