

RicENcode: the knowledge of cloned rice genes lost in the information of rice functional genomic studies

We have collected more than 2204 cloned rice genes and 303 gene families comprised of 3381 genes. For each gene, various information concerning the gene symbol, the genomic locus in the Nipponbare reference genome, the Genbank accession number, the title, journal, year, author affiliation, abstract of related publications and the text mining result of the publications were provided.

The data were deposited in Github as a repository (<https://github.com/andrewhzau/RICENCODE>). The companion web pages for this repository could be accessed at <http://andrewhzau.github.io/RICENCODE/>. Static web pages concerning all the information for a gene were created for every gene collected. The data were also deployed as an R Shiny application and could be accessed at <http://211.69.128.148:3838/ricencode/>.

Let's use the Shiny application (App) to query this database first!

Figure 1 shows the “Homepage” of this Shiny App, which displays the general information about this database.

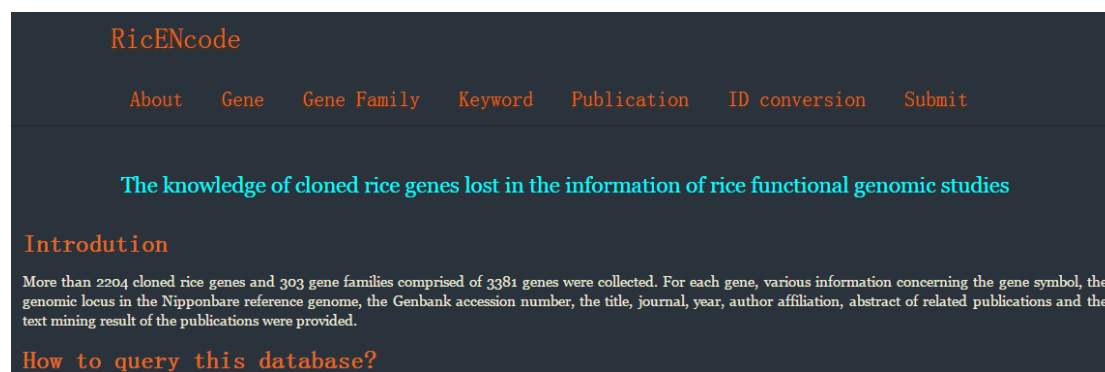


Figure 1. The Homepage of the Shiny application.

Following the link to “Gene” on the navigation bar opens a page of “Gene query interface” for cloned gene information (**Figure 2**).

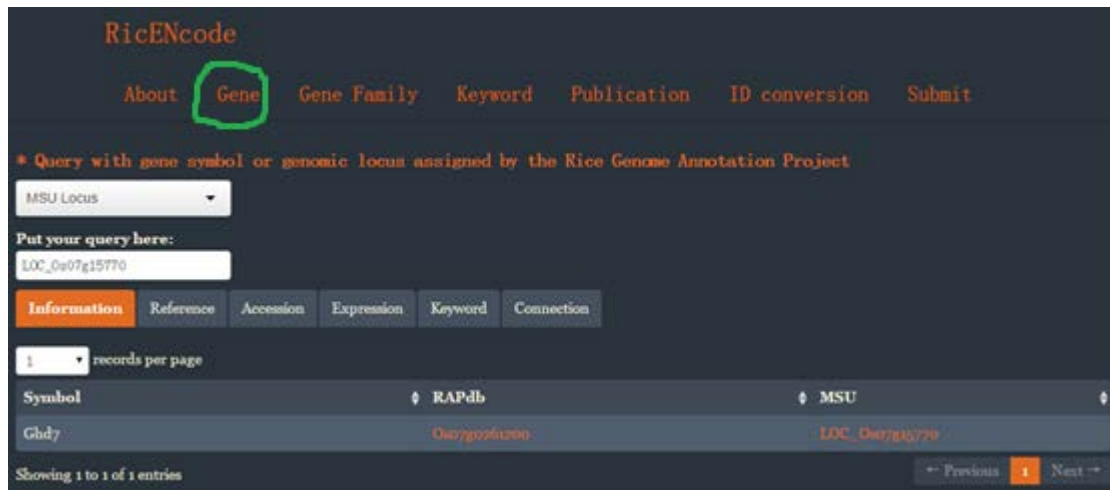


Figure 2. The “Gene” query interface to fetch cloned gene information.

