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# Race and Ethnicity in the Genome Era

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## *The Complexity of the Constructs*

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*The vast amount of biological information that is now available through the completion of the Human Genome Project presents opportunities and challenges. The genomic era has the potential to advance an understanding of human genetic variation and its role in human health and disease. A challenge for genomics research is to understand the relationships between genomics, race, and ethnicity and the implications of uncovering these relationships. Robust and scholarly discourse on the concept of race and ethnicity in genomic research should be expanded to include social and behavioral scientists. Interdisciplinary research teams are needed in which psychologists, as well as other social and behavioral scientists, work collaboratively with geneticists and other natural scientists.*

**W**ith the completion of the Human Genome Project, we have entered the “Genome Era,” a new frontier in science. The mysteries of knowing the genome have just begun to unravel. This era provides great promise for human health, but it also provides the potential for misunderstanding genomic information relating to disease, behavior, and human traits. One area that is particularly controversial is how the expanding scientific understanding of human genetic variation relates to the concepts of race and ethnicity.

This article provides us an opportunity to share with the readers of *American Psychologist* information about the Human Genome Project and genomics research as they relate to race and ethnicity. We propose several research areas that we believe are particularly important for the field of psychology as the genome era moves forward. As with all disciplines, genomics has its own jargon and terminology. A glossary of terms is included to assist the reader (see Table 1).

### **The Human Genome Project**

The ambitious goal of the Human Genome Project was to develop detailed genetic and physical maps of the human genome and determine the complete nucleotide sequence of human DNA (National Research Council [NRC], 1988). The idea to sequence the entire human genome was first proposed in discussions at scientific meetings organized in 1984 (Sinsheimer, 1989) and 1986 (Palca, 1986). A committee appointed by the NRC endorsed the concept in its 1988 report (NRC, 1988). In 1988, Congress appropriated funds to the Department of Energy (DOE) and the National

Institutes of Health (NIH) to begin planning the Human Genome Project. The planners established a 15-year time frame for completion of the project and an estimated price of \$3 billion. On October 1, 1990, the Human Genome Project officially began in the United States, though the project was international from the start, involving scientists from the United Kingdom, Germany, France, Japan, and China (U.S. Department of Health and Human Services & DOE, 1990).

On April 14, 2003, the Human Genome Project was pronounced complete, two years prior to the projected completion date and \$400 million under the budget estimates developed at the beginning of the project. The International Human Genome Sequencing Consortium, the group working on the project, had completed a “high-quality, comprehensive sequence of the human genome” (Collins, Green, Guttmacher, & Guyer, 2003), providing a powerful tool for understanding human biology and disease. Already, scientists have used this data to identify genes associated with many complex diseases, such as breast cancer, colon cancer, prostate cancer, and diabetes (see Florez, Hirschhorn, & Altshuler, 2003).

### **Ethical, Legal, and Social Implications of Genomic Research**

The importance of investigating the ethical, legal, and social implications of genomic research was recognized from the inception of the Human Genome Project. In its 1988 report, the NRC asserted the following:

Whatever its scientific merits, a concerted effort to map and sequence the human genome would have profound social significance. Human beings are fascinated with the reasons we are what we are, both for what those reasons tell us about ourselves and for the insights they give us into those around us. (p. 100)

To address these issues, the Ethical, Legal, and Social Implications (ELSI) Research Program was established in 1990 as an integral part of the Human Genome Project. The

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**Table 1**  
*Glossary of Terms*

