

KRDD: Korean Rice Ds-tagging Lines Database for Rice (*Oryza sativa* L. *Dongjin*)

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Abstract

The Korean Rice Ds-tagging lines Database (KRDD) is designed to provide information about Ac/Ds insertion lines and activation tagging lines using japonica rice. This database has provided information on 18,158 Ds lines, which includes the ID, description, photo image, sequence information, and gene characteristics. The KRDD is visualized using a web-based graphical view, and anonymous users can query and browse the data using the search function. It has four major menus of web pages: (i) a Blast Search menu of a mutant line; Blast from rice Ds-tagging mutant lines; (ii) a primer design tool to identify genotypes of Ds insertion lines; (iii) a Phenotype menu for Ds lines, searching by identification name and phenotype characteristics; and (iv) a Management menu for Ds lines.

Availability: The KRDD can be accessed at the web site of the National Institute of Agricultural Biotechnology (<http://www.niab.go.kr/RDS/>)

Keywords: Ac/Ds database, Ds phenotype, Ds-tagging line, insertion line, KRDD

Introduction

Rice is one of the most important cereal crops in Korea. It has become a model for monocot plants because of its small genome size (around 430 Mbp), ease of transformation, availability of genetic information, and economic importance (Goff *et al.*, 2002; Keller *et al.*, 2000, Sasaki *et al.*, 2005). In rice, insertion of mutant genes has been a powerful strategy for assessing gene func-

tion. The large-scale application of databases in T-DNA insertion sites requires considerable effort (Parinov *et al.*, 2000). But this database can easily be shared with the distribution of mutant materials and analysis of end sequence databases for T-DNA tagging lines in rice (An *et al.*, 2003).

The Activator/Dissociation (Ac/Ds) line has a variation in the transposition frequency and distribution pattern. The Ac element was shown to transpose at high somatic and transposition behaviors of an Ac/Ds system in rice (Enoki *et al.*, 1999; Greco *et al.*, 2003). The flanking sequence-tag database showed generation of an activation-tagging line in japonica rice (Jeong *et al.*, 2006). In this study, we obtained data on the characteristic information of the Ac/Ds family by analyzing insertion and activation tagging lines using japonica rice (*Oryza sativa* L. *Dongjin*). (Kim *et al.*, 2004; Park *et al.*, 2007).

Results and Discussion

The KRDD is designed to provide information about the Ac/Ds insertion line and activation tagging lines using japonica rice. This database has provided information on 18,158 Ds lines, including the ID, description, photo image, sequence information, and gene characteristics. Cross-links to other databases are also introduced to facilitate the access to individual clone information. The use of this database is free for non-commercial purposes. The KRDD is visualized using a web-based graphical view, and anonymous users can query and browse the data using the search function.

The KRDD homepage is shown in Fig. 1, and the stored data are visualized using a web-based graphical view. It has four major menus of web pages: (i) a Blast Search of a mutant line; Blast from rice Ds-tagging mutant lines; (ii) a primer design tool to identify genotypes of Ds insertion lines; (iii) a Phenotype menu for Ds lines, searching by gene name and phenotype characteristics among specific Ds lines; and (iv) a Management menu for Ds lines.

The Blast Search is searchable by selecting specific databases, consisting of DS Sequence, Indica Core, Japonica Core, Indica EST, Japonica EST, Indica Genome, Japonica Genome, Indica GSS, and Japonica GSS in *Oryza sativa*. The KRDD uses several reference databases to facilitate a comprehensive analysis of the genome sequence. These include the Entrez nucleotide database of the National Center for Biotechnology

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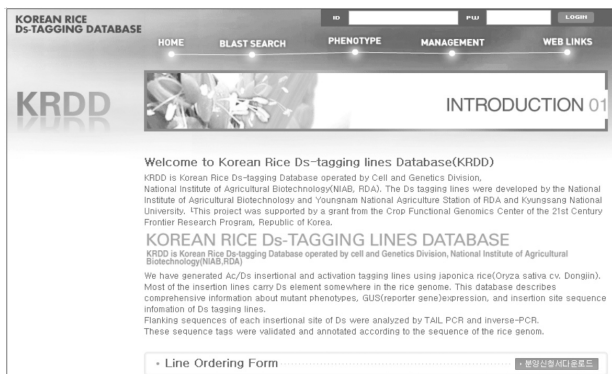


Fig. 1. Homepage of the KRDD. This database shows comprehensive information about mutant phenotypes and sequence information of Ds tagging lines.

