

The *Intermedium-C* gene in barley

Deploying Strudel to provide a facile interface between genetic map location in barley and comparative inference of the gene content of the interval using the rice and *Brachypodium* genomes

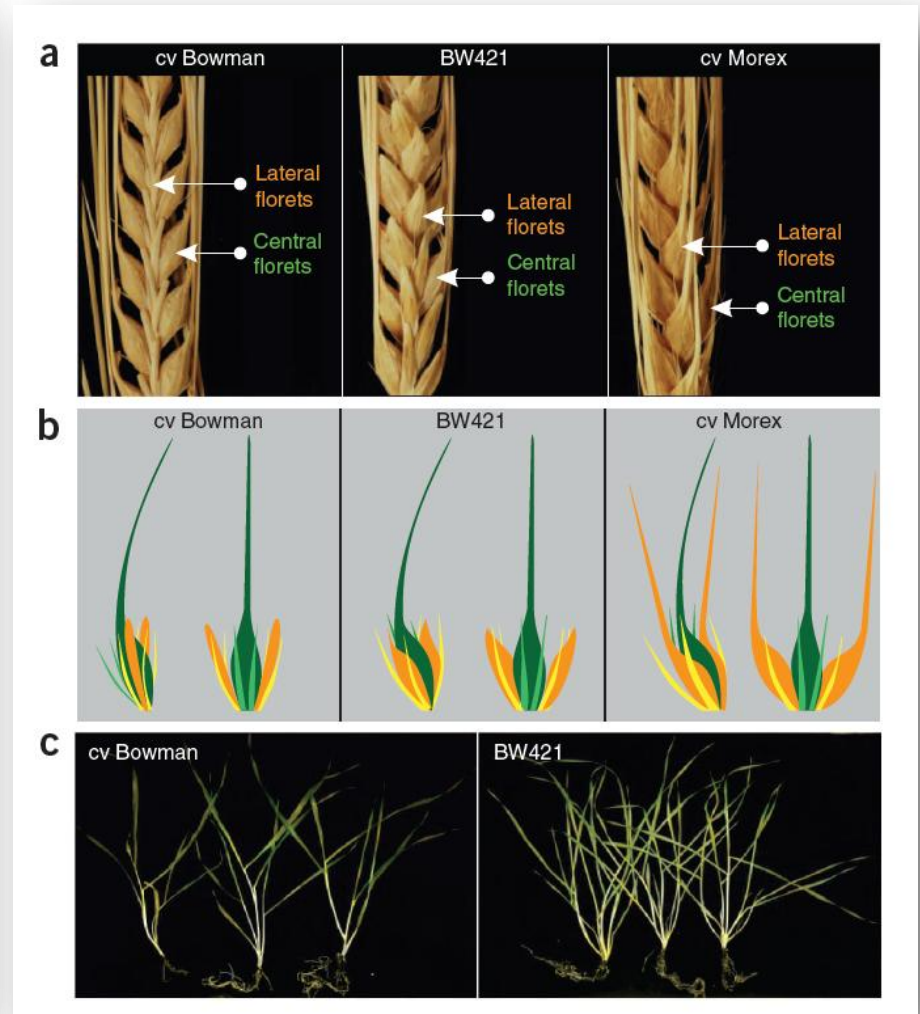
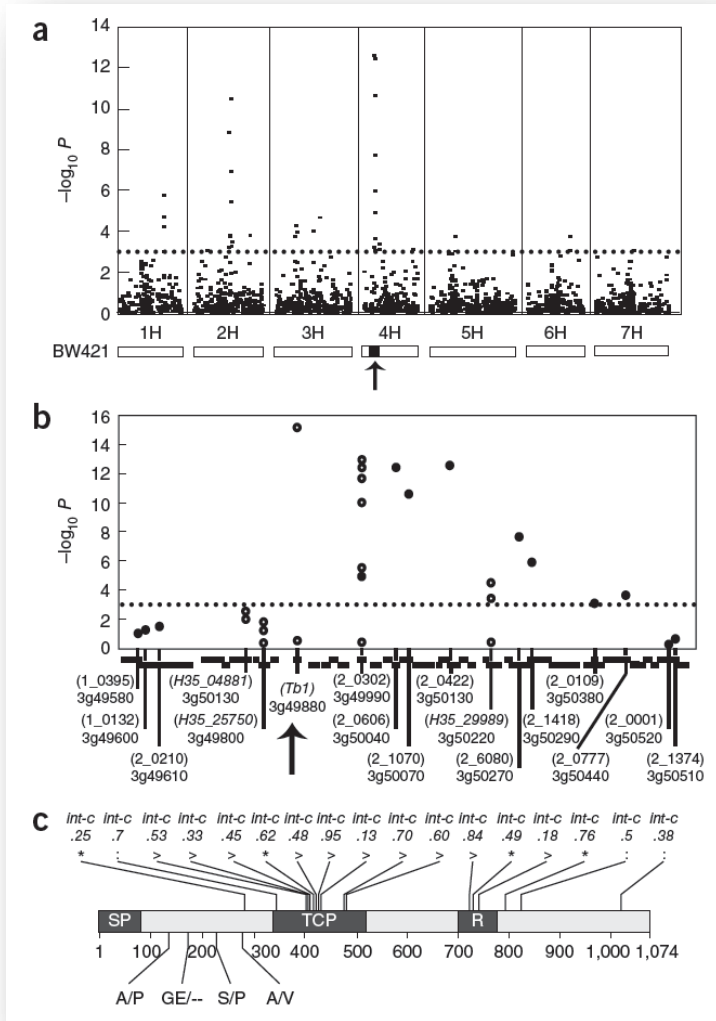
nature
genetics

INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1*

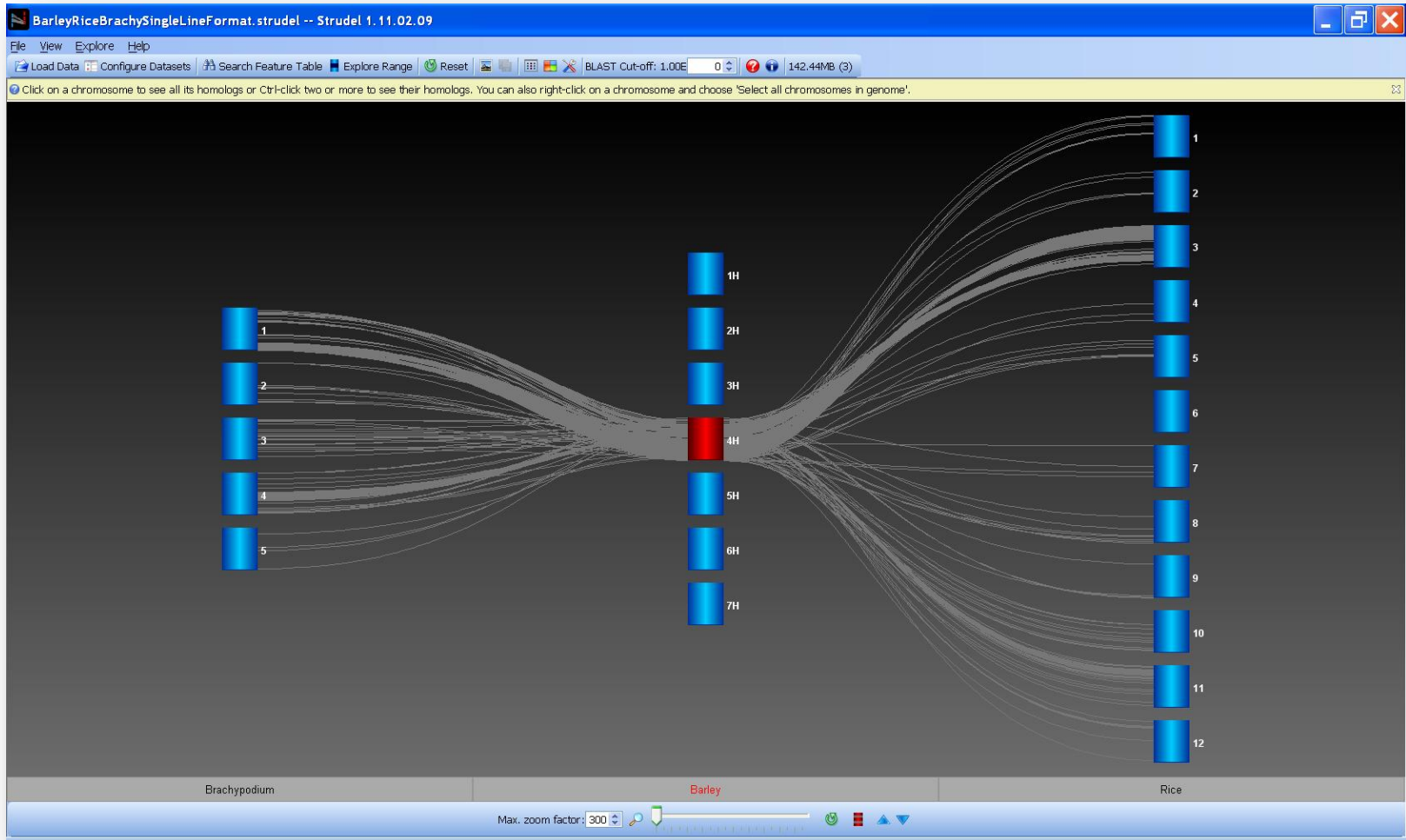
Luke Ramsay¹, Jordi Comadran¹, Arnis Druka¹, David F Marshall¹, William T B Thomas¹, Malcolm Macaulay¹, Katrin MacKenzie², Craig Simpson¹, John Fuller¹, Nicola Bonar¹, Patrick M Hayes³, Udda Lundqvist⁴, Jerome D Franckowiak⁵, Timothy J Close⁶, Gary J Muehlbauer⁷ & Robbie Waugh¹

