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e seek it here, we seek it there... Never before has the quest for genetic variation been so prominent in genetics research and it seems the more we seek, the more we find. A Highlight on page 934 describes one such successful search: an attempt to find the nucleotide variants in flies that underlie 'cryptic variation', which surfaces only under particular environmental or genetic conditions. In this respect, mapping the genetic basis of cryptic variation is similar to pharmacogenetics, as discussed by David Goldstein and colleagues on page 937, which aims to determine how and which genetic variation affects a patient's response to drugs. The field has been successful at identifying pharmacogenetic variation but needs to expand its selection of candidate genes beyond those that are involved in drug metabolism.

As for many research areas, advances in pharmacogenetics and gene mapping in general are contingent on technological and analytical developments. Two articles in this issue tackle progress on these fronts: Sobin Kim and colleagues (page 1001) discuss the mass-spectrometry-based approaches to faster and more accurate DNA sequencing, whereas Michael Stumpf and Gilean McVean (page 959) take us through the sophisticated statistical methods that are being developed to estimate recombination rates from population-genetic data.

Print subscribers will notice that their December issue has some extra girth, thanks to the addition of a supplement on RNA interference, which is sponsored by Qiagen and that features articles reprinted from Nature Reviews Genetics and other Nature Reviews journals. However, online-only subscribers will not miss out: these and other RNAi resources are freely available for six months in the associated web focus at http://www.nature.com/reviews/focus/rnai.



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