funRiceGenes

Comprehensive understanding and application of

rice functional genes

Part I

Display of information in this database as static web pages

https://funricegenes.github.io/

Welcome to funRiceGenes!

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A comprehensive database of functionally characterized rice genes

- 2800+ cloned rice genes [Download↓]
- 400+ gene families [Download↓]
- 400+ keywords [Download↓]
- 5000+ literatures [Download↓]
- 200+ interaction networks [Download↓]
- Contact: ywhzau at gmail.com
- Help manual [Download↓]

At the homepage of our database, we provide the download of the whole dataset in tidy format.

On-site search using Google or Bing

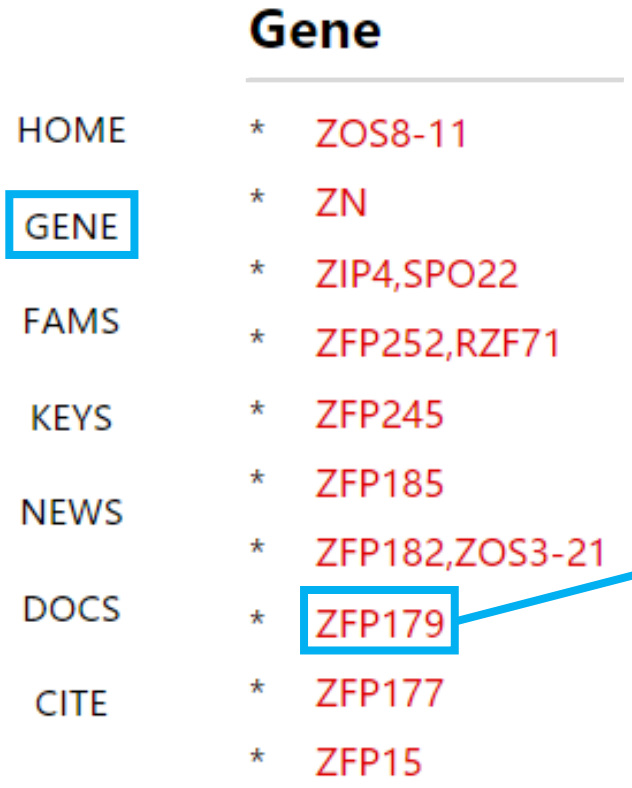
To search this site, please use Google or Bing with the following search pattern!

```
yourSearchKeyword site:https://funricegenes.github.io/
```

For example, to search this site with the keyword "domestication", open Google or Bing and type the following words:

```
domestication site:https://funricegenes.github.io/
```

https://funricegenes.github.io/



The GENE menu lists 2800+ cloned rice genes.

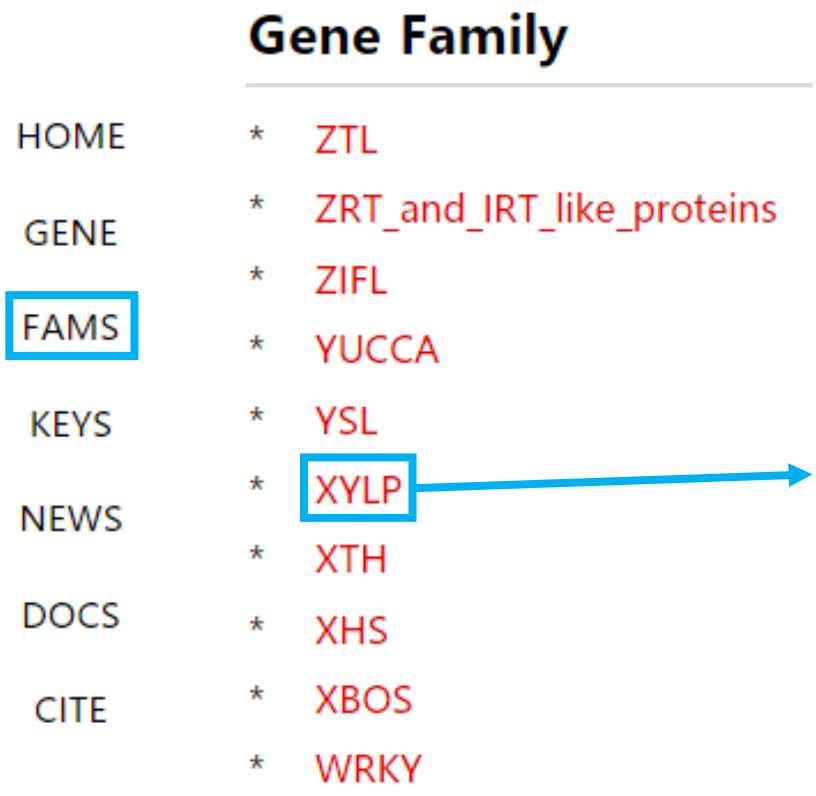
The detailed information of a gene is shown as a single page.

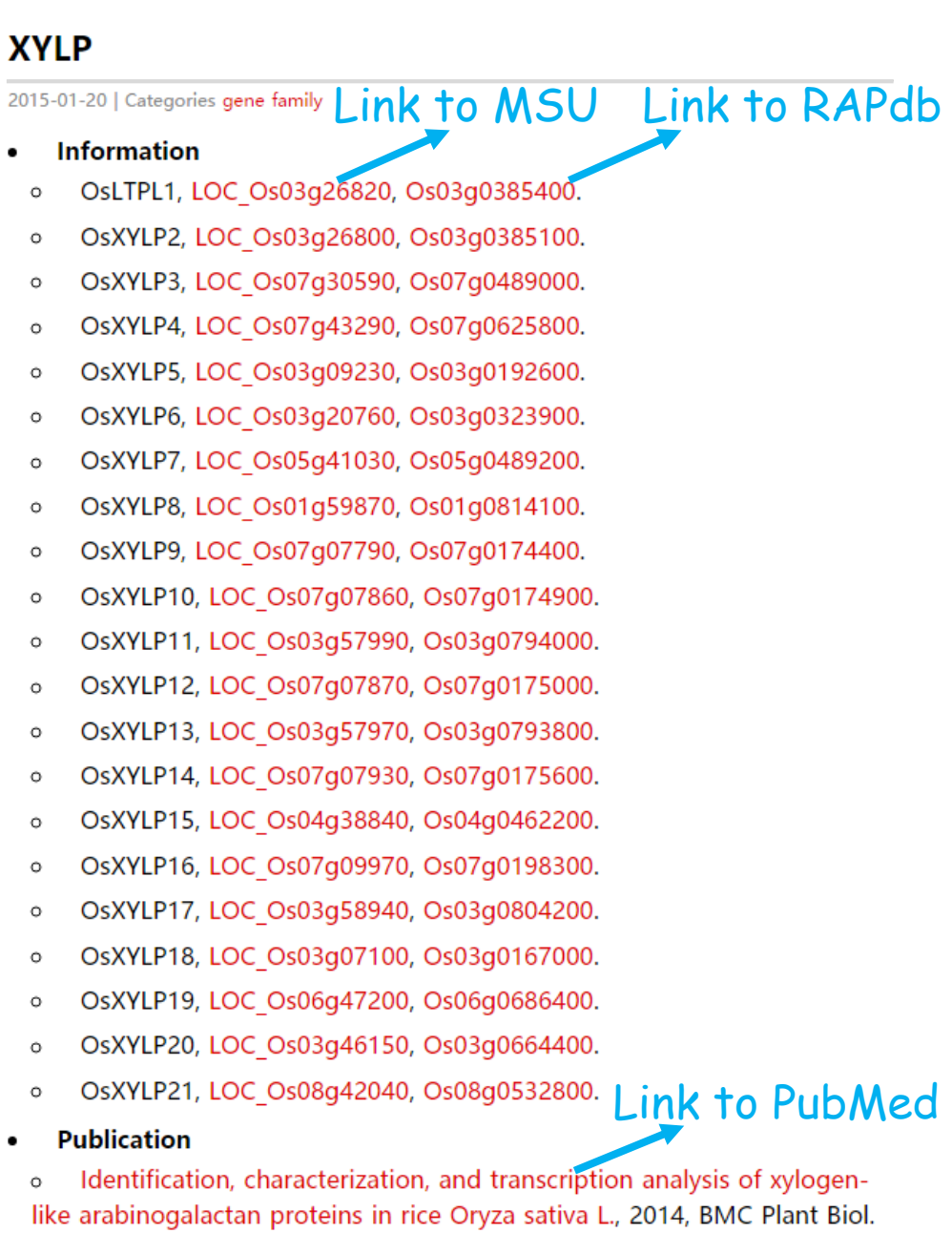
https://funricegenes.github.io/

ZFP179

2015-01-20 | Categories genes | Tags salt stress ABA seedling salt tolerance salt oxidative

