

NABIC marker database: A molecular markers information network of agricultural crops

Chang-Kug Kim, Young-Joo Seol, Dong-Jun Lee, In-Seon Jeong, Ung-Han Yoon, Gang-Seob Lee, Jang-Ho Hahn & Dong-Suk Park*

Genomics Division, National Academy of Agricultural Science (NAAS), Suwon 441-707, Korea; Dong-Suk Park - Email: dspark@rda.go.kr; Phone: +82-31-299-1625; Fax: +82-31-299-1652; *Corresponding author

Received September 27, 2013; Accepted September 30, 2013; Published October 16, 2013

Abstract:

In 2013, National Agricultural Biotechnology Information Center (NABIC) reconstructs a molecular marker database for useful genetic resources. The web-based marker database consists of three major functional categories: map viewer, RSN marker and gene annotation. It provides 7250 marker locations, 3301 RSN marker property, 3280 molecular marker annotation information in agricultural plants. The individual molecular marker provides information such as marker name, expressed sequence tag number, gene definition and general marker information. This updated marker-based database provides useful information through a user-friendly web interface that assisted in tracing any new structures of the chromosomes and gene positional functions using specific molecular markers.

Availability: The database is available for free at <http://nabic.rda.go.kr/gere/rice/molecularMarkers/>

Keywords: genetic database, molecular marker, NABIC marker.

Background:

Molecular markers are used in molecular biology to identify a particular sequence of DNA. To reveal the genomic relationship among molecular markers has become a necessary step for biology research. Molecular markers are required in a broad spectrum of gene screening approaches, ranging from gene-mapping within traditional 'forward'-genetics approaches through Quantitative Trait Loci (QTL) identification studies to genotyping studies [1]. The multiple molecular marker database based on various markers have been constructed for the purpose of displaying positional relationships among mapped markers in each chromosome [2]. The National Academy of Agricultural Science (NAAS, <http://www.naas.go.kr/>) developed a web-based database system to provide information about Single Nucleotide Polymorphism (SNP) and QTL markers in rice. The genetic marker database provides 7,227 SNP markers on each of 12 chromosomes by using genetic map in rice [3]. The NAAS has released a major update marker

ISSN 0973-2063 (online) 0973-8894 (print)

Bioinformation 9(17): 887-888 (2013)

database which provides 12,829 SNP markers information including gene location information on 12 chromosomes in rice [4]. In addition, NAAS genome information database provides information on expressed sequence tags for 10 species which are possible to detect specific markers and gene clone which mapped locus on a genetic map [5]. In 2013, we have released a major update that comprises various new features for annotation including 3,280 molecular markers analysis information. Enhanced methods to accuracy of gene annotation analysis information are included along with novel functionality that allows users to compare the different method for varying sets of molecular markers.

Methodology:

Dataset, design and development

The molecular markers were collected from the agricultural crops research project of NAAS. As a result of these projects, we have investigated 3,280 molecular markers on the genome and

other marker information. The integration-based molecular marker database is designed to provide molecular marker information on the genome of agricultural crops. This database has three major categories which consist of map viewer, RSN marker and gene annotation. It could be accessed by using a web-based graphical view and anonymous users can query and browse the data using the various functions. This database has developed an integrated system which platform was developed using MySQL, Hypertext Transfer Protocol and Hypertext Preprocessor language. The physical and logical scheme followed the standard principle of relational database by ERWin Data Modeler software (<http://www.ca.com>). This data was stored in an Oracle relational database management system (Oracle Database 10g, Redwood, CA, USA, <http://www.oracle.com/>).