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- Allele frequency:** The prevalence of a particular allele in a given population.
- Alleles:** Alternative forms of a single gene that differ in sequence or function.
- DNA (deoxyribonucleic acid):** The chemical inside the nucleus of a cell that carries the genetic instructions for making living organisms.
- Founder effect:** Variation of genetic drift, occurring when a few individuals separate from a larger population and establish a new group that is isolated from the original population, resulting in altered allele frequencies in the new population.
- Gene:** The functional and physical unit of heredity passed from parent to offspring. Genes are pieces of DNA, and most genes contain the information for making a specific protein.
- Genetic drift:** Unpredictable, chance fluctuations in allele frequency over time that have a neutral effect on the ability of a population to thrive and reproduce.
- Genetics:** The study of genes and their effects.
- Genome:** All the DNA contained in an organism or a cell, which includes both the chromosomes within the nucleus and the DNA in mitochondria.
- Genomics:** The integrated study of the functions of genes, their regulatory signals, and their interactions with the environment and other genes.
- Genotype:** The actual variations of genes present in an individual.
- Genotype frequency:** The proportion of total individuals in a population that are of a particular genotype.
- Haplotype:** A cluster of single nucleotide polymorphisms (SNPs), located near each other on a chromosome, that are inherited together.
- HapMap Project:** An international research project to chart human genetic variation by identifying and mapping haplotypes.
- Human Genome Project:** An international research project to map each human gene and to completely sequence human DNA.
- Mutation:** An alteration in the genetic sequence.
- Nucleotide:** One of the structural components, or building blocks, of DNA and RNA. A nucleotide consists of a base (one of four chemicals: adenine, thymine, guanine, and cytosine) plus a molecule of sugar and one of phosphoric acid.
- Phenotype:** The observable traits or characteristics of an organism—for example, hair color, weight, or the presence or absence of a disease. Phenotypic traits are not necessarily genetic.
- Protein:** A large complex molecule made up of one or more chains of amino acids, made from the sequence(s) of one or more genes. Proteins are required for the structure, function, and regulation of the body's cells, tissues, and organs.
- Selection:** A process that progressively eliminates individuals whose fitness is low, leaving individuals of higher fitness to survive and generate offspring.
- SNP (single nucleotide polymorphism):** A common variation of a single nucleotide at a particular point in the genetic sequence. SNPs occur in human DNA at a frequency of one every 1,000 bases. Pronounced "snip."

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*Note.* The following sources were helpful in compiling these terms: Hartwell et al. (2000); Lewin (2000); National Human Genome Research Institute [NHGRI], (n.d.). For NHGRI's "Talking Glossary of Genetic Terms," see [www.genome.gov/glossary.cfm](http://www.genome.gov/glossary.cfm)

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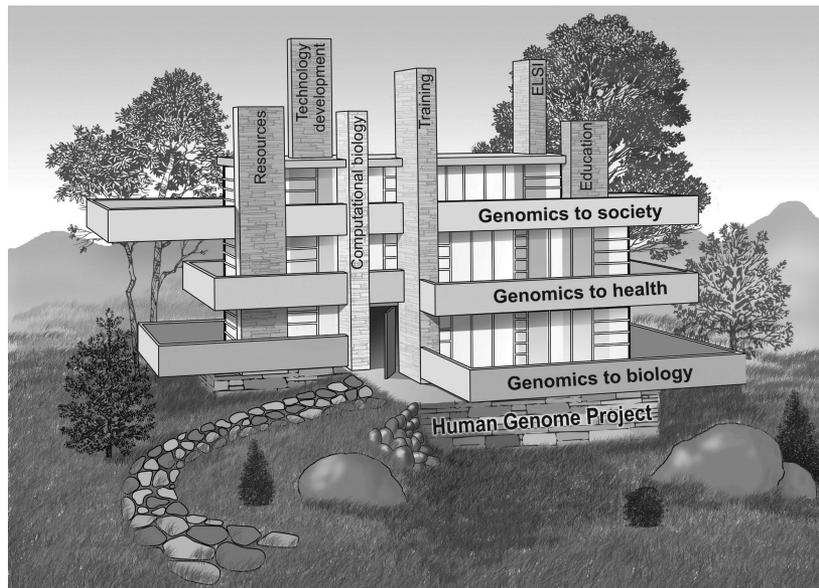
ELSI program provided a new approach to identifying, analyzing, and addressing the ethical, legal, and social implications of human genetics research in parallel with the basic science research.