Either gene symbol or genomic locus is available to fetch gene information using the drop-down menu (**Figure 3**).

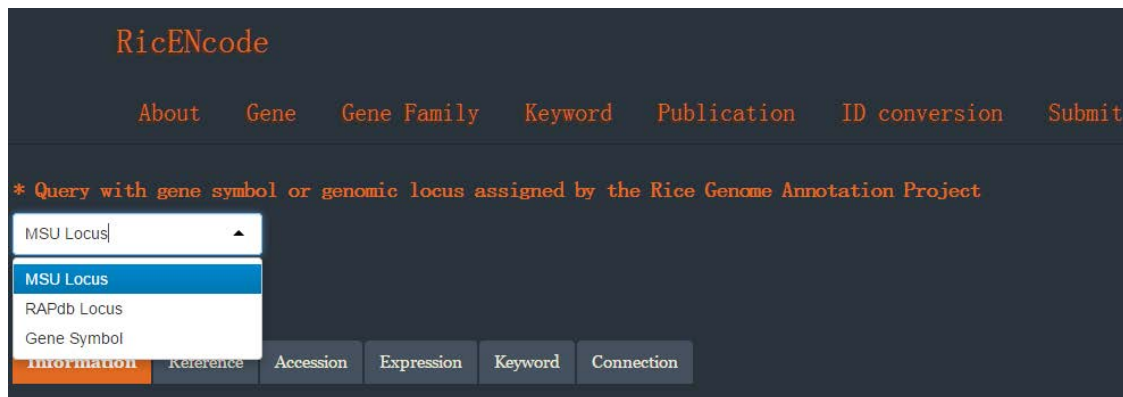


Figure 3. The drop-down menu for query in this database.

The links labeled “Information, Reference, Accession, Expression, Keywords, and Connection” leads to the corresponding information available for a given gene (**Figure 4**).

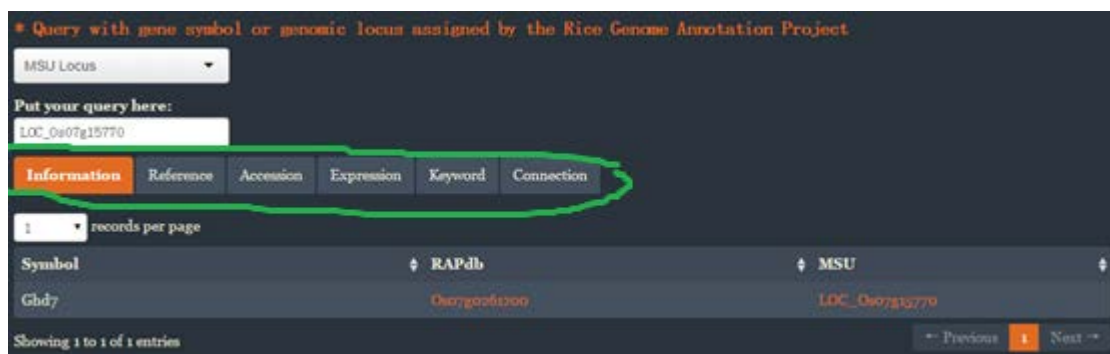


Figure 4. The corresponding information available for a specific gene.

The information on rice gene families can be accessed through the item “Gene Family”

on the navigation bar, which allows for searching of the gene symbol or genomic locus (Figure 5).



Figure 5. The “Gene family” query interface to fetch information on rice gene families.

You can also use the “Keyword” query interface on the navigation bar to search information in this database. Accordingly, the available keywords are listed in <http://andrewhzau.github.io/RICENCODE/tags.html>. For example, using the keyword “heading date” will get the results indicated in Figure 6.

