Human races and evolutionary medicine

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Presented at the congress on The future of life and the future of our civilization. Frankfurt May 2-6 2005

Summary

Data from the Human Genome Programme have clearly established that the human race is unique. Attempts to identify separately Black, Caucasian, Asian is not supported by biological data but is only based on socieconomic conditions. Evolutionary medicine takes the view that many contemporary diseases are likely to result from the incompatibility between our contemporary lifestyle and dietary habits and the conditions under which the evolutionary pressure had shaped our genetic inheritance. Assuming that human race is unique, it is now possible to identify new pathophysiological pathways through this paradigm.

Human race has always been a social construct reflecting in a given country, at a given period of time the status of the society, even the nomenclature has always been problematic with a mixture of phenotypic, geographical and even religious qualification, including black, African, negroes, or semite, white, Caucasian, or yellow, Asian, Asiatic, Hispanic…[Swynghedauw 2003]. Even self-identification is problematic, and in the last US Census 7 million persons identified themselves as member of more than one race; and 800,000 respondants said that they were both black and white [Schmitt 2001]. Finally, it is clear that race qualifies THE OTHER, and has been used throughout our history to justify the predominancy of a group of persons on another. Our recent, even very recent, history is full of examples which all illustrate how humankind may use such a vocabulary to cover ignorance or, still worst, tyranny.

Human race is inherently imprecise, based on appearance, surname, language…and has always been a social construct reflecting in a given country, at a given period of time the status of the society[1]. From a zoological point of view, animal races, as opposed to human "races", are a subtype of a species, inter-reproductive, phenotypically extremely well-characterized (with competitions) and isolated by geography or human wishes. By contrast, human race can't be accurately defined, are, in current practice, poorly-defined by vague phenotypic traits with many confounding factors, including socioeconomic status, educational level, religion, culinary customs, tribal affiliation…Nevertheless, despite of the lack of clear definitions « race » is a commonly utilised distinction utilised in most of biomedical publications.

Is the geographical distribution of a disease racial?

This is an important issue when studying evolutionary medicine, because it could not be possible to envisage medicine under these aspects if human race is not unique [Swynghedauw 2004].

Monogenic inherited diseases

The well-documented example of an overlap between race and a monogenic disease is that of Black Africans (considered as a race), and the geographical distribution of several inherited blood cell disorders, such as sickle disease and the Glucose-6-phosphate Dehydrogenase deficiency (caused by allele (A-)). Sickle disease is an inherited disease due to a mutation located on hemoglobin which protect against the severe forms of malaria when heterozygous but have reduced fitness compared to wild-type when homozygous, as a result of the clinical consequences of the red blood cell disease [reviewed in Jobling 2004]. Clearly the world map of malaria superimposed to that of the genetic disease, and the best way

[1] It is very common, for example, to say that most of the winners in the American team, during Olympic games, were Black and to attribute their physical condition to genetic predisposition, while it should be very simple to make a genome wide analysis to identify the corresponding genes or loci, or to refute the genetic thesis….which have never been done or even tried. Obviously the best explanation for the success of Black minority (like that of North-African minority in France for soccer players), is determined by the strong wish of those persons to climb into the social hierarchy

to explain the diffusion of the genetic mutation is selective pressure, but, clearly also, while sickle disease predominates in Black Africans, it also exists, with several historical birth places, in India, Spain and Arabia, and is not specific for the "Black" race.

AIDS, the most devastating new infectious disease, is most prevalent in several parts of Africa, and there is evidence that a few individuals show significant inherited resistance to the viral infection. One of the first loci conferring resistance to be identified was a chemokine receptor, CCR5, a cell surface protein which acts as a cofactor for HIV entry into the T cells. One of the variant of CCR5, D32, is not functional and, in homozygous form, is associated to resistance to HIV infection. The distribution of this variant over the world is now well-documented, the variant predominates in northwest Asia and northern Europe, and is not found in subsaharian Africa.

