

Introduction to Phytozome Plant comparative genomics portal

Simon Prochnik, US DOE - Joint Genome Institute
IITA, Nairobi, Kenya September 2010

Tuesday, September 21, 2010

1

Phytozome comparative plant genomics portal

- Introduction to the Phytozome portal v.5
- How you can use Phytozome to analyze cassava data
- Searching in Phytozome
- Viewing genes with the gbrowse genome browser

- workshop questions

- Preview of Phytozome v.6 which will be released in October

Tuesday, September 21, 2010

2

Phytozome v.5



Tuesday, September 21, 2010

3

<http://www.phytozome.net/>

The screenshot shows the Phytozome website interface. At the top, there is a navigation bar with the "phytozome" logo on the left and "JGI Joint Genome Institute" and "C I G Center for Integrative Genomics" on the right. Below the logo is a search bar and buttons for "Search", "BLAST", "Info", "BioMart", "Help", and "Contact". The main content area features a tree diagram titled "Phytozome: a tool for green plant comparative genomics". The tree has 16 branches, each labeled with a species name: *Populus trichocarpa*, *Ricinus communis*, *Medicago truncatula*, *Manihot esculenta*, *Glycine max*, *Cucumis sativus*, *Vitis vinifera*, *Arabidopsis lyrata*, *Zea mays*, *Arabidopsis thaliana*, *Sorghum bicolor*, *Carica papaya*, *Brachypodium distachyon*, *Mimulus guttatus*, *Oryza sativa*, *Selaginella moellendorffii*, and *Physcomitrella patens*, *Chlamydomonas reinhardtii*. To the right of the tree are two dropdown menus: "Explore a genome: Select an organism:" and "Find a gene family: Select node:". Below the tree is a "News" section with a list of recent updates, including "BLAST interface and Browser released for latest maize B73 genome assembly", "Peach genome released", "Phytozome v5.0 released", "Pseudomolecule maize assembly and annotation now available at Phytozome", and "Cassava genome released". Each news item includes a date, a brief description, and a "[more]" link.

Tuesday, September 21, 2010

4

phytozome JGI Joint Genome Institute C I G Center for Integrative Genomics

Search BLAST Info BioMart Help Contact

Phytozome: a tool for green plant comparative genomics

Explore a genome:
Manihot esculenta

- or -

Find a gene family:
Select node

Selected:
Manihot esculenta

cassava

Browse BLAST

[more info]

News

11 May 2010 **BLAST interface and Browser released for latest maize B73 genome assembly** The Maize Genome Sequencing Consortium [more]

1 Apr 2010 **Peach genome released.** Access to the Assembled Peach Genome is now available via Gbrowse and BLAST at Phytozome, [more]

8 Jan 2010 **Phytozome v5.0 released.** Version 5.0 of Phytozome is now available, and incorporates both updated and newly released plant [more]

23 Nov 2009 **Pseudomolecule maize assembly and annotation now available at Phytozome.** Maize version 4a.53 Pseudomolecule asse [more]

9 Nov 2009 **Cassava genome released.** Version 1.1 of the Cassava (Manihot esculenta) assembly and annotation is now available for dow [more]

Tuesday, September 21, 2010

5

Ways to get to your data: browsing and text/sequence searching

phytozome JGI Joint Genome Institute C I G Center for Integrative Genomics

Search BLAST Info BioMart Help Contact

Phytozome: a tool for green plant comparative genomics

Explore a genome:
Manihot esculenta

- or -

Find a gene family:
Select node

Selected:
Manihot esculenta

cassava

Browse BLAST

[more info]

- Whole database searching using links at top of web page:
 - Search = text search
 - BLAST/BLAT = sequence search
- Cassava specific searching using links on cassava organism page
 - Browse link takes you to the gbrowse genome browser
 - BLAST link takes you to a blast sequence search.

