FROM THE FDITORS

n the words of Ernst Mayr, "mutation is the ultimate source of all

Hodgkinson and Eyre-Walker (Review, p756) discuss insights from comparative genomics into how mutation rates vary across mammalian genomes. The emerging picture is of a complex range of influences on mutation rate — from neighbouring nucleotides to whole-chromosome

effects — but, in many cases, the molecular basis remains poorly

understood. A better understanding of regions of the genome that are particularly susceptible to mutation may be useful for studies of disease

Indeed, the data that are being produced by exome sequencing strategies for which are discussed in a Review by Bamshad and colleagues

(p745) — will provide a wealth of information on the distribution of protein-coding mutations. An average exome from an African American yields ~ 24,000 single-nucleotide variants, and resequencing gives the

Also, a Research Highlight on p741 explains a new strategy for genome-wide mapping of another type of mutation — translocation. And another Research Highlight (p740) suggests that we will need to broaden

our horizons when considering mutations to include epimutations:

Finally, the print copy of this issue is accompanied by a free Poster by Chang and Hannon on 'Tools for understanding and using small RNAs: from pathways to functions to therapies'. This Poster is also available free online and has been produced with kind support from Thermo Scientific.

DNA methylation changes that are carried across generations.

opportunity to identify rare as well as common events.

genetic variation". And yet, as illustrated by several articles in this

issue, much is still to be learnt about where and how mutations occur. A genome is not a level playing field when it comes to mutation.









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