AGEING

Predicting long life

Many of us hope for a long and healthy life, but it is widely accepted that achieving this depends on a complex combination of environment and genetics. A genome-wide association study of centenarians has now confirmed the importance of genetic variation in predisposition to exceptional long life and highlights the multifactorial nature of ageing.

Sebastiani and colleagues conducted a genome-wide association study of 801 unrelated Caucasians aged between 95 and 119 years and 926 controls with matched genetic backgrounds. They identified 70 SNPs that were associated with exceptional longevity ('longevity associated variants' (LAVs)), 33 of which were replicated with a different set of centenarians. To evaluate the combined effects of these variants, the authors built genetic risk models and tested their ability to predict exceptional or average lifespan. A combination of up to 150 SNPs could predict exceptional longevity with 77% accuracy.

The complexity of the genetics underlying longevity is emphasized by the authors' finding that groups of centenarians have distinct genetic signatures. One group, 'supercentenarians' (those at least 110 years old) have the greatest enrichment of LAVs.

What does this tell us about the alleles needed for longevity? Enrichment for LAVs correlated with lower prevalence for cardiovascular disease and diabetes. But the authors did not find a substantial difference in the numbers of disease-associated variants carried by centenarians and controls, so they suggest that LAVs might counter the effect of disease-risk alleles — an interesting hypothesis for further investigation.

Mary Muers

ORIGINAL RESEARCH PAPER Sebastiani, P. *et al.*
Genetic signatures of exceptional longevity in humans. *Science* 1 Jul 2010 (doi:10.1126/science.1190532)