Tuesday, September 21, 2010

6

Genome, feature coordinates

Scaffold overview

Annotation, feature details

Transcripts and alternative transcripts

Track visibility controls

Browser settings

User track/data upload

The screenshot displays the Phytozome genome browser interface for *Manihot esculenta*. At the top, it shows the scaffold overview for scaffold00234, positions 425,000 to 474,999. Below this, there are several tracks and control panels:

- Search:** A search bar with the current location `scf00234:425000..474999` and a search button.
- Overview:** A horizontal bar representing the scaffold with a yellow highlight indicating the current view.
- Details:** A detailed view of the scaffold with various tracks:
 - RepeatMasker:** Shows masked repeats as black bars.
 - Transcript:** Shows transcript models as lines with arrows indicating direction.
 - BLASTX Plant Peptides:** Shows BLASTX alignments as vertical bars with associated accession numbers.
 - BLASTX Plant ESTs:** Shows BLASTX alignments for ESTs.
 - Plant TA/EST/CDNA:** Shows plant-specific annotations.
 - BLASTX Plant Peptides:** Shows BLASTX alignments for peptides.
- Tracks:** A panel with checkboxes for various tracks:
 - Analysis:** VISTA Plot A. thaliana (TAIR5), VISTA Plot C. sativa, VISTA Plot M. truncatula v3.0, VISTA Plot R. communis, VISTA Plot S. soybean, VISTA Plot P. perla v2.0, VISTA Plot Rice v4, VISTA Plot: Wine grape.
 - Alignments:** BLASTX Plant Peptides, BLASTX Plant peptides, PASA Assembled EST, RepeatMasker.
 - General:** DNA sequence/GC content (zoom in to 100bp), Gaps, User Blast.
 - Transcripts:** At on, At off, Transcript.
- Display Settings:** Image Width (800), Cache tracks, Draggable tracks, Show tooltips, Highlight feature(s), Track Name Table, Highlight regions.
- Add your own tracks:** Upload a file, Add remote annotations, Enter Remote Annotation URL.

Tuesday, September 21, 2010

7

Protein page

- Gene locus viewer: transcript/gene models, ESTs, BLAST tracks
- Protein and nucleotide sequences for a gene model and BLAST analysis at Phytozome or against nr database with NCBI BLAST
- Detailed peptide homology (limited by species/clade)
- Gene Ancestry tracks evolution of the gene across the phylogenetic tree of plants

Tuesday, September 21, 2010

8

Protein Page top half

The screenshot shows the top half of a protein page on the Phytosome website. At the top, the Phytosome logo is on the left, and the Joint Genome Institute and Center for Integrative Genomics logos are on the right. Navigation buttons for Search, BLAST, Info, BioMart, Help, and Contact are present. The main title is "Manihot esculenta gene cassava22597.valid.m1". Below this are tabs for "About this gene", "Sequences", "Peptide Homologs", and "Gene Ancestry". The "Info" section contains a table with the following data:

Locus name	cassava22597.valid.m1
Transcript name	cassava22597.valid.m1
Description	
Links to external DBs	

The "Functional annotations" section shows a Pfam domain: Pfam:03138, Plant protein family. Below this is a "Protein domain view" showing a single yellow bar representing the protein domain from position 1 to 665.

Tuesday, September 21, 2010

9

Protein page bottom half

Go back to Gbrowse view by clicking here

The screenshot shows the bottom half of the protein page, displaying various genomic tracks. At the top, it says "Genomic view: Location: scaffold00234: 461372 - 468502 :: View in Gbrowse environment". Below this is a scale from 461k to 468k. The tracks include:

