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► **COVER:** 'Wove' by Patrick Morgan, inspired by the Review on p475.



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The advent of an exciting new technology or approach does not necessarily mean that it is wise to put aside traditional methods. Two Reviews in this issue highlight how combining the old with the new can provide promising new directions in diverse fields.

Mapping studies carried out in families using linkage analysis provided numerous breakthroughs in identifying the genetic basis of Mendelian disorders. But this approach fell out of fashion somewhat when association studies arrived, opening new doors for studying the genetic basis of common diseases. Now, however — as highlighted in the Review by Jurg Ott and colleagues (p465) — there is an increasing interest in combining linkage- and association-based approaches. Next-generation sequencing promises to further increase the utility of family-based approaches and increase the range of variants for which connections with disease can be established.

Restriction enzymes have been with us for so long that it is hard to imagine their use causing much new excitement. Again, however, combining their application with that of next-generation sequencing is driving a small revolution — in generating genome-wide sets of genetic markers. As discussed in the Review by John Davey and co-authors (p499), this approach is having a particular impact on smaller research communities for whom developing SNP arrays proves too expensive.

The print copy of this issue is accompanied by a free Poster by Ahmad Khalil and Jim Collins on the Applications of Synthetic Biology. This poster is also available [online](#) and has been produced with kind support from [OriGene Technologies](#) and its wholly owned subsidiary, [Blue Heron Biotechnology](#).

Finally, this month marks the launch of our new series on [Translational Genetics](#), which examines how knowledge about our genome is changing medical practice.

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