- **Information**
  - Symbol: ZFP179
  - MSU: LOC_Os01g62190 → Link to MSU
  - RAPdb: Os01g0839100 → Link to RAPdb
- **Publication**
  - Functional analysis of a novel Cys2/His2-type zinc finger protein involved in salt tolerance in rice, 2010, J Exp Bot.
  - Salt-responsive ERF1 regulates reactive oxygen species-dependent signaling during the initial response to salt stress in rice, 2013, Plant Cell. → Link to PubMed
- **Genbank accession number**
  - AK108227 → Link to GenBank
- **Key message**
  - The ZFP179 transgenic rice exhibited significantly increased tolerance to oxidative stress, the reactive oxygen species (ROS)-scavenging ability, and expression levels of a number of stress-related genes, including OsDREB2A, OsP5CS OsProT, and OsLea3 under salt stress
  - Our studies suggest that ZFP179 plays a crucial role in the plant response to salt stress, and is useful in developing transgenic crops with enhanced tolerance to salt stress
  - The real-time RT-PCR analysis showed that ZFP179 was highly expressed in immature spikes, and markedly induced in the seedlings by NaCl, PEG 6000, and ABA treatments
  - Through microarray analysis, a salt-responsive zinc finger protein gene ZFP179 was identified and subsequently cloned from rice seedlings
  - Overexpression of ZFP179 in rice increased salt tolerance and the transgenic seedlings showed hypersensitivity to exogenous ABA
- **Connection** → Link to PubMed
  - **OsProT~ProT**, **ZFP179**, Functional analysis of a novel Cys2/His2-type zinc finger protein involved in salt tolerance in rice, The ZFP179 transgenic rice exhibited significantly increased tolerance to oxidative stress, the

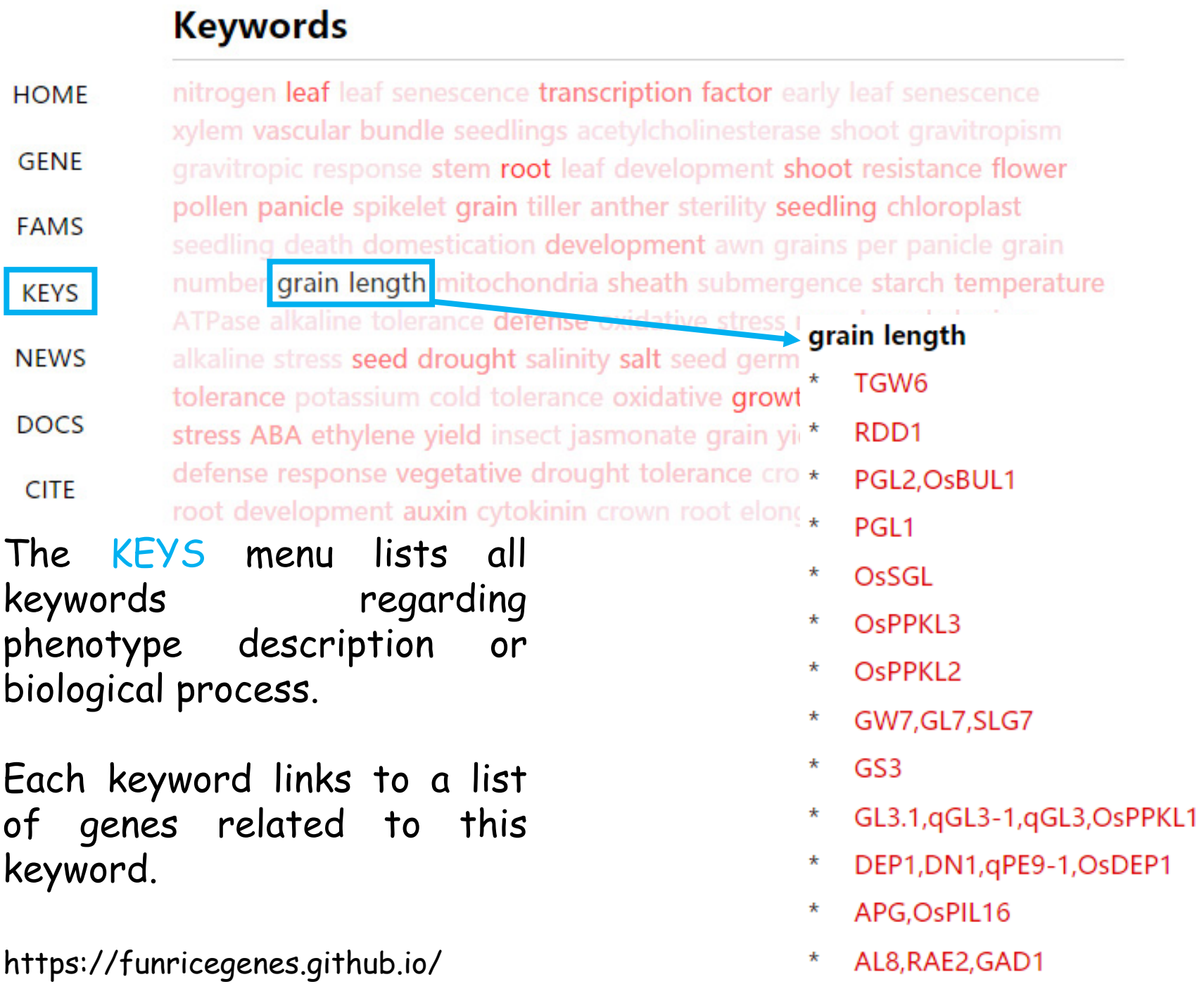




The FAMS menu lists 400+ rice gene families.

The detailed information of a gene family is shown as a single page.

https://funricegenes.github.io/



The KEYS menu lists all keywords regarding phenotype description or biological process.

Each keyword links to a list of genes related to this keyword.

https://funricegenes.github.io/

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News

- 2017/Mar/1 fix info
- 2017/Mar/1 add new accessions for OsGPCR
- 2017/Mar/1 add new pub.
- 2017/Mar/1 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 fix info
- 2017/Feb/27 add new info for gene: OsLBD3-7
- 2017/Feb/27 add new pub.
- 2017/Feb/27 PLA3 == OsLBD3-7

The NEWS menu shows the updating history of this database.

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Literatures

1. Cloning of a cDNA encoding an importin-alpha and down-regulation of the gene by light in rice leaves, 1998, Gene.
2. Molecular cloning of a novel importin alpha homologue from rice, by which constitutive photomorphogenic 1 COP1 nuclear localization signal NLS-protein is preferentially nuclear imported, 2001, J Biol Chem.
3. Mutations of genes in synthesis of the carotenoid precursors of ABA lead to pre-harvest sprouting and photo-oxidation in rice, 2008, Plant J.
4. A pair of orthologs of a leucine-rich repeat receptor kinase-like disease resistance gene family regulates rice response to raised temperature, 2011, BMC Plant Biol.
5. The ATP-binding cassette transporter OsABCG15 is required for anther development and pollen fertility in rice, 2013, J Integr Plant Biol.
6. ABCG15 encodes an ABC transporter protein, and is essential for post-meiotic anther and pollen exine development in rice, 2013, Plant Cell Physiol.

