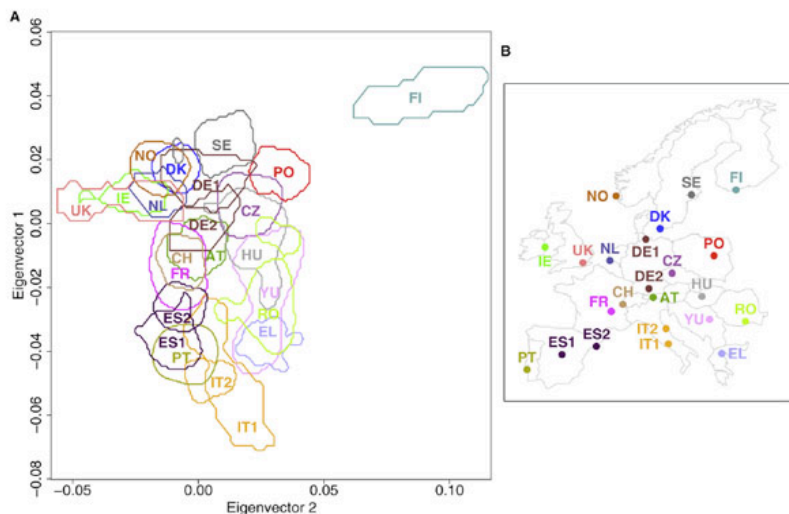


VISUAL SCIENCE

The Genetic Map of Europe



By NICHOLAS WADE
Published: August 13, 2008

Biologists have constructed a genetic map of Europe showing the degree of relatedness between its various populations.

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All the populations are quite similar, but the differences are sufficient that it should be possible to devise a forensic test to tell which country in Europe an individual probably comes from, said

Manfred Kayser, a geneticist at the Erasmus University Medical Center in the Netherlands.

The map shows, at right, the location in Europe where each of the sampled populations live and, at left, the genetic relationship between these 23 populations. The map was constructed by Dr. Kayser, Dr. Oscar Lao and others, and appears in an article in Current Biology published on line on August 7.

The genetic map of Europe bears a clear structural similarity to the geographic map. The major genetic differences are between populations of the north and south (the vertical axis of the map shows north-south differences, the horizontal axis those of east-west). The area assigned to each population reflects the amount of genetic variation in it.

Europe has been colonized three times in the distant past, always from the south. Some 45,000 years ago the first modern humans entered Europe from the south. The glaciers

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returned around 20,000 years ago and the second colonization occurred about 17,000 years ago by people returning from southern refuges. The third invasion was that of farmers bringing the new agricultural technology from the Near East around 10,000 years ago.

The pattern of genetic differences among present day Europeans probably reflects the impact of these three ancient migrations, Dr. Kayser said.

The map also identifies the existence of two genetic barriers within Europe. One is between the Finns (light blue, upper right) and other Europeans. It arose because the Finnish population was at one time very small and then expanded, bearing the atypical genetics of its few founders.

The other is between Italians (yellow, bottom center) and the rest. This may reflect the role of the Alps in impeding free flow of people between Italy and the rest of Europe.

Data for the map were generated by gene chips programmed to test and analyze 500,000 sites of common variation on the human genome, although only the 300,000 most reliable sites were used for the map. Dr. Kayser's team tested almost 2,500 people and analyzed the data by correlating the genetic variations in all the subjects. The genetic map is based on the two strongest of these sets of correlations.

The gene chips require large amounts of DNA, more than is available in most forensic samples. Dr. Kayser hopes to identify the sites on the human genome which are most diagnostic for European origin. These sites, if reasonably few in number, could be tested for in hair and blood samples, Dr. Kayser said.

Genomic sites that carry the strongest signal of variation among populations may be those influenced by evolutionary change, Dr. Kayser said. Of the 100 strongest sites, 17 are found in the region of the genome that confers lactose tolerance, an adaptation that arose among a cattle herding culture in northern Europe some 5,000 years ago. Most people switch off the lactose digesting gene after weaning, but the cattle herders evidently gained a great survival advantage by keeping the gene switched on through adulthood.

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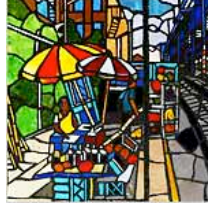


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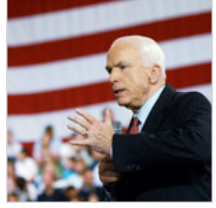
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