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NOVEMBER 24, 2009

Scientists Call for End to Race-Denial

Let's celebrate human genetic diversity

Bruce Lahn and Lanny Ebenstein *Nature*, 8 October 2009

Science is finding evidence of genetic diversity among groups of people as well as among individuals. This discovery should be embraced, not feared, say Bruce T. Lahn and Lanny Ebenstein.

A growing body of data is revealing the nature of human genetic diversity at increasingly finer resolution. **It is now recognized that despite the high degree of genetic similarities that bind humanity together as a species, considerable diversity exists at both individual and group levels (see box, page 728). The biological significance of these variations remains to be explored fully. But enough evidence has come to the fore to warrant the question: what if scientific data ultimately demonstrate that genetically based biological variation exists at non-trivial levels not only among individuals but also among groups? In our view, the scientific community and society at large are ill-prepared for such a possibility. We need a moral response to this question that is robust irrespective of what research uncovers about human diversity. Here, we argue for the moral position that genetic diversity, from within or among groups, should be embraced and celebrated as one of humanity's chief assets.**

The current moral position is a sort of 'biological egalitarianism'. This dominant position emerged in recent decades largely to correct grave historical injustices, including genocide, that were committed with the support of pseudoscientific understandings of group diversity. The racial-hygiene theory promoted by German geneticists Fritz Lenz, Eugene Fischer and others during the Nazi era is one notorious example of such pseudoscience. **Biological** egalitarianism is the view that no or almost no meaningful genetically based biological differences exist among human groups, with the exception of a few superficial traits such as skin colour. Proponents of this view seem to hope that, by promoting biological sameness, discrimination against groups or individuals will become groundless.

We believe that this position, although well intentioned, is illogical and even dangerous, as it implies that if significant group diversity were established, discrimination might thereby be justified. We reject this position. Equality of opportunity and respect for human dignity should be humankind's common aspirations, notwithstanding human differences no matter how big or

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small. We also think that biological egalitarianism may not remain viable in light of the growing body of empirical data.

Many people may acknowledge the possibility of genetic diversity at the group level, but see it as a threat to social cohesion. Some scholars have even called for a halt to research into the topic or sensitive aspects of it, because of potential misuse of the information. Others will ask: if information on group diversity can be misused, why not just focus on individual differences and ignore any group variation? We strongly affirm that society must guard vigilantly against any misuse of genetic information, but we also believe that the best defence is to take a positive attitude towards diversity, including that at the group level. We argue for our position from two perspectives: first, that the understanding of group diversity can benefit research and medicine, and second, that human genetic diversity as a whole, including group diversity, greatly enriches our species.

[...]

Box 2. Emerging understanding of human genetic diversity

Genetic diversity is the differences in DNA sequence among members of a species. It is present in all species owing to the interplay of mutation, genetic drift, selection and population structure. When a species is reproductively isolated into multiple groups by geography or other means, the groups differentiate over time in their average genetic make-up.

Anatomically modern humans first appeared in eastern Africa about 200,000 years ago. Some members migrated out of Africa by 50,000 years ago to populate Asia, Australia, Europe and eventually the Americas. **During this period, geographic barriers separated humanity into several major groups, largely along continental lines, which greatly reduced gene flow among them. Geographic and cultural barriers also existed within major groups, although to lesser degrees.**

This history of human demography, along with selection, has resulted in complex patterns of genetic diversity. The basic unit of this diversity is polymorphisms — specific sites in the genome that exist in multiple variant forms (or alleles). Many polymorphisms involve just one or a few nucleotides, but some may involve large segments of genetic material. The presence of polymorphisms leads to genetic diversity at the individual level such that no two people's DNA is the same, except identical twins. The alleles of some polymorphisms are also found in significantly different frequencies among geographic groups. An extreme example is the pigmentation gene SLC24A5. An allele of SLC24A5 that contributes to light pigmentation is present in almost all Europeans but is nearly absent in east Asians and Africans.

Given these geographically differentiated polymorphisms, it is possible to group humans on the basis of their genetic make-up. Such grouping largely confirms historical separation of global populations by geography. Indeed, a person's major geographic group identity can be assigned with near certainty on the basis of his or her DNA alone (now an accepted practice in forensics). There is growing evidence that some of the geographically differentiated polymorphisms are functional, meaning that they can lead to different biological outcomes (just how many is the subject of ongoing research). These polymorphisms can affect traits such as pigmentation, dietary adaptation and pathogen resistance (where evidence is rather convincing), and metabolism,

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For most biological traits, genetically based differentiation among groups is probably negligible compared with the variation within the group. For other traits, such as pigmentation and lactose intolerance, differences among groups are so substantial that the trait displays an inter-group difference that is nontrivial compared with the variance within groups, and the extreme end of a trait may be significantly over-represented in a group.

Several studies have shown that many genes in the human genome may have undergone recent episodes of positive selection — that is, selection for advantageous biological traits. This is contrary to the position advocated by some scholars that humans effectively stopped evolving 50,000–40,000 years ago. In general, positive selection can increase the prevalence of functional polymorphisms and create geographic differentiation of allele frequencies.

Link to Abstract

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