Link to PubMed

The DOCS menu lists all the literatures archived in this database.

https://funricegenes.github.io/

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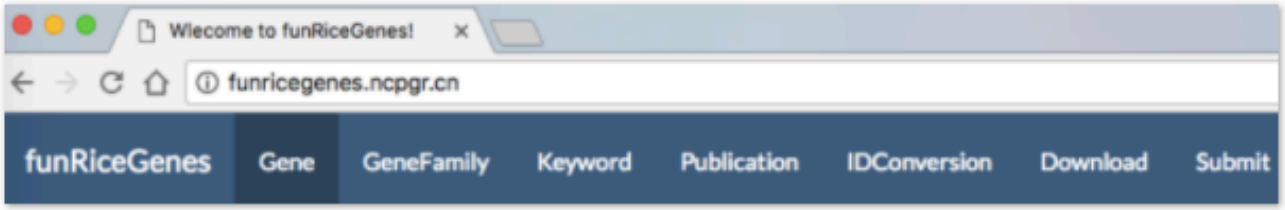
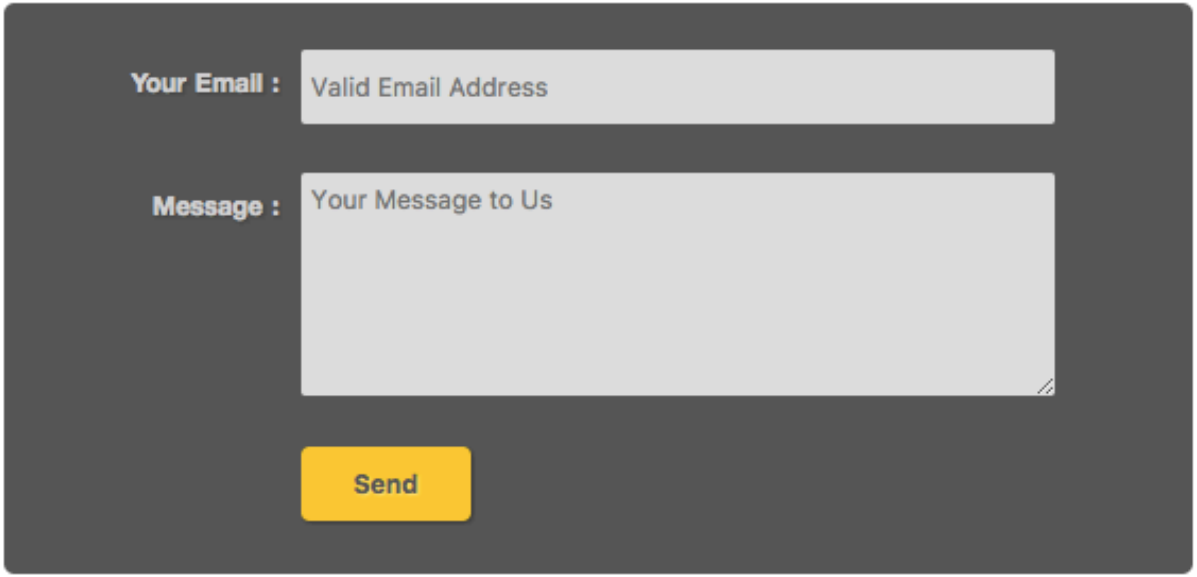
At the homepage of our database, we provide a link to a website allowing interactive query of this database.

To interactively query this database, go to the following site!



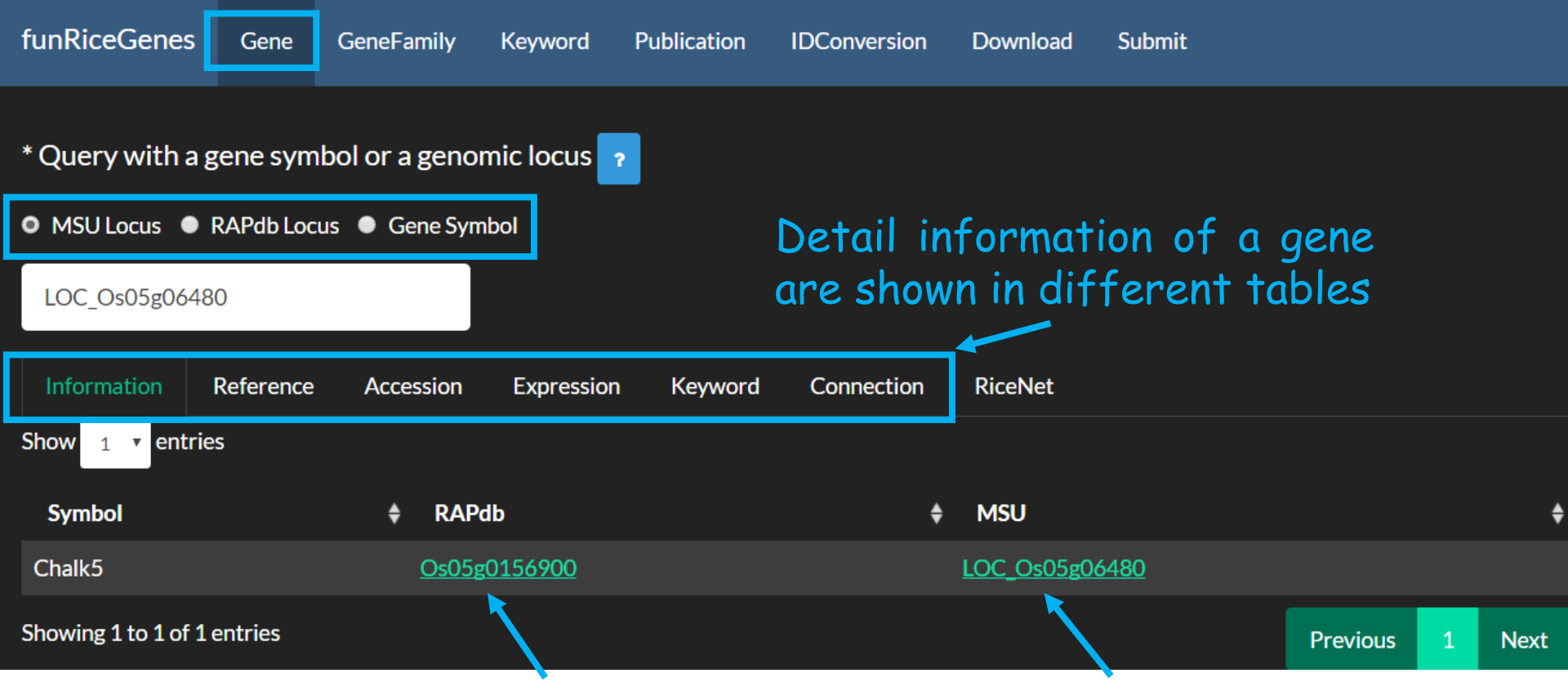
If you find any error information in our database or any functionally characterized rice genes missing from our database, please leave us a message.



