D4 DIRECT SUBMISSION SYSTEM AND LITERATURE ANNOTATION OF RICE GENES IN ORYZABASE

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Abstract

Oryzabase (http://www.shigen.nig.ac.jp/rice/oryzabase/) is a comprehensive rice science database [1]. It houses a variety of genetic resources, relevant literatures, gene dictionary, DNA sequences, and basic information such as developmental biology and anatomy. In order to keep the gene dictionary up-to-date, literature annotation has been conducted manually since 1995. However as the publication of journal articles increases year by year after genomic sequences were released, it became more difficult to update the dictionary timely and in high quality without sufficient annotators. To overcome this difficulty, we applied machine learning and text-mining to extract known and unknown genes from journals. The machine extraction followed by manual annotation achieved promising results and increased efficiency in manual annotation.
Furthermore a direct submission system where rice researchers can deposit new genes according to the standardized nomenclature [2] became operational in 2008. Recent advances will be introduced.

1.Kurata, N. and Y. Yamazaki., Oryzabase, An Integrated Biological and Genome Information Database for Rice. *Plant Physiology* (2006) 140, 12-17
2 Susan R. McCouch, Gene Nomenclature System for Rice, *Rice* (2008) 1:72-84

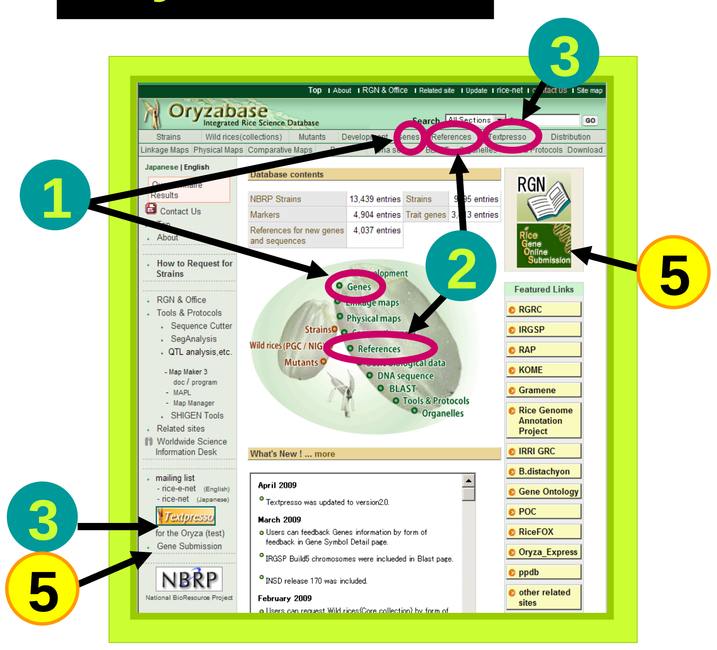
Future plan

Make the gene dictionary more up-to-date, accurate, and comprehensive.

- improve precision of machine extraction
- collaboration with RAP group on gene annotation
- encourage researchers to submit new genes before publication
- encourage researchers to give feedback on Oryzabase genes

Oryzabase HP

www.shigen.nig.ac.jp/rice/oryzabase/

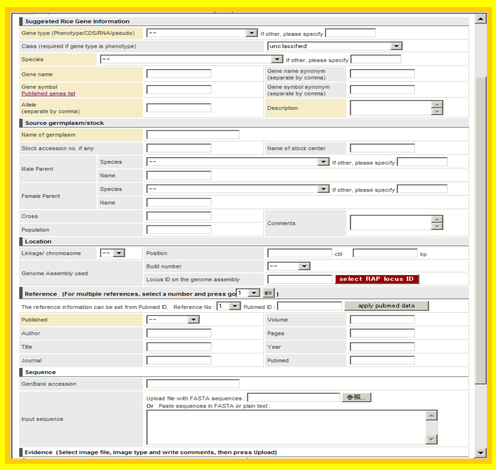


3 Rice Textpresso

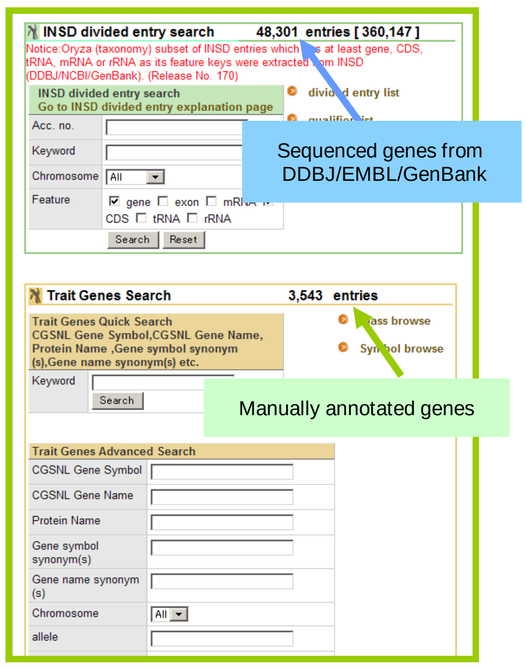
abstract (18889), title (18975)

