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Reading history through genetics: New method analyzes recent history of Ashkenazi and Masai populations

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Computer scientists at Columbia's School of Engineering and Applied Science have published a study in the November 2012 issue of *The American Journal of Human Genetics* (*AJHG*) that demonstrates a new approach used to analyze genetic data to learn more about the history of populations. The authors are the first to develop a method that can describe in detail events in recent history, over the past 2,000 years. They demonstrate this method in two populations, the Ashkenazi Jews and the Masai people of Kenya, who represent two kinds of histories and relationships with neighboring populations: one that remained isolated from surrounding groups, and one that grew from frequent cross-migration across nearby villages.

"Through this work, we've been able to recover very recent and refined demographic history, within the last few centuries, in contrast to previous methods that could only paint broad brushstrokes of the much deeper past, many thousands of years ago," says Computer Science Associate Professor Itsik Pe'er, who led the research. "This means that we can now use genetics as an objective source of information regarding history, as opposed to subjective written texts."

Pe'er's group uses computational genetics to develop methods to analyze DNA sequence variants. Understanding the history of a population, knowing which populations had a shared origin and when, which groups have been isolated for a long time, or resulted from admixture of

multiple original groups, and being able to fully characterize their genetics is, he explains, "essential in paving the way for personalized medicine."

For this study, the team developed the mathematical framework and software tools to describe and analyze the histories of the two populations and discovered that, for instance, Ashkenazi Jews are descendants of a small number—in the hundreds—of individuals from the late medieval times, and since then have remained genetically isolated while their population has expanded rapidly to several millions today.

"Knowing that the Ashkenazi population has expanded so recently from a very small number has practical implications," notes Pe'er. "If we can obtain data on only a few hundreds of individuals from this population, a perfectly feasible task in today's technology, we will have effectively collected the genomes of millions of current Ashkenazim." He and his team are now doing just that, and have already begun to analyze a first group of about 150 Ashkenazi genomes.

The genetic data of the Masai, a semi-nomadic people, indicates the village-by-village structure of their population. Unlike the isolated Ashkenazi group, the Masai live in small villages but regularly interact and intermarry across village boundaries. The ancestors of each village therefore typically come from many different places, and a single village hosts an effective gene pool that is much larger than the village itself.

Previous work in population genetics was focused on mutations that occurred very long ago, say the researchers, and therefore able to only describe population changes that occurred at that timescale, typically before the agricultural revolution. Pe'er's research has changed that, enabling scientists to learn more about recent changes in populations and start to figure out, for instance, how to pinpoint severe mutations in

personal genomes of specific individuals—mutations that are more likely to be associated with disease.

"This is a thrilling time to be working in computational genetics," adds Pe'er, citing the speed in which data acquisition has been accelerating; much faster than the ability of computing hardware to process such data. "While the deluge of big data has forced us to develop better algorithms to analyze them, it has also rewarded us with unprecedented levels of understanding."

Provided by Columbia University

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