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Understanding genetic mixing through migration

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Understanding the genetic ancestry of mixed populations, such as those found in North America, can not only help to detect their origins but also to understand the genetic basis of complex diseases, a scientist will tell the annual conference of the European Society of Human Genetics today. It is the first time that the genomes of individuals of admixed ancestry have been sequenced in such detail, says Dr. Francisco De La Vega of Life Technologies, Foster City, California, USA.

Working with Professor Carlos Bustamante and his team in the Department of Genetics at Stanford University, the scientists analysed the genomes of two people - one of African-American and one of Hispanic-Latino origin. The majority of the personal genomes sequenced to date come from individuals of either European, African, or Asian descent, because it is in these groups that most genetic disease association studies are being carried out. However, populations where genetic mixing through migration has taken place relatively recently make up a sizable proportion of the world's population, and have been not been well studied to date because of the complexity of dealing with the contributions of genes from different ancestries in disease.

"We set out to provide a better understanding of the genome structure in admixed populations by sequencing one African-American and one Mexican sample", said Dr. De La Vega. "By analysing genetic variants in mixed people whose frequency differs in the ancestral populations, we can work out the ancestry of different chromosomal segments in an individual. This has already been done in a number of different ways.

The difference with our work is that, by using whole genome sequencing using the SOLiD™ System, we can greatly increase the resolution of our analyses and achieve a very much clearer picture of the ancestry of genome sequences for the individuals studied.

"We already know that present-day African-Americans trace their ancestry to a rich mosaic of migrants from the mainly West African and Northern European populations who settled in North America and the Caribbean. Mexicans, on the other hand, are descendants of Meso-American indigenous populations - themselves derived from population migrations from Asia (through the Bering straits) - and largely Southern European (mainly Spanish) settlers", said Dr. De La Vega. "But the added value of our research is that we can show the approximate number of generations at which the genetic mixing occurred, estimate the rate at which admixture occurred, and understand better the genetic diversity in the ancestral populations."

To date there are few comprehensive studies of genetic diversity in native populations in the Americas, and by analysing them scientists can begin to piece together the population history of both the admixed and indigenous populations. They can also begin to analyse the contribution of native American genetic variants to the disease burden in the Americas of today, something which at present is relatively unknown.

"We believe that our work will help move forward genetic disease association studies in these admixed populations", said Dr. De La Vega. "This would not only provide valuable information on the genetic component of disease in these people, but would also help refine genetic association findings in other populations by replicating the findings in admixed samples. And the high resolution admixture maps we can generate can help in studies to map variants of disease whose prevalence is very different in the ancestral populations of admixed groups."

The scientists intend to follow up their work by sequencing many more genomes of different populations in the Americas in order to understand further differentiation within the continent and the frequency of the genetic variants. "The decreasing costs of sequencing genomes through new sequencing instruments such as those developed by Life Technologies, is making possible for the first time to compare at large scale genetic variants among and within populations" said Dr. De La Vega.

The scientists are also participants in the 1000 Genomes Project, an international research effort to sequence the genomes of at least 1000 subjects from a number of different ethic groups, and thus establish the most detailed catalogue of human genetic variation to date.

"The Project will sequence the genomes of around 500 admixed individuals from diverse populations including African-Americans from the South West and South East US, Afro-Caribbeans from Barbados, Mexicans from Los Angeles, Peruvians from Lima, Colombians from Medellin, and Puerto Ricans from Puerto Rico. We are incredibly excited about the inclusion of these populations in the Project, since we hope that the genomic resources developed by it will encourage the development of genetic studies in under-represented communities in the US and Latin America", said Professor. Bustamante, co-director of the study. "In the long run, the information obtained from such studies could become the basis of personalised genomic therapies for individuals of admixed origins."

Provided by European Society of Human Genetics