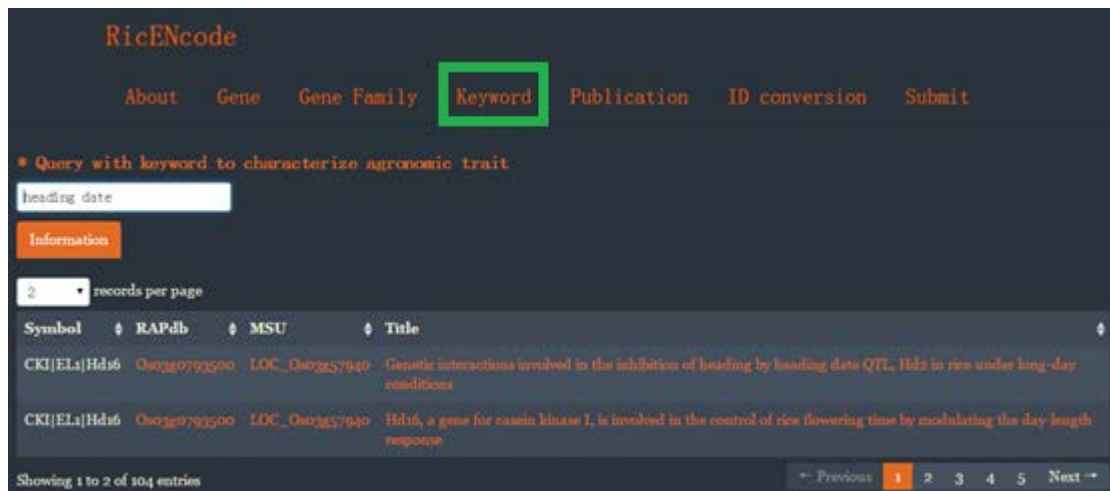


Figure 6. The “Keyword” query interface to fetch information in relation with the queried keyword.

The database provides alternative approaches to obtain information in cloned rice genes based on the “Publication” query on the navigation bar (Figure 7).

RicENcode

About Gene Gene Family Keyword **Publication** ID conversion Submit

* Query the title or abstract of collected publications

grain number

Result

1 records per page

Title	Year	Journal	Affiliation	Abstract	Gene
Cytokinin oxidase regulates rice grain production	2005	Science	Bioscience and Biotechnology Center, Nagoya University, Nagoya 464-8601, Japan.	Most agriculturally important traits are regulated by genes known as quantitative trait loci (QTLs) derived from natural allelic variations. We here show that a QTL that increases grain productivity in rice, Gm1a, is a gene for cytokinin oxidase/dehydrogenase (OsCKX2), an enzyme that degrades the phytohormone cytokinin. Reduced expression of OsCKX2 causes cytokinin accumulation in inflorescence meristems and increases the number of reproductive organs, resulting in enhanced grain yield. QTL pyramiding to combine loci for grain number and plant height in the same genetic background generated lines exhibiting both beneficial traits. These results provide a strategy for tailormade crop improvement.	Gm1a OsCKX2

Showing 6 to 6 of 11 entries

Previous 4 5 **6** 7 8 Next

Figure 7. The “Publication” query interface to fetch information from publications in rice functional genomics.

Besides fetching information from this database, users can also submit newly cloned genes to this database using “Submit” on the navigation bar (**Figure 8**).

RicENcode

About Gene Gene Family Keyword Publication ID conversion **Submit**

* Submit new Genbank accession to this database

Gene symbol Accession

Submit

* Submit new Expression information to this database

Gene symbol Expression Overexpression RNAi

Submit

* Submit new connection to this database

Gene symbol 1 Gene symbol 2 Title Evidence

Submit

* Submit new phenotype and expression figures to this database

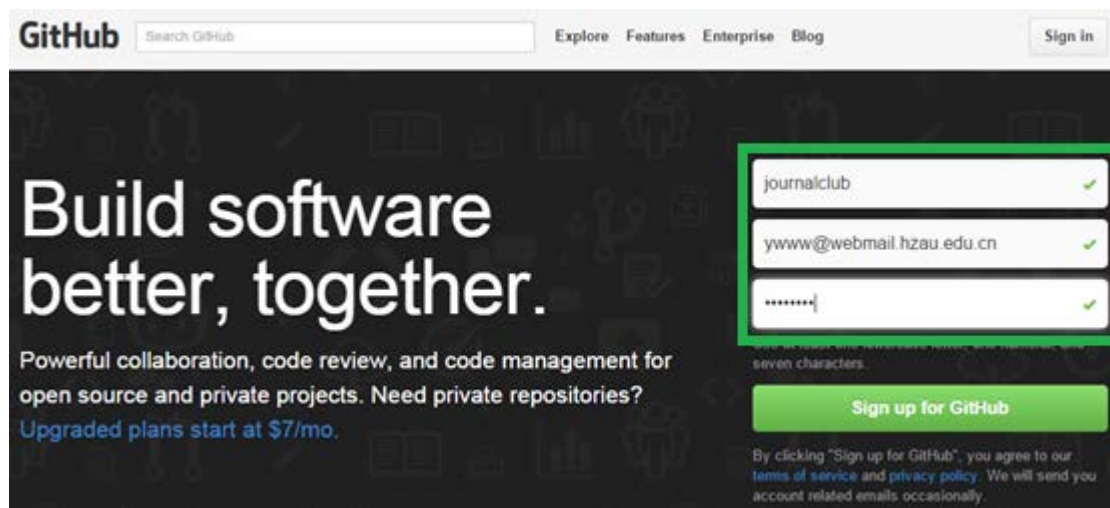
Gene symbol Phenotype Figure Expression Figure