- Transcript:** Shows the cassava22597.valid.m1 transcript with exons and introns.
- Alt_transcript:** Shows an alternative transcript.
- BLASTX Plant peptides:** Shows BLASTX results for various plant peptides, including Poptr|pt009751n.1, Poptr|pt031664n.1, Ricco|30072.m000984.1, Cucsa|Cucsa_340360.1.1, Clusa|Clusa8644070.1.1, Medtr|Medtr3g122820.1.1, and Medtr|Medtr7g012260.1.0.
- BLASTX Plant Peptides:** Shows BLASTX results for other plant species, including Arath|AT3003810.1.GX17H, Orysa|13105.m00417.GX19H, Arath|AT3630300.1.GX15H, Orysa|13104.m1817.GX2P, Arath|ATC600350.1.GX3P, Arath|AT3630300.1.GX17H, Arath|AT3602250.1.GX14H, Arath|AT4016680.1.GX30H, Orysa|13102.m05607.GX8M, Orysa|13101.m00754.GX22H, Arath|AT2003280.1.GX17H, and Arath|AT5615740.1.GX19H.
- RepeatMasker:** Shows masked repeats, including "AT_rich" 1 32.
- Plant TR/EST/cDNA:** Shows plant TR/EST/cDNA data.

Default tracks

Tuesday, September 21, 2010

10

Protein page - Sequences tab

[About this gene](#)
[Sequences](#)
[Peptide Homologs](#)
[Gene Ancestry](#)

[Genomic sequence](#)
[Transcript sequence](#)
[CDS sequence](#)
[Peptide sequence](#)
[Show all](#)
 key: [5' UTR exons](#) [CDS exons](#) [3' UTR exons](#)

- Genomic sequence [7131 nucleotides]
- Transcript sequence [2125 nucleotides]
- CDS sequence [1998 nucleotides]
- Peptide sequence [665 residues]

[BLAST this sequence:](#) [Phytozome](#) [NCBI](#)
[BLAST this sequence:](#) [Phytozome](#) [NCBI](#)
[BLAST this sequence:](#) [Phytozome](#) [NCBI](#)
[BLAST this sequence:](#) [Phytozome](#) [NCBI](#)





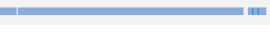

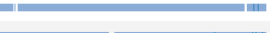

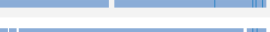

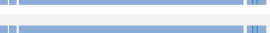

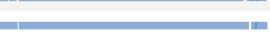

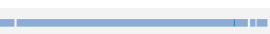

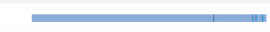

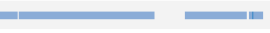

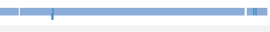



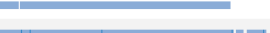

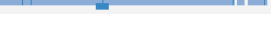


Tuesday, September 21, 2010

11

Protein page - Peptide homologs tab

[About this gene](#)
[Sequences](#)
[Peptide Homologs](#)
[Gene Ancestry](#)

Homolog filter

Org	Defline	MRSF Score	Similarity	
 Mes	cassava23954.valid.m1	MAL	3079 93.8%	
 Cpa	evm.model.supercontig_51.143	RPO	2577 83.9%	
 Vvi	GSVIVT00025295001	RPO	2576 84.2%	
 Ptr	POPTR_0019s05230.1: similar to expressed protein in Arabidopsis	MAL	2495 83.3%	
 Ath	AT3G03810.1: EDA30 (embryo sac development arrest 30)	RPO	2460 83.2%	
 Aly	477634	RPO	2444 82.6%	
 Gma	Glyma04g40730.1	EU1	2383 81.5%	
 Csa	Cucsa.340360.1	EU1	2377 80.5%	
 Ptr	POPTR_0013s05280.1	MAL	2369 76.7%	
 Rco	30072.m000984: conserved hypothetical protein	MAL	2324 78.3%	
 Mtr	Medtr1g008430.1: Hypothetical plant protein	EU1	2232 78.8%	
 Gma	Glyma06g14070.1	EU1	2202 72.6%	
 Mtr	Medtr3g122820.1: Hypothetical plant protein	EU1	2139 71.6%	
 Mgu	mgf010950m	EUR	2044 76.2%	

