

Geneticists reconstruct population history of New York City

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By combining genetic data, ancestry information, and electronic health records, scientists are able to identify neighborhood-level patterns of migration in the New York City area, according to research presented at the American Society of Human Genetics (ASHG) 2015 Annual Meeting in Baltimore. In addition to supplementing historical and census data, these sorts of findings can inform biomedical and public health efforts in New York and other locations, the study authors said.

"New York City is an important point of entry and immigration, and has long been one of the major 'melting pots' of the world. The population structure there is complex and interesting from a variety of perspectives, including the genetic one," said Gillian Belbin, MS, a graduate student at the Icahn School of Medicine at Mount Sinai (ISMMS) and first author on the study.

"These days, other cities such as London and Shanghai are reaching the same levels of diversity as New York, and many of our methods and findings can be applied to those cities' populations as well," added Eimear Kenny, PhD, Assistant Professor at ISMMS and senior author on the study.

Ms. Belbin and her colleagues are investigating a variety of questions related to migration into New York City, population transitions among its ethnic enclaves, and effects of historical events and trends on recent generations as well as during the last few centuries. They are using the ISMMS BioMe Biobank, an anonymized database of electronic health

record and genetic information from more than 32,000 ISMMS patients who have volunteered to share their medical data with researchers. The [genetic data](#), which includes about one million markers across the genome, is compared among individuals, among populations, and between current and ancestral populations to determine hidden patterns of relatedness, sort individuals into groups that share genetic characteristics, and find correlations with genes of medical relevance.

For example, the researchers identified a group of distantly related New York residents of Puerto Rican ancestry who were more likely than others to have Steel syndrome, a genetic skeletal and muscular condition characterized by short height, hip dislocation at birth, and spinal issues later in life. Last year, they were able to use this information to identify the gene that causes Steel syndrome, a finding that could lead to targeted screening for this condition among certain groups.

The researchers have also genetically compared groups of New Yorkers with ancestral populations outside of the city, producing analyses that enrich scientific understanding of [historical events](#). An example is the Garifuna people of Central and South America, a population that originated in the late 1600s when an African slave ship foundered off the coast of Venezuela. In the years that followed, the survivors of that event reproduced with Native populations, and many of their descendants form communities in New York today.

"What was interesting about Garifuna descendants in New York is that, unlike almost every other population in the Americas, they had no genetic evidence of European ancestry," Dr. Kenny said. "This reflects the initial historical event that brought their ancestors into contact as well as a lack of mixing with other groups since then."

The researchers are now conducting preliminary analyses of neighborhood-level data. "We want to understand how people belonging

to these smaller communities relate to one another, within and between communities, and how these patterns change over time," Ms. Belbin said.

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