The ELSI program for the Human Genome Project has assisted in the development of scholarship on important issues regarding genomic research; the use and interpreta-

tion of genetic information; the clinical integration of genetic advances; and the education of researchers, health professionals, and the public. For example, researchers funded through the National Human Genome Research Institute's (NHGRI) ELSI program have investigated the utility of various counseling strategies for breast cancer risk, the ethical and social issues in conducting genetics

## Figure 1

*The Future of Genomics Research Involves Applications to Biology, Health, and Society and Rests on the Foundation of the Human Genome Project*



Note. Reprinted from "A Vision for the Future of Genomics Research," by F. S. Collins, E. D. Green, A. E. Guttmacher, and M. S. Guyer, 2003, *Nature*, 422, p. 836.

research within indigenous populations, the societal impact of human genetic engineering, and the stigma of having a genetic disease (see [www.genome.gov/10001798](http://www.genome.gov/10001798)). The ELSI program provided an innovative model for directly linking the pursuit of a scientific program with the study of the ethical, legal, and social implications of the research and its outcomes. Similar programs have been launched by other NIH institutes (see [www.niehs.nih.gov/envgenom/elsi.htm](http://www.niehs.nih.gov/envgenom/elsi.htm) and [www.niehs.nih.gov/nct/elsi.htm](http://www.niehs.nih.gov/nct/elsi.htm)), and the value of considering scientific initiatives in parallel with their ethical ramifications for society has been echoed in other disciplines and countries (see [http://elsi.issp.sinica.edu.tw/about01\\_english.htm](http://elsi.issp.sinica.edu.tw/about01_english.htm)) (Roco & Bainbridge, 2001).

Today, NHGRI commits more than \$20 million annually from its budget to ELSI research, making NHGRI the largest supporter of research into the ethical, legal, and social implications of genetic research in the United States.

### The Future of Genomics Research

In conjunction with the completion of the Human Genome Project in April 2003, NHGRI published a vision for the future of genomics research (Collins et al., 2003). Informed by two years of scientific and public input through discussions, workshops, and individual consultations, the vision is meant to be an ambitious, inclusive set of challenges for the field of genomics.

This vision for genomics research is structured around a framework of three major themes—genomics to biology,

genomics to health, and genomics to society—and six crosscutting elements. The building in Figure 1 is a metaphor for the future of genomics research, built upon the foundation of the Human Genome Project. The future will involve using the findings of the Human Genome Project to advance an understanding of the structure and function of the human genome, to improve health, and to promote the use of genomics to maximize the benefit and minimize the harm of its applications within society.<sup>1</sup>

### Understanding Human Genetic Variation

One research challenge within the "genomics to biology" theme is the need to develop detailed information regarding heritable variation in the human genome. Although the vast majority of human genetic information is identical in all people, each individual's genetic code does differ slightly. Genomic researchers have found that any two human individuals are approximately 99.9% the same genetically, and it is hypothesized that the most important genetic material for human functioning is encompassed in that shared set. The 0.1% difference, although comparatively

<sup>1</sup> We recommend to the reader "A Vision for the Future of Genomics Research," by Collins et al. (2003), who present this blueprint for research in the genomic era. The text of this document can also be found at [www.genome.gov/1107524](http://www.genome.gov/1107524).

small, represents about three million differences between individuals' DNA. Whereas most of those differences probably have no effect on phenotype, a small fraction (perhaps about 200,000 common variants) are responsible for the genetic component of the differences in health, behavior, and other human traits (Cargill et al., 1999; Halushka et al., 1999; Li & Sadler, 1991; Wang et al., 1998).

To date, most genetics research has sought to correlate alterations in specific sections of DNA with defined phenotypic traits. Some phenotypic traits may be attributable to a single gene. Disorders that result from mutations in a single gene are considered single-gene disorders. However, the vast majority of phenotypic traits (including pharmacogenetic variability and the manifestation of common diseases) result from a complex interplay among multiple genetic and nongenetic factors (Goldstein, Tate, & Sisodiya, 2003; King, Rotter, & Motulsky, 1992). Although research thus far has produced great advances in the realm of single-gene disorders, resources for the identification and analysis of genetic variation within the human genome will need to be developed and made broadly available to the scientific community in order to decipher the more common complex interactions (Collins et al., 2003).