Ramsay *et al* 2011 Nature Genetics 43(2) 169-172

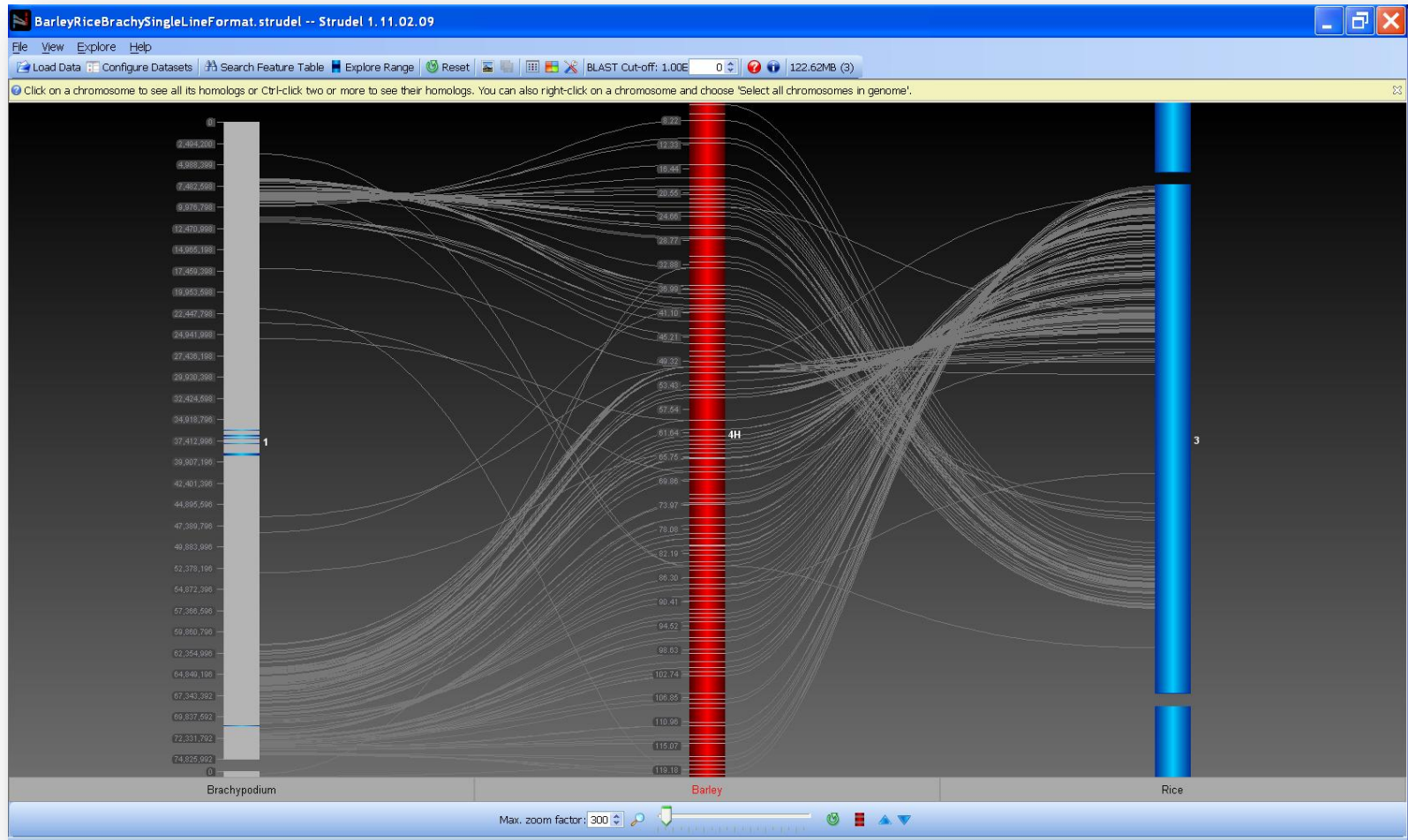
The int-C mutation has been genetically mapped to an interval on chromosome 4H of the barley SNP map



