Tripal

A web framework for genetic and genomic data

Drupal

Chado

CHADO

Chado: Biological database schema

Tripal

Goals

- Simplify construction of a community genomics websites
- Enable individual labs or research communities
- Encourage high-quality, standards-based websites for data sharing and collaboration
- Expand and reuse code

The Banana Genome Hub

CottonGen
a genomics, genetics and breeding resource for cotton

knowpulse
pulse crop breeding & genetic

GDR | Genome Database for Rosaceae

Genome Database for *Vaccinium*

Cacao Genome Database

PeanutBase

Fagaceae Genomics Web
genomic tools for chestnut, oak, beech, and other trees.

Citrus Genome Database

The Hardwood Genomics Project

GeneNet Engine v0.9
A network biology resource for genotype-phenotype relationship

Modules

- Organisms
- Stocks/Germplasm
- Phenotypes
- Genotypes

- Transcriptomes
- Genomes
- BLAST, KEGG, GO results
- Ontology tagging
- Genetic Maps
- Libraries

- Contact
- Project
- Pub

- Bulk Loader
- Jobs Management

Fagaceae Genomics Web

genomic tools for chestnut, oak, beech, and other trees.

Organisms

American Beech
American Chestnut
Chinese Chestnut
European chestnut
Japanese chestnut
Oak
Red Oak
White Oak

Project Information

Project Background
Project Phases and Objectives
Bioinformatic Methods
Outreach
Progress Reports
Project Team
Publications

Castanea mollissima

View   EST Assemblies   KEGG   Libraries

Details

Common Name	Chinese Chestnut
Genus	Castanea
Species	mollissima

Description

The Chinese chestnut is native to China and also to Taiwan and Korea. It grows close to sea level in the north of its range, and at altitudes of up to 2,800 m in the south of the range. The species prefers full sun and acidic, loamy soil, and has a medium growth rate. It is a deciduous tree growing to 20 m tall with a broad crown. The leaves are alternate, simple, 10-22 cm long and 4.5-8 cm broad, with a toothed margin. The flowers are produced in catkins 4-20 cm long, with the female flowers at the base of the catkin and males on the rest. The fruit is a densely spiny cupule 4-8 cm diameter, containing two or three glossy brown nuts; these are 2-3 cm diameter on wild trees.

Japanese chestnut
Oak
Red Oak
White Oak

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User login

Username: *
fgw_admin

Password: *
•••••••••
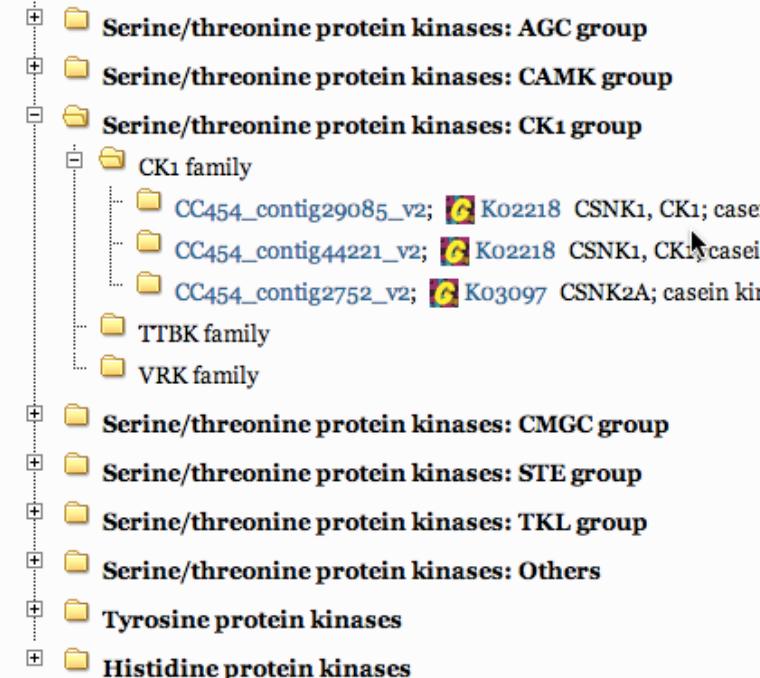
Any analysis with KEGG results related to this organism are available for viewing. For further information, see the analysis information page.

Analysis Results

KEGG BRITE

- KEGG Orthology (KO)
- KEGG pathway modules
- Photosynthesis proteins
- Cytochrome P450
- Proteoglycans
- Enzymes
- Protein kinases
- Peptidases
- Glycosyltransferases
- Lipid biosynthesis proteins
- Transporters
- Two-component system
- Bacterial motility proteins
- Bacterial toxins
- Transcription factors
- Ribosome
- Translation factors
- DNA replication proteins
- Chromosome
- Chaperones and folding catalysts

Hierarchy: Protein kinases

- ⊞ 📁 **Serine/threonine protein kinases: AGC group**
- ⊞ 📁 **Serine/threonine protein kinases: CAMK group**
- ⊟ 📁 **Serine/threonine protein kinases: CK1 group**
  - ⊟ 📁 CK1 family
    - 📁 CC454_contig29085_v2; 🅖 K02218 CSNK1, CK1; casei
    - 📁 CC454_contig44221_v2; 🅖 K02218 CSNK1, CK1; casei
    - 📁 CC454_contig2752_v2; 🅖 K03097 CSNK2A; casein kin
  - 📁 TTBK family
  - 📁 VRK family
- ⊞ 📁 **Serine/threonine protein kinases: CMGC group**
- ⊞ 📁 **Serine/threonine protein kinases: STE group**
- ⊞ 📁 **Serine/threonine protein kinases: TKL group**
- ⊞ 📁 **Serine/threonine protein kinases: Others**
- ⊞ 📁 **Tyrosine protein kinases**
- ⊞ 📁 **Histidine protein kinases**

