

Humans as a Model Organism: The Time Is Now

This issue of *GENETICS* features an article that signals the Editorial Board's intent for the journal to increase its presence in the human genetics arena. In its 98-year history *GENETICS* has featured many articles in which the subject species was *Homo sapiens*, but until recently those were largely in the realm of population genetics. We intend to maintain the journal as a high status, high visibility venue for communicating human population genetics research, because new sequencing technologies have made that field more important than ever.

But the journal has seldom published articles about identification of human genes and analysis of their function. We want that to change, because the depth of genetic analysis of humans is now approaching that possible with experimentally tractable organisms that have long been featured in the journal.

This is for primarily two reasons. First, remarkable advances in genomics and DNA sequence technologies enable facile identification of human genes and their DNA sequence variants that cause diseases and syndromes. Not so long ago it was a slog to map and clone a gene responsible for a phenotype (usually disease) in humans; today it is almost a cakewalk. Second, decades of work on a few experimental organisms have established them as models for the function of genes and pathways that are conserved throughout the tree of life and have provided sophisticated tools for analyzing those genes and exploring the pathways they are involved in. The function of the product of a human gene can often be determined by studying its ortholog(s) in a model organism. This marriage of model organism and human genetics is bringing in-depth understanding of human gene function, and it is doing so quickly.

The paper by Brooks *et al.* in this issue of *GENETICS* is a shining example of the power of enlisting model organisms

in the service of human genetics. In a Commentary, Hieter and Boycott tell how we are in the midst of an unprecedented era of human disease gene discovery, and how harnessing the analytical power of model organisms will be necessary to realize the ultimate goals of human genetics: an understanding of gene function, insights into the biology of disease, and the development of effective therapeutics.

The Editors of *GENETICS* want to extend the reach of the journal in the human genetics conversation. We seek submissions of papers, like Brooks *et al.*, that provide insight into human gene function and disease. More broadly, *GENETICS* (and our sister journal, *G3: Genes | Genomes | Genetics*) seek to publish papers that describe methodological and empirical studies of humans that advance understanding of fundamental concepts of genetics, such as:

- Methods for mapping loci that underlie human phenotypes.
- Comparative genomics.
- Genome organization and structure.
- Genome modification (epigenomics).
- Evaluation of mutation and recombination rates and their genomic variation.
- Human population genetics and genomics.
- Identification of genetic variants that cause disease.

We have recruited—and will continue to recruit—well-regarded, practicing human geneticists as Associate Editors to help us choose the best papers the field has to offer for publication in the journal. I look forward to *GENETICS* being part of a long and productive contribution of model organism and human genetics.

Mark Johnston, Editor-in-Chief