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• **LETTERS****A Primate Genome Project Deserves High Priority**

The initial goals of the Human Genome Project (HGP), to sequence the human genome and identify its constituent genes, are on the verge of being achieved. However, the scientific community recognizes that sequencing must be followed by understanding the manifold functions of human genes throughout the life-span, in health and in disease. In a *Science* interview (News Focus, 31 Mar., p. 2396), Francis Collins acknowledged this by saying, "Understanding what the sequence means will require us to make multiple comparisons....The arguments are quite strong for sequencing other mammals besides human and mouse...and for doing another primate."

In our opinion, one or more primate genomes should receive the highest priority (1, 2). An obvious candidate would be the chimpanzee genome, because it is more than 98% identical to the human genome (3). Because monkeys are much more appropriate for experimental purposes than apes, the genome of at least one of the commonly studied Old World primates should also be given high priority, for example, the rhesus macaque.

There are three fundamental reasons for analyzing primate genomes. First, we cannot fully understand human genome function until we have identified genetic features that underlie uniquely human anatomical, physiological, behavioral, and cognitive characteristics. To identify uniquely human aspects of gene structure and expression requires comparative data on related species. The mouse genome project will help, but analysis of rodent genomes can never tell us why we are not apes.

Second, there are compelling biomedical reasons for detailed comparisons with the chimpanzee genome (4). Several diseases differ in frequency and severity between chimpanzees and humans, including AIDS, Alzheimer's, cancer, and malaria. Understanding the genetic factors underlying these differences will help elucidate the etiology of such diseases and potentially increase our ability to control or cure them. There are also striking differences from human reproductive biology in apes (4), the genetic basis of which may help in understanding some major human reproductive disorders (4, 5). Finally, the enormous differences in cognitive abilities between humans and apes must also have a fundamental genetic basis, notwithstanding the powerful influence that environmental factors have on the realization of genetically defined potential. Comparative data on the genetic factors that influence behavior and cognition will help elucidate normal brain functions as well as mental illness in humans.

Third, there is an urgent need to provide better protection for wild populations of primates, especially the great apes, and to optimize conditions under which captive apes are maintained. If the HGP officially embraces a primate genome project, public awareness of the close evolutionary relationship between humans and other primates will improve. An increase in ethically appropriate studies on basic aspects of ape anatomy, physiology, and development (6) might also be a likely outcome, which would favorably impact both research and conservation programs. Of course, as with the HGP, a primate genome project must be accompanied by careful consideration of all relevant ethical, legal, and social issues.

We conclude that detailed analysis of one or more primate genomes is essential to full accomplishment of the overall goals of the HGP. We hope that the National Human Genome Research Institute will begin such studies in the immediate future, while also exploring potential collaborations with biotechnology companies, who may be independently interested in comparative primate genomics (7). The recent announcement of a Japanese project to compare gene expression in chimpanzees and humans (8) suggests that an international strategic plan should be developed to minimize redundancy and maximize information that should become a globally available public resource.

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