Tuesday, September 21, 2010

12

Protein page - Gene Ancestry tab

Node in phylogenetic tree List of protein families Membership of protein family

Gene families containing this gene:

SIZE	NODE	DESCRIPTION	A. esculenta	P. commutis	A. trichocarpa	A. thaliana	C. maritima	C. sinensis	A. thaliana	A. lyrata	C. papaya	V. vinifera	A. gossypium	S. tuberosum	Z. mays	G. sinense	B. distachyone	S. bicolor	M. domestica	A. thaliana	C. maritima	
572	Viridiplantae	Hypothetical gene (#23249114)	44	26	48	31	70	28	34	33	33	31	31	27	35	30	29	18	24	-	-	-
572	Embryophyte	Hypothetical gene (#23103069)	44	26	48	31	70	28	34	33	33	31	31	27	35	30	29	18	24	-	-	-
120	Tracheophyte	Hypothetical gene (#22962461)	9	5	10	6	17	6	6	6	8	6	7	7	10	7	7	3	-	-	-	-
20	Angiosperm	Hypothetical gene (#22928094)	2	1	2	2	2	1	1	1	1	1	1	1	2	1	1	-	-	-	-	-
15	Eudicot	Hypothetical gene (#22558210)	2	1	2	2	2	1	1	1	1	1	1	-	-	-	-	-	-	-	-	-
14	Rosid Pre-Duplication	Hypothetical gene (#22462745)	2	1	2	2	2	1	1	1	1	1	-	-	-	-	-	-	-	-	-	-
14	Rosid Post-Duplication	Hypothetical gene (#22423559)	2	1	2	2	2	1	1	1	1	1	-	-	-	-	-	-	-	-	-	-
10	Eurosid	Hypothetical gene (#22243378)	2	1	2	2	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5	Malpighiales	Hypothetical gene (#22076418)	2	1	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1	<i>Manihot esculenta</i>	cassava22597.valid.m1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Tuesday, September 21, 2010

13

Whole database searches: keyword, BLAST, BLAT

Or click on BLAST or BLAT query tabs and search by sequence

Keyword search **BLAST query** BLAT query

Gene Family Keyword Search

Enter gene symbol or name, function, domain name → SEARCH TERM: add trailing wildcard

SEARCH NODE:

SEARCH TYPE: Ontologies Symbols/Identifiers/Define Everything

FAMILY MEMBERS: Restrict organisms

- Keyword search might be “starch” or “drought” or “protein kinase”
- BLAST for general sequence searching
- BLAT for aligning transcript or peptide sequence to the genome, but taking splice sites into account

Tuesday, September 21, 2010

14

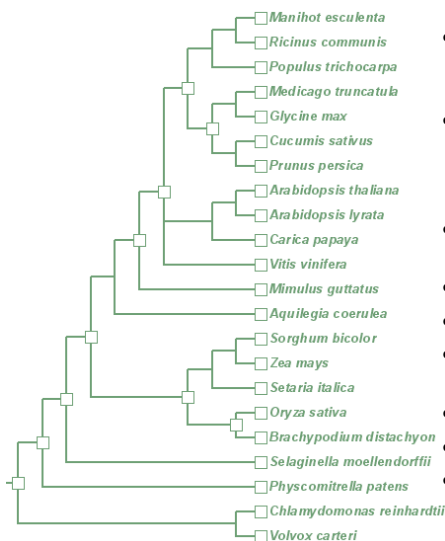
Bulk data download with BioMart

- Custom query for large datasets, e.g.
 - Sequences, gene regions, proteins for one or more whole genomes
- To build a query
 - Choose a dataset (genome or gene sequences)
 - Select search Filters, output data Attributes (additional datasets if desired)
 - Select Count to see how many records your search will return
 - Select Results to download the results of your search