Submit

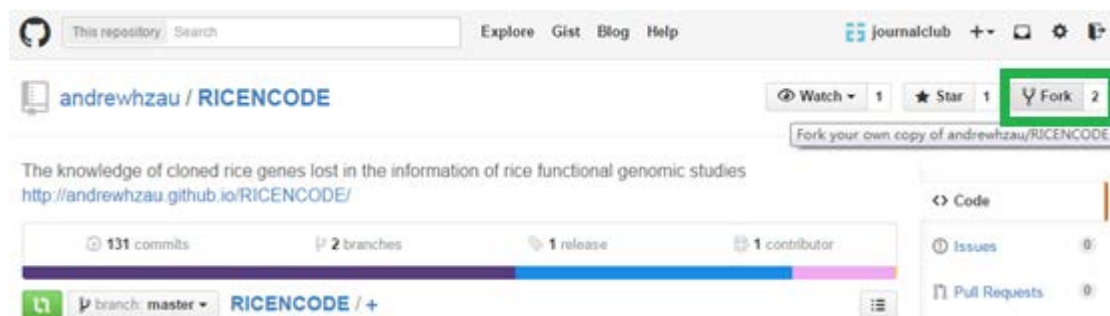
Figure 8. The interface for users to submit new information.

An alternative way to query or contribute to this database is to clone this database to your local computer. The following parts focus on this point step by step.

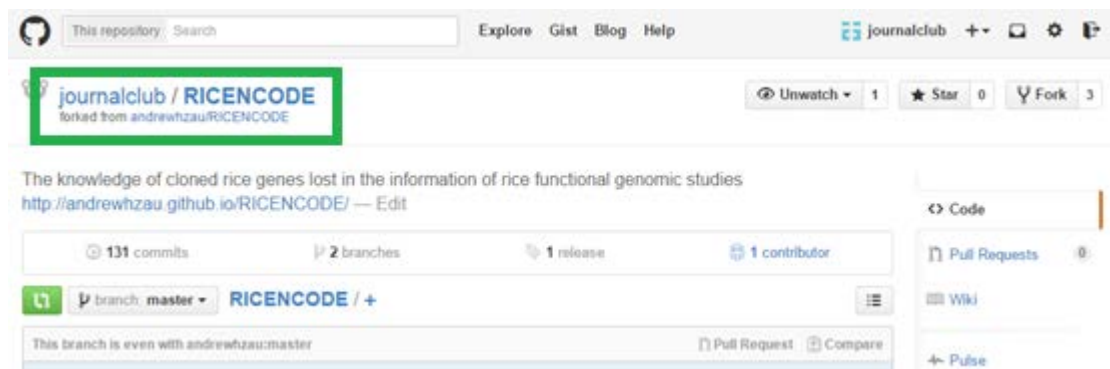
1. Go to <https://github.com/>, register a new account if you didn't have one. Here I created a new account named "journalclub".