The International HapMap Project (International HapMap Consortium, 2003) is a major new initiative that is currently exploring the nature of genetic variation across all the human chromosomes. The International HapMap Consortium, the project's research group, is composed of scientists and organizations from the United States, the United Kingdom, Canada, Nigeria, China, and Japan. The investigators are studying collective human genetic variation through a set of 270 DNA samples derived from northern and western Europe (U.S. residents living in Utah), East Asia (Japanese in Toyko and Han Chinese in Beijing, China), and West Africa (Yoruba in Nigeria). Through these efforts, more than half of the common DNA variants in the human species have already been discovered and placed in public databases. In addition, the HapMap project is determining how these variants correlate with their chromosomal neighbors. These correlated blocks of genetic variation are called *haplotypes*.

### **What Do We Believe We Know About the Relationship of Race, Ethnicity, and Genetics?**

Scientists have long been interested in human genetic variation. Human racial classification became a focus of scientific investigation by evolutionary biologists attempting to categorize individual humans on the basis of presumed patterns of biological difference. In the 18th century, scientists hoping to categorize humans taxonomically in the same way that they categorized other species asserted that all humans belonged to four (Linnaeus, 1758) and then five (Blumenbach, 1795) groups. These scientists attached hierarchical designations to these categorizations, claiming that differences in skin color, physiognomy, and geography were associated with scientifically measurable differences in character, aptitude, and temperament (Smedley, 1998). Studies supporting these claims have since been refuted as

severely flawed (Gould, 1981). Yet, in descriptions of human genetic variation, categorization of humans by "racial" and "ethnic" groups continues. Researchers must remain mindful of this historical legacy of the science of heredity as the genomic era unfolds.

Current genetic data also refute the notion that races are genetically distinct human populations. There are no gene variants that are present in all individuals of one population group and in no individuals of another. No sharp genetic boundaries can be drawn between human population groups. However, *frequencies* of genetic variants and haplotypes differ across the world.

The vast majority of common genetic variants present today existed in our common ancestral pool. This is not surprising, given the relative recency of the migration of humans out of Africa and the continuous exchange of DNA between populations. Trade, war, and exploration led to well-documented travel among peoples geographically distant from one another as far back as the Middle Ages, if not earlier (Smedley, 1999). However, because of evolutionary forces, such as genetic drift, founder effect, and selection, the frequencies of some genetic differences are not constant in all populations throughout the world. For example, certain versions of Class I alcohol dehydrogenase (ADH) genes that have been associated with a lower likelihood of alcoholism appear to exist in higher frequency in eastern Asian populations than in European or African populations (Osier et al., 2002).

In addition, because of our evolutionary past, variation itself is not spread evenly among population groups. Anthropological and genetic evidence strongly suggests that a small subset of the individuals in Africa some 30,000–50,000 years ago migrated in one or more waves out of northern Africa to subsequently populate the rest of the world (Cavalli-Sforza & Feldman, 2003; Goldstein & Chikhi, 2002; Jorde, Bamshad, & Rodgers, 1998; O'Rourke, 2003; Stringer, 2001). The genetic variation within that subset was smaller than that of the entirety of Africa, and that is reflected in today's patterns of genetic variation. There is greater genetic variation among African populations than there is in the rest of the world (Tishkoff & Verrelli, 2003; Watkins et al., 2003).

Still, researchers using new technologies have shown that DNA variation measured in humans from across the globe can be used to roughly categorize individuals into clusters based on the similarity of certain sections of their genetic code (Risch, Burchard, Ziv, & Tang, 2002; Rosenberg et al., 2002). Those categories—labeled by Risch and his colleagues as Africans, Caucasians, Pacific Islanders, East Asians, and Native Americans—loosely correspond to the social categories of race (Risch et al., 2002; Rosenberg et al., 2002). It should be noted, however, that these findings only result if one starts with individuals whose recent ancestors all derive from one geographic area—and of course that does not apply to an increasing proportion of individuals. It should also be noted that the number of "groups" is subject to the analysis of the data and the geographic areas of the world that are sampled. Human

genetic variation is a continuum across the world (Serre & Pääbo, 2004).