Barley chromosome 4H has syntenic regions with rice Os03g and Brachy1g



We can zoom to see these syntenic regions in more detail and identify inversions and other major re-arrangements



The Int-C barley map interval from Ramsay *et al* 2011

SNP	Consensus Map SNP	Barley Chr	Position (cM)
1_0132	11_0180	4H	24.59
1_0395	12_0092	4H	24.59
1_0562	12_0130	4H	24.59
1_0626	12_0146	4H	24.59
1_1060	12_0248	4H	24.59
1_1175	12_0287	4H	24.59
2_0210	11_0179	4H	24.59
2_0422	11_0406	4H	24.59
3_0394	12_0807	4H	24.59
2_0109	11_0084	4H	26.19
2_0302	11_0269	4H	26.19
2_0606	11_0569	4H	26.19
2_0680	11_0649	4H	26.19
2_1070	11_0995	4H	26.19
2_1418	11_1284	4H	26.19
2_0777	11_0752	4H	26.66
2_0001	11_0001	4H	28.15
1_0031	11_0044	4H	28.40
2_1374	11_1254	4H	28.40

This interval can be located onto the consensus genetic map of barley supplied as part of the example data set for Strudel. The above table show the conversion between the SNP names in the Ramsay *et al* paper and the SNP names in the Close *et al* consensus map*.

*Close *et al* (2009)Development and implementation of high-throughput SNP genotyping in barley BMC Genomics 10:582

The interval range of the barley map can be easily defined

The screenshot displays the Strudel 1.11.02.09 software interface. The main window title is "BarleyRiceBrachySingleLineFormat.strudel -- Strudel 1.11.02.09". The menu bar includes "File", "View", "Explore", and "Help". The toolbar contains "Load Data", "Configure Datasets", "Search Feature Table", "Explore Range", "Reset", and "BLAST Cut-off: 1.00E-04". The status bar shows "95.56MB (3)".

A dialog box titled "List features in range" is open, allowing the user to select a range for listing features. The dialog contains the following fields and options:

- Genome: Barley
- Chromosome: 4H
- Range start: 24.59
- Range end: 28.40
- Show all labels
- Show all homologies

The dialog has "Find" and "Cancel" buttons. The background shows a genomic map with chromosomes 1-12 on the right and Brachypodium, Barley, and Rice at the bottom. The status bar at the bottom shows "Max. zoom factor: 300".

Detailed information for the defined interval can be displayed along with HTML links to the appropriate genome resources

Selected region -- info and controls:

Info Controls

Filter by reference genome: <non...>

Show all labels

Show all homologies

Always highlight in white

Filter by name or annotation:

Click on a row to highlight a homolog (multiple selection: Ctrl-click). Click on a homolog name to show annotation in a web browser:

