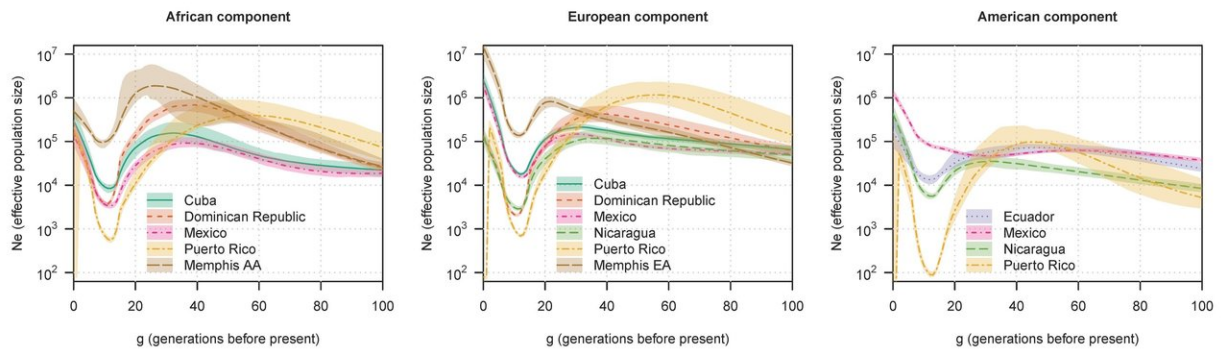


Genome study presents new way to track historical demographics of US populations

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In the African component, we see smaller estimated pre-admixture effective sizes for Cuba (150,000) and Mexico (100,000) than for the Dominican Republic (700,000), suggesting that the African ancestors of the former two populations came from smaller sub-populations of Africa than the African ancestors of the latter two populations. In the European component we see smaller estimated pre-admixture effective sizes for Cuba (200,000), Mexico (150,000), and Nicaragua (120,000) than for the Dominican Republic (400,000). In the American ancestral component, the estimated pre-admixture effective sizes are similar between Nicaragua (400,000), Ecuador (700,000), and Mexico (600,000). Credit: Sharon R. Browning and colleagues

Sharon Browning of the University of Washington and colleagues developed a method to estimate historical effective population size, which is the number of individuals who pass on their genes to the next generation, to reveal the shifting demographic history of U.S.

populations during the last several thousand years. They report their findings in a new study published May 24th, 2018 in *PLOS Genetics*.

Many populations in the U.S. are mixed, with ancestry from Europe, Africa, and the Americas. By looking at genome-wide data from several hundred individuals from a [population](#), scientists can learn not only the current effective [population size](#), but also the sizes of the [ancestral populations](#) that once contributed their genes. In the current study, researchers developed a method for estimating past effective population size and used it to analyze data from nine populations enrolled in a Latino health study, and from African-American and European-American populations in Pittsburgh and Memphis. They estimate that overall effective population sizes dropped substantially after the start of European and African immigration, reaching a minimum around 12 generations ago, but rebounded a few generations later. Researchers investigated these population size reductions, also known as bottlenecks, and found that the smallest bottleneck occurred in Puerto Rico, where the effective size at one point fell to just one thousand people.

The differences in historical effective sizes between these populations can be useful for understanding why individual groups face different health and disease risks. They can also be useful for scientists in selecting populations that will be most useful for studies that identify the genes linked to specific diseases.

Sharon Browning adds: "Admixed populations in the Americas are like ropes constructed by braiding together several different fibers, with the fibers representing different ancestral population groups. The genetic composition of those different groups is overall very similar, but is different enough so that we can distinguish the genetic material from each ancestry group and study its properties, which tells us about the histories of those populations."

We found that around 100 generations ago, which is approximately several thousand years ago, the effective sizes of the ancestral European, African and indigenous American populations contributing to current-day American populations were around several tens of thousands of individuals each. We also found clear signatures of the effects of migration and colonization, with reduced effective population sizes around 12 generations ago, which is approximately 300 years ago."

More information: Browning SR, Browning BL, Daviglus ML, Durazo-Arvizu RA, Schneiderman N, Kaplan RC, et al. (2018) Ancestry-specific recent effective population size in the Americas. *PLoS Genet* 14(5): e1007385. doi.org/10.1371/journal.pgen.1007385

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