

**Cover illustration**

Animal coat colour is a complex trait resulting from small contributions from many genes. (Image courtesy of P. Schermeister/Photolibary.com. Artwork by N. Spencer)

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QUANTITATIVE GENETICS

The father of modern quantitative genetics, R. A. Fisher, is credited with the observation: “Natural selection is a mechanism for generating an exceedingly high degree of improbability”. The truth in this is evident just from looking at evolutionary history — the improbable happens all the time. It is made possible by large reservoirs of genetic variation, the occurrence of mutations, and interactions between genes and the environment. Recent revolutions in genomics have allowed genetic variation to be described at an unprecedented level, pinpointing nucleotide changes that directly or indirectly affect phenotype. The result is a renaissance in quantitative genetics, particularly in the study of complex traits, enabling theories to be tested by experiment on a genome-wide scale.

One now common approach for examining complex traits in humans is the genome-wide association study, which compares variation across the genomes of two groups of individuals and looks for markers that are associated more with one group than the other, a strategy now being applied to plants and other organisms. After the variants linked to a trait have been identified by such approaches, the effects of these variants on the molecular networks (such as gene expression) in a cell or organism can be investigated. This Insight highlights progress in teasing apart the basis of complex traits in this way, as well as in determining the relative contributions of genetics and the environment to traits in various organisms, from plants to mice to the trio of the malaria parasite, its mosquito vector and the human host.

Genetics has always been a field in which studies in one organism are crucial for discoveries in another, and we hope that the articles in this Insight inspire crosstalk between specialists, as well as entice scientists from other fields. We are pleased to acknowledge the financial support of Monsanto, which contributed towards the distribution of this Insight. As always, *Nature* carries sole responsibility for editorial content and peer review.

Chris Gunter, Consultant Editor

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