Letters

Animal Research: A Position Statement

The following position statement was recently adopted by the deans of the 13 medical schools that make up the Associated Medical Schools of New York. The statement was drawn up in response to concerns expressed by faculty members over the continuing pressure from extremist groups in the animal rights movement, which has disrupted research in a number of institutions.

The Deans of the Associated Medical Schools of New York reaffirm in the strongest terms the obligation of our institutions to carry on the research programs that have expanded our knowledge of disease and led to life saving therapies. The use of laboratory animals is indispensable to much of this work, and we are gravely concerned that the actions of some organizations espousing an "animal rights" philosophy will threaten the continued progress of biomedical research.

In recent months, we have seen pressure from such extremist organizations disrupt ongoing research projects supported by public funds. Leadership among medical schools and universities must stand firm in the face of this pressure and insist that our institutions fully live up to the obligations they incur when they accept public and private research support.

AMS fully acknowledges that, along with the responsibility to fulfill our research role is the need for stewardship on behalf of those animals which are so vital to this work. All institutions conducting research must enforce appropriate standards for the care and use of laboratory animals. Research centers are currently subject to extensive laws, policies, guidelines and accreditation standards dealing with the use of animals in research.

The documentation of the benefits of such research not only to humankind, but also to animals themselves, is unchallengeable. Our disagreement is not with advocates of appropriate and respectful use of animals in a manner consistent with established guidelines for animal welfare, but with extremists who insist that no circumstances exist under which we can morally differentiate between the worth of the life of a human being and that of an animal. Such a philosophy is out of harmony with the tenets of most religions and codes of behavior in the world, and with the majority view in our society. Moreover, we cannot tolerate tactics of intimidation and violence which undermine our democratic traditions and threaten the principle of free scientific inquiry.

AMS pledges to the faculty in our member institutions that we will use every resource in our command to protect and preserve the right of scientists to pursue knowledge for the good of all people. Animal rights activists, no matter how well intentioned, will not be permitted to subvert the established mechanisms for conduct of responsible animal research and erode our obligations to society as physicians and scientists.

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Genetic and Linguistic Evolution

Richard T. O'Grady *et al.* (Letters, 31 Mar., p. 1651) question our conclusion that there is "considerable parallelism between genetic and linguistic evolution" (*1*, p. 6002). We address several incorrect statements in their comment. The eight points given below follow their numbering system, with additional letters to indicate separate concepts.

1A) We do not use *phenetic* similarity, as O'Grady *et al.* state; we measure *genetic* similarity based on gene frequencies for bona fide genetic polymorphisms. Nothing, short of DNA, is more "indicative of kinship." DNA data anlayzed so far agree (*2*) with our results. Ascertaining historical relationships, however, requires external evidence such as that which we have successfully used (*1*).

1B) Unlike thousands of evolutionary trees published in the past and not tested for statistical error, the validity of our genetic tree has been examined with the use of the bootstrap method (*3*). This new and powerful technique for determining statistical error is a breakthrough in taxonomy and in phylogenetic analysis.

1C) The bootstrap method uses random samples of genes (with replacement). The variation of results automatically tests the acceptability of missing values, enabling us to use many more genes than otherwise possible. The number of genes is of paramount importance for the accuracy of conclusions (*4*).

2A) We never spoke of "races," a concept which, for humans, is devoid of a useful scientific definition.

2B) The pooling method we used is far from arbitrary. Geographic propinquity involves considerable genetic similarity (*5*) as was tested in our results by analysis of variance within groups (*6*).

2C) Proving genetic discontinuity at the geographic level is unnecessary; discontinuity, likely to be rare, is easily erased by recent history.

2D) O'Grady *et al.* assert that we employed very small samples, "sometimes of single individuals." The average sample size for gene frequencies is well above 100 individuals. Small samples are rare and were avoided.

3) We included both "well-supported" linguistic families and those O'Grady *et al.* call "poorly supported" (Amerind, Altaic, Austric, and NaDene). Had we divided, for instance, Greenberg's Amerind family (*7*) according to older taxonomies [even those of the most extreme splitters (*8*), who are the main adversaries of the Amerind phylum], our conclusions would still be valid, for the lower taxonomic units preferred by others are even more clearly contained within the genetic Amerind cluster. The same is true for the other phyla.

4) We noted six exceptions to the rule that every linguistic phylum corresponds to one of the major genetic clusters. These are amply justified by language substitutions (*1*). Major genetic admixtures beween groups are associated with some of these exceptions; as populations speaking different languages merge, genes mix well, while only one language prevails (albeit with some borrowing or the partial survival of another language in some areas).

