

## ETHICS WATCH

### Genetics and social identity after the HapMap

Phase I of the [International HapMap Project](#) (HapMap) is now complete, and an analysis of its findings is being published<sup>1</sup>. Unlike the [Human Genome Project](#)'s signature message that all individuals have a 99.9% genetic similarity, HapMap will deliver a more mixed message about human genetic variation to scientists as well as the public:

that there are common variants that are found across populations, and that there are differences in frequencies of those variants and in genomic structures (such as linkage disequilibrium) between populations.

Although these two messages were evident even in the pre-sequence era, population-specific patterns of variation clearly will become a more significant aspect of genomics in the post-HapMap era, as will the social implications of that enhanced focus. HapMap might fuel the continuing debate about the biological relevance of group identities. Some participants in the debate have argued that differences in frequencies of genetic variants between groups make a relatively small contribution to the health disparities that are associated with social identities, and have been concerned about the adverse implications of designing genetic studies that explicitly make population and ancestral comparisons<sup>2</sup>. Others have argued that population-specific variants make significant contributions to understanding differences in the expression of complex traits, and have been concerned about the adverse scientific implications of ignoring social identities that serve as proxies for ancestry<sup>3</sup>.

Each perspective in this debate, which in the United States has focused on the biological meaning of race, emphasizes only one of the above messages.

The prospect of significant investments in infrastructure to support large-scale, population-based association studies (including prospective cohorts) presents the opportunity for a more nuanced framing of genetic variation research, one that could help to reduce potential damage to groups by educating both scientists and the public about the relationship between genetics and social identities.

The question is whether a middle ground can be established in what has become a polarized argument, in which both sides have conflated scientific and social issues. Categorizing individuals by identity, ancestry, locality, lifestyle or genetic markers (among other criteria) can be useful (and sometimes necessary) for biomedical research as well as clinical treatment<sup>4</sup>. However, those who are anxious to argue against the biological basis for race, for example, often make the mistake of denying the potential for racial and other social categories to be biologically informative. At the same time, treating any of these selectively defined categories as natural or fundamental ways of grouping individuals can have obvious adverse implications, both in scientific and social senses. Therefore, those who insist on maintaining racial and ethnic categories in biomedical research, for a contrasting example, often make the mistake of exaggerating claims for their genetic uniqueness and determinism, which only perpetuates practices that advantage one group over another.

We are at the beginning of an era in which genetic variation will become increasingly important in biomedical research and clinical treatment owing to theoretical and technological innovations in genomics. The challenge is to make similar innovations in how we frame that genomic information in the context of contingent social identities.

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#### URLs for web

**Human Genome Project:** [http://www.ornl.gov/sci/techresources/Human\\_Genome/home.shtml](http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml)  
**International HapMap Project:** [www.hapmap.org](http://www.hapmap.org)

**REFERENCES** <sup>1</sup>The International HapMap Consortium. A haplotype map of the human genome. *Nature* **437**, 1299–1320 (2005) | <sup>2</sup>Stevens, J. Racial meanings and scientific methods: changing policies for NIH-sponsored publications reporting human variation. *J. Health Polit. Policy Law* **28**, 1033–1087 (2003) | <sup>3</sup>Risch, N., Burchard, E., Ziv, E. & Tang, H. Categorization of humans in biomedical research: genes, race, and disease. *Genome Biol.* **3**, 1–12 (2002) | <sup>4</sup>Bamshad, M. Genetic influences on health: does race matter? *J. Am. Med. Assoc.* **294**, 937–946 (2005)