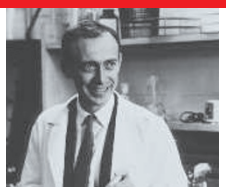

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JAMES WATSON'S DNA SEQUENCED
Discoverer of the double helix blazes trail for personal genomics.
www.nature.com/news

Genome miners rush to stake claims

This February, Laura Scott, a genetic epidemiologist at the University of Michigan, Ann Arbor, spent her holiday sitting in a ski lodge in front of her computer, "very occasionally trying to go out and ski". She was working on one of three papers that appeared online in *Science* in April, the same day that a competing group announced similar findings in *Nature Genetics*[1–4]. All four papers identify genes implicated in adult-onset diabetes, one of western society's commonest ailments. And all four are part of a new genetics gold rush that uses such 'genome-wide association studies' to flag disease-related genes. Hence Scott's indoor skiing trip: "The feeling was: 'It's gotta get out there'," she says.

As in any gold rush, prospectors are pursuing the spoils as quickly as their tools, skills and finances will allow. This week, *Nature* publishes the biggest pot of gold yet: a report tagging more than 20 genetic markers associated with seven common diseases, from bipolar disorder to hypertension, teased out from the DNA of 17,000 people (see page 661).

Science is always competitive. But human genetics is going through a particularly intense burst of activity. The race is to identify single-letter DNA variations that are more frequent in patients with common, complex diseases and thus serve as markers for susceptibility.

Technological advances that have come fully on-line only in the past 18 months are allowing geneticists to examine common diseases such as diabetes, which are caused by both environmental influences and by an unknown number of genes that contribute to different degrees. To find these small genetic influences, scientists must screen a thousand or more patients with each disease for hundreds of thousands of single-letter markers, and compare the results against similar screens of people without the disease.

Such studies are still expensive — costing, at minimum, nearly a million dollars — and there are only a limited number of strong genetic associations to be found for the most common diseases. So the race is on to be first to pick and publish this low-hanging fruit, which many expect to be collected within a year or two.

"If you've invested a large amount of money and a lot of time in doing one of these studies, you don't want to publish your paper a month after someone else has found the same things," says statistician Peter Donnelly of the University of Oxford, who is chairman of the Wellcome Trust Case Control Consortium and a lead author on today's study.

CMSP/SCIENCE FACTION

Trail of blood: many genes influence the development of common diseases such as diabetes.

Many scientists, including Donnelly, welcome the competition. A host of suspect genes published in the early days of the rush have turned out to be false positives. The way that results today are being confirmed through multiple, overlapping findings published near-simultaneously by competing groups "is fantastic for the field", says Donnelly.

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In some cases, the prospectors are working together in the hope of improving their claims. The authors of the three papers on diabetes that appeared in *Science*, for instance, agreed months before publication to pool their initial data to improve their chances of identifying truly significant genetic variants.

A working group at the US National Institutes of Health (NIH) that today publishes a set of proposed standards for genome-wide association studies (see page 655) stresses the desirability of simultaneously publishing independent replication of results. It notes, however, that some work may be so important as to justify its publication before it has been replicated.

The results published by Donnelly and colleagues today do not include independent replication. "The referees were unanimous that this advance was powerful enough as a landmark not to necessitate the conditions recommended by the NIH," says Philip Campbell, *Nature*'s editor-in-chief. Indeed, the pace of the field means that several other groups have already confirmed and published some genetic links highlighted in this paper.

Many of these findings will lead to genetic tests to identify those at greater risk of common disease. But tests may be of limited use without an obvious intervention, such as statin drugs for those at increased risk of heart disease. Patients must now wait for cell biologists to discover how the suspect genes do their damage — and for drug companies to exploit those findings. ■

Meredith Wadman

1. Diabetes Genetics Initiative of Broad Institute of Harvard and MIT, Lund University, and Novartis Institutes of BioMedical Research *Science* **316,** 1331–1336 (2007).
2. Zeggini, E. *et al. Science* **316,** 1336–1341 (2007).
3. Scott, L. *et al. Science* **316,** 1341–1345 (2007).
4. Steinthorsdottir, V. *et al. Nature Genet.* **39,** 770–775 (2007).