5) O'Grady *et al.* state, "Only Greenberg's controversial Amerind phylum corresponds with the grouping of individual races within a major cluster." Older genetic clusters are expected to include more than one linguistic phylum.

6) They also state, "Neither of the linguistic superphyla, Nostratic and Eurasiatic, precisely corresponds with the genetic data tree." The union of these two sets, plus Amerind (as discussed previously) (*1*), does so very closely, providing reciprocal confirmation of the two trees.

7A) O'Grady *et al.* measure the agreement between our genetic tree and the linguistic one, finding an undefined and unreferenced "Consistency Index" of 0.48, with unspecified standard error. If it is the index suggested in (*9*), it does not fit quasi-continuous traits such as gene frequencies, but only character states [see, however, (*10*)]. It has been shown that this index is negatively correlated with the size of the tree (*11*), and in our case 0.48 may therefore be a high value.

7B) O'Grady *et al.* write that "the remaining 52% of the association must be attributed to the independent origin of a language in more than one race, or to the replacement of one language by another." Are O'Grady *et al.* serious in suggesting that identical languages can arise independently in different parts of the world?

8A) Why should one expect correspondence between phylogenetic and linguistic relationships? ask O'Grady *et al.* Both the differentiation between languages and that between genes are strongly affected by common factors: (i) time since fission followed by segregation of the relevant populations into geographically separate groups and (ii) extent of residual exchanges between groups after fission. The extent of genetic exchange is correlated with that of cultural (including linguistic) exchange, since geographic, ecological, and even linguistic barriers tend to act similarly on both.

8B) O'Grady *et al.* state that "linguistic relationships reflect a much later period in

human history than the genetic relationships." They do not specify, however, any basis for their belief. Our data provide the first evidence that "much later" translates on average into a factor of 5 or 10. Genetic data indicate that most human linguistic phyla known today must have arisen approximately 25,000 to 8,000 years ago, while Khoisan, Indopacific, and Australian arose perhaps 30,000 to 50,000 years ago. In contrast, modern humans are more than 100,000 years old. While our dates for the origin of linguistic phyla seem more convincing than the few statements in the linguistic literature, they do not necessarily disagree with them.

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Erratum: In Eliot Marshall's article "Bomb factories of the 21st century" (News & Comment, 20 Jan., p. 305), it was erroneously reported that the Department of Energy proposed to close down the Mound Facility in Miamisburg, Ohio. In fact the department suggested shifting all radiation-related work (amounting to 30% of the total) to other sites.

Erratum: In figure 3B (p. 699) of the report "Calicheamicin γ_1^I and DNA: Molecular recognition process responsible for site-specificity" by N. Zein *et al.* (12 May, p. 697), the stereo pair was incorrectly printed and inverted. The correct representation is a mirror image of what was shown.

Agency for International Development

Announcement of
Malaria Vaccine Research & Development
Request for Applications
[RFA-ST/H-89-001]

Background. For more than 20 years, the United States Agency for International Development (A.I.D.) has supported a program of applied research in malaria vaccine development. Currently, the primary research foci of the Malaria Vaccine Research & Development Project include:

—the identification and characterization of malaria parasite antigens, with emphasis on asexual, sporozoite, and liver stages of the parasite by immunochemical and/ or molecular biological methods, for development of vaccine candidates;

—the elucidation of the importance of identified antigens and B-cell and T-cell epitopes in providing a protective immune response in naturally acquired human malaria and in relevant animal models, including appraisals of strain specificity of protective immunity;

—the elucidation of humoral and cellular effector mechanisms of protective immunity to malaria and the development of *in vitro* correlates of protective immunity;

—the modification of the structure and/or mode of presentation of antigens, which have been shown to have a role in protection, in an attempt to increase their ability to induce a protective immune response;

—the testing of vaccine candidates for immunogenicity, safety, and efficacy in appropriate animal models, including non-human primates.

Proposals. A.I.D. is soliciting proposals for Cooperative Agreements describing a program for malaria vaccine research. In general, the range of activities requested in the RFA is as outlined above. However, there is a special interest in proposals whose major emphasis is on development of vaccines that induce responses mimicking natural immunity (*i.e.*, a state characterized by protection from disease but not necessarily from infection) thus allowing restimulation of immunity through natural exposure to parasites. It is the intent of A.I.D. to support 3-year research programs. **Only U.S. institutions are eligible for these grant awards.**

Applications. The American Institute of Biological Sciences (AIBS) will process all applications. **Proposals must be received by September 1, 1989.** The complete RFA and detailed information on the application process may be obtained from:

American Institute of Biological Sciences
1800 North Kent Street (Suite 930)
Arlington, Virginia 22209
fax: 703-527-4404