https://funricegenes.github.io/

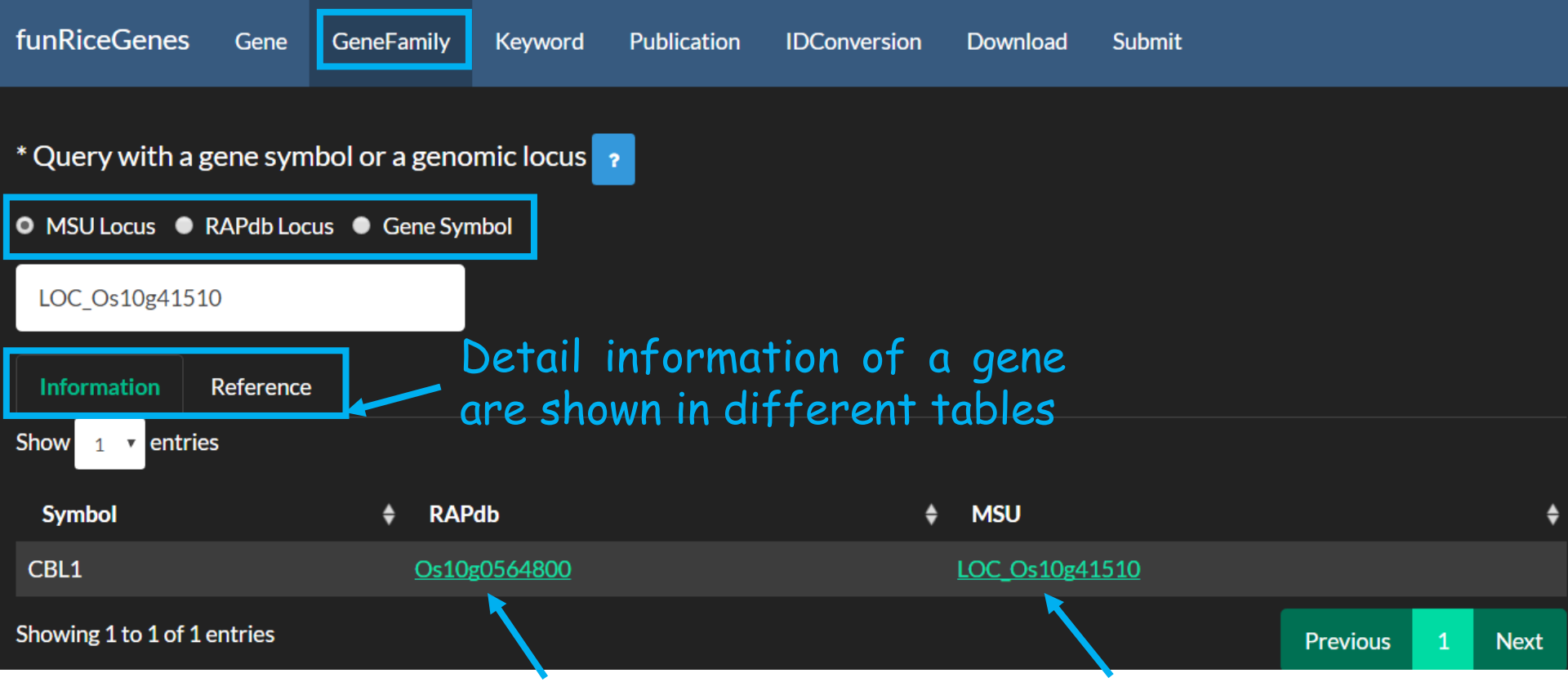
Part II

Interactive query of this database



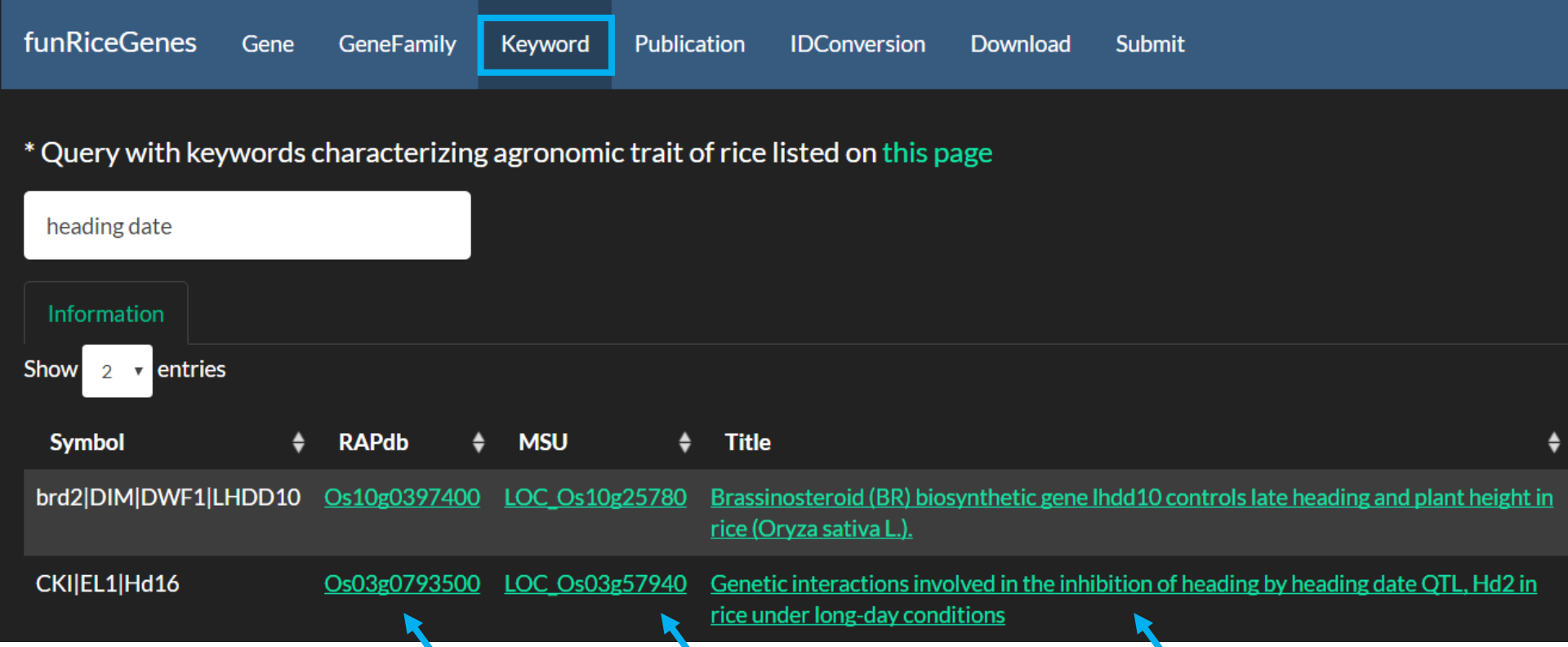
The Gene menu allows query of 2900+ genes using a MSU/RAPdb genomic locus or a gene symbol.

http://funricegenes.ncpgr.cn/



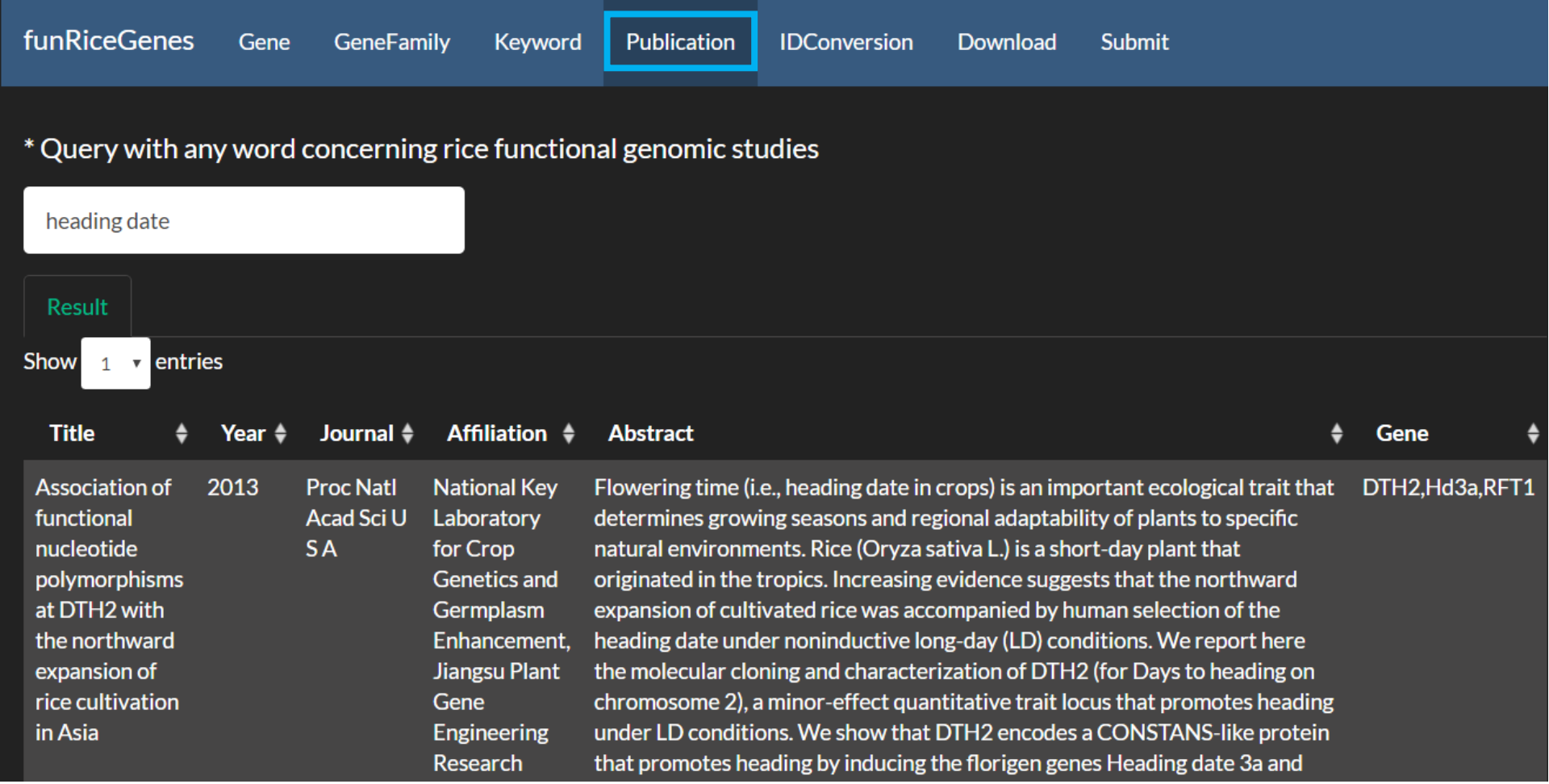
The GeneFamily menu allows query of 5000+ gene family members using a MSU/RAPdb genomic locus or a gene symbol.

