

ANALYSIS

Monsanto releases rice data to academia

On April 4, Monsanto (St. Louis, MO) announced it has completed a “working draft” genetic map of the rice genome and that it will share the information freely with academic researchers. Although most praise the decision—the first time a large multinational corporation has agreed to disclose so much information about an important crop to the academic world—some question the availability of the data and the eventual cost of using it.

The map, which was compiled under contract by the laboratory of Leroy Hood of the University of Washington (Seattle), covers locations on all 12 rice chromosomes of the *Oryza sativa* (*japonica* variety) rice genome, but is not a complete sequence of any of them. Monsanto’s database is a shotgun library of 80,000 bacterial clones of the genome, which is estimated to contain between 40,000 and 50,000 genes: data includes a few hundred base pairs from each end of each clone and provide 5X coverage of the genome.

According to Gerard Barry, a Monsanto research genomics leader, Monsanto will release the data by mid-July to the International Rice Genome Sequencing Project (IRGSP), a public effort comprising researchers in Japan, China, India, Taiwan, Korea, Thailand, Canada, France, UK and US. Monsanto’s data will help researchers fill in the gaps between sections that have already been sequenced.

Roger Beachy, director of the Donald Danforth Plant Science Center (St. Louis, MO), a nonprofit agricultural research institute that is working on rice genetics, says Monsanto’s decision to release the data will save researchers three to four years in sequencing the entire rice genome, bringing the project’s scheduled completion to around 2004 or 2005. “It’s a very good deal,” he says. “I wish someone would do the same for corn and other crops.”

Monsanto, now a wholly owned subsidiary of Pharmacia Corp. (Peapack, NJ), says it is releasing the data so that both it and academic researchers will eventually be able to develop new strains of GM rice that can improve nutrition, tolerate greater cold or heat, or use up less land for cultivation, for example.

Completion of the IRGSP, along with a similar project to sequence the cruciferous plant *Arabidopsis thaliana*, will allow researchers to identify more effectively the location of genes controlling important traits such as yield or hardiness. “To have the rice genome as a model crop along with

Arabidopsis gives us some powerful tools for functional genomics,” says Beachy.

Under the agreement between Monsanto and the IRGSP, any academic researcher can access the data. The Japanese Ministry of Agriculture, Forestry and Fisheries (MAFF; Tokyo) is leading the IRGSP, and Monsanto’s data will be kept on MAFF’s computer server. Researchers will need a password to access it, according to Joachim Messing, director of the Plant Genome Initiative at Rutgers University, an IRGSP member.

One researcher, however, wonders why Monsanto doesn’t just deposit the information in GenBank, a free Internet-based database that contains genetic sequences from rice, *Arabidopsis*, and 65,000 other organisms, and is maintained by a division of the US National Institutes of Health. “The thing that concerns me is the access issue,” says Joe Ecker, who is leading the *Arabidopsis* sequencing project at the University of Pennsylvania. “When it says freely available, that means I can go to GenBank and get it. This [access via IRGSP] is better than not having [the information], but it’s not freely available.”

Monsanto’s Barry counters that Monsanto is simply trying to restrict potential commercial competitors from using the rice genome information.

However, academic researchers who want to use the information must still agree to give Monsanto first right of refusal to negotiate a nonexclusive license for any patents that result from the data. But Monsanto does not require restrictive “reach-through” rights that require researchers to pay for further uses of the technology—rights that have traditionally been imposed by private companies and academic institutions on proprietary material. “We just want the first option,” says Barry.

Detlef Weigel, a plant biologist at the Salk Institute, points out that a researcher who discovers something of commercial importance using the Monsanto rice data would have to negotiate a deal with Monsanto. “In principle it’s fantastic that they [Monsanto] want to make it [the rice data] accessible,” says Weigel. “But we would need to see the details to see how steep the price tag is for discovering something later on.”

Eric Niiler

GM food regulatory terms debated

The country that is about to introduce the strictest regulations in the world concerning safety of GM foods—Japan—has been chosen to chair a working group that will draft the guiding principles on risk analysis and risk assessment of foods derived from biotechnology. However, the resulting guidelines are unlikely to be as draconian as might be expected because two key concepts of the risk assessment process up for discussion, “traceability” and “familiarity,” have many countries perplexed—most notably Japan, whose officials seem reluctant to use the terms in the context of food-safety regulation.

The GM food-safety working group is part of the ad hoc Intergovernmental Task Force on Foods Derived from Biotechnology, which was established by the global food standards body, the Codex Alimentarius Commission. The task force is charged with developing “standards, guidelines and principles on foods derived from biotechnology or traits introduced into foods by biological methods” by 2003, and it was at its first meeting in the middle of March in Chiba, Japan, that France proposed “traceability” and “familiarity” be included in the task force agenda.

Japan’s Ministry of Health and Welfare (MHW; Tokyo), which will take a leading

role in the working group, says that applying the terms to GM foods is a daunting task. “It is unclear at the moment what the implications of the two concepts are, as they have not previously been used by Codex, and are new to most of us,” says Itaru Nishimoto, director-general of MHW’s environmental health bureau.

The concept of “familiarity” in environmental risk assessment has already been defined by the Organization for Economic Cooperation and Development (OECD) as the understanding of characteristics of an organism and its introduced trait, the environment into which the organism is introduced, and the interactions between them. Although Nishimoto accepts and understands “familiarity” as a form of environmental risk management, “its application [to food safety] in relation to a precautionary approach would have to be considered carefully,” he says.

“Traceability”—mechanisms by which particular substances can be followed from source to final product through record tracking of trade routes and labeling—is seen as “ambiguous” when applied to

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