Phenotype View

iden No	Ds17004	Description	unspliced-genomic 33 kDa secretoryprotein, putative, expressed
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Photo Information

There is no photo file.

Sequence information

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ATACCTGGAAGGCTCTGGTGGCGGACC AATTGCTTCACTGTTCTTACAATTGTCACCTCTCAGATGGTTGTGA
AAACTGACGTCCCTTTGTGGAAACCGCCTTGGACCACCGTGTGACAGTGGATACATCTGGCTTACC GCCTTTTC
CGTTTCTTTTCCGGTATATCGAAGTCCTCC AAGCCCTTGGATCGTTTTTTGCCACCACTGCTACTCGATGGCCA
GGCTGGCAACTCGGTCTCGCTGCTTGCCTACTCCATGTTTCATCCGCGCATGAATCTGAACCAAGATTAAAACGTG
CAACGGAAATTTGGAATCAAGTGTACTACCTCTTTTCAAGTTAC AAGACTTTCTAGCATTGTCCACATCTATCTATTCT
ATCTATTATTATTAAAATAGCTCTAAAAGAAGACACCAAGTTCGCTGTGGGGGCTAGAAAATTTCCACATTAATCGA
AGAAAAGAGAAACTATTTTGTATCTGTTAGTTATAGCTG
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Gene Characteristic

Chr No.	Description	Gene	Score	E-Value	Clone	BAC Acc
03	unspliced-genomic 33 kDa secretoryprotein, putative, expressed	LOC_Os03g19840	22	0.004	OSJNB0011G21	AC118669

Fig. 2. Typical result page of search for a DS line. The phenotype view page shows Ds line information, including the ID, description, photo information, sequence information, and gene characteristics.

Information (NCBI) for homology searches and Rice Genome Annotation version 5 of the Institute for Genomic Research (TIGR).

The Phenotype View can be searched using Ds sequence information that includes chromosome location (cM) in relation to anchored genetic markers. To integrate genetic maps with Ds sequences, we searched bacterial artificial chromosome (BAC) and P1-derived artificial chromosome (PAC) clones for each chromosome that contained Ds-flanking DNA. As shown in Fig. 2, a phenotype view window shows that all analysis results for a sequence are integrated in the Ds-tagging mutant line. The gene characteristic was designed based on the concept of the Primer design tool throughout the TIGR annotation database. The DS position of chromosome was calculated by the Primer design tool program.

A simplified view of the KRDD data model integrates

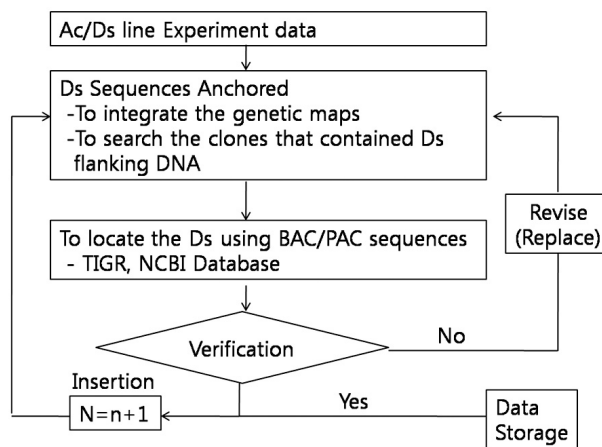


Fig. 3. System flowchart of KRDD. Data collected from users are stored in the KRDD. All registration results are visualized using a web-based graphical view and are made accessible via the Internet.

several programs for search and analysis of Ds line structures (Fig. 3). The physical schema of the database is shown schematically in Fig. 4. It is designed specifically to provide an efficient system and a comprehensive database for Ds lines. It is a very simple model, based on only two core types of objects.

The interface is prepared to submit and analyze each sequence. To prevent disclosure, a user needs to register and enter a password, which serves as security control. The improvement of data quality can be made in the 'Verification' section of the database manager, which allows the user to modify, delete, and add information. The total information on 18,158 Ds lines is collected by the system and then is made available to the public via the Internet. The KRDD will collect additional information and develop a useful tool for Ac/Ds line information.