http://funricegenes.ncpgr.cn/



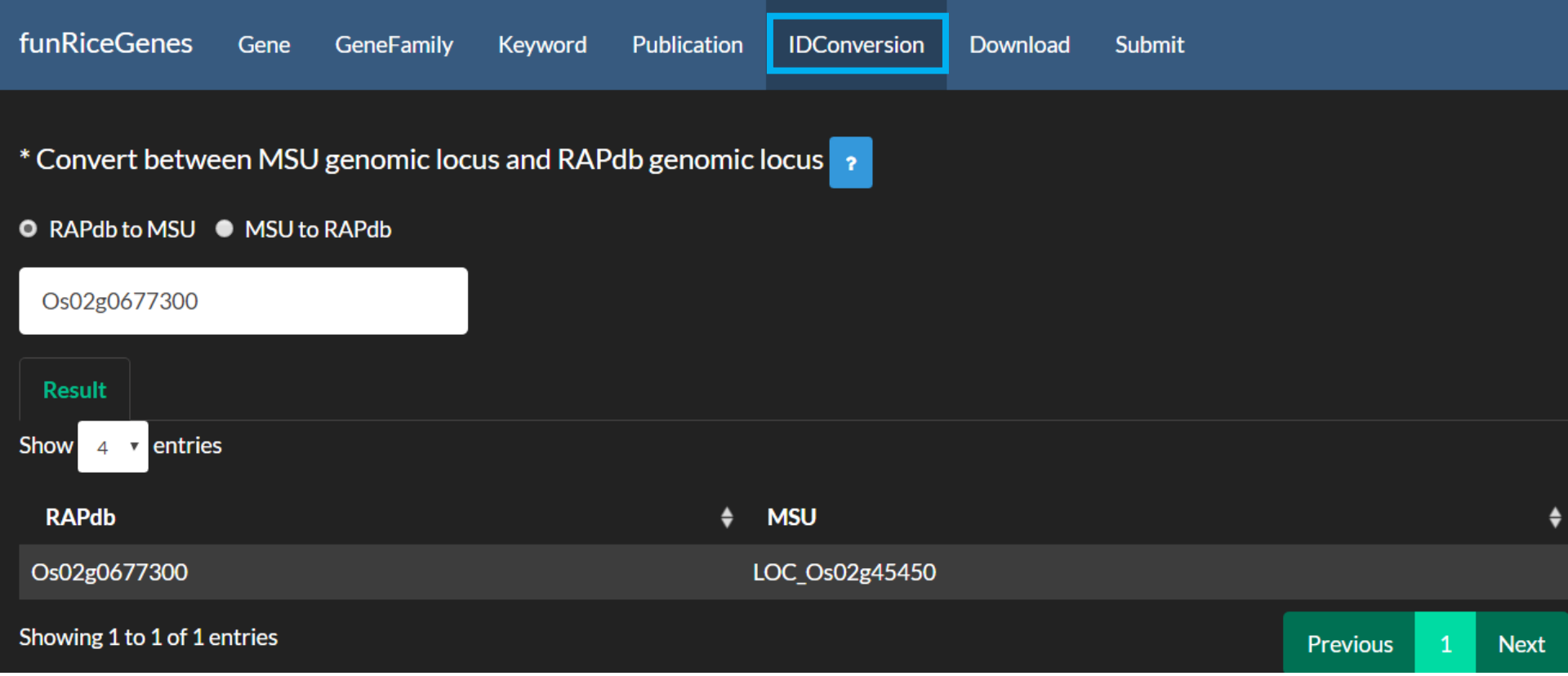
The Keyword menu allows query of the database with keywords regarding phenotype description or biological process.

http://funricegenes.ncpgr.cn/



The Publication menu allows query of the titles and abstracts of all publications archived in this database with any word.