4 Feedback to a gene

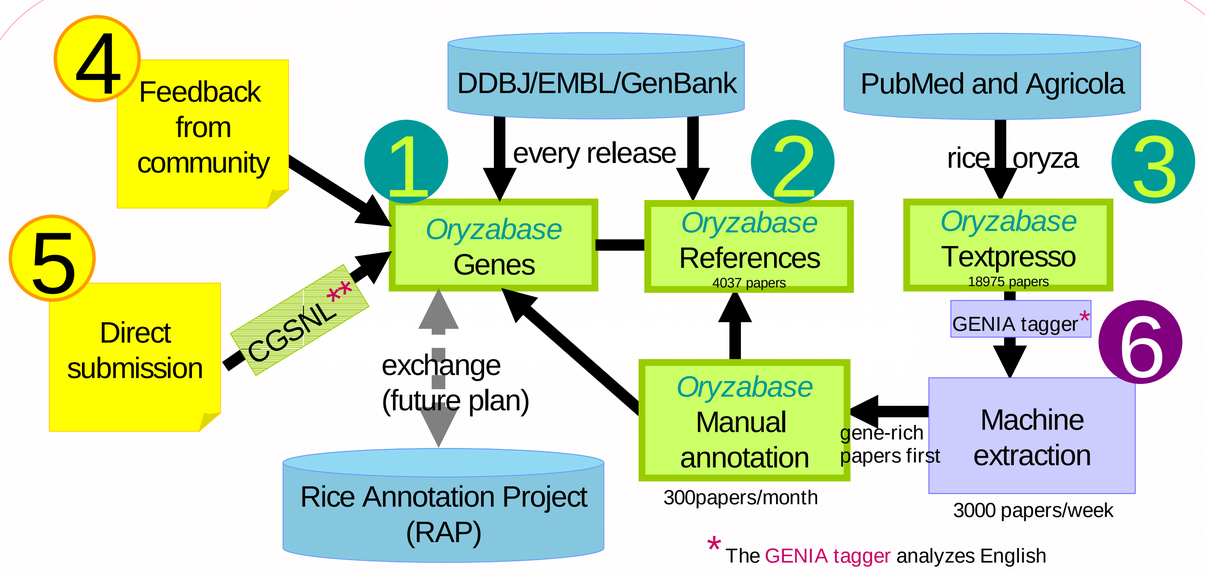
5 on-line gene submission system



1 *Oryzabase* genes



Oryzabase gene annotation flow



**The Committee on Gene Symbolization, Nomenclature and Linkage

*The GENIA tagger analyzes English sentences
and outputs the base forms, part-of-speech tags,
chunk tags, and named entity tags. The tagger
http://www-tsujii.is.s.u-tokyo.ac.jp/GENIA/tagger/
specifically tuned for biomedical text such as MEDLINE abstracts.

6-1 Materials used for machine extraction

Oryzabase Gene Dictionary (as referencedata)
Rice DNA marker name (from RGP)
WordNet Dictionary for general words

GENIA Tagger (Corpus)*
- **Protein**
- **DNA**
- **RNA**
- **Cell Line**
- **Cell Type**

