Oral Communication Abstract – 3B.01

EUGENICS, 'RACIAL SCIENCE' AND HUMAN GENETICS

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Racial science, Scientific racism, Geneticists' Manifesto, UNESCO Statements on Race, IQ debate

What has the relationship been between the scientific study of race and racism? Has "racial science" always meant "scientific racism"?

In order to answer these questions, this contribution will survey three topical moments which structured the international debate on science and race during the twentieth century: the publication of the Geneticists' Manifesto in 1939; the negotiation of several UNESCO Statements on Race in the 1950s and 1960s; the IQ debate in the 1960s and 1970s.

IMPROVING THE ACCURACY OF DEMOGRAPHIC MODELS USING WHOLE-GENOME SEQUENCE DATA

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Whole- genome sequence, human demography, 1000 Genomes project

Accurate knowledge of human genome sequence variation is important for the study of human disease inheritance and understanding of the history of human populations. Demographic models inferred from genetic data can explain patterns of genome variation and have been successfully used to decipher the history of human migrations within a framework of archaeological evidence. Demographic models are also essential to distinguish signals of natural selection from patterns of neutral variation resulting from demographic processes. This has important implications for mapping genes underlying complex human diseases.

Current models represent simple approximations to the true complexities of human history. Still, in some respects, they have also offered good fits to empirical data and often the quality of the empirical data has been the limiting factor. Indeed, it has been shown that the use of unbiased empirical data sets can considerably improve the accuracy of model predictions. A major bias in empirical data comes from the fact that most consist of Single Nucleotide Polymorphisms (SNPs) that were discovered in a small set of samples then genotyped in a larger set, so that rare alleles tend to be missed or over-represented and a description of the true distribution of allele frequencies is not achieved. Data sets for analysis of evolutionary history without this bias do exist but have been small and not representative of the whole human species. Thus, significant contributions and new exciting insights are expected from the use of unbiased empirical data.

The 1000 Genomes Project now provides a nearly unbiased resource describing human genetic variation, including SNPs and structural variants. Within this project, genome sequences of 2,500 anonymous people from 27 populations distributed around the world are being produced. At the moment, the 1000 Genomes Pilot Project has generated low-coverage sequence data over the complete genomes of 179 individuals from four HapMap samples, discovering 14.5 million SNPs, 8 million of which are novel, with their genotype in each individual, and many structural variants.

We are exploring ways of calibrating the existing models of human evolution using the newly-available pilot sequence data from the 1000 Genomes Project, with a view to then applying these methods to additional populations.

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VARIABILITY OF TASTE AND SMELL GENES ALONG THE SILK ROAD

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Silk Road, Population studies, genetics of taste, food preferences

Thanks to the scientific expedition Marcopolo2010 (www.marcopolo2010.it) we have studied approximately 20 different communities from Georgia to China. Their genomes have been analyzed with 700,000 genetic markers. All the data were then analyzed with PCA. Preliminary results demonstrate the similarity between the Kazakh populations (different populations are largely overlapping) and the extreme homogeneity' of those located in the Zerafshan Valley (Tajikistan). Additional data indicate that ethnically and linguistically isolated populations such as those of the Pamir, are now losing their uniqueness. As a matter of fact, they are characterized by a mixture of unique and peculiar individuals together with individuals close to those living in other regions of Tajikistan. Finally, surprising was the situation of the Uzbeks Quarshie, falling off sharply from all other populations examined. Apart from this general view, we tested phenotypes and genotypes related to taste, smell, hearing and vision. As regards taste we were able to demonstrate a gradient of distribution from west to east of supertaster for PROP/PTC bitter compounds. Moreover, food preferences are the main factor driving food intake and choice. Although taste has been widely studied especially in regards of pure tastes such as bitter or sweet perception, the relationship between taste related genes and food preferences has seldom been explored. The Silk Road has been the root through which spices and silk have come from the far east to Europe creating a particular mixture of population along it. However up to now no one has studied the way this populations are genetically related to each other. We have thus created a genetic map based on whole genome single nucleotide markers. We have used this knowledge to test 26 genes related to taste and how this genes influence food preferences. In particular we have found that TAS1R gene which encodes the sweet receptor is associated to alcohol related foods; PCLB2, a gene related to smell is associated to liking of hot tea; the capsaicin receptor TPRV1 is associated to white/red radish; and finally ITPR3 is associated to many foods including Lamb, Sheeps Cheese, Fava Beans and Watermelon significantly, but it shows to influence up to 35 more foods. These knowledge will help understand better the effect of admixture of this populations and will help clarify the genetic relationship between taste, smell and food preferences.