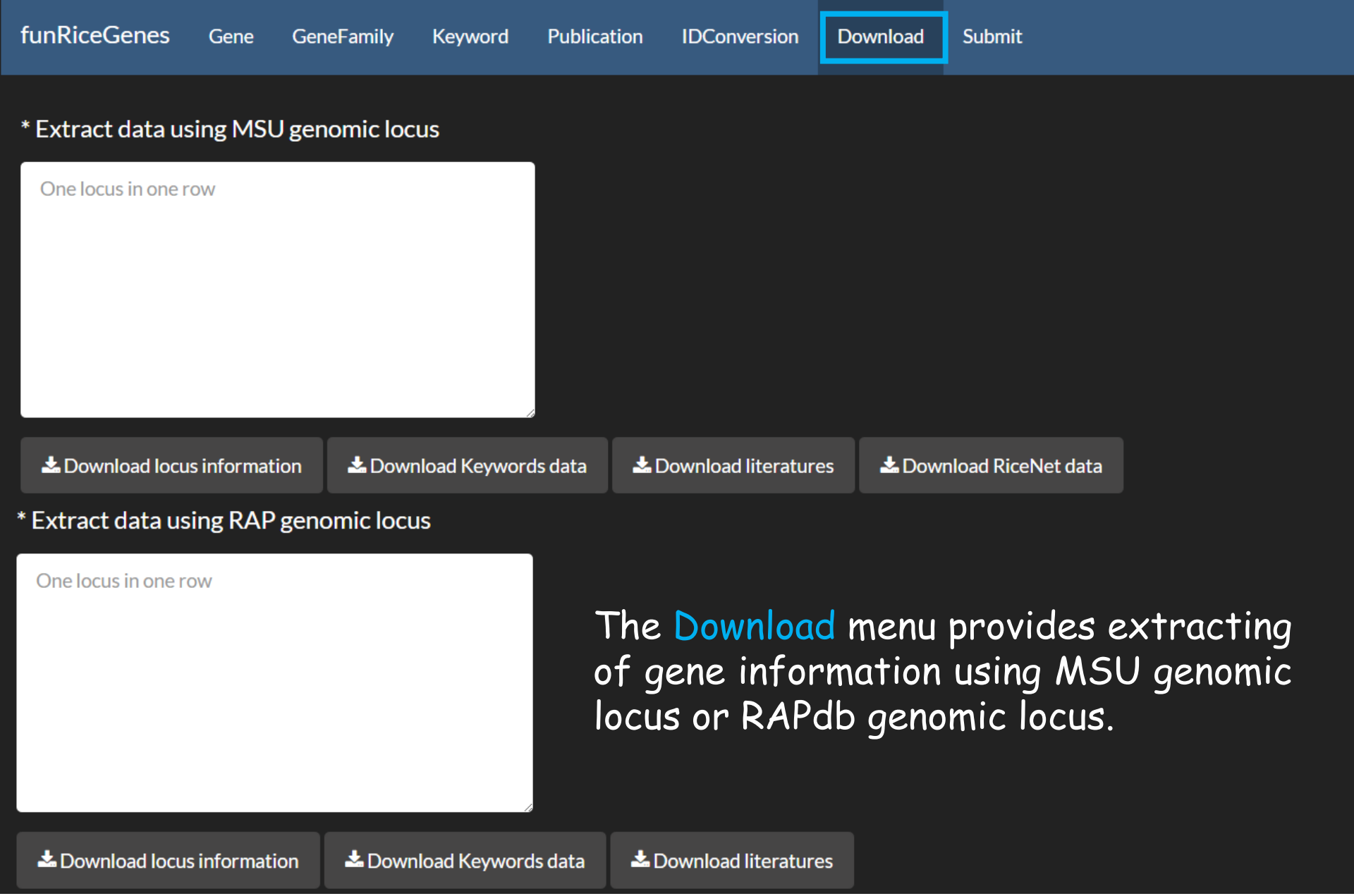
http://funricegenes.ncpgr.cn/



The IDConversion menu provides a tool to convert between a MSU genomic locus and a RAPdb genomic locus.

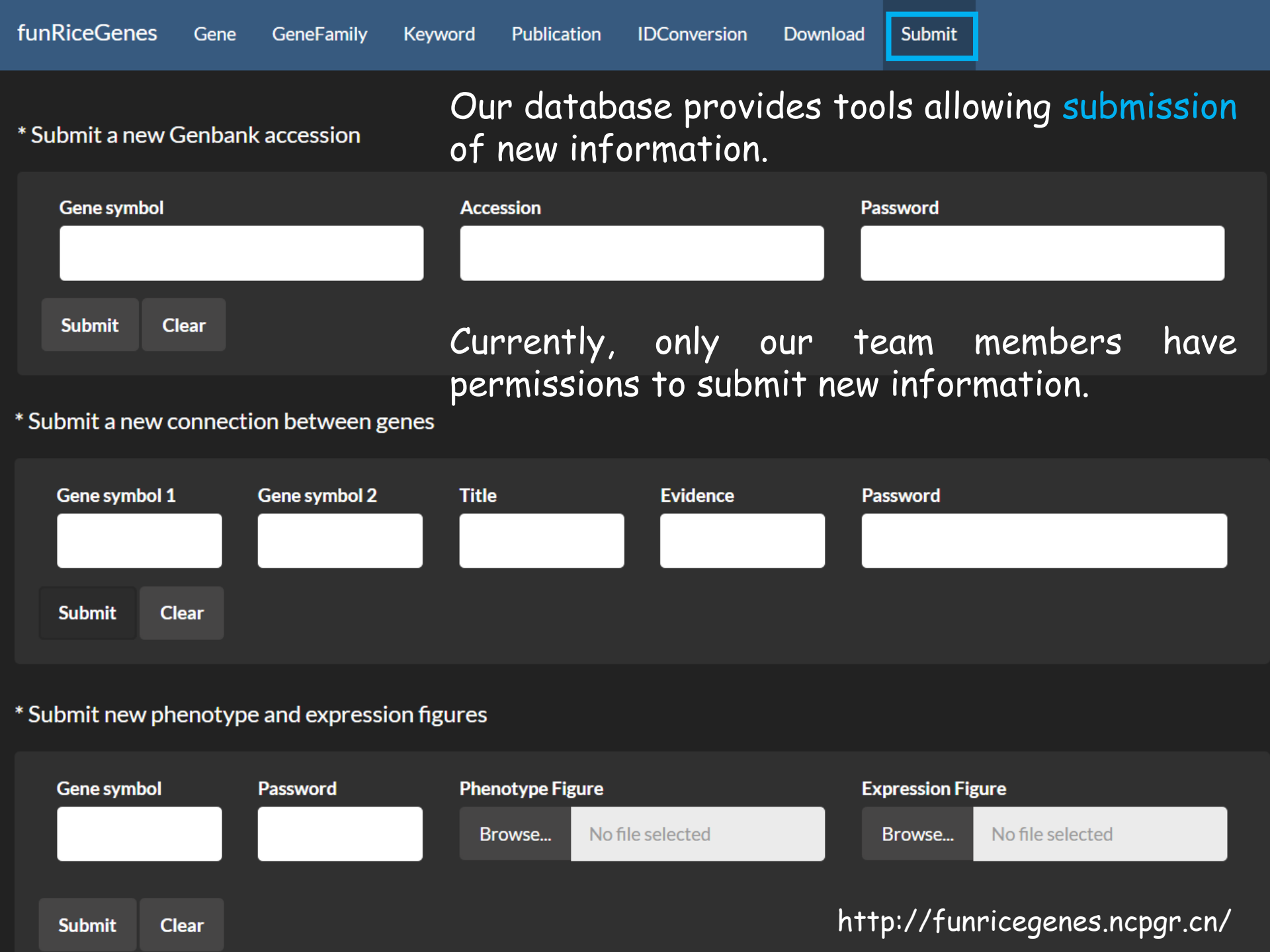
Batch query is supported.

http://funricegenes.ncpgr.cn/



The Download menu provides extracting of gene information using MSU genomic locus or RAPdb genomic locus.

http://funricegenes.ncpgr.cn/


funRiceGenes
Gene
GeneFamily
Keyword
Publication
IDConversion
Download
Submit
Our database provides tools allowing submission of new information.
* Submit a new Genbank accession
Gene symbol
Accession
Password
Submit
Clear
Currently, only our team members have permissions to submit new information.
* Submit a new connection between genes
Gene symbol 1
Gene symbol 2
Title
Evidence
Password
Submit
Clear
* Submit new phenotype and expression figures
Gene symbol
Password
Phenotype Figure
Browse...
No file selected
Expression Figure
Browse...
No file selected
Submit
Clear
http://funricegenes.ncpgr.cn/

Link to https://funricegenes.github.io/

http://funricegenes.ncpgr.cn/

Part III

Add new records to this database

What's new for 'rice alert' in PubMed ☆

发件人：My NCBI <efback@ncbi.nlm.nih.gov>
时　间：2017年9月12日(星期二) 上午8:00 (UTC-04:00 阿根廷、巴西时间)
收件人：ywhzau <ywhzau@gmail.com>

This message contains My NCBI what's new results from the National Center for Biotechnology Inforn
Do not reply directly to this message.

Sender's message:

Daily email alert from PubMed

Sent on Tuesday, 2017 September 12
Search: **(((rice[Title]) OR rice[Title/Abstract]) OR oryza[Title]) OR oryza[Title/Abstract]**

View complete results in PubMed (results may change over time).

Edit saved search settings, or unsubscribe from these e-mail updates.

PubMed Results

Items 1 - 6 of 6

1. Plants (Basel). 2017 Sep 9;6(3). pii: E37. doi: 10.3390/plants6030037.

Impact of Silicon in Plant Biomass Production: Focus on Bast Fibres, Hypotheses, and Perspectives.

https://www.ncbi.nlm.nih.gov/pubmed/24723033

J Plant Res. 2014 May;127(3):423-32. doi: 10.1007/s10265-014-0631-5. Epub 2014 Apr 11.

Functional conservation of the glycosyltransferase gene GT47A in the monocot rice.

Zhang B[1], Zhao T, Yu W, Kuang B, Yao Y, Liu T, Chen X, Zhang W, Wu AM.