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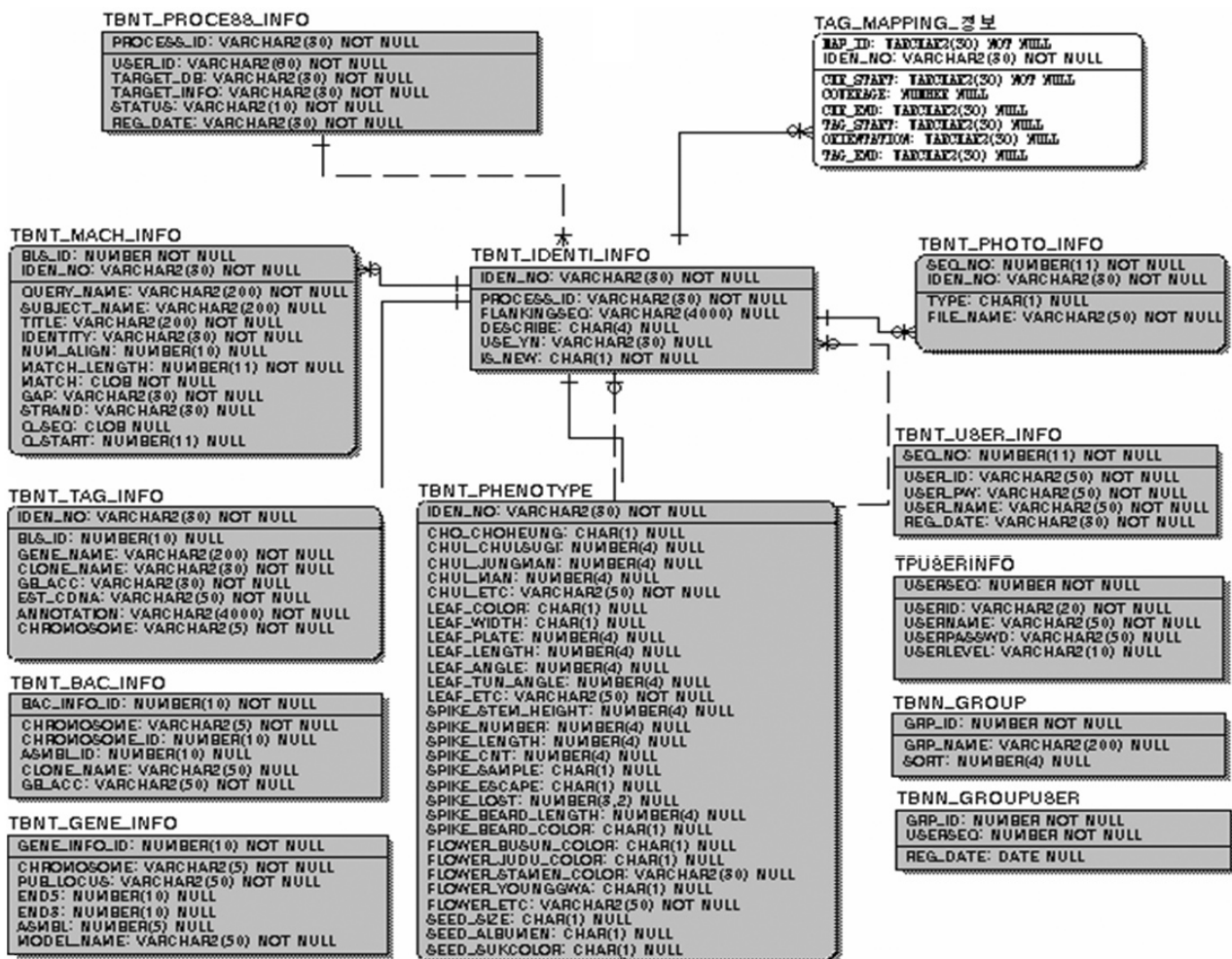


Fig. 4. The physical schema of the database. Each box represents a separate entity, implemented as a database table. Lines between entities indicate a relationship exists. Some tables and columns have been omitted to make the diagram more concise.

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