Target n...	Target posi...	Target chromos...	Homolog	Homolog gen...	Homolog chromos...	Homolog posi...	BLAST e-y...	Homolog annotation
12_10626	24.59	4H	LOC_Os03d49510	Rice	3	2.817328E7	0.0	phosphatidylinositol-4-phosphate 5-kinase, putative, expressed
12_10626	24.59	4H	Bradi1g11530	Brachypodium	1	8577640.0	0.0	
12_10395	24.59	4H	LOC_Os03d49580	Rice	3	2.8229248E7	0.0	eukaryotic peptide chain release factor subunit 1-1, putative, expressed
12_10395	24.59	4H	Bradi1g10900	Brachypodium	1	7931948.0	0.0	
12_10395	24.59	4H	Bradi1g10880	Brachypodium	1	7919251.0	0.0	
11_10132	24.59	4H	LOC_Os03d49600	Rice	3	2.82384E7	0.0	Os3glu7 - beta-glucosidase, exo-beta-glucanase, expressed
11_20710	24.59	4H	LOC_Os03d49610	Rice	3	2.82471E7	0.0	Os3holu8 - beta-glucosidase, exo-beta-glucanase, high similarity to Os3holu7, expressed

We can zoom in for more detail

BarleyRiceBrachySingleLineFormat.strudel -- Strudel 1.11.02.09

File View Explore Help

Load Data Configure Datasets Search Feature Table Explore Range Reset BLAST Cut-off: 1.00E 96.72MB (3)

Click on a chromosome to see all its homologs or Ctrl-click two or more to see their homologs. You can also right-click on a chromosome and choose 'Select all chromosomes in genome'.

Brachypodium Barley Rice

Max. zoom factor: 300

Selected region -- info and controls:

Info Controls

Filter by reference genome: <non...>

Show all labels

Show all homologs

Always highlight in white

Filter by name or annotation:

Target n...	Target posi...	Target chromos...	Homolog	Homolog gen...	Homolog chromos...	Homolog posi...	BLAST e-v...	Homolog annotation
12_10626	24.59	4H	LOC_Os03g49510	Rice	3	2.817328E7	0.0	phosphatidylinositol-4-phosphate 5-kinase, putative, expressed
12_10626	24.59	4H	Bradi1g11530	Brachypodium	1	8577640.0	0.0	
12_10395	24.59	4H	LOC_Os03g49580	Rice	3	2.8229248E7	0.0	eukaryotic peptide chain release factor subunit 1-1, putative, expressed
12_10395	24.59	4H	Bradi1g10900	Brachypodium	1	7931948.0	0.0	
12_10395	24.59	4H	Bradi1g10880	Brachypodium	1	7919251.0	0.0	
11_10132	24.59	4H	LOC_Os03g49600	Rice	3	2.82384E7	0.0	Os3bglu7 - beta-glucosidase, exo-beta-glucanase, expressed
11_20210	24.59	4H	LOC_Os03g49610	Rice	3	2.82471E7	0.0	Os3hlu18 - beta-xylosidase, exo-beta-xylosanase, high similarity to Os3hlu17, expressed

We can link to the orthologous region in rice via the MSU browser and scan for candidate genes

