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REVIEWS

GENETICS



OUT OF THIN AIR
Diversity, fine-tuning and integration in transcriptional responses to hypoxia

Induced pluripotent stem cells
Comments from leading researchers on prospects and problems

► **COVER:** 'Aeration' by Patrick Morgan, inspired by the review on p821.



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Certain technologies have changed the face of genetic research — notable examples being DNA cloning, Sanger sequencing and PCR. Now, next-generation sequencing is making waves that are being felt across genetics and genomics.

As sequencing costs continue to fall, we will see a rapid increase in the number of completely sequenced species, recently highlighted by plans to sequence 10,000 vertebrate genomes. In the human genetics community, projects such as 1000 Genomes are underway, in which the sequencing of many individuals will provide an unprecedented view of human genetic diversity. The ability to sequence bacterial genomes cheaply and at speed is already reaping rewards in areas such as experimental evolution. For example, the Research Highlight on page 815 reports two recent studies that resequenced large numbers of bacterial genomes to gain insights into the nature of adaptation. The routine sequencing of larger genomes will require even cheaper technologies, but in the meantime high-throughput sequencing of targeted regions will remain important. An In Brief article on page 817 discusses two recent papers that describe advances in both areas.

The applications of high-throughput sequencing extend beyond genomes. In his Review on page 833, Alain Jacquier notes the importance of RNA-seq to our increasing appreciation of the complexity of eukaryotic transcriptomes. And two Research Highlights, on pages 816 and 818, show how sequencing can be combined with other techniques to map long-range interactions between chromosomal regions and to chart DNA methylation patterns at high resolution.

The various ways in which these technologies are advancing research will be charted in our ongoing article series on applications of next-generation sequencing.

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