Implementation and Features:

The molecular marker database features three major functions: map viewer, RSN marker and gene annotation. Map viewer provides molecular markers information including sequence and location information on chromosome using a genetic map. The marker viewer allows that users can access the information of updated 7,250 markers in 2013 (**Figure 1a**). RSN marker menu provides the localization information with marker name, chromosome region, gene definition, and product. Users can view a table of detailed information for updated 3,301 RSN markers using keyword search or inputting identification number (**Figure 1b**). Gene annotation menu provides a table of detailed annotation information for additional 3,280 molecular markers in 2013. An annotation table provides specific information such as marker name, identification number, expressed sequence tag information, gene definition and general marker information. In the detail table, users can view a specific information table through GO, MIPS, EC, SNP and Marker view tables. For the example, result by clicking a specific accession number in the 'GO' menu shows a detail information table among three categories: biological process, cellular component, molecular function (**Figure 1c**).

Discussion and Future work:

The molecular marker database of NAAS consists of three major functional categories: map viewer, RSN marker and gene annotation. The database provides 13,831 molecular markers including 7250 marker locations, 3301 RSN marker property, 3280 molecular marker annotation information in agricultural plants. Users are assisted in tracing any new structures of the chromosomes and gene positional functions using specific molecular markers. In the future, NABIC continually provides related services to professional genomic research institutes and

societies. The integration-based molecular marker database provides information through a user-friendly Web-interface from searching marker sequences to related genome location analysis. We plan to develop an integrated marker database that combines a molecular marker database and the other genetic marker database for agricultural crops.

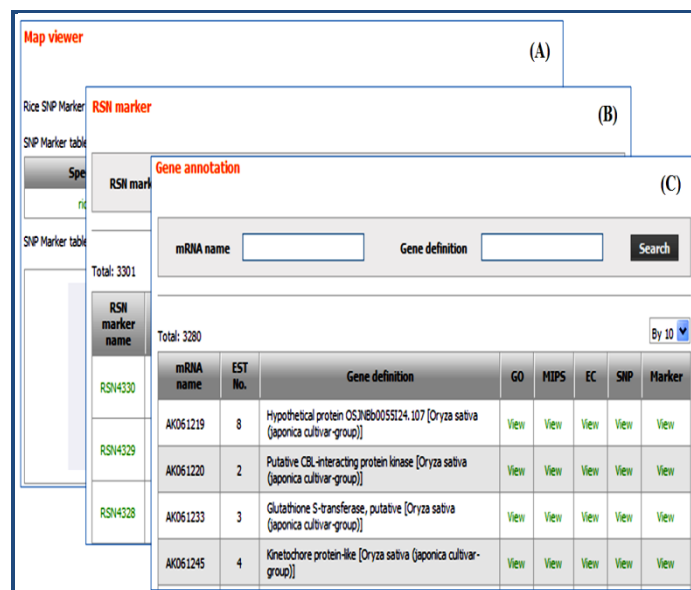


Figure 1: A web snapshot of the molecular marker database is shown. The individual menus have a hypertext sub-menu that can access linked windows with additional information. **A)** The map viewer; **B)** RSN marker; **C)** gene annotation menu table

Acknowledgement:

This study was conducted with support from the Research Program for Agricultural Science & Technology Development (Project No. PJ006651) of the National Academy of Agricultural Science, and the Next-Generation BioGreen 21 Program (SSAC, grant number PJ009614), Rural Development Administration, Republic of Korea.

References:

- [1] Rudd S *et al.* *Nucleic Acids Res.* 2005 **33**: D628 [PMID: 15608276]
- [2] Katsumi S *et al.* *Nucleic Acids Res.* 2000 **28**: 97 [PMID: 10592192]
- [3] Kim C *et al.* *Bioinformatics* 2008 **3**: 61 [PMID: 19238232]
- [4] Kim C *et al.* *Bioinformatics* 2009 **4**: 269 [PMID: 20975922]
- [5] Kim C *et al.* *Bioinformatics* 2012 **8**: 1059 [PMID: 23275706]

Edited by P Kanguane

Citation: Kim *et al.* *Bioinformatics* 9(17): 887-888 (2013)

License statement: This is an open-access article, which permits unrestricted use, distribution, and reproduction in any medium, for non-commercial purposes, provided the original author and source are credited