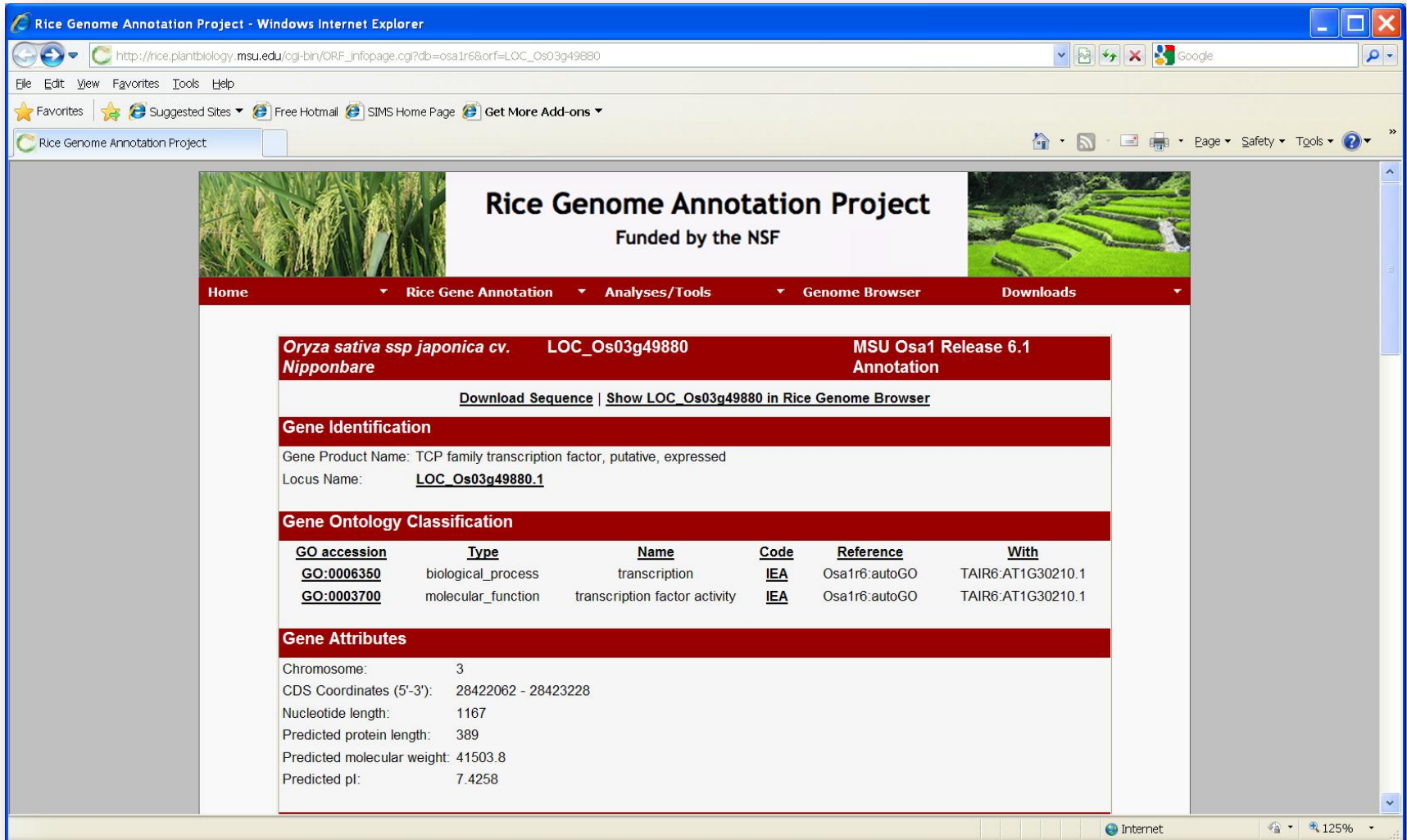
The screenshot displays the Rice Genome Annotation Project Rice Genome Browser interface. The browser window title is "Rice Genome Annotation Project Rice Genome Browser - Release 6.1: Chr3:28355669..28516718 - Windows Internet Explorer". The address bar shows the URL "http://rice.plantbiology.msu.edu/cgi-bin/gbrowse/rice/#search".

The main content area is titled "Details" and shows a genomic map of a region on chromosome 3, spanning from approximately 28350k to 28510k. The map includes a scale bar at the top and a list of gene annotations below. The annotations are organized into two sections:

- MSU Osa1 Rice Loci:** This section lists various gene models and their descriptions. Key entries include:
 - LOC_Os03g49810: hypothetical protein
 - LOC_Os03g49820: hypothetical protein
 - LOC_Os03g49830: expressed protein
 - LOC_Os03g49840: hypothetical protein
 - LOC_Os03g49850: hypothetical protein
 - LOC_Os03g49860: hypothetical protein
 - LOC_Os03g49870: transposon protein, putative, Mariner sub-class
 - LOC_Os03g49880: TCP family transcription factor, putative, expressed
 - LOC_Os03g49890: hypothetical protein
 - LOC_Os03g49900: zinc finger, C3HC4 type domain containing protein, expressed
 - LOC_Os03g49910: pentatricopeptide, putative
 - LOC_Os03g49920: retrotransposon protein, putative, Ty1-copia subclass
 - LOC_Os03g49930: integral membrane protein, putative, expressed
 - LOC_Os03g49940: expressed protein
 - LOC_Os03g49960: expressed protein
 - LOC_Os03g49970: hypothetical protein
 - LOC_Os03g49980: retrotransposon protein, putative
 - LOC_Os03g49990: GRHS family tran
- MSU Osa1 Rice Gene Models:** This section shows the gene models for the above loci, including their coordinates and orientations. For example, LOC_Os03g49810.1 is located at approximately 28355k and is transcribed to the right. LOC_Os03g49940.1 is located at approximately 28495k and is transcribed to the right. LOC_Os03g49960.5, LOC_Os03g49960.1, LOC_Os03g49960.1, and LOC_Os03g49960.2 are clustered together at approximately 28495k and are transcribed to the left.

