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Omer Gokcumen

State University of New York at Buffalo, gokcumen@gmail.com

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Evolution, Function and Deconstructing Histories: A New Generation of Anthropological Genetics

Omer Gokcumen^{1*}

¹Department of Biological Sciences, State University of New York at Buffalo, Buffalo, New York, USA.

*Correspondence to: Omer Gokcumen, Department of Biological Sciences, State University of New York at Buffalo, 109 Cooke Hall, Buffalo, NY 14260 USA. E-mail: gokcumen@gmail.com.

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It has been an amazing decade for anthropological genetics. Our questions have remained the same, profound inquiries about human nature and diversity. But thanks to an array of new technologies, our answers become infinitely more insightful and accurate. A click away, we now have access to thousands of whole modern human genomes and hundreds of ancient individuals with genome-wide data. Our comparisons of these genomes become even more meaningful because we now know much more about what a variant at a given location of the genome may do to the expression of genes, the functioning of proteins, the cellular phenotypes, or the processes in our organs. These new datasets build upon existing concepts. A DNA sequence is still a DNA sequence, and a quantitative trait locus still marks a variable site that is associated with a given trait. What changed is the massive amount of data generated, not for a single gene, but for the

entire genome, and not for a single individual, but for thousands. In this ocean of data, a new generation of genomic anthropologists has emerged, tackling fundamental questions of biological anthropology with novel computational know-how and with a stronger appreciation of functional genetics. The future for genetic anthropology has never been brighter.

This quantitative revolution in how we study human variation and evolution has allowed for qualitative leaps in our perception of humanness. In the first article of this special issue, Harris and DeGiorgio provide a thorough conceptual summary of the state-of-the-art methods that are applied to genomic data to understand admixture between populations and species. Such methods have recently revealed that a tiny fraction of our variation is shared with now extinct species, such as Neanderthals. The data are so rich that even that tiny fraction amounts to tens of thousands of variants, which allow us to reveal signatures of recent admixture events from the archaic humans into modern human populations. The possibility of an admixture between Neanderthals and humans has been a major focal point in the field for decades. And ten years ago, genetic anthropology had little to say. Now, genomic approaches lead the way not only describing the more precise timing and nature of such admixtures, but also their impact on contemporary human populations. Touching on these issues, Hawks' article describes how admixture can leave signatures that influence how we understand population histories. Excavating these signatures allows us to paint a more accurate and bias-free picture of human diversity.

Similarly, when it comes to the evolution of our biological features that are key to our survival and underlie our variation, genomic approaches reveal new empirical zing to existing paradigms, such as the evolution of our immune system, our senses, and our cognitive abilities. Blending animal and cell-line models, it is now possible to measure the functional and

evolutionary impact of genetic variation. In her article, Brinkworth touches on this exciting new front and makes a compelling case explaining the genetic diversity of the human immune system within the context of never-ending and ever-changing pathogenic pressures. Such approaches even allow direct estimation of the health of now extinct species, as is done here by Berens, Cooper, and Lachance.

Maybe the most immediately visible impact of this quantitative revolution is the empirical definitiveness that it brought to studies of population history. As described by Antelope, Marnetto, and Huerta-Sanchez, it is now possible to reconstruct the genetic histories of contemporary and ancient peoples with unprecedented power. Sometimes our findings fit well with established histories and expected evolutionary trajectories, but sometimes they do not. Regardless, genomics studies increasingly establish themselves as definitive narratives for human variation in the public sphere. In my opinion, this is largely a positive development, given that genetic studies tend to deconstruct rather than support ethnocentric narratives of human diversity. However, a continuous and vigorous debate remains crucial as genomic anthropology has become a central discipline in our discussions with regard to human uniqueness and diversity. It is now a time to revisit old questions, ask new ones, and even stumble upon questions that we did not even know existed. To rephrase Haldane's prophetic words, in the vast ocean of genomic data, we now realize that human evolution is stranger than we imagined.

A note on the origins of this special issue: American Association of Anthropological Genomics (AAAG), as a young and dynamic organization, is at the forefront of the exciting new venues in applying genomics technologies to anthropological questions. In 2016, Aaron Sams and I have organized the annual AAAG symposium, which was entitled: "Ancient alleles in modern

populations: Ancient structure, introgression, and variation-maintaining adaptive forces.” This special issue is mainly based on contributions by the speakers in this symposium, building upon the rigorous discussions during the symposium. As such, I like to thank all the speakers for the symposium, my co-organizer Aaron Sams, my colleagues in AAAG, as well as the editors of Human Biology.

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