Resource Summary Report

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Comparative Saccharinae Genomics Resource

RRID:SCR_008153
Type: Tool

Proper Citation

Comparative Saccharinae Genomics Resource (RRID:SCR_008153)

Resource Information

URL: http://csgr.pgml.uga.edu/

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Description: The objective of this project is to develop physical maps of the sorghum and rice genomes, based on BAC contigs that are cross-linked to each other and also to genetic maps and BAC islands for other large-genome crops and a library of ca. 50,000 expressed-sequence tags (EST''s) and corresponding cDNA clones, from diverse sorghum organs and developmental states. It also aims to improve understanding of genetic diversity and allelic richness that might be harbored ex situ (in gene banks) or in situ (in nature), and refine techniques for assesing allelic richness and Expedite data acquisition and utilization by a sound parnership between laboratory scientists and computational biologists. Specific goals of developing physical maps of sorghum and rice genomes include: -Enrich cross-links between sorghum and rice by mapping additional rice probes on sorghum. -Apply mapped DNA probes to macroarrays of sorghum, sugarcane, rice, and maize BACs. -Fingerprint 10x BAC libraries of Sorghum bicolor and S. propinquum. Libraries presently 3x and 6x respectively, to be expanded to 10x each. -Use fragment-matching (BAC-RF) method to determine locus-specificity in polyploids. - Contig assembly based on 1-3, plus rice BAC fingerprints generated under a separate Novartis project. -Evaluate methodology for rapid high-throughput assignment of new ESTs to BACs. -Conduct genomic sequencing in a region duplicated in both sorghum and arabidopsis. Selected BACs from sorghum(2), sugarcane, maize, rice, wheat. By improving the understanding of genetic diversity and allelic richness, the goal is to: -Sequence previously mapped sorghum DNA probes. -Discover & characterize 100 single nucleotide polymorphisms (SNPs) from cDNA markers. -Develop colorimetric high-throughput genotyping assays, and utilize to assess genetic diversity in geographically- and phenotypically-diverse sorghums. -Develop colorimetric high-throughput asssays for identifying phytochrome allelic variation, and apply these assays to a core collection representing a large set of genetic resources. -Support informatics group to streamline cataloging of DNA-level information relevant to large genetic resources collections. Lastly, the goals of expediting data acquisition and utilization include: -A new web-based resource for 3D-integration and visualization of structural and functional genomic data will be developed. -New sequence assembly and alignment software SABER (Sequence AssemBly in the presence of ERror), and PRIMAL(Practical RIgorous Multiple ALignment), will be evaluated with reference to existing standards (PHRED, PHRAP). -Specialized image processing and image analysis tools will be developed for acquistion and interpretation of qualitative and quantitative hybridization signals. To deal expeditiously with large volumes of data, parallel processing approaches will be investigated. Sponsors: * National Science Foundation (NSF) * National Sorghum Producers * University of Georgia Research Foundation (UGARF) * Georgia Research Alliance (GRA)

Synonyms: CSGR

Resource Type: data or information resource, data processing software, portal, topical portal, software application, database, software resource, image processing software

Keywords: fingerprint, genetic, alignment, allele, allelic, arabidopsis, bac, biologist, cdna, clone, colorimetric, computational, contig, crop, diverse, diversity, dna, genome, genotyping, locus, macroarray, maize, map, marker, nucleotide, organ, phenotypically, physical, phytochrome, polymorphism, polyploid, probe, rice, sorghum, sugarcane, undergraduate, wheat, k-12 program

Funding:

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Old URLs: http://csgr.agtec.uga.edu/

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Ratings and Alerts

No rating or validation information has been found for Comparative Saccharinae Genomics Resource.

No alerts have been found for Comparative Saccharinae Genomics Resource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.