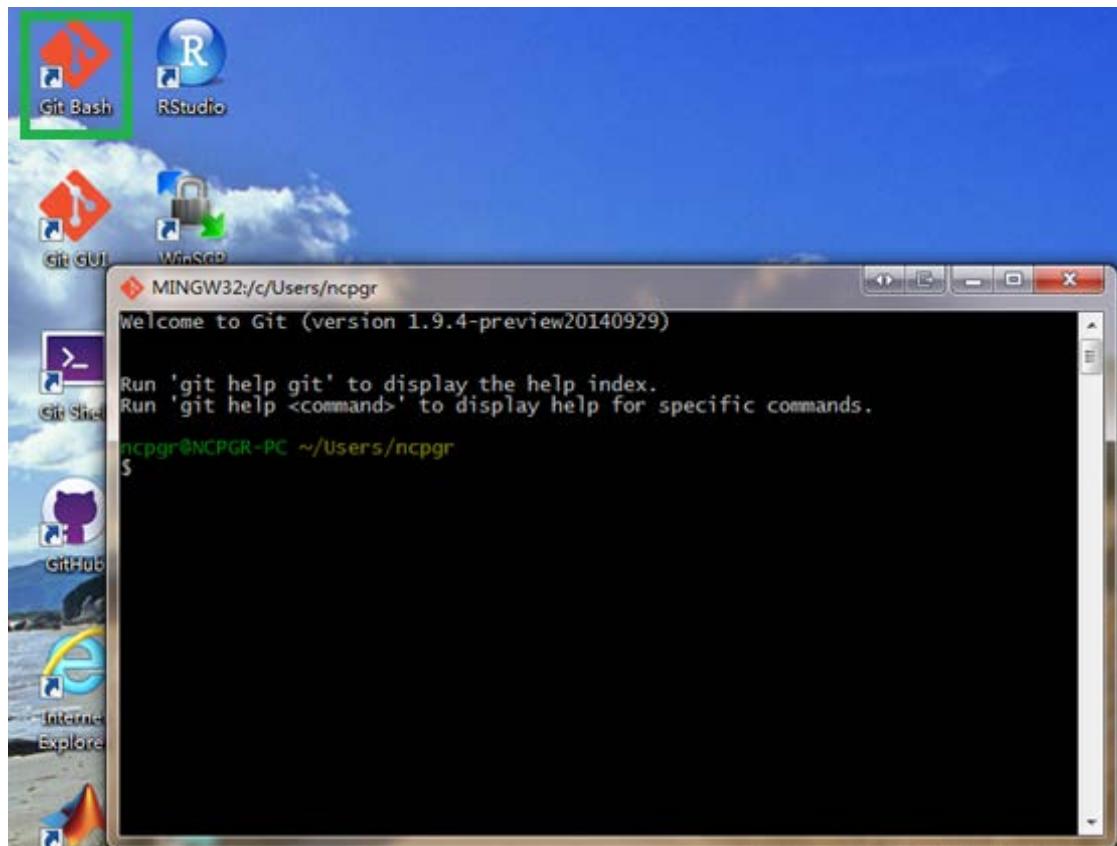
2. Sign in your Github account and then go to <https://github.com/andrewhzau/RICENCODE>. Fork this repo by clicking the "Fork" on the top right.



When the "fork" was done, you will see the repo "RICENCODE" under your account: <https://github.com/journalclub/RICENCODE>.



3. Go to <http://msysgit.github.io/>, download Git and install it on your local computer. When it's done, open "Git Bash" which would probably be on the Desktop of your computer.



4. Configure **your** Github account information (**should be different from mine**) using the following commands.


```
MINGW32:/c/Users/ncpgr
ncpgr@NCPGR-PC ~/Users/ncpgr
$ git config --global user.name "journalclub"
ncpgr@NCPGR-PC ~/Users/ncpgr
$ git config --global user.email "ywww@webmail.hzau.edu.cn"
ncpgr@NCPGR-PC ~/Users/ncpgr
$
```

5. Clone the RICENCODE repo to your local computer using the following commands.

```
MINGW32:/G/DATA
ncpgr@NCPGR-PC /G/DATA
$ cd /G/DATA/
ncpgr@NCPGR-PC /G/DATA
$ git clone https://github.com/journalclub/RICENCODE.git
Cloning into 'RICENCODE'...
remote: Counting objects: 21905, done.
Receiving objects: 12% (2717/21905), 2.29 MiB | 217.00 KiB/s
```

