Southern Europeans have North African genes

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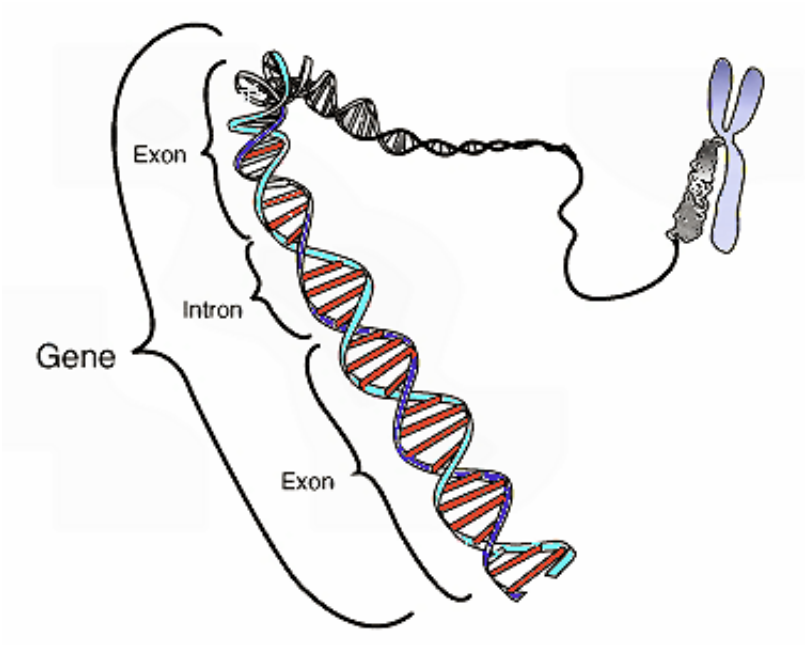

This image shows the coding region in a segment of eukaryotic DNA. Credit: National Human Genome Research Institute

(Phys.org) —Southern Europeans are more genetically diverse than Northern Europeans. Geneticists have several different explanations for this phenomenon, one of which is migration from Africa to southern Europe. However, previous studies, which have relied on samples from sub-Saharan populations, have not revealed much shared ancestry between Africans and Europeans. Recognizing that there are many genetic differences between Northern and sub-Saharan Africans, Carlos

Bustamante of Stanford University and his colleagues performed a DNA analysis that included North African populations. The study, published in the *Proceedings of the National Academy of Sciences*, shows high levels of shared ancestry between Southern Europeans and North Africans.

Population geneticists have formulated three hypotheses to explain the greater genetic diversity of Southern Europeans. One says that about 20,000 years ago, people from all over Europe retreated southward to escape advancing glaciers. When the glaciers receded, only a small segment of the original population recolonized the North.

A second explanation, associated with the Neolithic revolution and the development of agriculture in the Near East, about 10,000 years ago, is that people from the Near East migrated westward to Europe, with gene flow varying in different parts of the continent.

The third hypothesis says that Southern Europe's high genetic diversity was caused by recent migration from Africa to Southern Europe, related to the Roman conquest of North Africa and the Moorish occupation of the Iberian peninsula. However, previous studies suggested that Europeans and Africans share only between 1 and 3 percent of their genomes, making this scenario unlikely.

These studies looked at populations from sub-Saharan Africa but excluded North African populations. To correct this oversight, Bustamante and his team analyzed data from DNA samples of 2,099 individuals in 43 different populations, including seven from North Africa and three from Spain. They found much higher levels of gene flow from Africa to Europe than earlier studies had indicated.

Evidence of North African descent was highest in the Iberian Peninsula and the Canary Islands, with up to 20 percent of individual genomes reflecting shared ancestry. The analysis showed that North Africans must

have migrated to Spain at least 240 to 300 years ago.

Basques who live on the Iberian Peninsula were an exception. They showed lower levels of shared ancestry with North Africans, closer to those of Europeans from further north.

The researchers also looked at the relationship between disease risk and their suggested migration patterns. They studied 134 diseases and found that most of them followed inheritance patterns consistent with their interpretation. However, people from North Morocco and the Western Sahara had a higher risk of multiple sclerosis than expected, while Canary Islanders had a lower risk.

More information: Gene flow from North Africa contributes to differential human genetic diversity in southern Europe, Published online before print June 3, 2013, doi: 10.1073/pnas.1306223110

Abstract
Human genetic diversity in southern Europe is higher than in other regions of the continent. This difference has been attributed to postglacial expansions, the demic diffusion of agriculture from the Near East, and gene flow from Africa. Using SNP data from 2,099 individuals in 43 populations, we show that estimates of recent shared ancestry between Europe and Africa are substantially increased when gene flow from North Africans, rather than Sub-Saharan Africans, is considered. The gradient of North African ancestry accounts for previous observations of low levels of sharing with Sub-Saharan Africa and is independent of recent gene flow from the Near East. The source of genetic diversity in southern Europe has important biomedical implications; we find that most disease risk alleles from genome-wide association studies follow expected patterns of divergence between Europe and North Africa, with the principal exception of multiple sclerosis.

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