Race and ethnicity are complex sociopolitical constructs. They are variable and fluid, changing over time and differing throughout the world (see, e.g., Harris, Consorte, Lang, & Byrne, 1993; Jacobson, 1998; Snowden, 1983). How can researchers reconcile what may at first blush seem contradictory claims?

### ***The Series of Weak Correlations***

The real connections between genetic variation and self-identified race travel through several intermediate steps. It is true that variation in specific genes can increase the likelihood of developing certain diseases and/or human traits. These are not deterministic “DNA oracles,” however—the role of the environment is extremely important for nearly all behaviors and common diseases, and gene–environment interactions are complex and dynamic. As a result, the presence of specific susceptibility genes is far from a perfect predictor of the true probability of experiencing a given illness or exhibiting a given trait.

At the present time, most of the specific gene variants involved in particular traits have not yet been discovered (Collins et al., 2003). However, researchers do have the tools with which to study variation across the entire genome in a set of individuals and to try to correlate that with health outcomes. Variation across the genome, in turn, can correlate with ancestral geographic origin, but this correlation is far from perfect. Ancestral geographic origins, in turn, correlate to some degree with self-identified race or ethnicity, but as noted earlier, this relationship is blurry and context dependent. So when it comes to the relationship between self-identified race and the genetic contribution to the likelihood of developing a disease or a given trait, self-identified race is a surrogate for ancestral geographic origin, which is a surrogate for variation across the genome, which is a surrogate for variation in disease-relevant alleles, which is a surrogate for individual disease risk (Collins, 2004).

### ***The Current Interdisciplinary Conversation***

An interdisciplinary conversation on issues of race, ethnicity, and genetics is beginning to occur. A number of researchers have published articles in which they discuss and debate the value of the use of the concept of self-identified race in genomics research (Bamshad & Olson, 2003; Bamshad, Wooding, Salisbury, & Stephens, 2004; Burchard et al., 2003; Cooper, Kaufman, & Ward, 2003; Kittles & Weiss, 2003; Phimister, 2003). Others have asserted the need for clarity of definitions of terms used to categorize populations in human genetic variation studies (Sankar & Cho, 2002). A number of meetings have been held in the last two years that have brought scientists, policymakers, and the public together to begin a broader conversation on these important issues (e.g., American Anthropological Association, 2004; Michigan Center for Health Disparities, 2004; National Human Genome Center, Howard University, 2003; Stanford Center for Biomedical Ethics, Stanford School of Medicine, 2003). The NHGRI also held a round-

table in March 2004 that brought together approximately 35 external scholars, researchers, and scientists from various disciplines to discuss the current knowledge on race, ethnicity, and genomics; the future research directions needed; and science policy development.

## **The Need to Engage Psychosocial and Behavioral Researchers**

One finding of these meetings is the need for an expanded interaction between geneticists and social and behavioral science researchers. Geneticists continue to forge ahead, investigating the genetic component of disease, treatment response, and behavioral traits. Yet as a group, they are not trained to investigate the psychosocial impact of their research. Biomedical research needs psychologists and other social and behavioral researchers to play an essential role in understanding the genetic component of behavioral traits. Genomic research aims to tease apart the complex interaction of genes and environment, yet geneticists as a whole do not possess the expertise to measure much of the environmental component. The ability to improve health depends on the involvement of researchers who do possess this expertise.

Interdisciplinary research teams are needed in which psychologists, as well as other social and behavioral scientists, work collaboratively with geneticists and other natural scientists to ask the right research questions, assess the right variables in the right ways, and conduct methodologically rigorous studies. We believe that research teams spanning the disciplines will generate extremely valuable knowledge in the years to come.

