

COMMENTARY

Human populations are not biologically and genetically discrete

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Science relies on the validity of concepts, especially when these come from other disciplines. The differentiation of human groups according to phenotypic appearance, for example the colour of their skin, seemed so obvious that after centuries only genetics could fundamentally revise this concept. For 50 years, attempts have been made to break away from racial categorization, among others in the recent Jena Declaration of 2019 (Fischer et al., 2019). There is no biological justification for categorizing people into discrete groups; on the contrary, racism seeks a biological legitimization in its justification.

This Special Issue takes up the enormous challenge of how to deal with the realization that ‘race’ in humans is not a scientifically tenable category but that ‘race’ permeates psychological processing (Editorial of this Special Issue) especially in fields of psychology, for which the term is constitutive, such as the ‘other-race-effect’. Other sciences may be curious to see how psychology discusses the downgrading of ‘races’ to groups of increasingly higher resolution or, for example, the individual-differences approach, and finally how giving up a concept may open new doors and provide new opportunities.

People have been categorizing each other based on appearance for millennia, as is still shown by the ongoing controversy on ancient Egyptian ‘races’. In the 19th century, early evolutionary thinking began to remodel this practice of classifying human groups using phenotypes, culminating in ideas of superior human ‘races’ and eugenics. An influential figure here is Herbert Spencer, who conceived the term ‘evolution’ before and differently from Darwin (Köchy, 2007), and from whom the expression ‘survival of the fittest’ originated. He founded ‘biological Spencerism’ in Victorian England (Freeman et al., 1974), Social Darwinism (even before German biologist Ernst Haeckel) and the supposedly biologically based form of white superiority. According to his theory, different groups of people would have inherent and distinct characteristics, which are displayed, for example, in the colour of their skin. Those characteristics would be linked to the population ancestry of its bearer.

Differences between human populations were further imagined using biological concepts, such as morphospecies, reflecting a static worldview, in which species were defined by certain characteristics selected by systematists. In essence, human groups were seen as immutable ‘classes’ (Mahner & Bunge, 1997). This, however, does not reflect objective biology but rather represents a flawed construct of the human mind. Taxonomy is a rather static way of thinking, uninfluenced by the idea of evolution.

The central question was, and still is, the relationship of between-group variation (intergroup variation) to individual variability within a group (intragroup variation). Our view of human biological history

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began, however, to transform in the 1960s with the advent of molecular biology and its application to population genetics (Lewontin, 1972). Molecular evidence provided new criteria to observe speciation processes and taxonomic divisions, which were readily applied to human populations. After early studies on simple biological markers such as blood groups, mitochondrial DNA and Y-chromosomes (Cavalli-Sforza et al., 1994), recent years have seen an explosion of studies on human genetic diversity due to the advent of high-throughput DNA sequencing technologies, deciphering the genomes of millions of people. These genomic studies focus on polymorphic sites in the human genome, that is variants in the DNA sequence, also known as single nucleotide polymorphisms (SNPs) that vary between individuals and that change over time according to stochastic processes of neutral evolution. Most of these SNPs are not located in genes and therefore have no effect on phenotype. Populations that have recently separated still have many SNPs in common, only over many generations this proportion would decrease. Each person carries between 4 and 7 million SNPs and millions of larger structural variants, compared to the human reference genome (The 1000 Genomes Project Consortium, 2015). There are orders of magnitude more such genetic variants than morphological traits on which classical taxonomy was based.

With genomic analysis, the genetic history and relatedness of populations can be traced in detail, while also explicitly disproving earlier and current notions of ‘race’. Studies revealed that the genetic variability within any given human population is almost as high as the variation between human populations (The 1000 Genomes Project Consortium, 2015). Not even one position in the genome has been found that represents a fixed difference between all individuals of two continental populations. This fact also includes genetic variation contributed from extinct human lineages, such as Neanderthal DNA in non-Africans, and Denisovan DNA in contemporary people from Southeast Asia and Oceania. It is rather the frequencies of genetic variants that differ between human populations. Humans are a relatively young species in evolutionary terms; the genetic effects of geographic isolation that resulted from settling the entire world in the last 50,000 years are minor and have been often overwritten by secondary admixture events (Lazaridis et al., 2016).

A small subset of this genetic variation *will* have phenotypic consequences. An example of local adaptation are genes involved in skin pigmentation polymorphism. Increased melanin levels giving rise to darker complexion are selected for in lower latitudes in order to protect from UV radiation, while lower melanin levels giving rise to lighter complexion are favourable in higher latitudes to facilitate Vitamin D synthesis which depends on UV exposure (see also Editorial of the Special Issue Box 1). The later mechanism is known since the 1930s (Murray, 1934), however, only analysis of human genomes from the past has shown that Ice Age European hunter gatherers were mostly dark-skinned, and the high prevalence of light-skin pigmentation was only reached in Europe during the Bronze Age (Mathieson et al., 2015). Our current understanding is that early dark-skinned farming societies had to adapt to low Vitamin D diets and higher latitudes by developing light-skin pigmentation to spread into central and northern Europe (Krause & Trappe, 2019).

Categorizing human groups based on skin colour makes thus little sense, as this trait reflects latitude as a proxy for UV exposure rather than population history. Skin pigmentation is additionally far from a binary trait with countless tones that change gradually in relationship to proximity to the equator. Gradients of variability are the rule in human populations and not discrete boundaries. Genome-wide association studies (GWAS) with increasing sample size and ethnic diversity, like a recent one concerning tobacco and alcohol consumption (Saunders et al., 2022), show that ancestry has weak predictive power, emphasizing that phenotypic- and underlying genetic variation are present deep within human ancestry rather than only existing between them. Last but not least, it is not only a problem of variability perception, but also of face recognition abilities and here of qualitative differences between the perception of familiar and unfamiliar faces (Jenkins et al., 2018), which are closely related to the topic of this Special Issue.

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CONFLICT OF INTEREST STATEMENT

Both authors declare no conflict of interest.

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