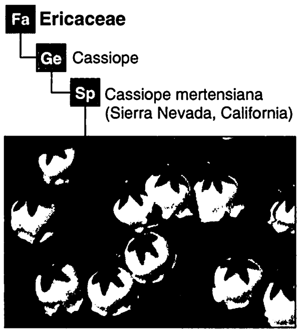
types, including the nascent SIS and existing repositories like the Nature Conservancy's Natural Heritage Network (www.heritage.tnc.org/), as well as the resources indicated in Fig. 1 of our Viewpoint article in the special issue ("Interoperability of biodiversity databases: biodiversity information on every desktop," p. 2313).

We offer three additional observations. First, databases of natural history collections are not static but are constantly updated, as species identifications and phylogenetic relationships are improved and as new specimens are added to the collections. Second, one of the GBIF's major goals is to catalyze the completion of the Catalog of Names of Known Organisms. The catalog will serve biological databases of every type, enabling the SSC's specialist network to make linkages among their own and other databases. And third, it is precisely the long time series and the large samples present in many collections that allow historical trends and population variability to be studied and brought to bear on conservation decision-making. Even if some previous collection sites have disappeared, fuller understanding of historical ranges and habitats can be gleaned from collections. Such insights contribute to wise decisions on how to manage species or habitats.



Specimen data alone are insufficient for making informed conservation decisions. Estimates of current conditions are also needed. Given this proviso, specimen data in large quantities are tremendously useful for making all kinds of biodiversity-related decisions, as evidenced by several recent papers (*1*).

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2. We thank J. Soberon for comments and suggestions.

Smith and his coauthors are right. The interoperability frameworks being developed in biodiversity informatics can link all manner of biodiversity record types and should be available to serve a wide range of biodiversity disciplines, including those of the conservation community. Indeed, applications ranging from germplasm resources to agroforestry and marine biota are already in process, and bringing together information from different sectors within the biodiversity community is itself an important goal. Several programs mentioned in my Viewpoint article ("The quiet revolution: biodiversity informatics and the Internet," p. 2309) and in other articles in the special issue are already under way. One program, Species Analyst, is experimenting with observational and museum records. Another program, Species 2000, will link the conservation, publishing, and germplasm worlds. Such programs will assure that applications will not just focus on historical data. A good example of cross-discipline interoperability is the network of botanic garden, gene bank, wild flora, genetic, and ecological resource systems within the big network of the German agency ZADI (Centre for Documentation and Information in Agriculture).

Smith *et al.* emphasize that a dynamic biodiversity information system on the Internet needs to synthesize information from resources that are themselves kept current and dynamic. Time scales may vary, but it is easy to envision moments when conservation alert systems, germplasm stock catalogs, and museum accessions databases all need to be updated on an immediate day-to-day basis. In other cases, even where the underlying information changes daily, users may not wish for reference systems and standards to be reissued too frequently. Several taxonomic systems are experimenting with fixed annual editions. Whatever the time scale, expectations that "living" systems in all sectors will be continuously updated are important.

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Collaborations Tailored for Bioinformatics Projects

As long-term participants in international collaborative research projects related to biodiversity informatics, we strongly support the activities described in *Science*'s special issue of 29 September and believe that they should be carried out worldwide and that all data should be shared by all countries. Moreover, the collaborations under way should receive more attention, not only technologically, but also conceptually.

The conventional pattern of collaboration—funds come from mainly developed countries and raw data from mainly developing countries—is in need of reform. Many developing countries are willing to contribute to global data systems, but they may also be concerned that without foreign technical assistance their own data systems could not be maintained after completion of the collaborative projects. As an ancient Chinese proverb says, "Give a man a fish and he will eat for a day; teach him how to fish and he will eat for the rest of his days." The availability of core technology and advice rather than money is more important for a successful collaboration between developed and developing countries. We believe that the biodiversity data "fishing expedition" would benefit from attention to this issue.

At present, the establishment of close collaborations between biodiversity scientists in developing countries and more highly trained computer scientists and engineers from developed countries is still a necessary and valuable step during the development phase of biodiversity informatics systems, for, as another Chinese proverb suggests, "It is better to go back and make a net than to stand by the pond and long for fish."