Tuesday, September 21, 2010

15

Phytozome v.6 protein family construction



- 12 core genomes: *Sorghum*, *Selaginella*, *Brachypodium*, rice, *Arabidopsis*, peach, *Mimulus*, grape, *Physcomitrella*, *Chlamydomonas*, poplar
- double-affine Smith-Waterman alignment score provides distance metric between pairs of proteins, normalized to the best score of either of the proteins in a pair against itself. Score is in range 0 to 1.
- subtract score from shuffled proteins to account for random noise
- at a given node, combine all MBH relationships within ingroups
- add paralogs if their score is better than best score to outgroup
- repeat at next most ancient node until whole tree has been traversed.
- Add unique and consistent MBH from non-core proteomes
- Make MSA and HMM for each family and sweep in singletons
- Break up large families based on E-value and coverage

Tuesday, September 21, 2010

16

Phytozome extras

- Only a few features are covered here.
- Explore on your own
- Most items on your screen show you more information if you click on them or move the mouse over them.
- Try some phylogenetic analysis on your own.
- Explore the help

Tuesday, September 21, 2010

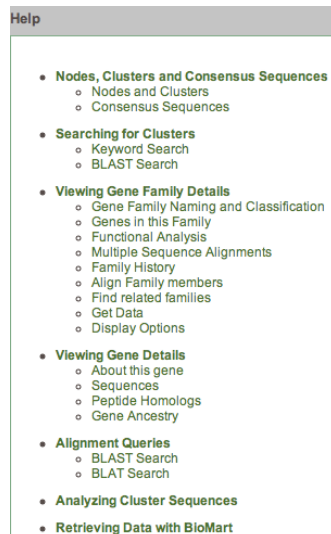
17

Help pages

Help link is in the menu at the top of every screen





Help topics



Tuesday, September 21, 2010

18

Workshop questions part 1

- Alpha amylase is an enzyme involved in starch mobilization by starting the degradation process.
- The gene has been cloned in cassava. This workshop will use Phytozome to compare gene models in cassava to the cloned alpha amylase gene.
- The gene in cassava is MEamy2 and has the Genbank accession DQ011041. Find this in the GenBank nucleotide database. (Published in PMID: 16297635)
- Get the sequence by changing the display to FASTA. Copy the sequence from GenBank and BLASTN against the masked cassava genome using an E-value cutoff of 1e-10.
- How many hits are there? Which ones look reasonable and why? Can you tell the difference between the Feature scale and Target scale diagrams of the hits?
- Click on the  in the UserBlast track heading  UserBlast
- In the Packing menu, select 'Expand & Label'. Zoom out by selecting Show 10 kb. Turn on the 454 EST tracks (PASA assembled EST and PASA aligned EST/ cDNA) and click on update image.
- Try BLAT with max intron size 5 kb. Compare the results to BLASTN. Which exons are different?

Tuesday, September 21, 2010

19

Workshop questions part 2

- Although there is a good gene model in this genomic region we are looking at in the browser, how can we decide if this is the gene model that best matches the MEamy2 gene? Let's investigate whether we are looking at the correct gene region.
- Click on the gene in the region in the Transcript track. It is called cassava43869.valid.m1.
- What domains are present in the protein?
- If you click on the Peptide Homologs tab, what is the most similar protein in Phytozome to MEamy2?
- In the Gene Ancestry tab, click on the Viridiplantae family with 51 members. Turn on display of the cassava members in the Display Options tab. How many cassava paralogs are there?
- Display the transcript sequence of the gene model cassava43869.valid.m1 in the Sequences tab and BLAST this against NCBI. Choose the nr/nt database at NCBI. What is the top hit? How much of the gene model hits the sequence in NCBI? What is the rest of the sequence?