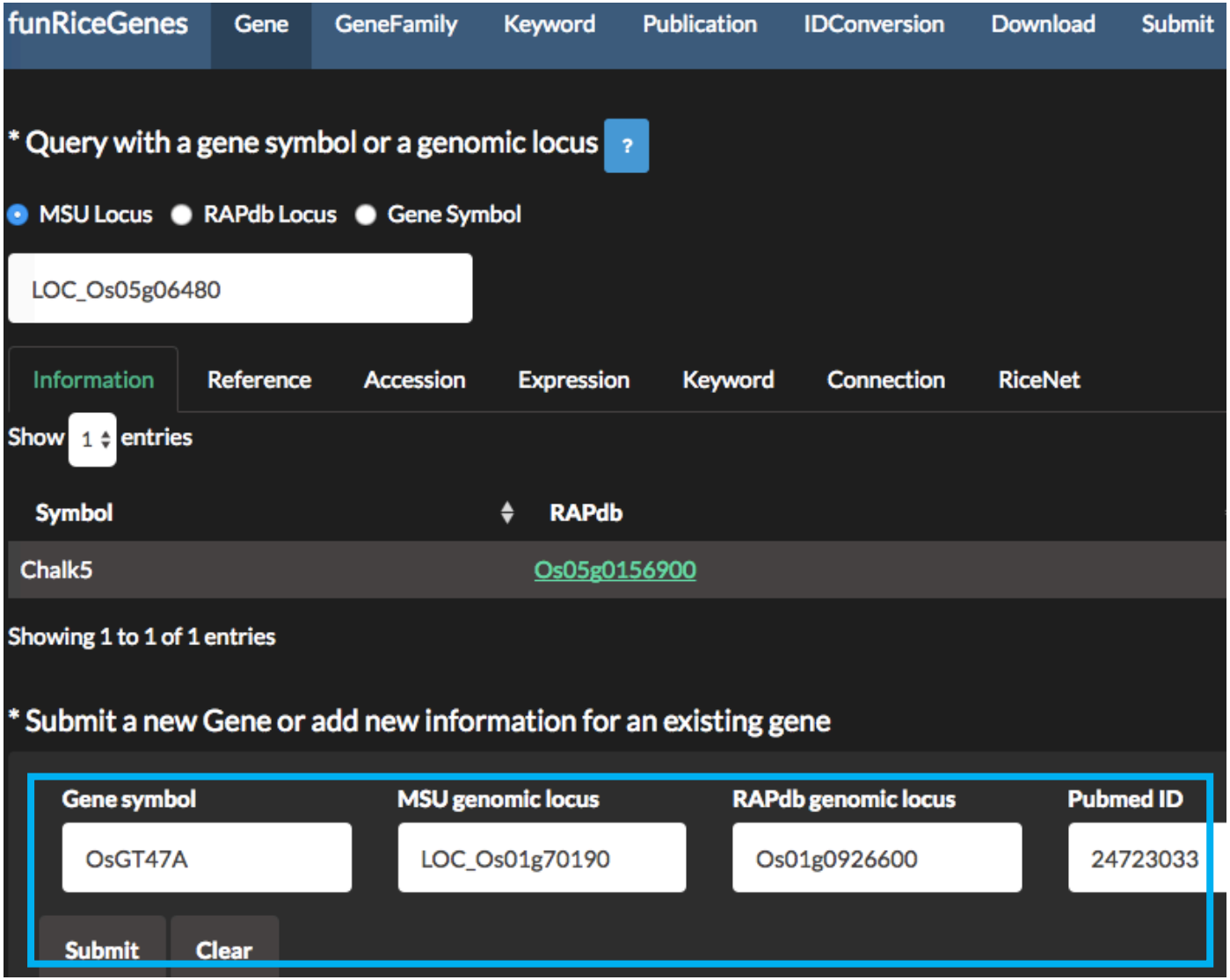
Author information

Abstract

Glucuronoarabinoxylan is the major hemicellulose in grass cell walls, yet the mechanism of xylan synthesis in monocot plants is still unclear. Unraveling the genes involved in the biosynthesis of xylan in rice will be very important for the utilization of rice straw as a source of bioenergy in the future. In this report, we investigated the functional role of a rice gene homologous to Arabidopsis IRREGULAR XYLEM10 (IRX10), belonging to the glycosyl transferase (GT) gene family 47 (GT47), in the biosynthesis of xylan. The protein sequence of OsGT47A from rice exhibits a 93.49% similarity to IRX10, which is involved in the biosynthesis of glucuronoxylan in Arabidopsis. Phylogenetic analysis of the GT47 glycosyl transferase family in the rice genome revealed that OsGT47A is a closely related homolog of IRX10 and IRX10L. Expression pattern analysis showed that the OsGT47A gene is highly expressed in the rice stem. Overexpression of OsGT47A in the irx10 irx10L double mutant rescued the plant growth phenotype and restored secondary wall thickness. Analysis of monosaccharides indicated that the rescued plants had levels of xylose identical to those of the wild type plants, and the fluorescence signals were restored in the complementation plants by xylan immunolocalization. The OsGT47A complementation under the native promoter of Arabidopsis IRX10L (ProIRX10L) partially rescued the double mutant, indicating that OsGT47A is functionally equivalent to IRX10L. Together, these results suggest that the IRX10 homolog OsGT47A exhibits functional conservation and is most likely involved in xylan synthesis in rice.

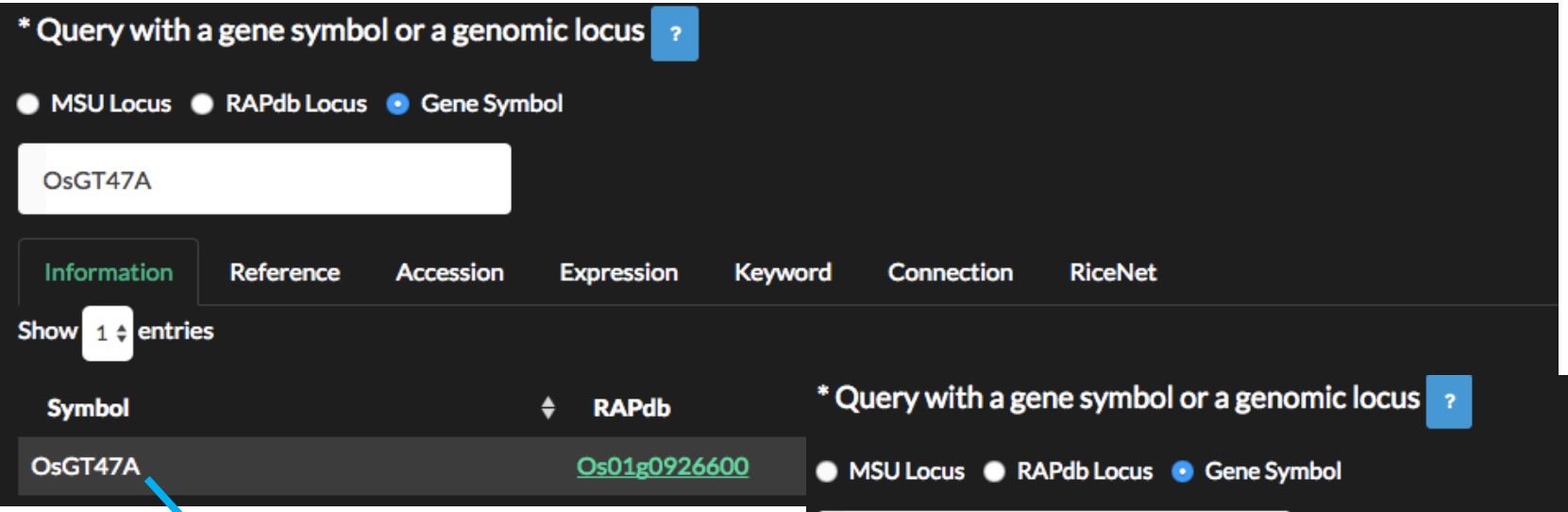
PMID: 24723033 DOI: 10.1007/s10265-014-0631-5

We identified from the email alert a PubMed record (24723033) which described the cloning of a rice gene (*OsGT47A*).
We further identified the genomic locus LOC_Os01g70190 and Os01g0926600 assigned by the MSU and the RAPdb database by manually searching of the full text of this paper at https://link.springer.com/article/10.1007%2Fs10265-014-0631-5.

