mechanisms that differentiate healthy from disease states. In that regard, those nonhuman primate species that are used extensively as models in biomedical research offer many more opportunities for scientific advancement through gene expression studies than do chimpanzees.

Regarding the goal of defining the genetic changes that underlie human uniqueness, it is not only peripheral to the NIH mission but also is not well served by a sequencing-first approach. Most sequence differences between humans and chimpanzees will be functionally neutral, and simple comparison of sequences will not identify the few functional changes among the large number of neutral substitutions.

We urge the National Human Genome Research Institute (NHGRI) and the National Center for Research Resources to consider carefully the scientific value of sequencing the chimpanzee genome by comparison with investing equal resources in supporting gene expression research and developing detailed gene maps of nonhuman primates that are extensively used in biomedical research. The potential health benefits of these research activities in well-characterized, widely-used Old World monkey models will be much greater than those obtained from sequencing the chimpanzee genome.

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Response

In our original letter we presented the arguments in favor of a primate genome project and suggested that the project should focus both on the chimpanzee, because it is our closest evolutionary relative, and on one of the well-studied Old World monkeys, which would be more suitable for experimental purposes and for studies of gene expression. Thus, we have a substantial area of agreement with VandeBerg and colleagues. However, we disagree with their statement that "a focus on chimpanzee genomics would have little impact on future opportunities and progress in biomedical research." The potential relevance of chimpanzee genome data for understanding such diseases as AIDS, Alzheimer's, malaria, and others has been presented elsewhere (*1*).

VandeBerg and colleagues also say that "the goal of defining the genetic changes that underlie human uniqueness [is] peripheral to the NIH mission." This implies that the genes involved in human uniqueness are never involved with human disease, a highly unlikely assumption. For example, genes that underlie bipedal locomotion may be involved in many malfunctions of the musculoskeletal system, and genes that mediate specific aspects of human cognition are likely to be involved in mental illness. In general, it will not be possible to separate genomic information relevant to human evolution from that relevant to human disease. The close similarity of the chimpanzee and human genomes also increases the likelihood of finding disease-related differences quickly. Furthermore, any genomic differences found between Old World monkeys and humans will be easier to interpret if the corresponding regions of the chimpanzee genome are also available.

We did not mean to imply that a primate genome project should begin with or be limited to total sequencing of the chimpanzee genome. Our hope is that NHGRI (and other funding agencies in the United States and elsewhere) will consider a variety of approaches to primate genomics that may advance our understanding of human genetic function in health and disease. Suggestions such as those made by VandeBerg and colleagues will contribute to the decisions that must be made by the administrators of the funding agencies. The main purpose of our letter was to emphasize the need to give high priority to genomic studies on primates, rather than limiting comparative genomics to nonprimate mammals in the immediate future.

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Transgenic Crops in China

In his News Focus report entitled "Asia gets a taste of genetic food fights" (25 Aug., p. 1279), Dennis Normile states that in China there are four transgenic crops (six varieties) in commercial cultivation and five transgenic crops in field trials or in development, but this is not so.

In China, the study of transgenic crops began in the early 1990s; the first field trial of a transgenic crop occurred in 1994. Up to now, there are three transgenic crops (cotton, tomato, sweet pepper) and 12 varieties in commercial cultivation (*1*), eight of which are transgenic cotton varieties (*2*). There are seven crops

TRANSGENIC CROPS IN CHINA* (1)

Commercial cultivation	Environment release	Field trials
Cotton (eight varieties)	Cotton (at least 15 other varieties)	Cotton (more than 20 other varieties)
Sweet pepper (three varieties)	Maize	Rice
Tomato (one varieties)	Tomato	Tobacco
	Potato	Peanut
	Rice	Casaba
	Poplar	Chinese cabbage
	Tobacco	Sweet potato

*Authorized by the Office of Agricultural Biological Genetic Engineering Safety Administration of the Ministry of Agriculture of China (OFABGESA).

in environment release, seven crops in field trials (*1*), and at least 20 other crops in development.

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Unite Efforts and Conquer Mysteries of Artificial Genetics

In his News Focus article "Creation's seventh day" (14 Jul., p. 232), Robert F. Service highlights some recent work in artificial genetics, emphasizing the controversy that might surround "a new life form" and the distinctive personalities of some scientists who have taken up the challenge. Entertaining reading, of course, but amid the discussion of personalities it remains most important to identify ways that artificial genetics might change the landscape of science. Here are just two.

First, why is it so difficult to move in vitro artificial genetics into a living cell? Buried in this question are the mechanisms by which living systems achieve precision when precision is important—in particular, in DNA replication (*1, 2*). Efforts to implement artificial genetics show that we understand far less about the enzymology and chemistry of precision than we thought (*2*), especially where DNA is involved. Second, since the Enlightenment, science has divided itself into two traditions, one from natural history, the other known as "physical science." Explanations in natural history use models of the past, consistent with physical laws, but not determined by them. Physical science explanations use universal models of atomic structure or mathematics. The two traditions are often adversarial in the culture, in academic departments, and (consequently) in education. Research in artificial genetics shows that if these two traditions can be joined, the combination has great power (*3*). For example, precision in biology will be better understood when we understand the history through which precision evolved. But only a few U.S. research laboratories have the advantage of moving smoothly from geology to evolution to chemistry to informatics. How should we join these traditions? A challenge, for sure.

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