6. Go to <http://cran.r-project.org/>, download the newest R program and install it on your local computer.

7. Go to <http://www.rstudio.com/>, download the newest RStudio and install it on your local computer.

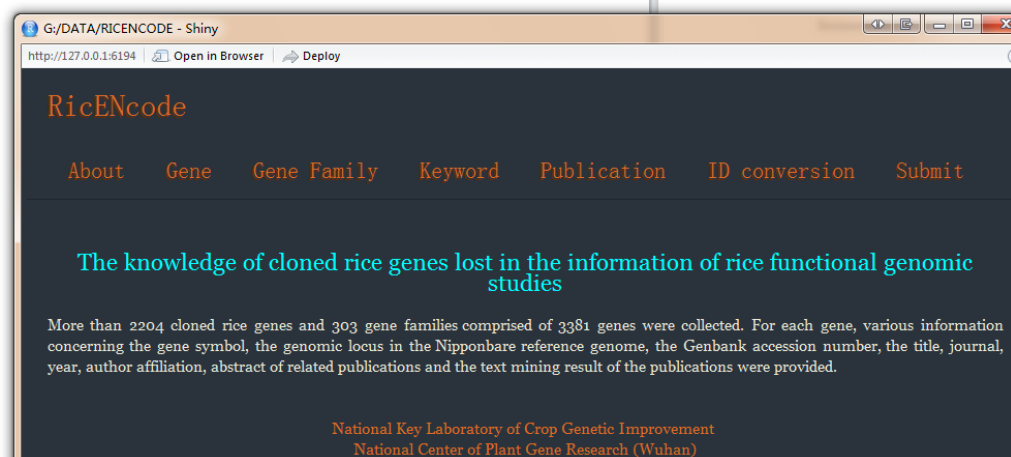
8. Open Rstudio on your local computer and install the Shiny package by typing the following command in your R console.

```
install.packages("shiny", dep=T); install.packages("RCurl", dep=T)
install.packages("XML", dep=T); install.packages("stringr", dep=T)
install.packages("plyr", dep=T)
```

9. Run the following command in Rstudio (**The path of “RICENCODE” on your computer might be different from mine**).

```
library(shiny)
runApp("G:/DATA/RICENCODE")
```

```
> runApp("G:/DATA/RICENCODE")
Listening on http://127.0.0.1:6194
```



10. Let's submit a newly cloned rice gene in the following publication to this database.

Note: Since this gene would appear in this database after this submission, you may want to submit another newly cloned rice gene absent from this database.

[Mol Genet Genomics](#), 2014 Nov 4. [Epub ahead of print]

The rice (*Oryza sativa* L.) LESION MIMIC RESEMBLING, which encodes an AAA-type ATPase, is implicated in defense response.

Fekih R¹, Tamiru M, Kanzaki H, Abe A, Yoshida K, Kanzaki E, Saitoh H, Takaqi H, Natsume S, Undan JR, Undan J, Terauchi R.

Author information

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Abstract

Lesion mimic mutants (LMMs) provide a useful tool to study defense-related programmed cell death (PCD) in plants. Although a number of LMMs have been identified in multiple species, most of the candidate genes are yet to be isolated. Here, we report the identification and characterization of a novel rice (*Oryza sativa* L.) lesion mimic resembling (*lmr*) mutant, and cloning of the corresponding LMR gene. The LMR locus was initially delineated to 1.2 Mb region on chromosome 6, which was further narrowed down to 155-kb using insertions/deletions (INDELs) and cleavage amplified polymorphic sequence markers developed in this study. We sequenced the open reading frames predicted within the candidate genomic region, and identified a G-A base substitution causing a premature translation termination in a gene that encodes an ATPase associated with various cellular activities type (AAA-type) protein. RNA interference transgenic lines with reduced LMR transcripts exhibited the lesion mimic phenotype similar to that of *lmr* plants. Furthermore, expression of the wild-type LMR in the mutant background complemented the lesion phenotype, confirming that the mutation identified in LMR is responsible for the mutant phenotype. The pathogenesis-related (PR) genes PBZ1 and PR1 were induced in *lmr*, which also showed enhanced resistance to rice blast (*Magnaporthe oryzae*) and bacterial blight (*Xanthomonas oryzae* pv. *oryzae*), suggesting LMR is a negative regulator of cell death in rice. The identification of *lmr* and cloning of the corresponding LMR gene provide an additional resource for the study of PCD in plants.

PMID: 25367283 [PubMed - as supplied by publisher]

Fill in some forms and then click "submit".

*** Submit new gene to this database**

Gene symbol LMR	MSU genomic locus LOC_Os06g03940	RAPdb genomic locus Os06g0130000
<input type="button" value="Submit"/>		

*** Submit new publication to this database**

Gene symbol LMR	Title The rice (<i>Oryza sat</i>	Year 2014	Journal Mol Genet Genomics	Affiliation Iwate Biotechnology	Abstract Lesion mimic mutant
<input type="button" value="Submit"/>					

11. You can also submit newly cloned genes or add new publication for existing genes or add new publications not on cloned rice genes but focus on aspects of rice functional genomics progress, using the “Submit” under the item “Gene” on the navigation bar.

