Using Gramene For Maize-Rice Genome Comparisons

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Maize, commonly referred to as corn in the United States, has been considered a unique plant since the time that the indigenous peoples of the Americas developed it to be their staple food. It is central to many sacred mythologies and creation stories which are still honored today (1, 2). Maize was introduced from the New World to the Old World in the 1400's, and it was planted between the harvesting of spring and winter crops, filling an important niche as a summer crop (1). Today, the United States, China, the European Union, Brazil and Mexico are the world’s largest producers of maize (3). Together, the US and China produce approximately 60% of the world maize crop (4). Maize accounts for 15-20% of the total daily calories in the diets of more than 20 developing countries, located mainly in Latin America and Africa (5, 6). 68% of the land devoted to maize is located in the developing world, however only 46% of maize production occurs there, indicating the need for improving yields in developing countries where it is a major source of direct human consumption for many of the poor (7).
Maize Queries

Gramene Database information on Zea mays

Pre-designed Zea Queries

- Show me all the maize markers in Gramene.
- Show me all the maize QTL in Gramene.
- What are the best maps to use to compare maize to rice?
- Show me a syntenic region between maize and rice.

Show me all the maize markers in Gramene.

- To perform this query, open the Markers database by using the main navigation bar of Gramene.
- Use the Marker navigation bar to open the Marker Search function.
- Type "*" in the "Marker Name" box and select "Maize" from the "Species" drop-down menu.

Show me all the maize QTL in Gramene.

- To perform this query, open the QTL database by using the main navigation bar of Gramene.
- Use the QTL navigation bar to open the QTL Simple Search function.
- Type "*" in the "Search for" box and select "Maize" from the "Species" drop-down menu.
- A QTL search results page will appear with a list of all Maize QTL in Gramene.
- Note: Maize can be replaced by another species to perform similar QTL searches.

- In the "Restrict Reference Sets By" section, select maize from the "All Species" field, and then click on "Submit."
- A Matrix results table will appear. Down the page vertically, all the maize maps will appear. Across the page horizontally, all the other maps in CMap will appear.
- Scroll horizontally until you reach the rice section. The numbers in the individual cells indicate the number of correspondences the maps contain, i.e., the greater the number, the better the maize map to compare to rice.
- Note: Maize can be replaced with any other species in Gramene to perform similar searches.

Show me a syntenic region between maize and rice.

- Using the above example, examine the numbers in the Matrix table.
- The GR TIGR Assembly and IBM2 Neighbors 2004 have a large number of correspondences. Selecting that number will display a Matrix table that will display the individual number of correspondences for each chromosome.
- Maize chromosome 1 and rice chromosome 3 have a large number of correspondences. Selecting that number will display a comparative map view of the two maps.
Gramene Modules

- **Genomes [Ensembl]**
  - ESTs, markers, genes, etc. from Poaceae on rice, maize & Arabidopsis
- **BLAST**
  - Sequence similarity search to genomes
- **Maps [CMap]**
  - Comparative map viewer
  - Genetic, physical, sequence & QTL maps
- **Markers**
  - Find markers and map positions
  - View marker details
- **Proteins**
  - Grass proteins from Swissprot & TrEMBL
  - Cellular locations and functions
- **Genes**
  - Genes and alleles associated with phenotype
- **QTL**
  - Quantitative trait loci from major cereal crops
- **Ontologies**
  - Controlled vocabularies
- **Literature**
Maize Genome Browser

Browse the Maize genome (Zea mays)

Current Release

Assembly
The Gramene Browser for maize presents results from the Maize Genome Sequencing Project. Further details are available from the MaizeSequence.org web site.

Accessioned BAC Browser
- The BAC database contains the 504 full-length Zea mays clones deposited with GenBank as of 26-Jan-2006.
- Sequences from various grass species including rice and maize were mapped to the BACs using the Gramene pipeline. E.g. AC149836. Mapping results for the sequence data sets are available in detailed form.
- Gene models were predicted using the FGENESH HMM-based ab initio gene prediction program, and their domains annotated using interproscan. E.g. FGENESH0005329
- Putative orthologs between rice, Arabidopsis and maize gene models were generated using Ensembl's compara pipeline. E.g. FGENESH0005329

Maize Agarose FPC Map
- The FPC database contains the 721 contigs from the AGI 19 Jul 2005 agarose map. [more] [citation]
- Accessioned BACs within the FPC map have been highlighted. E.g. ctg3
- Syntenic regions between the maize FPC map (AGI maize FPC map released on April 5, 2006) and the rice genome (TIGR v4) were estimated, and loaded into Ensembl. E.g. Maize chr9 Vs Rice
- The accessioned BACs will be merged into the FPC map database in the near future.