Tuesday, September 21, 2010

20

Background reference Cassava alpha amylase

<http://www.ncbi.nlm.nih.gov/pubmed/16297635>

Plant Physiol Biochem. 2005 Sep;43(9):821-7. Epub 2005 Oct 4.
Isolation and characterization of an alpha-amylase gene in cassava (*Manihot esculenta*).
Tangphatsornruang S, Naconsie M, Thammarongtham C, Narangajavana J.
National Center for Genetic Engineering and Biotechnology, 113 Phaholyothin Road, Klong 1, Klong
Luang, Pathumthani 12120, Thailand. sithichoke.tan@biotec.or.th
Abstract

The roots of cassava plants (*Manihot esculenta* Crantz) accumulate starch as their major form of carbohydrate reserve. Starch accumulation and properties are determined by a balance between starch biosynthesis and degradation processes. Alpha-amylases (EC 3.2.1.1) are alpha-1,4 endoglycolytic enzymes, responsible for the mobilization of stored carbohydrate reserves by initiating the degradation process. Alpha-amylase genes have been shown to be differentially expressed at various developmental stages and environmental conditions through the action of plant hormones such as abscisic acid (ABA) and gibberellic acid (GA). In this study, we isolated an alpha-amylase gene from cassava tuberous roots (designated as MEamy2, GenBank accession number DQ011041). The deduced product of MEamy2 is 407 amino acid residues in length, with a calculated molecular mass of 46.7 kDa and an isoelectric point of 8.66. Southern blot analysis showed that the MEamy2 is present as a single copy in cassava genome. It shares the highest homology with AMY8 from apple fruit. The predicted structural model of MEamy2 contains three domains, active sites and starch-binding domain that are common with other plant alpha-amylases. RT-PCR analysis showed that the MEamy2 gene expression was induced in cassava roots within 2 hours after treatment with GA, but not ABA.

PMID: 16297635 [PubMed - indexed for MEDLINE]

Tuesday, September 21, 2010

21

Phytozome v.6



Tuesday, September 21, 2010

22

Species > Tools > Info > Help > Contact Us

phytozome

Species in Phytozome v6.0

Click here to search/browse/BLAST Phytozome genes and genomes

- Manihot esculenta*
- Ricinus communis*
- Populus trichocarpa*
- Medicago truncatula*
- Glycine max*
- Cucumis sativus*
- Prunus persica*
- Arabidopsis thaliana*
- Arabidopsis lyrata*
- Carica papaya*
- Vitis vinifera*
- Mimulus guttatus*
- Aquilegia coerulea*
- Sorghum bicolor*
- Zea mays*
- Setaria italica*
- Oryza sativa*
- Brachypodium distachyon*
- Selaginella moellendorffii*
- Physcomitrella patens*
- Chlamydomonas reinhardtii*
- Volvox carteri*

Welcome to Phytozome!

Phytozome is a joint project of the Department of Energy's Joint Genome Institute and the Center for Integrative Genomics to facilitate comparative genomic studies amongst green plants. Families of orthologous and paralogous genes that represent the modern descendants of ancestral gene sets are constructed at key phylogenetic nodes. These families allow easy access to clade specific orthology/paralogy relationships as well as clade specific genes and gene expansions. As of release v6.0, Phytozome provides access to twenty-three sequenced and annotated green plant genomes which have been clustered into gene families at sixteen evolutionarily significant nodes. Where possible, each gene has been annotated with PFAM, KOG, KEGG, and PANTHER assignments, and publicly available annotations from RefSeq, UniProt, TAIR, JGI are hyper-linked and searchable.

Using Phytozome: How do I ...

- find genes?
- ... find a family?
- BLAST?
- find a paralog?

Announcements

[3 Sep 2010] **Welcome to Phytozome version 6.0!** some (optional) random text can go here.

[24 Nov 2009] **Cassava genome is released** here too.

