

Great Ape Phenome Project?

We applaud the notion recently highlighted by Ann Gibbons (News Focus, 4 Sept., p. 1433) about "Pushing a primate genome project." There is much to be learned by comparing human genomic sequences with those of other primates, particularly those of our closest evolutionary cousins, the great apes. This information can also be obtained by noninvasive methods that would not harm these individuals. However, part of the value of the Human Genome Project lies in interpreting genomic data in the context of the large body of existing information about humans, ranging from the biochemistry of cells to the physiology of organ systems to the functional output of complex systems like the brain. In contrast, the corresponding information about the great apes is limited. We suggest that the funding of such a Great Ape Genome Project should be complemented by a "Great Ape Phenome Project," which would support comparative studies of humans and apes at all levels, from expression patterns of messenger RNA, to biochemistry and cell biology, all the way to neural systems and cognitive functions. Not to do so would be like funding the Human Genome Project without supporting much of the rest of the National Institutes of Health. Indeed, with the exception of gross deletional or nonsense mutations, the significance of most genomic sequence differences found between humans and apes will not be obvious unless such a detailed comparative phenotypic database is also available. Notably, such a database could be obtained without undue harm to the primate subjects, with the use of ethical principles similar to those guiding human experimentation. Such a project would also heighten awareness of the urgent need to protect and conserve these endangered hominoids who are so closely related to us.

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