An ad-hoc committee, commissioned by the Maize Genetics Executive Committee met in Chicago on May 17, 2004, to prepare a report defining the "gold standard" for the maize genome - that is, what the community agrees is the best possible genome resource to enable the best science to be done. Another goal was to generate a timetable towards achieving the "gold standard" and to make a recommendation for how the data should be released. The committee's report, which has been presented to the National Science Foundation is below.

Gold standard:

The maize genome-sequencing project must provide the complete sequence and structures of all maize genes and their locations (in linear order) on both the genetic and physical maps of maize.

The gene space of B73 (gene sequences and adjacent regulatory regions) should be finished quality to Bermuda standards. If applicable, the sizes of gaps between the genes should be estimated and draft sequences of repetitive DNA between genes presented where possible. The sequence must be fully integrated with the genetic and physical maps. To obtain the complete species gene space it may be necessary to sequence multiple inbred lines.

Annotation should include gene models, predicted exon/intron structure, incorporation of EST and full-length cDNA data, gene ontology, and relationship with homologs in other organisms, including but not limited to the other sequenced plant genomes. Annotation should be coordinated with existing maize community and comparative databases with the eventual goal of generating complete curation of the genomic sequences to a standard set by established model organism databases.

Time line:

Stage I: Sequences on pilot projects should be fully available by Sept. 04. See http://www.maizegenome.org/ for details of these projects.

Stage II: The goal of this stage is to have a draft sequence of ALL gene space for B73 placed on the BAC physical map, with each gene located to a BAC within the first year. It is expected that this stage will include non-curated automated first pass annotation (gene structure predictions and tentative functional annotation) that will be concurrent with first year sequencing. The cost of proceeding to the next stage, *i.e.* finishing the sequence should be discussed in proposals. Added values of proposed strategies that yield additional information such as gene order, estimation of gap size and draft sequences of repetitive DNA between genes should be discussed. Another consideration to be addressed is to what extent the proposed strategy captures the entire species gene space (different inbred lines can vary in gene content).

Stage III: The goal of this stage is to complete the ordering of B73 genes within each BAC and to finish B73 gene space to Bermuda standards. An additional goal is to obtain high quality draft sequence of complimentary gene space from other inbred lines if B73 does not contain at least 95% of species gene space.

This stage will also include more complete curation of the genomic sequences to a standard set by established model organism databases. It is anticipated that these efforts will entail development and application of novel maize-specific or maize-trained bioinformatics tools. Proposals for this task may be in connection with or independent of the sequencing projects, but should leverage and augment the existing maize and cereal database resources.

Data Release:

All sequence data, including trace files, will be automatically deposited with GenBank within 24h, or at most within a week, after production. Trace files will also be provided simultaneously to MaizeGDB (www.maizegdb.org) and Gramene (www.gramene.org). An important goal is to support existing integrated databases and analytic tools for the management of maize genomics data and make them available to the worldwide research and development community.

Committee Members:
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