(1) To only submit an new publication focus on aspects of rice functional genomics progress, fill in only the fourth form (“Pubmed ID”).

(2) To submit an new publication for existing genes, fill in the first (“Gene symbol”) and the fourth (“Pubmed ID”) forms.

(3) To submit an newly cloned gene, fill in all the four forms. This is all that you need to do!

*** Submit new Gene or add new information for existing genes in one shot**

Gene symbol	MSU genomic locus	RAPdb genomic locus	Pubmed ID
<input type="text" value="LMR"/>	<input type="text" value="LOC_Os06g03940"/>	<input type="text" value="Os06g0130000"/>	<input type="text" value="25367283"/>
<input type="button" value="Submit"/>			

12. Open “Git Bash” and push the newly add data to the Cloud.

```

ncpgr@NCPGR-PC /G/DATA/ricencode (master)
$ cd /G/DATA/ricencode

ncpgr@NCPGR-PC /G/DATA/ricencode (master)
$ git add -A

ncpgr@NCPGR-PC /G/DATA/ricencode (master)
$ git status
On branch master
Your branch is up-to-date with 'origin/master'.

Changes to be committed:
  (use "git reset HEAD <file>..." to unstage)

        new file:   data/Gene/Abstract/L/LMR/Keyword.trait
        new file:   data/Gene/Abstract/L/LMR/LMR.exp.png
        new file:   data/Gene/Abstract/L/LMR/LMR.pheno.png
        new file:   data/Gene/Abstract/L/LMR/acc-AK070084
        new file:   data/Gene/Abstract/L/LMR/expression.info
        new file:   data/Gene/Abstract/L/LMR/gene.info
        new file:   data/Gene/Abstract/L/LMR/reference.info
        modified:   geneInfo.table
        modified:   geneKeyword.table
        modified:   reference.table

ncpgr@NCPGR-PC /G/DATA/ricencode (master)
$ git commit -m "add new gene LMR"
[master 0fbc099] add new gene LMR
10 files changed, 19 insertions(+)
create mode 100644 data/Gene/Abstract/L/LMR/Keyword.trait
create mode 100644 data/Gene/Abstract/L/LMR/LMR.exp.png
create mode 100644 data/Gene/Abstract/L/LMR/LMR.pheno.png
create mode 100644 data/Gene/Abstract/L/LMR/acc-AK070084
create mode 100644 data/Gene/Abstract/L/LMR/expression.info
create mode 100644 data/Gene/Abstract/L/LMR/gene.info
create mode 100644 data/Gene/Abstract/L/LMR/reference.info

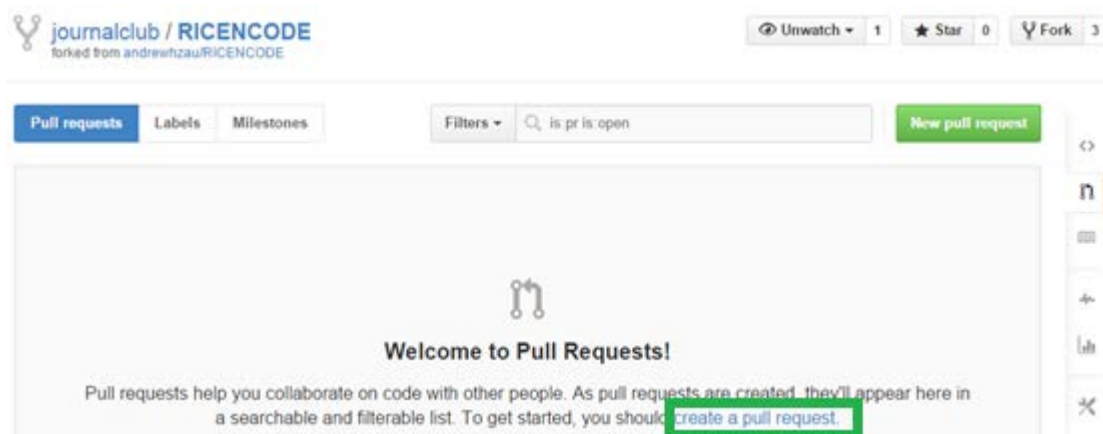
ncpgr@NCPGR-PC /G/DATA/ricencode (master)
$ git push -u origin master
Username for 'https://github.com': journalclub
Password for 'https://journalclub@github.com':

