FROM THE FDITORS





GENETICS



COVER: 'Root about' by Patrick Morgan, inspired by the Review on p305.





enetic and genomic approaches are revolutionizing many aspects of infectious disease research. This was a clear message from a conference held in March, jointly organized by the American Society of Human Genetics, The Human Genome Organization and Nature Publishing Group. The meeting — Genetics and Genomics of Infectious Diseases (www.nature.com/natureconferences/ ggid2009/index.html) — was unusual in bringing together researchers working on a diverse range of infections and in emphasizing the importance of both pathogen biology and host response. Particular excitement surrounded the acceleration of pathogen genome sequencing using next-generation technologies and its applications — from identifying the specific genetic changes that have taken place in the evolutionary history of pathogens to increasing the power of molecular epidemiology.

But the meeting also prompted reflection and re-evaluation. For example, with all the emphasis that is placed on developing new technologies and investigating interesting biological questions, there is a danger that money and effort are diverted away from translating existing tools and knowledge into applications that will save lives. For instance, array-based genotyping already provides the potential for useful new diagnostic tools — but only if this technology is adapted so that it can be used to generate results quickly. cheaply and in settings that may be far removed from the nearest laboratory.

On a different note, this month we launch a series of articles on the design and analysis of genome-wide association studies (www.nature.com/ nrg/series/gwas/index.html). We kick off with the Review by John Ioannidis and colleagues on page 318, which discusses the steps between the initial identification of an association signal and the validation of a causal variant — in many cases a process that is far from straightforward.

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