

Lawyer Gets Top Science Post

NEW DELHI—A prominent lawyer has been appointed India's new science minister. Prime Minister Manmohan Singh this week appointed Congress Party spokesperson Kapil Sibal to oversee the new government's science, technology, and oceans portfolio.

Sibal, 56, holds a law degree from Harvard University and is well known in India for his work on AIDS policy. He also sits on the board of the New York-based International AIDS Vaccine Initiative. Sibal told *Science* that he hopes to revamp India's system for assessing genetically modified products and would seek new rules to foster greater use of animal trials. "It is absurd to [use] humans [as] guinea pigs," he said.

Although Sibal has little technical training, researchers are happy with the appointment. Sibal is "a breath of fresh air," says polymer engineer Raghunath Anant Mashelkar, director-general of the Council of Scientific and Industrial Research in New Delhi. —PALLAVA BAGLA

UC Faculty Back Bid for Two Weapons Labs

Faculty support for the University of California's (UC's) management of two nuclear weapons laboratories is growing. A poll of 3271 UC faculty members released last week found that 67% favored having the university system enter a pending competition for contracts to manage the Department of Energy's (DOE's) Los Alamos National Laboratory in New Mexico and Lawrence Livermore National Laboratory in California. That reverses a similar 1990 poll, in which 64% opposed continued management of the labs, which UC has run for 60 years.

The new poll, conducted by the academic senate, did identify some apprehension. Three-quarters of the faculty expressed concerns about plans to build plutonium "pits"—the heart of nuclear weapons—at Los Alamos. "Clearly, even those faculty supportive of the labs find weapons-component manufacturing a bitter pill to swallow," said astronomer George Blumenthal, vice chair of the senate body.

Meanwhile, a U.S. National Research Council panel on laboratory contracting said earlier this month that a single government committee overseeing a simultaneous competition of both contracts was the best way to pick a contractor "most likely to maintain the coordination between the labs." Last November, a DOE advisory panel came to the opposite conclusion, saying a double competition might be too much to pull off for the department and interested bidders. A decision is expected later this year. —DAVID MALAKOFF

approval, more resources be spent on testing, and communications be adequate to monitor landings.

At the press conference, Pillinger made light of the recommendations, calling them "motherhood statements." "We gave Beagle the best shot we could within the constraints imposed on us," he said. "If you want to add some spice to people's lives, you have to take some risks." Others see a more serious take-home message. "It's a pretty thorough indictment of the way the project was man-

aged," says space policy analyst John Logsdon of George Washington University in Washington, D.C.

Pillinger said he would be pushing ESA to launch a new Beagle at the earliest opportunity. Southwood said ESA will consult with the scientific community first, but he foresees a simple lander, to be launched in 2009, again focusing on astrobiology. He hoped to have a plan in place for a meeting of European ministers this fall. —DANIEL CLERY

With reporting by Richard Kerr.

MAMMALIAN BIOLOGY

More Genomes, But Shallower Coverage

For the human genome, nothing less than perfection was acceptable: Each DNA base was supposed to be correctly identified and in its proper position. But for a host of other mammals now in sequencers' sights, perfection may be too slow and expensive.

The National Human Genome Research Institute (NHGRI) is considering a proposal from a new advisory committee to turn its sequencing centers loose on decoding the DNA of a dozen or so mammals. Elephants and bats are among the top candidates, all of which will be based on how distant they are from humans and one another on the mammalian family tree. But in a policy shift that is being hotly debated—and could be approved as early as next month—the centers would make only a quick pass at the sequence of each species. For the human and mouse genomes, repeated passes identified each base seven times or more. Now the plan is to drop this 7× coverage to 2×. As a result, the new data would consist of thousands of small pieces of DNA too disjointed to put back together in a whole genome sequence.

An important reason for taking this approach is money: Less coverage means lower cost, and that means researchers will get four genomes for the price of one. "You have the possibility of sequencing lots of organisms quickly," says Edward Rubin, director of the Department of Energy (DOE) Joint Genome Institute in Walnut Creek, California.

But others worry that there just won't be enough data to work with. Michael Lynch, an evolutionary genomicist at Indiana University in Bloomington, says, "You are just

going to be left with a hodgepodge of data." Adds Maja Bucan, a geneticist at the University of Pennsylvania in Philadelphia, "I don't think that 2× is good enough for the kind of biology that we want to do." Without extensive data, researchers will have trouble trying to understand a genome's overall structure.

Although the new approach could produce a hodgepodge, at least it will be extensive enough to compare with the more fully detailed human, mouse, and rat genomes, says developmental geneticist William Gelbart of Harvard University. And researchers will be able to find new genes and regulatory regions that they can't find when they compare just a few sequences. Already, the analysis of the poodle genome, which had just 1.5× coverage, demonstrated that skimming a genome can yield useful information (*Science*, 26 September 2003, p. 1898). Some researchers even argue that they could get away with sketchier coverage. "The idea is to find the sweet spot where there's enough information but [the genome] is not too expensive," Gelbart explains.

Having multiple genomes to compare will pay big dividends, says NHGRI Director Francis Collins. For example, researchers should be able to find hidden regulatory elements common to most species. Besides, Collins argues, 2× is just "a starting point." Lynch and others wonder, however, whether sequencers will ever complete these genomes, once the quick-and-dirty approach has yielded its initial trove of data.

—ELIZABETH PENNISI



Next up? Bats are among the leading candidates for sequencing.

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