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Tools of the Trade in Vaccine Design

Michael Hagmann provides a good account in his News article "Computers aid vaccine design" of the potential that computer algorithms and computer modeling have for predicting what parts of an antigen (what epitopes) would be most likely to elicit a strong immunological response and hence be well suited as a target for vaccines (special issue, Frontiers in Cellular Immunology, 6 Oct., p. 80). This exciting technology will undoubtedly yield important immunotherapeutics for both cancer and infectious diseases. In the article, however, there are a few inaccuracies that we wish to clarify.

First, Hagmann says that Hans-Georg Rammensee at the University of Tübingen, Germany, defined motifs for major histocompatibility complex (MHC) class I proteins, and our group did the same for epitopes for MHC class II proteins. But, in fact, both groups defined both types of motifs and compiled class I and class II databases.

Second, it is stated that we use a matrix-based algorithm similar to the one developed by J. Hammer and F. Sinigaglia's group at Hoffmann-La Roche, which suggests that their method was developed first. Without detracting from the outstanding

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work of this group, we published the matrix method in 1989 (*1*), several years before the first description of the method by Hammer and colleagues.

Third, James Kazura, a malaria immunologist at Case Western Reserve University School of Medicine, is quoted as saying that "a brute-force approach where you test every single peptide [in a given protein] is obviously not possible for financial and logistical reasons." Yet, we have done just that in a study performed in collaboration with K. Melief and M. Kast (*2*). Our group has been working for more than 15 years developing high-throughput assays to evaluate binding of specific peptides to a large panel of MHC molecules. Our current throughput is about 10^6 assays per year and is easily scalable. It is the basis of our functional genomics programs. Other groups have developed large assay capacity as well.

Lastly, regarding the computer algorithms based on artificial neural networks that are capable of "learning" as more data are supplied, it is worth mentioning that these alogrithms are in fact less efficient at predicting whether a peptide will bind a MHC molecule than are the matrix methods we, Hammer, Rammensee, and others use (*3*). The method used for prediction, however, is not as important as the size of the database available to train the system or derive the matrix for predicting binding capabilities. The larger the database, the more accurate the prediction. Hence, our group has been amassing a large database that currently contains binding constants for more than 50,000 different MHC-peptide combinations. Such large amounts of data are critical in trying to identify peptides capable of binding many different MHC variants, "a must for a widely applicable vaccine," as Hagmann points out. In terms of the overall success rate of our method, in various studies performed in collaboration with leading academic investigators, epitopes from various disease indications (hepatitis B and C viruses, HIV, and *Plasmodium falciparum*) were studied (*4*). The success rate of epitope prediction from these studies ranged from 85 to 100%. Results from these studies have been incorporated in the design of several different experimental vaccines that are now in the early stages of clinical and preclinical development.

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CREDIT: (TOP) M. KLIMEK/THE LIASON AGENCY NETWORK; (MIDDLE AND BOTTOM) RICK KOZAK

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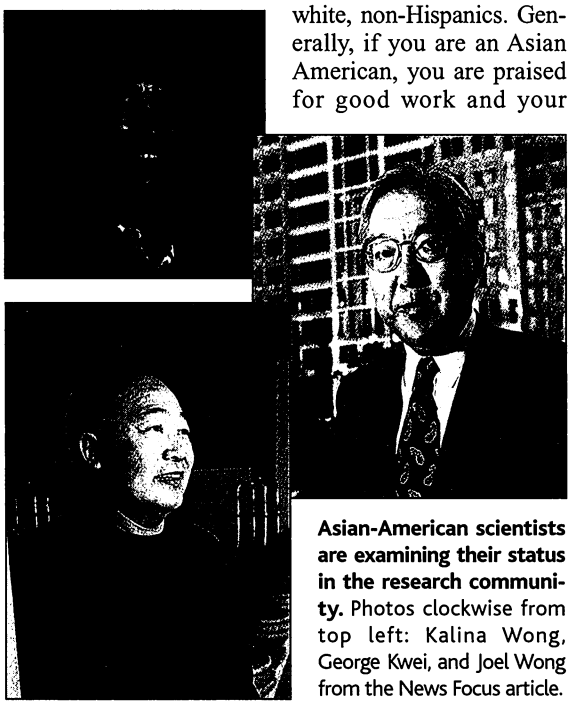
"Diamond Ceiling" for Asian Americans