Entry Points

Lookup an Accessioned BAC
BAC: AC007410 (30650bp) Go

Lookup an AGI FPCntig
FPC: ctg1 (2101248bp) Go

Browse by FPC Map Chromosome

Lookup a Chromosome Location
Chr: 1 from 1M - 2M Go

FPC Synteny Vs. Rice Genome
Maize Chr 1 vs. Rice Go
Rice Genome Viewer
Rice Genome - Detailed View
Maize Maps

- Physical
- Genetic
  - IBM 2002
  - IBM neighbors 2002
  - IBM2 neighbors 2004
  - SSR IBM 2001
  - BNL 1996
  - UMC 1998
  - CU 1999

- Bin
- QTL
  - MISCU H123/AG19 BC1 QTL 2003
  - NCSU B73/Mo17 QTL 1992
  - INRA Io/F2 Composite QTL 1996
  - Iowa Mo17/H99 RI QTL 1996
  - CIMMYT Ac7729/Ac7643S QTL 1996
  - Bologna Os420/Iab78 QTL 1998
Maize Bin Map
Maize chr 1
Maize chr 1
Rice chr 8 - maize chr 1
## Marker Database

### View Maize RFLP "CSU675"

**Details**
- **ID**: 4273
- **Name**: CSU675

**Source/Library**
- csu675a(prh)
- csu675b(prh)
- CSU675E3
- csuh00675

**Map Positions (8)**

<table>
<thead>
<tr>
<th>Species</th>
<th>Map Type</th>
<th>Map Set</th>
<th>Name</th>
<th>Chr.</th>
<th>Start</th>
<th>Stop</th>
<th>Map Links</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oryza sativa</td>
<td>Sequence</td>
<td>Gramene Annotated Nipponbare</td>
<td>CSU675</td>
<td>8</td>
<td>24,568,487</td>
<td>24,568,660</td>
<td>View in Genome</td>
<td>View Comparative Map</td>
</tr>
<tr>
<td>Sorghum bicolor</td>
<td>Genetic</td>
<td>Paterson 2003</td>
<td>CSU675</td>
<td>1</td>
<td>3.8 cM</td>
<td></td>
<td>View Comparative</td>
<td></td>
</tr>
<tr>
<td>Zea mays</td>
<td>Genetic</td>
<td>IDM neighbors</td>
<td>csu675a(prh)</td>
<td>1</td>
<td>479 cM</td>
<td></td>
<td>View Comparative</td>
<td></td>
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### Associations (5)

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<th>Direction</th>
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<th>Analysis</th>
<th>Assoc. Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>To</td>
<td>AA072449</td>
<td>EST</td>
<td>Zea mays</td>
<td>gss_poaceae</td>
<td>shared_synonym</td>
</tr>
<tr>
<td>To</td>
<td>SOG0631</td>
<td>OVERGO</td>
<td>Zea mays</td>
<td>SOG_OVERGO</td>
<td>related_probe</td>
</tr>
<tr>
<td>From</td>
<td>AA072449</td>
<td>EST</td>
<td>Zea mays</td>
<td>gss_poaceae</td>
<td>shared_synonym</td>
</tr>
<tr>
<td>From</td>
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<td>Maize Bin</td>
<td>Zea mays subsp. mays</td>
<td>bin_marker</td>
<td>bin_marker</td>
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<tr>
<td>From</td>
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<td>Maize Bin</td>
<td>Zea mays subsp. mays</td>
<td>bin_marker</td>
<td>bin_marker</td>
</tr>
</tbody>
</table>
Ontologies

- Plant ontology
  - Plant structure (morphology, organs, tissue and cell types)
  - Growth stages
- Trait ontology
  - Plant traits and phenotypes
- Gene ontology
  - Molecular functions
  - Biological processes
  - Cellular components
- Environment ontology
- Taxonomy ontology
### Summary for Gramene taxonomy Term: Zea mays (GR_tax:014450)

| Term Name | Zea mays  
| Synonym   | Zea mays var. japonica.  
| Aspect    | Taxonomy  
| External References | NCBI_taxid:4577  
| Derivation |  

