A Quantitative Trait Loci Resource and Comparison Tool for Pigs: PigQTLDB

A.S. Leaflet

Zhi-Liang Hu , Associate scientist
James Reecy, Assistant professor, and
Max Rothschild, Distinguished professor of animal science

Summary and Implications

The Pig Quantitative Trait Loci (QTL) database has gathered all pig QTL data published during the past 10 years. The database and its peripheral tools make it possible to compare, confirm and locate on pig chromosomes the most feasible location for a gene responsible for quantitative trait important to pig production.

Introduction

The ultimate goal of QTL studies is the identification of the gene(s) responsible for the phenotypic variation observed in a particular trait. However, it is a challenging task to combine results from different research projects involving QTL studies for positional candidate gene or marker searches from information scattered in many publications, each described in different ways (Bidanel and Rothschild, 2002). The pig QTL database we developed can be used for easy search and comparison of QTL results from different studies, derived from different populations, and obtained with perhaps different testing methods. With overlapping QTL results from different studies, it will be easier to confirm and narrow down QTL regions that may help to speed up the positional search for underlying genes.

Material and Methods

All QTL data are from published journal papers and reports. The data are organized into related tables and loaded into MySQL, a relational database software. The programs to make worldwide web user interface to the data is written in Perl/CGI. The communication between the database and the web server is made possible with Perl DBI/DBD. Perl GD library was employed to draw QTL map graphs "on the fly". All data and tools are hosted on a RedHat linux server located at the Iowa State University.

Results

To date, **791** QTL from **73** publications have been curated into the database. Those QTLs represent **219** different traits. The pig QTL database can be accessed with this URL: http://www.animalgenome.org/QTLdb/. The main features and functions include:

Graphical display of QTL data from different studies.

Figure 1 is a snap shot of the QTL locations mapped to pig chromosome 7. This shows how it is possible to easily find the area where multiple reported QTL for a trait is located, and how it may be aligned with the pig genome map (Rohrer et al., 1996).

Dynamic link of pig QTL data with related information from other databases

QTL data in the PigQTLdb can be linked to related information in the public domain. These data have also been submitted to the Gene and Map Viewer resources at the NCBI, where the information about markers has been matched to marker records in NCBI's UniSTS database. The data are retrievable from NCBI via Gene, Map Viewer, and UniSTS. This tool can be used for other species as well.

Figure 1. A snap shot of the QTL mapped to pig chromosome 7, displayed with a "QTL Mapper" tool.

References

Bidanel, J. P. and Max F. Rothschild, 2002. Current Status of Quantitative Trait Loci Mapping in Pigs. Pig News and Information, 2002, Vol. 23, No. 2

Rohrer, G. A., L. J. Alexander, H. Zhiliang, T. P. L. Smith, J. W. Keele, and C. W. Beattie. 1996. A comprehensive map of the porcine genome. Genome Research 6:371-391.