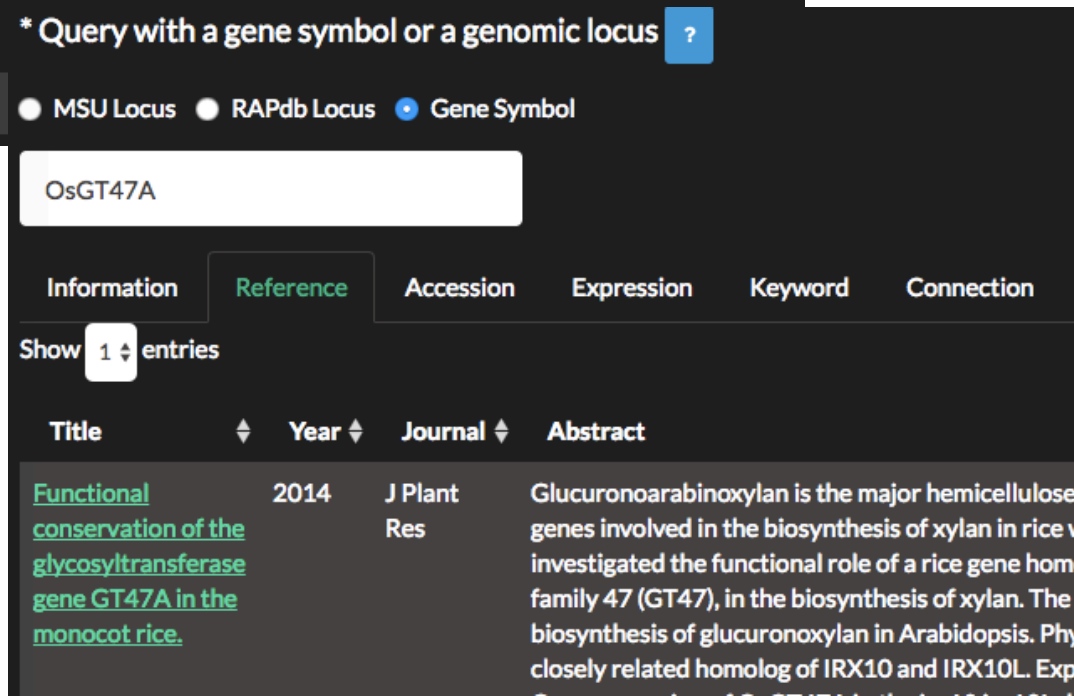


Then go to http://funricegenes.ncpgr.cn/.
In the Gene menu, fill in the four cells "Gene Symbol", "MSU genomic locus", "RAPdb genomic locus" and "Pubmed ID" and click the "Submit" button.
Then the Shiny application will extract information on this gene from the publicationand add all the information to this database.

Once succeeded, the Shiny application will give a popup message.



Now, gene *OsGT47A* is included in this database!



Part IV

Deploy the Shiny application on local computer

The content of the Shiny application (http://funricegenes.ncpgr.cn/) was deposited in Github (https://github.com/venyao/RICENCODE). You can deploy the Shiny application on local computer.

Step 1: Install R and Rstudio

Before running the app you will need to have R and RStudio installed (tested with R 3.3.3 and RStudio 1.0.143).
Please check CRAN (https://cran.r-project.org/) for the installation of R.
Please check https://www.rstudio.com/ for the installation of RStudio.

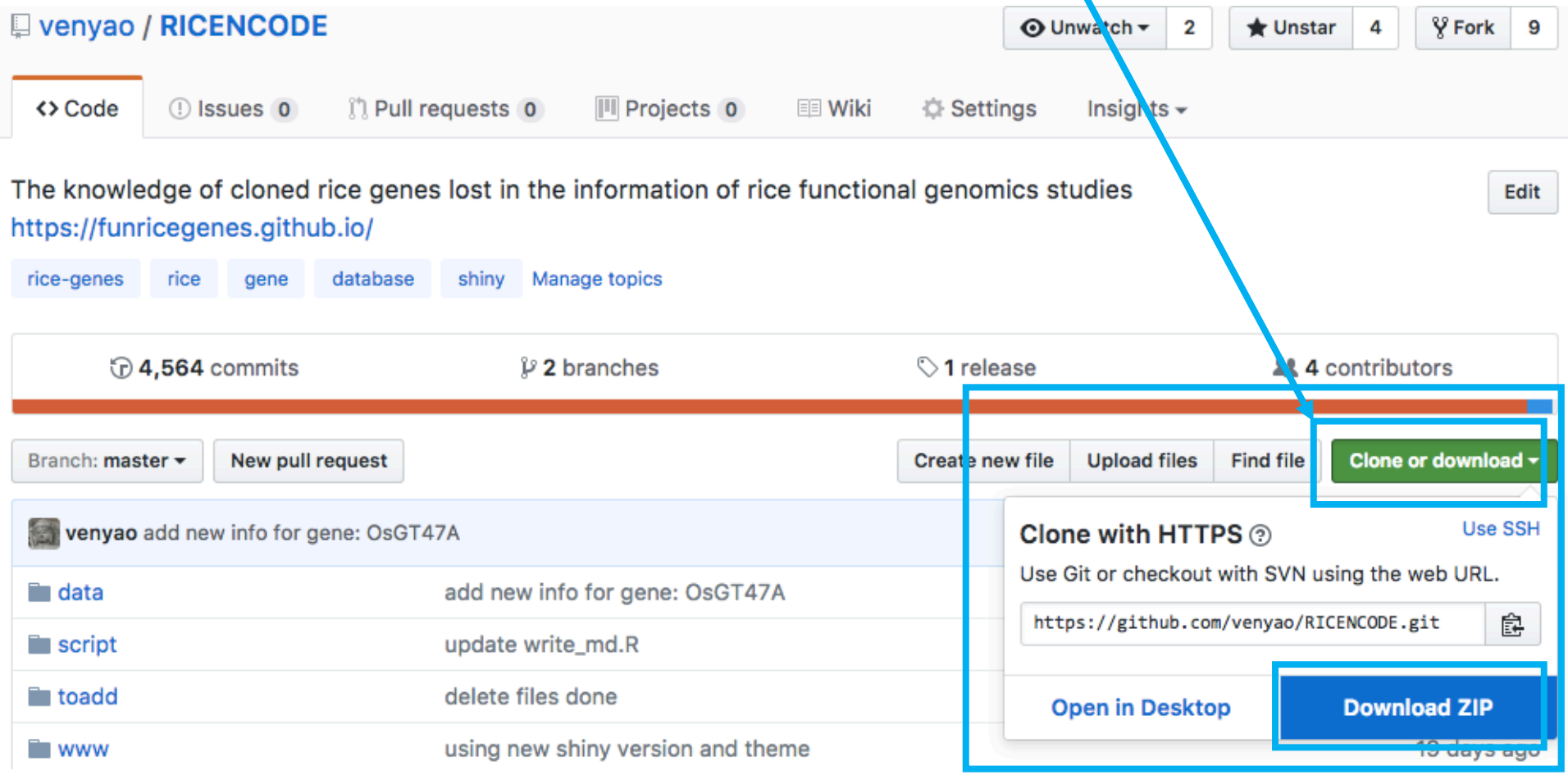
Step 2: Install the R Shiny package and other packages required by the Shiny application

Start an R session using RStudio and run these lines:

```
# try http:// if https:// URLs are not supported
install.packages("shiny")
install.packages("shinythemes")
install.packages("shinyBS")
install.packages("RCurl")
install.packages("XML")
install.packages("stringr")
install.packages("plyr")
```

Step 3: Download the content of the Shiny application

Go to https://github.com/venyao/RICENCODE
Download the content of the Shiny application as a ZIP file.



Step 4: Launch the Shiny application

Unzip the ZIP file downloaded in Step 3 into a directory.
Start an R session using RStudio and run these lines:

```
library(shiny)
runApp("~/RICENCODE/", launch.browser = TRUE)
```

The first parameter of runApp is the directory where the content of this Shiny application are stored. In this directory, you can find two R scripts server.R and ui.R.

Then your browser will open the Shiny application.