[23 Nov 2009] **Maize version 4a.53 Pseudo-chromosome browser and BLAST interface are now available**

News

[8 Jan 2010] **Phytozome v5.0 released.** Version 5.0 of Phytozome is now available, and incorporates both updated and newly released plant genomes. Eighteen genomes (eleven of which

[23 Nov 2009] **Pseudomolecule maize assembly and annotation now available at Phytozome.** Maize version 4a.53 Pseudomolecule assembly and annotation from

[23 Nov 2009] **Phytozome v4.1 released.** Version 4.1 of Phytozome is now available, with several new features. Gene Pages (e.g., here) now exist for every gene in Phytozome, providing

[9 Nov 2009] **Cassava genome released.** Version 1.1 of the Cassava (*Manihot esculenta*) assembly and annotation is now available for download, browsing and BLAST searching. It will be

:: Go to the news page to view all the news ::

Early release genomes

None available at this time

Info

- Release notes
- Plant Genomics resources

JGI Joint Genome Institute ©2010 University of California Regents. All rights reserved CIG Center for Integrative Genomics

Tuesday, September 21, 2010

23

Start here

Species > Tools > Info > Help > Contact Us

Species in Phytozome v6.0

Click here to search/browse/BLAST Phytozome genes and genomes

- Manihot esculenta*
- Ricinus communis*
- Populus trichocarpa*
- Medicago truncatula*
- Glycine max*
- Cucumis sativus*
- Prunus persica*
- Arabidopsis thaliana*
- Arabidopsis lyrata*
- Carica papaya*
- Vitis vinifera*
- Mimulus guttatus*
- Aquilegia coerulea*
- Sorghum bicolor*
- Zea mays*
- Setaria italica*
- Oryza sativa*
- Brachypodium distachyon*
- Selaginella moellendorffii*
- Physcomitrella patens*
- Chlamydomonas reinhardtii*
- Volvox carteri*

Using Phytozome: How do I ...

- find genes?
- ... find a family?
- BLAST?
- find a paralog?

Announcements

[3 Sep 2010] **Welcome to Phytozome versio** some (optional) random text can go here.

[24 Nov 2009] **Cassava genome is release** here too.

[23 Nov 2009] **Maize version 4a.53 Pseudo-BLAST interface are now available**

News

[8 Jan 2010] **Phytozome v5.0 released.** Version 5.0 of Phytozome is now available, and newly released plant genomes. Eight

[23 Nov 2009] **Pseudomolecule maize asse** available at Phytozome. Maize version 4a.53 Pseudomolecule asse

[23 Nov 2009] **Phytozome v4.1 released.** Version 4.1 of Phytozome is now available, Gene Pages (e.g., here) now exist for ever

[9 Nov 2009] **Cassava genome released.** Version 1.1 of the Cassava (*Manihot escul* is now available for download, browsing an

:: Go to the news page to view

Tuesday, September 21, 2010

24

Choose cassava genome

Tuesday, September 21, 2010

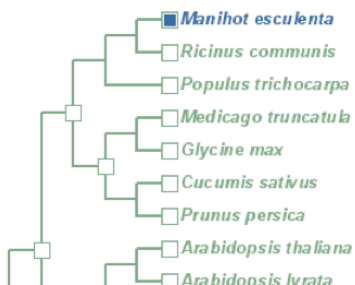
25

cassava genome options

Download bulk data: annotations, sequences

Information on cassava project and annotations

go to Gbrowse v2.0 genome browser



Tuesday, September 21, 2010

26

Gbrowse 2.0 genome browser

Main control tabs

Turn tracks on and off

Upload extra data

Location on genome

Search

Genomic region in increasing levels of detail on subsequent tracks

Genes

Alternative splice forms

EST assemblies

Protein homology from other plants

Tuesday, September 21, 2010

27

The Phytozome Team

Daniel Rokhsar

David Goodstein
Shengqianq Shu
Richard Hayes
Therese Mitros
Russell Howson

Cassava Genome Project
Steve Rounsley
Cassava genome and EST sequencing
454 Roche (Chinnappa Kodira), JGI (Dan Rokhsar)
Assembly
Brian Desany, Steve Rounsley
Annotation
Simon Prochnik

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CHI1231.

Tuesday, September 21, 2010

28