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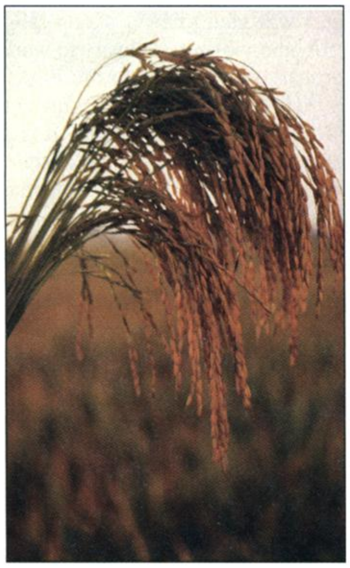
Why Finishing the Rice Genome Matters

A MAJOR PUBLICLY FUNDED GENOME sequencing effort is quietly nearing a milestone. The International Rice Genome Sequencing Project (IRGSP) (http://rgp.dna.affrc.go.jp/rgp/press_releas20011225.htm) has an announced goal of completing a 10-fold redundant draft of a japonica strain of rice by the end of 2002. The primary goal of this ambitious international sequencing effort, the first of a major food crop, is to produce a finished-quality product. The value of draft sequencing to exploit coarse regional syntenic relationships and find genes in a map-based sequence has been established; nevertheless, we do not yet understand how to value a finished sequence or under what conditions its high cost is warranted.



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There are compelling reasons for achieving a publicly available finished rice genome sequence. Rice, at a compact 430 Mb, is only one-sixth the size of the human and maize genomes and provides the sequencing template for all the grasses. This includes every significant grain crop (including sorghum, maize, barley, oat, and wheat), most of which have enormous genomes that are not feasible to sequence at current costs (e.g., wheat has a tetraploid genome estimated at 16 Gb, about five times the size of the human genome). Complete discovery of all rice genes and alignment with the robust genetic map will not only allow immediate fine-grain syntenic leveraging across all the grain genomes but will also provide a critical foundation for all comparative work in agricultural species. Moreover, rice, as a model species, is the plant in which the function of most cereal genes will be discovered.

Not finishing the rice genome will put a surcharge on every grains-related research project in the future. This will be especially true as researchers attempt to understand and harness genes responsible for traits such as disease/drought/salinity tolerance, faster germination time, or nutritional quality in crops such as corn, wheat, barley, rye, oat, sorghum, sugarcane, and millet, as well as rice.

Population growth, loss of arable land, and climatic changes will increasingly challenge the need for continued growth in food supplies. We will need a "Green Gene" revolution to meet this challenge, and completing the rice genome promptly will be the most important step we can now take. We challenge the countries and corporations involved with rice sequencing to find creative and cooperative ways to help the IRGSP complete a finished rice genome by the end of 2003. The potential approach of merging public and private data could form an enhanced draft of the rice genome, similar to Celera's handling of the human genome. Conventional finishing of the IRGSP's bacterial artificial clones (BAC), the Gold Standard option, would be a more easily achieved result. [In fact, one collaboration is already producing results. The Monsanto BACs, which underlie 30% of the BAC/PAC (P1 artificial clone) sequences submitted, have greatly speeded submission of rice sequence to public databases.]

Finishing the rice genome sequence is clearly an opportunity to do something now to benefit all humankind.

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Collaborating on the Rice Genome

MANY INDEPENDENT EFFORTS HAVE NOW been made to sequence portions of or all of the rice genome. The finished rice genome will be instrumental in cereal crop improvement and will serve as a foundation for other cereal genomes. With so much rice sequence now generated, it's time to consider merging these efforts toward a common goal of a finished and accurate genome sequence. Syngenta is making its rice draft sequence available to support the international project (IRGSP). We encourage all genome sequencing groups to join together in establishing a collaborative effort to complete a finished rice genome sequence in the most efficient and timely fashion.

All parties involved in rice genome sequencing are invited to participate. I recommend that participating parties provide sequence assemblies and raw chromatogram data to facilitate finishing of the rice genome and establish an assembly and finishing strategy that maximizes the use of existing data and the current sequencing efforts. In addition, assemblies, quality files, and chromatograms should be made available to all participating parties upon completion. Participating parties should not

Letters to the Editor

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