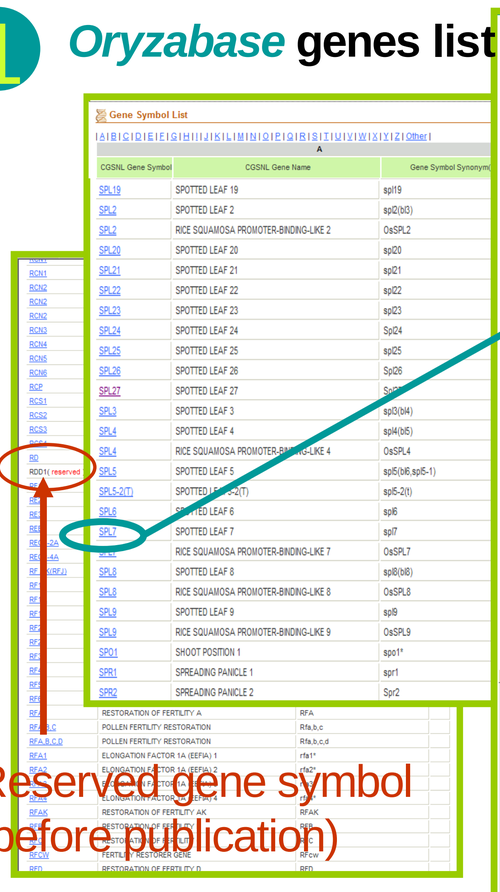
6-2 Result of natural language processing

Journal	Number	Manually extracted genes (A)	Machine extracted genes (B)	Match (C) %	Precision (D=C/B)%	Recall (E=C/A) %	F-value 2x(DxE)/(D+E)
Nature/Science	127	85	206	67	32.5	78.8	46
TAG*	103	47	171	33	19.3	70.2	30.3
Plant Cell etc.	233	226	656	181	27.9	80.8	41.5
Total	463						

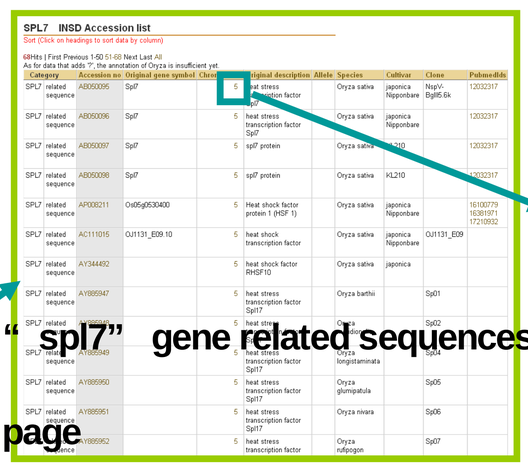
6-3 To improve precision

-- Use correlation of author and gene class
-- Use correlation of author and co-author
-- Improve quality of dictionary
-- Adjust GENIA Corpus to rice related words

1 *Oryzabase* genes list



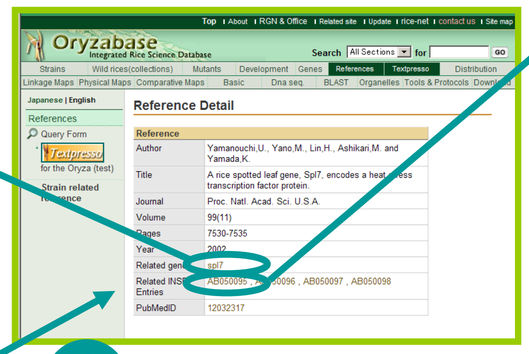
“spl7” gene related sequences



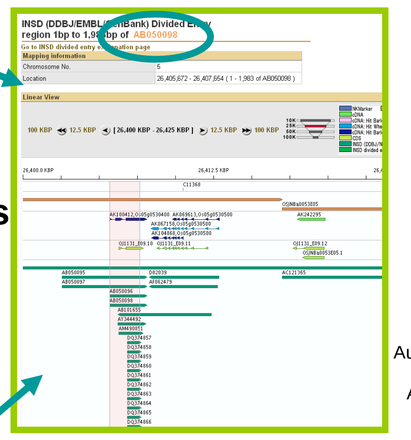
“spl7” gene page

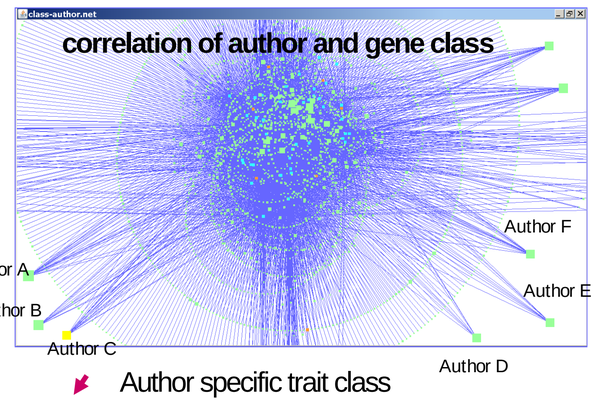
Photo from A. Yoshimura

2 *Oryzabase* Reference



Oryzabase Genome viewer





Author specific trait class