CC454_contig29085_v2

Name CC454_contig29085_v2

Accession ID2751432

Sequence
```
GTCTTAACGATTCAATCAAACTCTCTCTGTTGTCTGAATGTCTCAAAAAC
ACACAATGCCTCCTCTCTCTcCTYCTTCTTCTTCTTCTTCACTTTGATAA
TTCCTGTTTCCAATTCTGCCCTCGCTCTCTCATCTTATCTTCATCTCTGT
CCTCCCCACATCTCCGCCGTCGATTGCTTTTCCCATTTTCCACTCTCTGG
ACGGTCCGGATTGCTTGATCGAGGATTCTCGGAGCTATGGAGCCCCGAGT
TGGAAACAAGTTTCGACTCGGCAGAAAGATCGGTAGTGGATCGTTCGGAG
AGATCTATCTCGGTACTAACATTCAGACCAATGAGGAGGTTGCAATTAAG
CTTGAAAATGTCAAGACAAAGCACCCCCAATTGCTGTATGAATCGAAGCT
GTATAAAATACTACAGGGAGGAACTGGAATTCCGAATGTGAGATGGTTTG
GCGTTGAAGGAGACTACAATGTTCTTGTGATGGATTTATTGGGACCCAGT
CTTGAAGATTTATTCAACTTTTGCAGTAGGAAATTGTCCCTTAAGACTGT
ACTTATGCTTGCAGATCAGATGATCAATCGAGTTGAGTTTGTTCATTCCA
AGTCATTTCTACACCGAGATATAAAGCCTGACAACTTTCTTATGGGTTTA
GGAAGGCGTGCAAATCAGGTTTACGTCATTGACTTTGGTCTGGCTAAGAA
GTATAGAGATGCTTCAACCCATCAACATATTCCTTATAGAGAAAATAAGA
ATTTAACAGGAACTGCAAGATATGCGAGCATGAATACTCACCTCGGCATT
GAACAAAGCCGCAGGGATGATTTAGAGTCACTTGGATATGTTCTTATGTA
TTTCTTAAGAGGAAGTCTTCCTTGGCAGGGACTGAAAGCAGGAACTAAGA
AGCAAAAGTATGAGAAGATCAGTGAGAAGAAAGTTTCGACATCCATTGAG
GCTTTATGTCGTGGTTATCCTACAGAGTTTGCTTCATACTTCCATTACTG
CCGTTCTCTACGATTTGATGATAAACCGGATTATGCGTATCTCAAAAGAC
TCTTCCGTGACCTTTTCATTCATGAAGGCTTCCAGTTTGATTACGTGTTT
GATTGGACCATTTTGAAATATCAGCAGTCCCAGATTGCCACTCCACCTGC
TCGTGTTCTTGGTCCTGGTGCTGGACCCAGCTCTGGCATGCCACCAATAG
CTGCAAATGCTGATAGACAATCAGGTGGGGAAGAAGGTAGACTTACTGGT
```

Blast Hits to TAIR7 Peptides

Analysis Date: 11-17-2009 ([Blast: CC454_contigs_v2_vs_TAIR7_pep_20070425](#))
Best 10 Hits Shown | [Show Best 25 Hits](#)
Note: Click a description for more details.

Match Name	E value	Identity
[AT1G72710.1](#)	8.71347e-179	68.95%

casein kinase, putative | chr1:27376215-27379840 FORWARD

```
HSP 1
Score: 624.009 bits (1608), Expect = 8.71347e-179
Identity = 322/467 (68.95%), Postives = 357/467 (76.45%), Query Frame = 3
Query:   237 MEPRVGNKFRLGRKIGSGSFGEIYLGTNIQTNEEVAIKLENVKTKHPQLLYESKLYKILQGG
             MEPRVGNKFRLGRKIG GSFGEIYLGTNIQTNEEVAIKLENVKTKHPQLLYESKLYK+LQGG
Sbjct:     1 MEPRVGNKFRLGRKIGGGSFGEIYLGTNIQTNEEVAIKLENVKTKHPQLLYESKLYKVLQGG
```

GO terms assigned to this feature

Accession	Category	Term
GO:0006468	biological_process	protein amino acid phosphorylation
GO:0005524	molecular_function	ATP binding
GO:0004672	molecular_function	protein kinase activity
GO:0004674	molecular_function	protein serine/threonine kinase activity

Why use Tripal?

- Its open source
- Much of the stuff you need for a website is already there
- Github
- APIs!
  - Tripal Theming API: allows customization of the look-and feel of the site through API function calls and template files.
  - Tripal Module Development API: allows addition of new or custom functionality through module development.
- Reasonably good documentation (we additions!)
- Friendly developers
- Responsive mailing list

Dive in!

- To theme a site
  - Knowledge of PHP
  - Knowledge of Chado and relationships between tables (at least tables where data of interest is stored).
  - Understanding of the Tripal theming API
  - Understanding of how Drupal theming works
- To development new content modules
  - Above PLUS
  - Understanding of the Drupal API
  - Understanding of the Tripal API (described here)

Tripal.info

Future

- Integration with iPlant and other data analysis resources
- Semantic Web and Ontology integration
- Modules for new data types
  - Geospatial
  - Environmental
  - Breeding

- Growing a great open source community!

Thanks

- Developers
  - Stephen Ficklin
  - Lacey Anne Sanderson
  - Chun Huai Chen

- PIs
  - Dorrie Main (University of Washington)
  - Kirsten Betts (University of Saskatchewan)
  - Jill Wegrzyn (University of Connecticut)