Editorial

As a result of popular demand, *Human Genomics* is being re-launched as an online quarterly publication. The primary goal of this peer-reviewed journal remains the same *viz.* promotion and review of genomics approaches that are tailored to providing answers to the most important and interesting questions in biomedical research. More specifically, *Human Genomics* provides a forum for the publication of primary research and reviews on the application of genomics research in drug discovery and medicine. Recognising the critical role of genomics data analysis and modelling, the Journal will pay particular attention to the statistical and computational methods and tools required for interpreting genomics data. The inclusion of a diverse range of such computational approaches in a single forum is expected to facilitate the flow of information across the many different aspects of human genomics and thereby facilitate 'unblocking' of this methodological bottleneck in human genomics research. The expertise of the Editorial Board is intentionally extensive and covers bioinformatics, genomics, proteomics, neurogenetics, human genetics, clinical genetics, cancer genetics, epidemiology, genomic diversity, human evolution and primate genetics, population genetics, statistical genetics, microarrays, pharmacogenetics, pharmacogenomics and evolutionary genomics.

I would like to welcome David Ross, the new Associate Editor, and David Cooper, Larry Hunter and Carsten Wiuf as new members of the Editorial Board.

The field of human genomics is rapidly evolving. Given this protean nature, we continue to be inclusive in coverage and not to provide a strict description of what the Journal will cover. We certainly do not feel in a position to predict which directions are likely to be the most promising in the coming years. It is therefore easier to recognise the kind of work that should be included rather than to define it.

Obvious examples include the following:

- Linkage disequilibrium association mapping of complex and multifactorial diseases and traits, and relevant methods
- Comparative, functional and structural genomics
- Assessment of the functional consequences of gene variations associated with disease and drug response
- Biology of repetitive elements
- Origin and divergence of human genes
- Protein structure and human variation
- Quantitative genetics and development
- Epigenetics/epigenomics
- Human variation and disease
- Genomic redundancy
- Human gene families
- Statistical analyses of comparative genomics data
- Regular updates on human genome completion and annotations
- Human proteomics

In this issue, the first of the re-launched *Human Genomics*, we are publishing one guest editorial, one review and five research papers, which are accompanied by a gene annotation update, a book review and a software review; the latter three will be regular features of the Journal.

One of the most important challenges in human genomics is to localise and identify the genetic variation associated with disease phenotypes. Collins and colleagues open this issue with a guest editorial on candidate gene and genome-wide association studies of lung cancer.

Mitochondria play a central role in critical metabolic pathways, apoptosis and ageing-related

neurodegenerative diseases. Mancuso *et al.* present an impressive review on mitochondrial DNA sequence variation and neurodegeneration, where they discuss the role of the mitochondrial haplogroups in the pathogenetic cascade leading to major neurodegenerative disorders.

Zhang *et al.* have performed a genome-wide analysis using public databases on the US National Cancer Institute (NCI)-60 human cancer cell lines and identified genes whose expression levels or genotypic variation are correlated with the cytotoxicity of perifosine, an alkylphospholipid with anticancer activity.

Sen *et al.* have utilised deviation from Hardy–Weinberg equilibrium (HWD) as a tool to investigate the magnitude and direction of genotyping error in published association studies. The authors have focused on the pattern of HWD across a set of studies, rather than on HWD in individual studies.

Lind *et al.* report on the association between *ALDH1A1* and alcohol consumption behaviour and susceptibility to problem drinking or alcohol dependence in a Finnish population. In the next paper, Aquilante *et al.* report on polymorphisms in drug transporter genes and drug-metabolising enzyme genes affecting inter-individual variability in rosiglitazone pharmacokinetics in humans. The last research paper, by Hsu *et al.*, describes *CYP2C19* variants in three different ethnic and geographically isolated regional populations of Papua New Guinea.

In the Gene Completions and Annotation section, Nebert *et al.* provide a comprehensive update on the olfactory receptor gene superfamily, that represents the largest in the human genome, consisting of 390 putatively functional genes and 465 pseudogenes. Also in this issue, Liu *et al.* provide a very informative survey of genetic simulation software for population and epidemiological studies. The book, *Biosimulation in Drug Development*, is also reviewed and covers the panoply of modelling applications in drug development.

The Publisher, the Editorial Board and the Editor of the Journal are committed to serving and interacting with the research community in building a bridge between genomics and biological questions of human genetics. If you are interested in writing for the Journal then please get in contact with us.

Welcome back to *Human Genomics*!

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