Seven new genetic regions linked to type 2 diabetes

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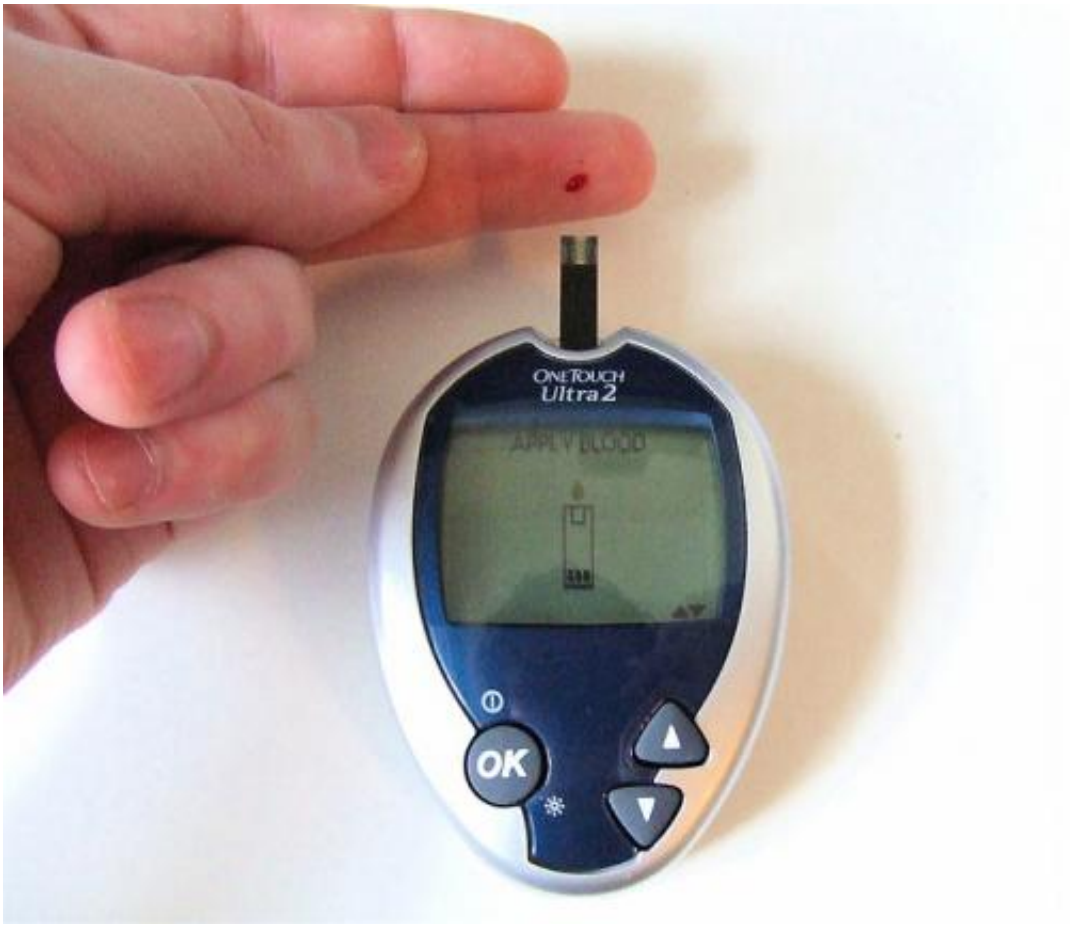

Blood glucose monitoring. Credit: Wikipedia

Seven new genetic regions associated with type 2 diabetes have been identified in the largest study to date of the genetic basis of the disease.

DNA data was brought together from more than 48,000 patients and 139,000 healthy controls from four different ethnic groups. The research was conducted by an international consortium of investigators from 20 countries on four continents, co-led by investigators from Oxford University's Wellcome Trust Centre for Human Genetics.

The majority of such 'genome-wide association studies' have been done in populations with European backgrounds. This research is notable for including DNA data from populations of Asian and Hispanic origin as well.

The researchers believe that, as more genetic data increasingly become available from populations of South Asian ancestry and, particularly, African descent, it will be possible to map genes implicated in type 2 diabetes ever more closely.

'One of the striking features of these data is how much of the genetic variation that influences diabetes is shared between major ethnic groups,' says Wellcome Trust Senior Investigator Professor Mark McCarthy from the University of Oxford. 'This has allowed us to combine data from more than 50 studies from across the globe to discover new genetic regions affecting risk of diabetes.'

He adds: 'The overlap in signals between populations of European, Asian and Hispanic origin argues that the risk regions we have found to date do not explain the clear differences in the patterns of diabetes between those groups.'

Among the regions identified by the international research team are two, near the genes ARL15 and RREB1, that also show strong links to elevated levels of insulin and glucose in the body – two key characteristics of type 2 diabetes. This finding provides insights into the ways basic biochemical processes are involved in the risk of type 2

diabetes, the scientists say.

The genome-wide association study looked at more than 3 million DNA variants to identify those that have a measurable impact on risk of type 2 diabetes. By combining DNA data from many tens of thousands of individuals, the consortium was able to detect, for the first time, regions where the effects on diabetes susceptibility are rather subtle.

'Although the genetic effects may be small, each signal tells us something new about the biology of the disease,' says first author Dr Anubha Mahajan of Oxford University. 'These findings may lead us to new ways of thinking about the disease, with the aim ultimately of developing novel therapies to treat and prevent diabetes. There's every reason to expect that drugs acting on these biological processes would have a far larger impact on an individual's diabetes than the genetic effects we have discovered.'

Principal investigator Dr Andrew Morris, also of the Wellcome Trust Centre for Human Genetics at Oxford University, says: 'The findings of our study should also be relevant to other common human diseases. By combining genetic data from different ethnic groups, we would expect also to be able identify new DNA variants influencing risk of heart disease and some forms of cancer, for example, which are shared across ethnic groups. It has the potential to have a major impact on global public health.'

The paper 'Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility' is to be published in the journal *Nature Genetics* on Sunday 9 February 2013.

More information: Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility, DOI: 10.1038/ng.2897

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