RiceQTLPro: an integrated database for quantitative trait loci marker mapping in rice plant

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Abstract:
The National Agricultural Biotechnology Information Center (NABIC) in South Korea reconstructed a RiceQTLPro database for gene positional analysis and structure prediction of the chromosomes. This database is an integrated web-based system providing information about quantitative trait loci (QTL) markers in rice plant. The RiceQTLPro has the three main features namely, (1) QTL markers list, (2) searching of markers using keyword, and (3) searching of marker position on the rice chromosomes. This updated database provides 112 QTL markers information with 817 polymorphic markers on each of the 12 chromosomes in rice.

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

Background:
The Quantitative Trait Loci (QTL) is essentially a statistical creation that identifies a particular region of the genome as containing one or more genes. The QTL analysis is the phrase used currently to study this genetic variation, to locate the genes responsible and to explore their effects and interactions. QTL databases have become a routine tool for complex traits analysis in functional genomic research and QTL mapping is widely used due to its simplicity and concept **[1].** To increase the importance of QTL analysis, various databases have been constructed for comparative detection and prediction of genome structure. The NIAB genetic marker database (http://nabic.niab.go.kr) provided QTL markers which have been systematically aligned to the sequence on the 12 chromosomes in rice **[2]**. The GRAMENE QTL database (http://www.gramene.org/qtl/) provides QTL identified for numerous agronomic traits in plants, and genetic maps have been systematically aligned to the rice sequence where they can be searched as standard genomic features **[3-4].** The QTLNetwork is a mapping tool to identify main effect QTLs,

epistatic QTLs and QTL- Environment effects in several crop species **[5].** The Q-TARO Database (http://qtaro.abr.affrc.go.jp/) focused on QTL information which views the genomic location of a target QTL or to compare target QTLs.

Methodology:
Dataset
The QTL markers were collected from the Korea rice (*Oryza sativa*) genome project of National Academy of Agricultural Science (NAAS, http:// http://www.naas.go.kr/) and the New Bio-Green 21 project (http://atis.rda.go.kr/). In addition, QTL information was collected through international public institutes and collaborative university.

Development and marker design
The platform was developed using MYSQL and Oracle relational database management system. To construct a loci database with genetic map, we analyze the collected QTL markers using the Haldane mapping function method. Using the MapMaker/Exp 3.0 program with integrated rice genome

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explorer (INE, http://ine.dna.affrc.go.jp/giot/) method, QTL map was developed in two stages as polymorphic markers and QTL markers. The Logarithm of the Odds (LOD) score was analyzed with MapMaker/QTL 1.1 program using a range of recombination frequency value which was computed using