Researchers have demonstrated the association of certain genes with schizophrenia (Berry, Jobanputra, & Pal, 2003), depression (Ryu et al., 2004), panic disorder (Lam et al., 2004), attention-deficit/hyperactivity disorder (Acosta, Arcos-Burgos, & Muenke, 2004), alcoholism (Dick & Froud, 2003), and autism (Bespalova & Buxbaum, 2003), among others. Researchers are also beginning to search for the genetic underpinnings of more controversial behavioral characteristics, such as novelty seeking (Benjamin, Patterson, & Greenberg, 1996; Ebstein et al., 1996), aggression (Mikics, Kruk, & Haller, 2004), sexual orientation (Bupree, Mustanski, Bocklandt, Nievergelt, & Hamer, 2004), monogamy (Lim, Hammock, & Young, 2004), and antisocial behavior (Caspi et al., 2002). This research is in its infancy, and few gene variants have been validated in humans as influencing these characteristics. To make clinical use of this information requires much more than the association of a particular gene with a particular behavioral trait or disease. These studies, and their potential findings, have many social implications and implications for clinical psychology that deserve study. In this area, especially, interdisciplinary research collaborations will enhance the rigor of the research, the development of the scientific questions, and the generation of valuable knowledge.

Social and behavioral scientists also have an important role to play in the investigation of how discoveries in human genetics will ultimately affect conceptualizations of

the constructs of race and ethnicity. Already, research on human genetic variation is affecting society in new ways. For example, some researchers (Shriver et al., 2003) and genetic ancestry services (African Ancestry, 2003) maintain that they can provide a statistical prediction of the geographic ancestry of any genetic sample, even if the ancestry of that individual is complex. The emergence of such genetic ancestry companies, some of which seem to claim a level of precision in defining ancestry that is incompatible with current knowledge of population genetics, raises new questions for the social and psychological implications of an understanding of identity, ancestry, ethnicity, and race (Shriver & Kittles, 2004). Research is needed to study the social and psychological implications of social identity that is based on the estimation of personalized genetic histories. For example, social and behavioral scientists are needed to investigate how information about human genetic variation and race is communicated by the media, pharmaceutical companies, and scientists, and how such information is received by the public.

As genomic studies advance understandings of human traits, disease risks, and health outcomes, the scientific community must guard against the potential societal harm this young science may bring. Poorly designed research or even the poor communication of well-designed research must be avoided, as either misrepresentation may oversimplify or inflate the role of genetic factors. Such indiscretions can significantly increase the potential of this research to stigmatize populations and/or individuals (Foster & Sharp, 2003; Greely, 2001; Juengst, 1998; Lee, Mountain, & Koenig, 2001). It is therefore important, especially when using race and ethnicity as variables in behavioral genetics research and as factors in clinical decision-making, that one recognize their fluidity, imprecision, and extremely indirect connection to human genetic variation.

This research must continue to be expanded in order to fully engage the social and behavioral science research communities. There are many important research questions that psychology and behavioral genetics researchers are poised to address. We believe those important questions include the following:

1. What are the implications, for both individuals and society, of uncovering any genomic contributions that there may be to traits and behaviors?
2. How do individuals understand the genetic risks of disease? What influence does such understanding have on behavioral change?
3. What is needed to train behavioral science researchers to take full advantage of the new and powerful tools of genomics to study human genetic variation contributions to human traits and behaviors? What is needed to train behavioral science researchers to study the implications of these findings?
4. What is needed to form collaborative, interdisciplinary research teams among social, behavioral, and genomic scientists?
5. How should researchers most appropriately use the concepts of race, ethnicity, and ancestry as research vari-

ables in the study of the genomic contribution to human traits and behavior?

6. How do natural and social scientists communicate complex topics of human genetic variation in a racialized society, and how should those topics be communicated?

Although rapid progress is being made in understanding the human genome, the intersection of genomics and psychology is just beginning to be explored. We remain optimistic about the benefits that genomic advances will provide for those suffering from psychological disorders, and there is good reason to believe that the incorporation of genomics into behavioral research will generate new insights and avenues of investigation. While retaining this enthusiasm, we remain wary of the abuses of the past and the potential for genomic research to harm those who have historically been most vulnerable. We hope that by forging ahead with scientifically rigorous research and accompanying that research with deep inquiry into social, ethical, and legal implications, the promise of genomics will become a reality for all peoples.

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