Scientists and engineers of Asian-American descent are intelligent, hard-working, and motivated individuals, yet they are seldom rewarded. It is not just the Department of Energy (DOE) laboratories that treat Asian Americans as "high-tech coolies" and do not promote them into leadership positions, as Andrew Lawler discusses in his News Focus article "Silent no longer: 'model minority' mobilizes" (10 Nov., p. 1072); the situation is widespread in academia and industry as well. According to statistics from the Department of Education (*1*), only about 1.6% of those of executive/administrative/managerial rank in fall 1993 were Asian or Pacific Islanders, whereas about 86% were white, non-Hispanics. Generally, if you are an Asian American, you are praised for good work and your loyalty to the organization, but most promotions and other forms of reward and recognition seem to be reserved for other colleagues.


Asian-American scientists are examining their status in the research community. Photos clockwise from top left: Kalina Wong, George Kwei, and Joel Wong from the News Focus article.

In my opinion, it is not just a "glass ceiling," but it is becoming a more hardened "diamond ceiling" as more Asian Americans excel in all areas of science and technology. The solution may not be to litigate all such matters, but considering the injustice and agonizing experiences suffered by Wen Ho Lee, the Asian-American community needs to wake up and get organized. United, we can raise awareness and get what is legally, morally, and rightfully due to us as Asian Americans. It is a matter of pride for all Asian Americans that they have maintained high work ethics, and it is time that we stand up and be counted for what we deserve.

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1. Available at www.ed.gov/NCES/

CORRECTIONS AND CLARIFICATIONS

Policy Forum: "Surveillance and privacy" by R. Bayer and A. L. Fairchild (8 Dec., p. 1898). Notes 2 and 5 were inadvertently omitted from the text. They should have appeared at the end of the third and seventh paragraphs, respectively.

NetWatch: "Krill stuff" (24 Nov. p. 1459). The Antarctic krill *Euphausia superba* was erroneously described as a copepod. Also, the NetWatch item "Growing a book of science" (13 Oct. p. 227) should have indicated that a movie explaining the seasons shows how Earth's tilt changes "relative to the sun."

Letters: "Thoughts on the causes of tree mortality in Appalachia" by H. S. Neufeld (17 Nov., p. 1301). The species names of the trees were either misspelled or incorrect. The proper ones are as follows: red spruce (*Picea rubens*), Fraser fir (*Abies fraseri*), and balsam woolly adelgid (*Adelges picea*).

Perspectives: "Nitrogen on the moon" by R. H. Becker (10 Nov., p. 1110). Some of the labels in the accompanying figure were incorrect. On the arrow marked "Solar wind," the labels should have read "$^{14}N/^{36}Ar \approx 37$" and "$^{15}N/^{14}N \sim 0.0028$ or ~ 0.0045." On the arrow marked "Meteorites," the label should have read "$^{15}N/^{14}N \sim 0.0037$." The labels on top of the cube should have read "$^{14}N/^{36}Ar \approx 370$" and "$^{15}N/^{14}N \sim 0.0028$ to ~ 0.0045."

Reports: "Invasive plants versus their new and old neighbors: a mechanism for exotic invasion" by R. M. Callaway and E. T. Aschehoug (20 Oct., p. 521). The figure that appeared with the legend to Fig. 3 was Fig. 2 and vice versa. Figure 2 described biomass, and Fig. 3 illustrated reduced ^{32}P uptake of bunchgrass species.

Reports: "Optically defined multifunctional patterning of photosensitive thin-film silica mesophases" by D. A. Doshi *et al.* (6 Oct., p. 107). In Fig. 1, the "greater than" symbol indicating the relation between the variables n_{irr} and n_{unirr} in the diagram for Scheme 3 was incorrect. The symbol should have been "less than."