the expertise of the national laboratories.

Similarly, the facilities are becoming increasingly important for the development of clean-up strategies for environmental situations that have been difficult to manage. There are many cases where the scientific issues that underlie the interaction of toxic materials with the environment are poorly understood and where bringing some science to bear might greatly increase the effectiveness of clean-up work or sharply reduce its cost. For example, samples of mixed waste from the nuclear weapon production sites (for example, Fernald and Hanford) are regularly brought to the Stanford Synchrotron Radiation Laboratory for x-ray absorption spectroscopy analysis. Such analysis, which provides information about the ionic states of toxic elements, as well as the nature of their bonding to their neighbors, is expected to lead to new treatment protocols.

For both the industrial and the environmental researchers, a major shortcoming of these facilities is their limited operations schedule. The proposed funding initiative would provide major increases in operating time at these facilities for a relatively small fraction of their total operating budgets, for the reasons cited in Lawler's article.

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Sunlight and Melanoma: An Answer from MTS1 (p16)

The incidence of malignant melanoma has been increasing for several years at a rate of 5% per year, probably as a result of changes in lifestyle. The etiology of such a tumor is a controversial topic. Despite the evidence of a peculiar incidence of the disease in fair-skinned populations, no convincing data are at present available about the relation between melanoma development and sunlight exposure (*1*).

Recently, the demonstration of a peculiar pattern of p53 gene mutations has been reported in some sun-related skin tumors, in particular in squamo- and basocellular carcinomas by Brash *et al.* (*2*) and in atypical fibroxanthoma by our group (*3*). In these neoplasms a high frequency of C:G to T:A mutations at dipyrimidine sites, together with tandem CC to TT transitions, were detected. This pattern of mutation constitutes a sort of hallmark of ultraviolet (UV)-

Proposed Constitutional Amendment

A proposed amendment to the AAAS Constitution will be considered by the AAAS Council at its 19 February 1995 meeting. The Council now has the authority and responsibility to elect Fellows, but no matching authority to revoke Fellow status. At its meeting on 4 December 1992, the Committee on Council Affairs endorsed the following amendment to Article VII, Section 1, of the Constitution enumerating the duties of the Council. It would be added as a new provision (i).

> *To consider, on a proposal by the Committee on Council Affairs, the revocation of Fellow status of an individual who has been so elected from among members of the Association.*

The current provision (i) would be relettered (j), and current provision (j) would be relettered (k).

This information about the proposed amendment is published in accordance with the Association's Constitution. Article IX calls for publication of any proposed amendment at least 30 days prior to the Council meeting at which it will be considered. If the Council approves the amendment, it will be submitted to the AAAS membership for mail ratification during the 1995 general election.

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AAAS Scientific Freedom, Responsibility and Law Program

induced DNA damage. UV radiation induces distinctive DNA mutations, typically at dipyrimidine sites, with a prevalence of single, and in particular double, CC to TT transitions (*4*). The evidence of a specifically UV-induced mutational pattern confirms the relevance of sunlight in the etiology of these skin neoplasms. Unfortunately, the low frequency of p53 gene abnormalities has prevented such an analysis in malignant melanomas.

In a recent report, "A cell cycle regulator potentially involved in genesis of many tumor types" (15 April, p. 436), Alexander Kamb *et al.* reported the identification of a new oncosuppressor gene, named MTS1, corresponding to a previously identified inhibitor (p16) of cyclin-dependent kinase 4. This gene maps to a genomic region (chromosome 9p21) that is frequently altered in malignant melanoma and, in fact, table 2 of the report shows the mutational analysis of a series of 14 melanoma cell lines as a confirmation of the role of MTS1 alterations in melanoma induction.

Further important information about the biology and etiology of melanoma can be inferred from this report. An excess of C:G to T:A transitions at adjacent pyrimidines emerges from an in-depth analysis of the MTS1 mutational spectrum of the 14 melanoma cell lines tested. In particular, 15 out of 18 mutations detected were C:G to T:A transitions, and 14 of these were at dipyrimidine sites. Moreover, two cell lines (SK-MEL-61 and SK-MEL-150) carried a tandem CC to TT mutation. As this peculiar mutational pattern is induced specifically by UV radiation, the report by Kamb *et al.* provides molecular evidence of the central role of UV radiation in the pathogenesis of melanoma, which strongly supports a "sunlight etiology" for this type of tumor.

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Response: Maestro and Boiocchi point out an important feature in some of our published data, namely, that the type of mutation observed in melanoma cell lines, apart from deletions, is the same as reported by Brash and coworkers for TP53 mutations induced by ultraviolet light in nonmelanoma skin cancers (*1*). We have made the same observation (*2*).

There are actually two conclusions that can be drawn from these data. First, as Maestro and Boiocchi state, the results suggest strongly that the melanoma CDKN2 mutations were induced by ultraviolet radiation, providing strong circumstantial support for the view that melanoma is at least partly a result of exposure to sunlight. Second, the findings imply that the point mutations arose in vivo before establishment of the cells in culture. This lends further credence to the notion that many MTS1 mutations occur during tumor formation and are not simply an artifact of cell culture.

Both these inferences are important and quite solid. The latter conclusion, that CDKN2 mutations occur in vivo, adds to the accumulating evidence that p16 is a bona fide tumor suppressor gene whose inactivation in vivo is causal to tumor formation.

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