Human Population Genetics and Genomics
https://doi.org/10.47248/hpgg2303010001

Editorial

Human Population Genetics and Genomics: An Open Access Journal of Our Own

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Received: 27 Feb 2023
Accepted: 28 Feb 2023
Published: 4 Mar 2023

The origins of population genetics can be traced back to the rediscovery of Mendel's pioneering experiments in 1900 [1] and what is now referred to as the Hardy-Weinberg law published in 1908 [2]. However, it was the work of Sewall Wright, J.B.S. Haldane, and Ronald Fisher over the next three decades that forged population genetics into the discipline we recognize today [3,4]. Their contributions established population genetics as a uniquely quantitative and mathematical branch of biology. As tools to uncover molecular variation were developed and applied to natural populations, significant advances in population genetics were made by integrating empirical data with rigorous theoretical models [5]. Nonetheless, the relevance of population genetics to other biological disciplines, beyond its obvious significance in understanding the genetic basis of evolution, was not always appreciated.

But then a funny thing happened. As genome sequencing projects started to come to fruition, the relevance and broad purview of population genetics became impossible to ignore. This was perhaps most obvious in the wake of the Human Genome Project when the first large-scale catalogs of human genomic variation were being constructed. Population genetics provided the intellectual framework to quantify, characterize, and interpret the increasingly large collections of human genetic variation. Formerly esoteric population genetics concepts, such as linkage disequilibrium, were repurposed into utilitarian tools to guide the design of genome-wide association studies. Additional examples of population genetics principles finding pragmatic applications include delineating the dynamics of cancer cell evolution, decomposing total variation of high-dimensional molecular phenotypes into within versus between population components, and determining optimal ways of imputing missing genotype data in individuals to improve the power of mapping disease genes.

The march of human population genetics to prominence accelerated with the rise of second-generation sequencing and the ensuing deluge

of whole-genome sequence data sets. The wealth of genomic data ushered in the golden era of human population genetics and genomics [6]. The large number of human genomes that have been sequenced has led to many methodological innovations in population genetics that are providing fascinating insights into the evolutionary forces that shape extant patterns of human genomic variation. Population genetics analysis of ancient DNA (aDNA) from Neanderthals, Denisovans, and modern humans has revealed dramatic new insights into human history and how admixture among hominins influenced the genomes of contemporary individuals. Despite all the surprising things we have already learned from aDNA, it seems likely this is just the tip of the iceberg. For instance, the field of ancient environmental genomics, where sequencing dirt can reveal stories of Neanderthal history [7], is in its nascent stages and seems poised to reveal new stories of human and hominin evolution. More broadly, third generation sequencing will soon facilitate *de novo* assembly of individual genomes providing access to previously inaccessible parts of the human genome. In short, human population genetics and genomics plays a central role in addressing fundamentally important problems in basic and biomedical science.

Despite the broad significance, diversity, and growth in human population genetics and genomics research, there are surprisingly no journals specifically dedicated to this area. The recently launched Open Access journal *Human Population Genetics and Genomics* (HPGG) was conceived to remedy this important gap. Although numerous journals are interested in publishing some narrow aspect of human population genetics work, HPGG will be home to the full spectrum of human population genetics and genomics research. Indeed, we are interested in empirical studies of human genomic diversity, experimental and functional studies of evolutionarily interesting genetic variation, development of novel experimental technologies for sequencing and functional genomics, statistical and methodological development, descriptions of new software and computational tools, gene-culture interactions, and theoretical population genetics studies to name a few. The scope of HPGG is broad because population genetics and genomics is inherently broad and interdisciplinary.

I am excited to be Editor-in-Chief of the first journal specifically dedicated to providing a forum for human population genetics and genomics research. Although starting a new journal is fraught with challenges, I am nevertheless optimistic HPGG will be successful. Perhaps the most important harbinger of things to come is the exceptional advisory and editorial board of prominent scientists whose interests encompass the same breadth in scope as the journal. Their experience, wisdom, and enthusiasm are a tremendous resource that will help ensure the science HPGG attracts and publishes is top notch and worthy of respect.

This is an exciting opportunity for our community to have a journal of its own. Our goal is for HPGG to be your first choice when considering where to submit your population genetics and genomics work. We will accomplish this goal by providing an open access platform with a rigorous and efficient peer review process that rapidly publishes the highest quality and most creative work being done in human population genetics and genomics. We are interested in receiving your best manuscripts and hearing from you how HPGG can best serve its authors and the community of scientists whose work falls under the broad purview of human population genetics and genomics.

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Cite this article: Akey JM. Human Population Genetics and Genomics: An Open Access Journal of Our Own. Hum Popul Genet Genom. 2023;3(1):0001. https://doi.org/10.47248/hpgg2303010001.