- **all (all)** #512041
  - [i] Magnoliophyta (GR_tax:017503) #117906
    - [i] Liliopsida (GR_tax:017503) #117905
      - [i] commelinids (GR_tax:017504) #117904
        - [i] Poales (GR_tax:014481) #117904
          - [i] Poaceae (GR_tax:013699) #117904
            - [i] PACAD clade (GR_tax:013697) #16260
              - [i] Poaceae (GR_tax:013699) #15509
                - [i] Andropogoneae (GR_tax:012443) #14562
                  - [i] Zea (GR_tax:014447) #12989
        - [i] Zea mays (GR_tax:014450) #12713
          - [i] Zea mays subsp. huehuetenangensis (GR_tax:014451) #0
          - [i] Zea mays subsp. mexicana (GR_tax:014452) #0
          - [i] Zea mays subsp. parviglumis (GR_tax:014453) #45
          - [i] Zea mays subsp. ramosa (GR_tax:014454) #0
          - [i] Zea mays subsp. mays x Zea mays subsp. parviglumis (GR_tax:017762) #0
          - [i] Zea mays subsp. mays x Zea perennis (GR_tax:017763) #0

- [i] Zea (GR_tax:014447)

### Parent Term (1)
- [i] Zea mays subsp. huehuetenangensis (GR_tax:014451)
- [i] Zea mays subsp. mexicana (GR_tax:014452)
- [i] Zea mays subsp. parviglumis (GR_tax:014453)
- [i] Zea mays subsp. ramosa (GR_tax:014454)
- [i] Zea mays subsp. mays x Zea mays subsp. parviglumis (GR_tax:017762)
- [i] Zea mays subsp. mays x Zea perennis (GR_tax:017763)

### Child Terms (7)
- [i] Zea mays subsp. huehuetenangensis (GR_tax:014451)
- [i] Zea mays subsp. mexicana (GR_tax:014452)
- [i] Zea mays subsp. parviglumis (GR_tax:014453)
- [i] Zea mays subsp. ramosa (GR_tax:014454)
- [i] Zea mays subsp. mays x Zea mays subsp. parviglumis (GR_tax:017762)
- [i] Zea mays subsp. mays x Zea perennis (GR_tax:017763)

### Total Number of Annotations:
- 12713 objects, 12713 associations
- QTL (1681) Marker species (3) Gene (6680) Protein (4330)

### QTL:
- Zea mays (1681)

### Marker species:
- Zea mays (1)
- Zea mays subsp. mays (2)

### Gene:
- Zea mays subsp. mays (6680)

### Protein:
- Zea mays (4210) Zea mays subsp. mays (75) Zea mays subsp. parviglumis (45)
Gene Ontology

Summary for GO Term: defense response (GO:0006952)

**Term Name**
defense response

**Synonym**
antimicrobial peptide activity, defence response, defense/immunity protein activity, GO:0002217, GO:0042829, physiological defense response.

**Aspect**
Biological Process

**Definition**
Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.

**External References**
GOC:go_curators

**Source Ontology Database Link**
The GO browser of Gene Ontology Database.

Total Number of Annotations:
1346 objects, 1359 associations

**Gene:**
- Oryza sativa(9)
- Ensembl rice gene(470)
- Ensembl maize gene(18)
- Ensembl arabidopsis gene(368)
- Protein(181)

**Protein:**
- Arabidopsis thaliana(368)
- Aegilops ventricosa(7)
- Lolium perenne(13)
- Oryza sativa (indica cultivar-group)(14)
- Secale strictum(1)
- Triticum monococcum(2)
- Triticum turgidum subsp. durum(5)
- Avena sativa(7)
- Hordeum vulgare(72)
- Hordeum vulgare subsp. vulgare(3)
- Hordeum vulgare subsp. vulgare(3)
- Oryza officinalis(3)
- Oryza rufipogon(7)
- Oryza sativa(26)
- Seccharum sp.(1)
- Secale cereale(1)
- Sorghum bicolor(17)
- Pennisetum glaucum(3)
- Thinopyrum intermedium(3)
- Triticum aestivum(48)
- Triticum aestivum/Thinopyrum intermedium alien addition line(2)
Defense response proteins in maize

- Rust resistance-like protein RP1-2
- Rust resistance protein Rp1-kp3
Gramene Staff

• Pl’s
  – Lincoln Stein
  – Susan McCouch
  – Doreen Ware
  – Pankaj Jaiswal
  – Ed Buckler

• Curators
  – Junjian Ni
  – Noel Yap
  – Isaak Tecle
  – Dean Ravenscroft
  – Chih-Wei Tung

• Developers
  – Ken Youens-Clark
  – Shuly Avraham
  – Liya Ren
  – Will Spooner
  – Payan Canaran
  – Sharon Wei
  – Terry Casstevens
  – Jim Thomason

• Coordinators
  – Chengzhi Liang
  – Claire Hebbard