The interface includes a "Clear highlighting" button and an "Update Image" button. At the bottom, there is a "Tracks" section with a "Region" checkbox and options for "All on" and "All off". The status bar at the bottom shows "Done" and "Internet".

The MSU rice resource gives us more detail on the rice orthologue of TB1



Rice Genome Annotation Project
Funded by the NSF

Home | Rice Gene Annotation | Analyses/Tools | Genome Browser | Downloads

Oryza sativa ssp japonica cv. Nipponbare **LOC_Os03g49880** **MSU Osa1 Release 6.1 Annotation**

[Download Sequence](#) | [Show LOC_Os03g49880 in Rice Genome Browser](#)

Gene Identification

Gene Product Name: TCP family transcription factor, putative, expressed
Locus Name: [LOC_Os03g49880.1](#)

Gene Ontology Classification

GO accession	Type	Name	Code	Reference	With
GO:0006350	biological_process	transcription	IEA	Osa1r6:autoGO	TAIR6:AT1G30210.1
GO:0003700	molecular_function	transcription factor activity	IEA	Osa1r6:autoGO	TAIR6:AT1G30210.1

Gene Attributes

Chromosome: 3
CDS Coordinates (5'-3'): 28422062 - 28423228
Nucleotide length: 1167
Predicted protein length: 389
Predicted molecular weight: 41503.8
Predicted pI: 7.4258

We can do the same for Brachypodium using the MIPS Brachypodium Gbrowse interface

The screenshot displays the MIPS Brachypodium Gbrowse interface in a Mozilla Firefox browser window. The address bar shows the URL: <http://mips.helmholtz-muenchen.de/gbrowse/plant/cgi-bin/gbrowse/brachy/#search>. The browser title is "Brachypodium distachyon: chr01_pseudomolecule:8029867..8229866".

The interface includes a search bar with the text "chr01_pseudomolecule:8029:" and a "Go" button. Below the search bar, the "Data Source" is identified as "Brachypodium distachyon". Navigation controls for "Scroll/Zoom" are visible, including "Show 200 kbp" and a "Flip" checkbox.

The main content area is divided into several tracks:

- Overview:** A horizontal bar representing the chromosome region from 0M to 70M.
- Region:** A detailed view of the region from 8030k to 8220k.
- DNA/GC Content:** A line graph showing GC content, with values ranging from 34% to 67%.
- transcript:** A track showing gene models and transcripts. Key entries include:
 - Bradi1g11027.1: putative protein
 - Bradi1g11040.1: 1-phosphatidylinositol-4-phosphate 5-kinase activity (Blast200)
 - Bradi1g11050.1: putative protein
 - Bradi1g11060.1: Zea Maize teosintebranded1 (tbl) ortholog, syntenic to Sb01g010690, Os
 - Bradi1g11070.1: RING, subfamily zinc finger (C3HC4-type RING finger) famil
 - Bradi1g11080.1: putative protein
 - Bradi1g11090.1: homolog of DELLA a gene involved i
 - Bradi1g11100.1: putative protein
 - Bradi1g11101.1: protein serine
 - Bradi1g11110.1: putative prote

At the bottom, the "Tracks" section includes options for "Analysis" (All on / All off) and checkboxes for "Blast Against Displayed Sequence", "GeneFinder Features", and "Restriction Sites".

And get to detailed information of the Brachypodium orthologue of TB1

Brachypodium distachyon project - Mozilla Firefox

http://mips.helmholtz-muenchen.de/plant/brachypodium/reports.jsp/geneticElement.jsp?gene=Bradi1g11060.1

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Member of HELMHOLTZ GEMEINSCHAFT

Brachypodium distachyon project

Element Report

Name: Bradi1g11060.1 **Version: 1**

Element type: transcript

Description: Zea Maize teosintebranched1 (tb1) ortholog, syntenic to Sb01g010690, Os03g49880, ZmEvi041455.02.

Comment: ID=Bradi1g11060.1;Parent=Bradi1g11060

Contig: [chr01_pseudomolecule](#)

Gene features

Size (bp): 1158

Spliced size (bp): 1158

Start: 8129288

Stop: 8130445

Subelements:

Type	Start	Stop	Size
exon	1	1158	1158

References

Confidence: Class_2

mips
münchen information center
for protein sequence

Done

BB 107 217 142 otaio