Multigenic diseases

Multigenic diseases include cancer, cardiovascular diseases which are consequences of atherosclerosis, hypertension or diabetes, but which also have a strong, frequently predominant, environmental components []. Tobacco smoking is one of these components, but there also nutritional, psychological, socioeconomic and genetic determinants, which all play a role. Epidemiologists have published tables which allow to calculate a global risk by weighing and measuring these different factors. In spite of the absence of indisputable and clear definition, it is now well-accepted that Black Americans[2] have more risk than White of suffering from cardiovascular diseases (mortality for the total population, in number of deaths per 100,000 : 247.8 ; Black population : 316.9 ; White : 243.5) , including myocardial infarction (177.8 ; 211.6 ; 176.5) and stroke (57.9 ; 78.8 ; 56.4) [Mentah 2005].

Can human « race » be a proxy for genetic variations?

The answer is clearly no. The genetic diversity is too inequally distributed, the skin color is a multigenic trait which can't be linked with any genetic locus and, finally, a given "race" did not correspond to genetic markers.

Apportionment of genetic diversity

The genetic diversity is not equally distributed throughout the world. The first major point is that 83-88% of autosomal variations (the same is rue for mitochondrial markers, Y chromosome or microsatellites) is found within population between individuals, not between populations or races. A programme called STRUCTURE allow to identify four different groups of people based on the apportionment of genetic polymorphisms [Wilson 2001] and showed that the two classifications, that obtained with STRUCTURE, and the usual race classification do not clearly superimposed. Studies of the genetic of the populations have definitely demonstrated that the origins of humankind (homo sapiens sapiens) was in West

[2] The inclusion in this category was based on self-assignation

Africa 100,000 years ago, followed by one, probably two migrations through the actual Suez to disseminate in Europe, Asia and America (reached 10-15,000 years ago). There are many confirmations of these view, including considerations based on languages classification. Finally, genetic diversity, as calculated using F_{st} is higher in Africans than in any other continents in the world [Cavalli-Sforza 2001].

Skin color, can't be a proxy for human race

The first reason is that the biological determinants of skin color are diverse and far from being simple and monogenic, the trait is multigenic, and includes melanosome density, eumelanine and/or pheomelanin content, at least, 13 genes for the regulation of the expression of these genes, including MC1R, are highly polymorphic receptor with more than 30 variants with 5 synonymous haplotypes in Africa and 13 non synymous out of Africa, which indicates a strong selective functional pressure in Africa [Parra 2004]. To establish a genetic link between skin color and behavior or any given multigenic disease is an impossible and hopeless task due to the highly complex nature of the two groups of partners. A study comparing the degree of skin pigmentation in five populations of various ranges of pigmentation have shown that pigmentation was weakly associated to genetic markers [Parra 2004].

The socioeconomic level

The major confounding factor when studying « race » inequalities is the socioeconomic status. For example, black American community when compared to non black showed major differences in terms of average household income (+ 25.3% in favour of non black) and high-school diploma (+ 50%), the two most commonly employed markers of the socioeconomic status.
Indeed, the deathrate ratio, workers+employees/management+liberal professions, in men 25-54 years, in a French study was on average above 1 for every cause of death, including cancer, cardiovascular disease, workers and employees having a risk of death 2.9 higher than the others [Lang 2000]. These results have been confirmed by many many studies.

Suggested guidelines for using race/ethnicity in biomedical publication

As a consequence several authors have suggested a sort of guideline for biomedical authors [Kaplan 2003, Swynghedauw 2003] which is as follow:

- The reason for categorization should be specified.
- The way in which individuals were assigned to a given category should be specified, even when for self assignment.
- Racial/ethnicity is not a proxy for genetic variation, but more a proxy for socioeconomic status.
- To distinguish between race/ethnicity as a risk factor or as a risk marke
- All relevant confounding factors should be considered (insurance status, diet, education, religion, tribal affiliation, psychological factors…) and principally socioeconomic status.

- To avoid terminology (as Caucasian) that implies an immutable attribute of an individual.

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