Ancestry.com analyses user DNA samples to build migration maps of North America

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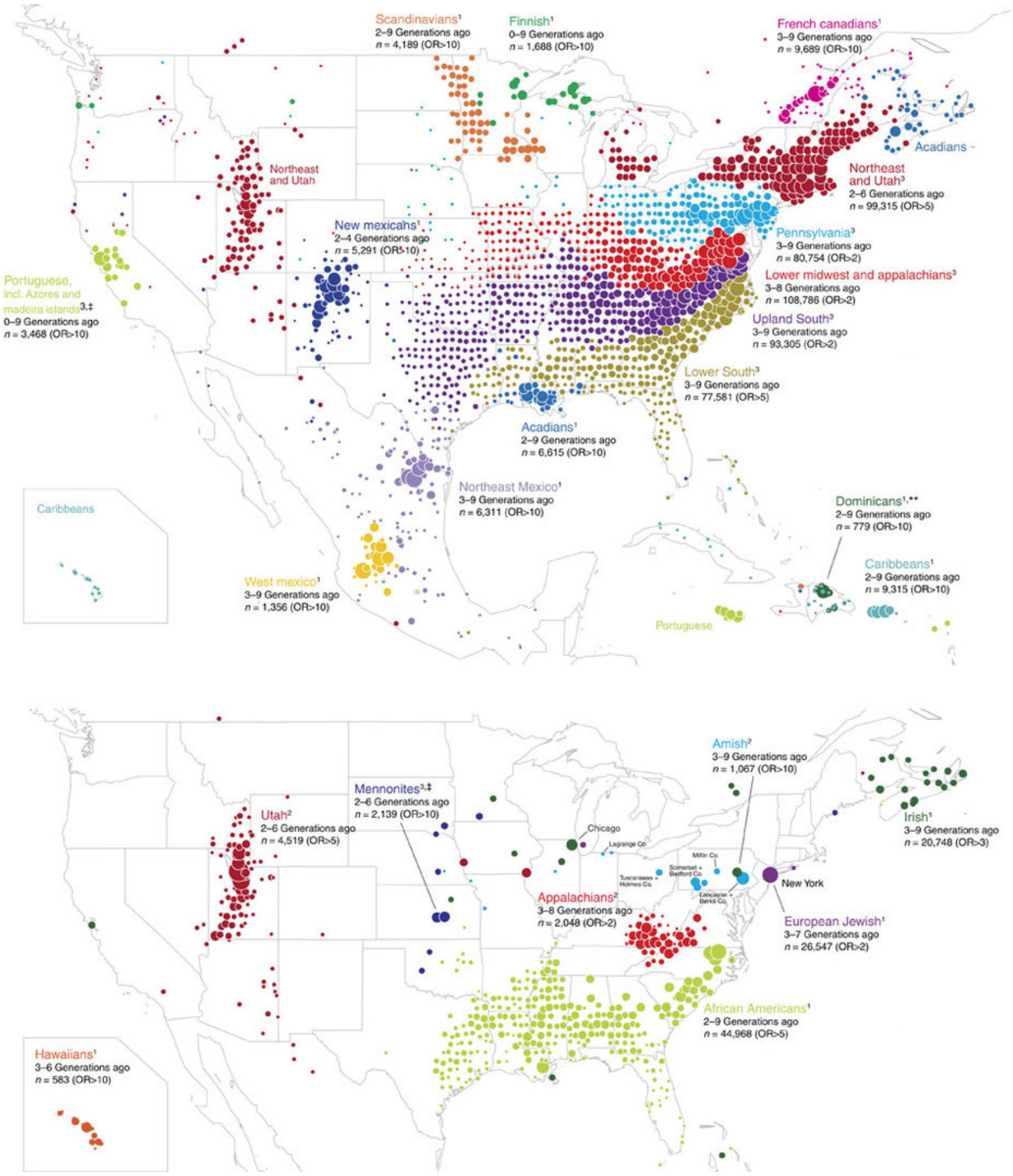

Distribution of ancestral birth locations in North America associated with IBD clusters. Points show pedigree birth locations that are disproportionately assigned to each cluster. Only birth locations with OR>x within indicated generations y–z are plotted, in which parameters x, y, z are chosen separately per cluster to better visualize the cluster's historical geographic concentration. For each cluster,

points are independently scaled by the number of pedigree annotations. Note that clusters are separated into two maps only for clarity. Also note that the concentration of Puerto Rican ancestors in Hawaii probably reflects their arrival there in the early 1900s. Maps were generated with the maps R package using data from the Natural Earth Project (1:50 m world map, version 2.0). These data are made available in the public domain (Creative Commons CC0). Credit: *Nature Communications* (2017). DOI: 10.1038/ncomms14238

(Phys.org)—A team of researchers at Ancestry, the people behind Ancestry.com, has used genotype data gathered from user kit samples and family tree information to create maps of post-colonial North American migration patterns. In their paper published in the journal *Nature Communications*, the team describes how they gathered information from their databases, analyzed it, and used it to plot the course of human migration across North America.

As the researchers note, genetic studies of pre-colonial North America have provided an accurate picture of early human migration and settlement patterns, but to date, the same cannot be said for the period after white people arrived.

Ancestry.com allows customers to use DNA kits to collect and submit their own DNA samples—users get a family history profile and Ancestry gets data that can be used to create profiles. To date, Ancestry has user data on more than 3 million people. In this new effort, the team used genotype data from approximately 700,00 people, along with their family tree profiles, to create migration and cultural cluster maps of North America. In all, they used their tools to create 60 genetically tied communities that arose during the 1800s to the 1900s. To fill in additional information and to offer explanations of why migration patterns developed the way they did, the team worked with historians at Harvard University. By putting all the pieces together, the team created

maps of both cultural clusters and the movements of people as they spread across North America.

Using the historical information in their databases, the researchers looked even farther into the past for some groups—identifying the regions in Europe from which some people migrated. As one example, they were able to show, generation by generation, where in France settlers came from that populated parts of Canada, some of whom later migrated to parts of northern New England.

Notably, the maps created by Ancestry are likely to offer more than just historical amusement; they could provide the foundation for studies about people with different genotypes who are more or less susceptible to diseases or cancers. And perhaps even more exciting is that the database will only grow bigger as more customers send in their data, offering maps that will one day offer unprecedented historical information.

More information: Eunjung Han et al. Clustering of 770,000 genomes reveals post-colonial population structure of North America, *Nature Communications* (2017). DOI: 10.1038/ncomms14238

Abstract
Despite strides in characterizing human history from genetic polymorphism data, progress in identifying genetic signatures of recent demography has been limited. Here we identify very recent fine-scale population structure in North America from a network of over 500 million genetic (identity-by-descent, IBD) connections among 770,000 genotyped individuals of US origin. We detect densely connected clusters within the network and annotate these clusters using a database of over 20 million genealogical records. Recent population patterns captured by IBD clustering include immigrants such as Scandinavians and French Canadians; groups with continental admixture such as Puerto

Ricans; settlers such as the Amish and Appalachians who experienced geographic or cultural isolation; and broad historical trends, including reduced north-south gene flow. Our results yield a detailed historical portrait of North America after European settlement and support substantial genetic heterogeneity in the United States beyond that uncovered by previous studies.

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