

Just Awards?

The article about the "Molecule of the Year" award (20 Dec., p. 1706) prompts me to write with a concern I have had ever since the award was announced. The concept of recognizing a major discovery each year is commendable. But the name "Molecule of the Year," while clever, seems biased and unrepresentative of the broadly based science that AAAS and *Science* aspire to represent.

No one denies that some of the most exciting research being done today is in the disciplines of molecular biology and biochemistry. Nor do I have any argument with the selection of buckminsterfullerene for this year's award. But surely the prime science results of each year cannot be expected always to lie in the areas of molecular biology and biochemistry. What if the most exciting discovery were a new concept in elementary particle physics, or a new class of objects in astrophysics? What if cold fusion had turned out to be correct? Would these still be called "Molecule of the Year"?

I get the message that my kind of science is second-class and is not likely to produce an award-winning discovery. To me it seems analogous to writing in the masculine gender and then being told that masculine really is neuter and thus includes everyone. The editor of *Science* may believe that molecular science really includes all science, but the net result seems biased to me.

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Response: Morrison is correct—we should consider all areas of science for special recognition, and we have done so by awarding "Molecule of the Year" to the polymerase chain reaction, a method, in 1989; to diamonds, an engineered material, in 1990; and to the buckyball, a molecule, in 1991. Our award runners-up have been selected from areas ranging from cosmology to social science. We meant the name "Molecule of the Year" to be symbolic of scientific discovery in general. However, we are open-minded and invite readers to suggest a more appropriate name for this award.

—DANIEL E. KOSHLAND, JR.

Florida Dentist Case: Research Affiliation and Ethics

We wish to clear up some misconceptions and errors that were contained in the News & Comment article "The case of the Florida

dentist" (24 Jan., p. 392) by Joseph Palca.

Although Palca notes that one of us (L.G.A.) has no financial connection to the case, the clear implication in the caption of the photo accompanying the article (p. 393) is that Lionel Resnick, Stanley Weiss, and one of us (L.G.A.) are all part of the "defense team of experts." In fact, neither of us is part of any defense team, and we began our investigation independently in August 1990. We first contacted the Florida AIDS office in October 1990 and corresponded with the Centers for Disease Control (CDC) shortly thereafter. At the suggestion of the CDC we wrote directly to Gerald Myers at Los Alamos National Laboratory in December 1990, offering to collaborate on a statistical analysis of the sequence data. After 4 months, Myers declined our offer by phone. It is therefore incorrect to state that one of us (L.G.A.) was "recruited" by Resnick for help on this project. Only after our analysis was complete and a manuscript was nearly completed did we learn of a financial connection between Resnick and Weiss and CIGNA Dental Health of Florida. Neither of us has had any connection to CIGNA or any legal group involved in the case, nor do we have any direct or indirect financial interest in the case. Our research is funded solely by our institutions, the National Science Foundation (L.G.A.) and the National Institutes of Health (R.W.D.).

We are also particularly concerned about the implication that our use of the Freedom of Information Act to obtain data from the CDC was possibly unethical. It is standard practice, particularly in the field of molecular phylogenetics, for any data used in a publication to be included in the paper, submitted to the recognized international sequence databases, or be made available on request. The CDC had published three reports in *Morbidity and Mortality Weekly Report* that included statements about the similarities of sequences as well as a phylogenetic tree based on those sequences, although the data on which these analyses were based were not included. These published reports were being discussed widely and were being cited as the basis for public policy. We neither requested nor obtained any data that had not already been the basis of published work.

We are confident that we have in no way behaved unethically and that our critique of the CDC's analyses stands entirely on its own merit. We have no interest in promoting any particular result; we only feel that this case deserves careful consideration by the scientific community and that the data and analyses should be subject to peer review.

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Biopesticides and Resistance

The letter by M. K. Harris (6 Sept., p. 1075) and the Research News article by Ann Gibbons (1 Nov., p. 646) about the development of resistance in insects to insecticides and to transgenic plants that express the *Bacillus thuringiensis* (*Bt*) gene give the mistaken impression that little has been accomplished in this discipline and that *Bt* research is breaking new, totally unexplored ground. We believe the vast literature on conventional pesticide resistance management, as well as ongoing research with engineered plants, was not adequately addressed in these statements.

Experiments that have been done to test deployment strategies for transgenic cotton include those by one of us (D.A. and co-workers) in which two *Bt* gene constructions were introduced into 56 different plant populations that had three unrelated mechanisms of resistance to lepidopterous insects. This is making it possible to assess the benefit of pyramiding different types of genetic resistance (1). Several insect management strategies are being tested (2), including high-dose expression of *Bt* proteins in transgenic cottons, the creation of "refugia" (refuges provided for sensitive insects within a population so they will not be exposed to *Bt*), tissue-specific or inducible expression, or both, of foreign gene products such as *Bt* (to reduce overall insect population exposure), mixed seed or mosaic plantings, insertion of combinations of two or more foreign genes into the plant genome by using *Bt* or other proteins that affect Lepidoptera, and cultivation of *Bt* transgenic cottons by using certain agronomic practices to reduce exposure time. Our research has not shown that *Bt* can be deployed without resistance problems, but assertions that *Bt* transgenic cotton (and other plants) will not work are premature.

Agricultural scientists have dealt with insect and pathogen adaptation to conventionally bred resistant cultivars for nearly a century. The public rarely notices the loss of resistance genes to pest adaptation unless a highly visible crisis such as the 1970 Southern corn leaf blight epidemic occurs. Biotechnology has focused on the problems of pest adaptation, but funded research initiatives or incentive programs for good management practices have not materialized in legislation. Commitment from public institutions has been minimal for the development of sustainable approaches to conventional pest resistance breeding, and the analogous situation with transgenic plants has generated interest, but no additional resources. Without action by public agencies, engineered plants may be developed