maximum likelihood algorithm between markers. In 2014, we have released a major update for QTL mapping using Haldane's mapping function method [6] with LOD score and recombination frequency value.
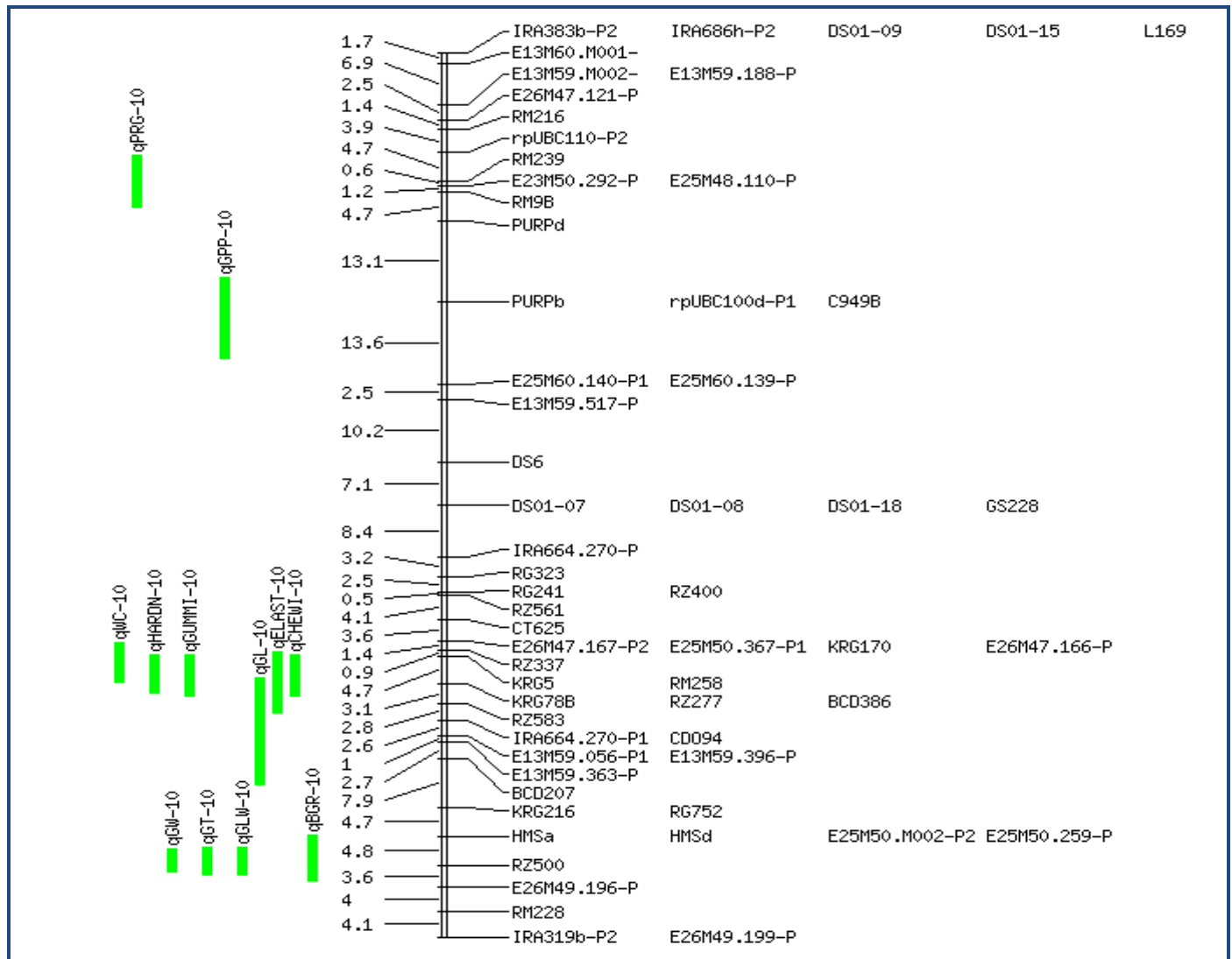

Figure 1: A snap shot of QTL position linkage map. The view page shows the genetic map on the 10 chromosome in rice plant.

Implementation and features
The NABIC has developed an integrated web database which is comprised of QTL markers for genetic variation and markers position search tools. The RiceQTLPro database provides information through a genetic map of about 112 QTL markers with 817 polymorphic markers on each of the 12 chromosomes in rice. The database has three major parts and functions such as QTL markers list, searching of markers, and map of QTL markers position. Users can detect a mapped locus of specific QTL markers with associated trait. In addition, users can view a table of detailed information by clicking the linked QTL marker **(Figure 1).**

The QTL marker locus is displayed on the left while the genetic markers as polymorphic marker are displayed on the right and QTL names are shown next to each vertical green bar. The QTL

marker list table shows the peak LOD value and their genetic parameters. The user can directly specify the viewer to view the genomic location of a target QTL. The specific marker information is displayed by selecting chromosome map with both information on associated traits and a mapped locus on a genetic map. The position of QTL markers are displayed by trait categories, allowing the locations of QTLs of each trait to be easily compared. Using the RiceQTLPro database, a user can access the individual information table for genome structure analysis by clicking a linked their respective hypertext.

Utility and future developments
The RiceQTLPro database provides information through genetic map of about 112 QTL markers with 817 polymorphic markers on each of the 12 chromosomes in rice. Users can trace the new structures of the chromosomes and gene positional

functions through comparisons using our QTL marker database. In the future, NAAS plans to develop an integrated genetic linkage map that combines an SNP marker database and a QTL marker database for rice.

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