```

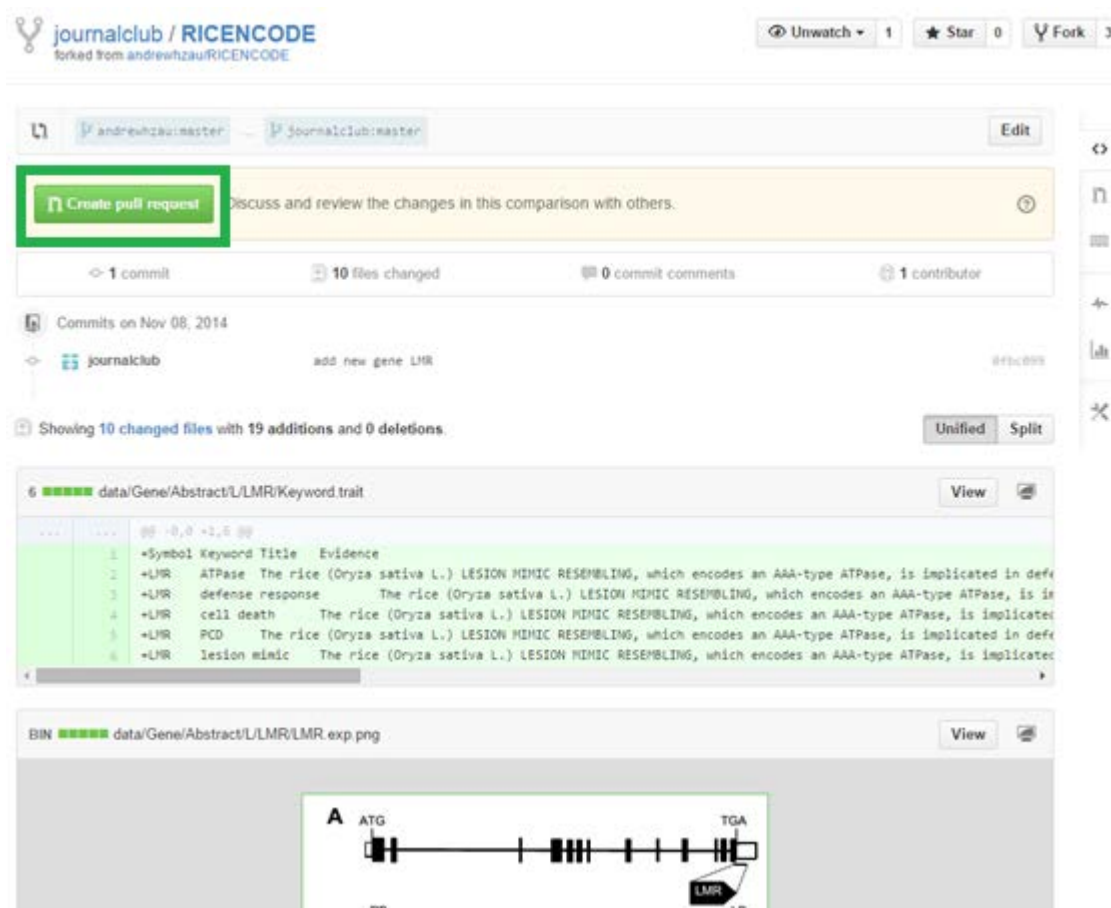
13. Sign in your Github account and go to the repo: <https://github.com/journalclub/RICENCODE>. Click “Pull Requests”.



Then click “create a pull request” in the new page.



Then you will see the newly add data not in my original repo (andrewhzau). Click “Create pull request” on the topleft.



14. Finally, when I login my Github account (andrewhzau), I can merge your pull request into my repo and all the data were updated.

The knowledge of cloned rice genes lost in the information of rice functional genomic studies
<http://andrewhzau.github.io/RICENCODE/> — Edit

133 commits
2 branches
1 release
1 contributor

branch: master
RICENCODE / +

Merge pull request #1 from journalclub/master ...
add new gene LMR

andrewhzau authored just now
latest commit 96a0a3f184

data
.add new gene LMR
12 minutes ago