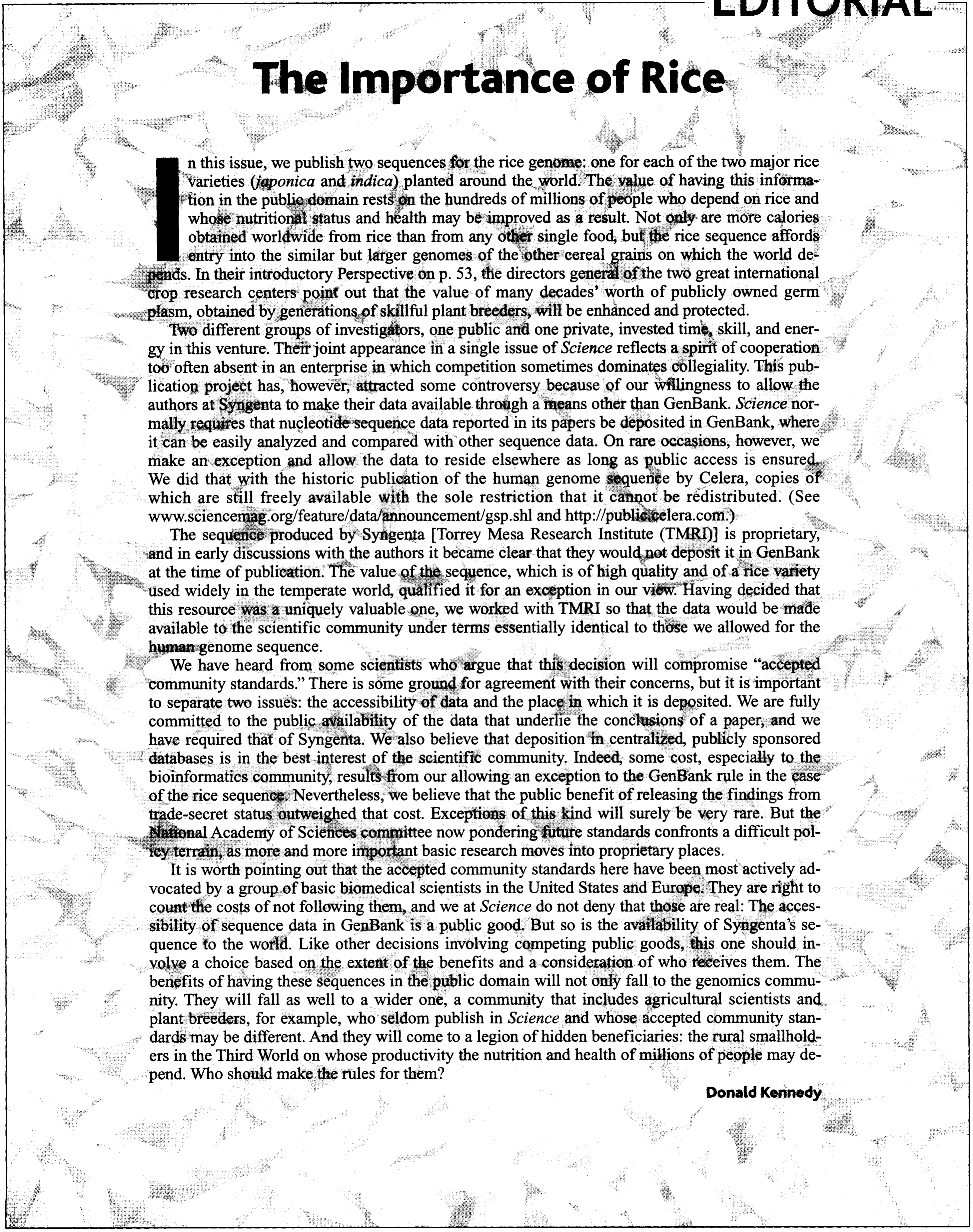

# The Importance of Rice

In this issue, we publish two sequences for the rice genome: one for each of the two major rice varieties (*japonica* and *indica*) planted around the world. The value of having this information in the public domain rests on the hundreds of millions of people who depend on rice and whose nutritional status and health may be improved as a result. Not only are more calories obtained worldwide from rice than from any other single food, but the rice sequence affords entry into the similar but larger genomes of the other cereal grains on which the world depends. In their introductory Perspective on p. 53, the directors general of the two great international crop research centers point out that the value of many decades' worth of publicly owned germ plasm, obtained by generations of skillful plant breeders, will be enhanced and protected.

Two different groups of investigators, one public and one private, invested time, skill, and energy in this venture. Their joint appearance in a single issue of *Science* reflects a spirit of cooperation too often absent in an enterprise in which competition sometimes dominates collegiality. This publication project has, however, attracted some controversy because of our willingness to allow the authors at Syngenta to make their data available through a means other than GenBank. *Science* normally requires that nucleotide sequence data reported in its papers be deposited in GenBank, where it can be easily analyzed and compared with other sequence data. On rare occasions, however, we make an exception and allow the data to reside elsewhere as long as public access is ensured. We did that with the historic publication of the human genome sequence by Celera, copies of which are still freely available with the sole restriction that it cannot be redistributed. (See www.sciencemag.org/feature/data/announcement/gsp.shl and http://public.celera.com.)

The sequence produced by Syngenta [Torrey Mesa Research Institute (TMRI)] is proprietary, and in early discussions with the authors it became clear that they would not deposit it in GenBank at the time of publication. The value of the sequence, which is of high quality and of a rice variety used widely in the temperate world, qualified it for an exception in our view. Having decided that this resource was a uniquely valuable one, we worked with TMRI so that the data would be made available to the scientific community under terms essentially identical to those we allowed for the human genome sequence.

We have heard from some scientists who argue that this decision will compromise "accepted community standards." There is some ground for agreement with their concerns, but it is important to separate two issues: the accessibility of data and the place in which it is deposited. We are fully committed to the public availability of the data that underlie the conclusions of a paper, and we have required that of Syngenta. We also believe that deposition in centralized, publicly sponsored databases is in the best interest of the scientific community. Indeed, some cost, especially to the bioinformatics community, results from our allowing an exception to the GenBank rule in the case of the rice sequence. Nevertheless, we believe that the public benefit of releasing the findings from trade-secret status outweighed that cost. Exceptions of this kind will surely be very rare. But the National Academy of Sciences committee now pondering future standards confronts a difficult policy terrain, as more and more important basic research moves into proprietary places.

It is worth pointing out that the accepted community standards here have been most actively advocated by a group of basic biomedical scientists in the United States and Europe. They are right to count the costs of not following them, and we at *Science* do not deny that those are real: The accessibility of sequence data in GenBank is a public good. But so is the availability of Syngenta's sequence to the world. Like other decisions involving competing public goods, this one should involve a choice based on the extent of the benefits and a consideration of who receives them. The benefits of having these sequences in the public domain will not only fall to the genomics community. They will fall as well to a wider one, a community that includes agricultural scientists and plant breeders, for example, who seldom publish in *Science* and whose accepted community standards may be different. And they will come to a legion of hidden beneficiaries: the rural smallholders in the Third World on whose productivity the nutrition and health of millions of people may depend. Who should make the rules for them?

**Donald Kennedy**

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