

10-2005

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# A QTL Resource and Comparison Tool for Pigs: PigQTLDB

## Abstract

During the past decade, efforts to map quantitative trait loci (QTL) in pigs have resulted in hundreds of QTL being reported for growth, meat quality, reproduction, disease resistance, and other traits. It is a challenge to locate, interpret, and compare QTL results from different studies. We have developed a pig QTL database (PigQTLdb) that integrates available pig QTL data in the public domain, thus, facilitating the use of this QTL data in future studies. We also developed a pig trait classification system to standardize names of traits and to simplify organization and searching of the trait data. These steps made it possible to compare primary data from diverse sources and methods. We used existing pig map databases and other publicly available data resources (such as PubMed) to avoid redundant developmental work. The PigQTLdb was also designed to include data representing major genes and markers associated with a large effect on economically important traits. To date, over 790 QTL from 73 publications have been curated into the database. Those QTL cover more than 300 different traits. The data have been submitted to the Entrez Gene and the Map Viewer resources at NCBI, where the information about markers was matched to marker records in NCBI's UniSTS database. Having these data in a public resource like NCBI allows regularly updated automatic matching of markers to public sequence data by e-PCR. The submitted data, and the results of these calculations, are retrievable from NCBI via Entrez Gene, Map Viewer, and UniSTS. Efforts were undertaken to improve the integrated functional genomics resources for pigs.

## Disciplines

Agriculture | Animal Sciences | Cell Biology | Genomics

## Comments

This article is from *Mammalian Genome* 16 (2005): 792, doi:[10.1007/s00335-005-0060-9](https://doi.org/10.1007/s00335-005-0060-9).

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## A QTL resource and comparison tool for pigs: PigQTLDB

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Received: 23 April 2005 / Accepted: 16 June 2005

### Abstract

During the past decade, efforts to map quantitative trait loci (QTL) in pigs have resulted in hundreds of QTL being reported for growth, meat quality, reproduction, disease resistance, and other traits. It is a challenge to locate, interpret, and compare QTL results from different studies. We have developed a pig QTL database (PigQTLdb) that integrates available pig QTL data in the public domain, thus, facilitating the use of this QTL data in future studies. We also developed a pig trait classification system to standardize names of traits and to simplify organization and searching of the trait data. These steps made it possible to compare primary data from diverse sources and methods. We used existing pig map databases and other publicly available data resources (such as PubMed) to avoid redundant developmental work. The PigQTLdb was also designed to include data representing major genes and markers associated with a large effect on economically important traits. To date, over 790 QTL from 73 publications have been curated into the database. Those QTL cover more than 300 different traits. The data have been submitted to the Entrez Gene and the Map Viewer resources at NCBI, where the information about markers was matched to marker records in NCBI's UniSTS database. Having these data in a public resource like NCBI allows regularly updated automatic matching of markers to public sequence data by e-PCR. The submitted data, and the results of these calculations, are retrievable from NCBI via Entrez Gene, Map Viewer, and UniSTS. Efforts were undertaken to improve the integrated functional genomics resources for pigs.

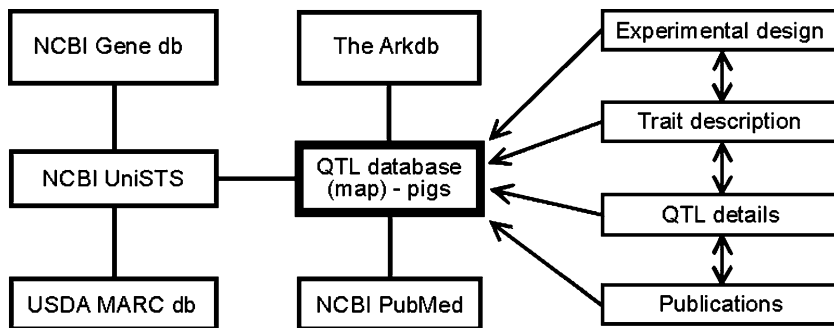
### Introduction

Quantitative trait loci (QTL) have been mapped for some of the most economically important traits in pigs, such as meat quality, fertility, and disease resistance. They are based on several genetic linkage maps (Archibald et al. 1995; Marklund et al. 1996; Rohrer et al. 1996). These data allow researchers to narrow down genomic regions and identify the genetic factors that contribute to trait variations (Bidanel and Rothschild 2002).

The ultimate goal of QTL studies is the identification of the actual gene(s) responsible for the phenotypic variation observed in a particular trait. While many QTL are overlapping on the same genomic region and others add new regions for certain traits, it is possible to combine results from different QTL studies for positional candidate gene or marker searches. However, several challenging factors limit the accurate dissection of targeted QTL information. First, the QTL information within the public domain is scattered in many publications; the data are the result of independent studies that used similar or different statistical analysis methods. Second, QTL represent statistical evidence for cosegregation of traits and markers within a particular experimental population. However, there is no tool that combines QTL data for comparisons among experiments. Third, pig production traits are defined and measured in many different ways in different laboratories and/or countries and there is a lack of standardized nomenclature to define similar traits for meaningful comparisons. While the accuracy of QTL locations depends on a number of factors, such as marker density of the linkage map, the design of the experiment, the size and structure of the resource population, the method to establish significance threshold, etc., the precise location of a

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**Fig. 1.** Conceptual database structure of PigQTLdb showing how QTL data are organized and linked to external public databases.

true QTL maybe approximated with multiple QTL mapping results from several studies.

We developed an integrated QTL database and visualization tool, pig QTL database (PigQTLdb), to easily search and compare QTL results from different studies, derived from different resource populations, and obtained using a variety of statistical testing methods. Users of PigQTLdb can electronically confirm and/or narrow down more promising chromosomal regions from overlapping QTL results. This tool should speed up the positional search for underlying genes.

#### Material and methods

**Data.** All QTL data entered into the PigQTLdb are from published papers and reports. Over 50 parameters/data types are subjected for raw data collection. These included QTL location (chromosome, location, location span), flanking markers (at suggestive and/or significant test levels), peak markers, test statistics (LOD score, least square means,  $p$  values,  $F$  values, variance), QTL effects (dominance effect, additive effect), candidate genes, and traits and their measurements. The data are organized into related tables in a relational database. The database structure is designed to enable dynamic links to external data resources (Fig. 1). The base map for displaying marker locations was developed with mapping data mainly from USDA-MARC (Meat and Animal Research Center) (Rohrer et al. 1996). Markers defining a QTL that were not on the MARC map were interpolated to form a consensus map with the comparative framework of ArkDB (Hu et al. 2001). When a marker defining the peak, the left, or the right boundary of a QTL is found to be on the MARC map, the MARC map location of this marker is inputted directly into the PigQTLdb. When there is no marker at the point where the QTL curve goes past the significance threshold, the reported map location is translated into MARC map location by interpolation with the aid of map locations of adjacent common markers.

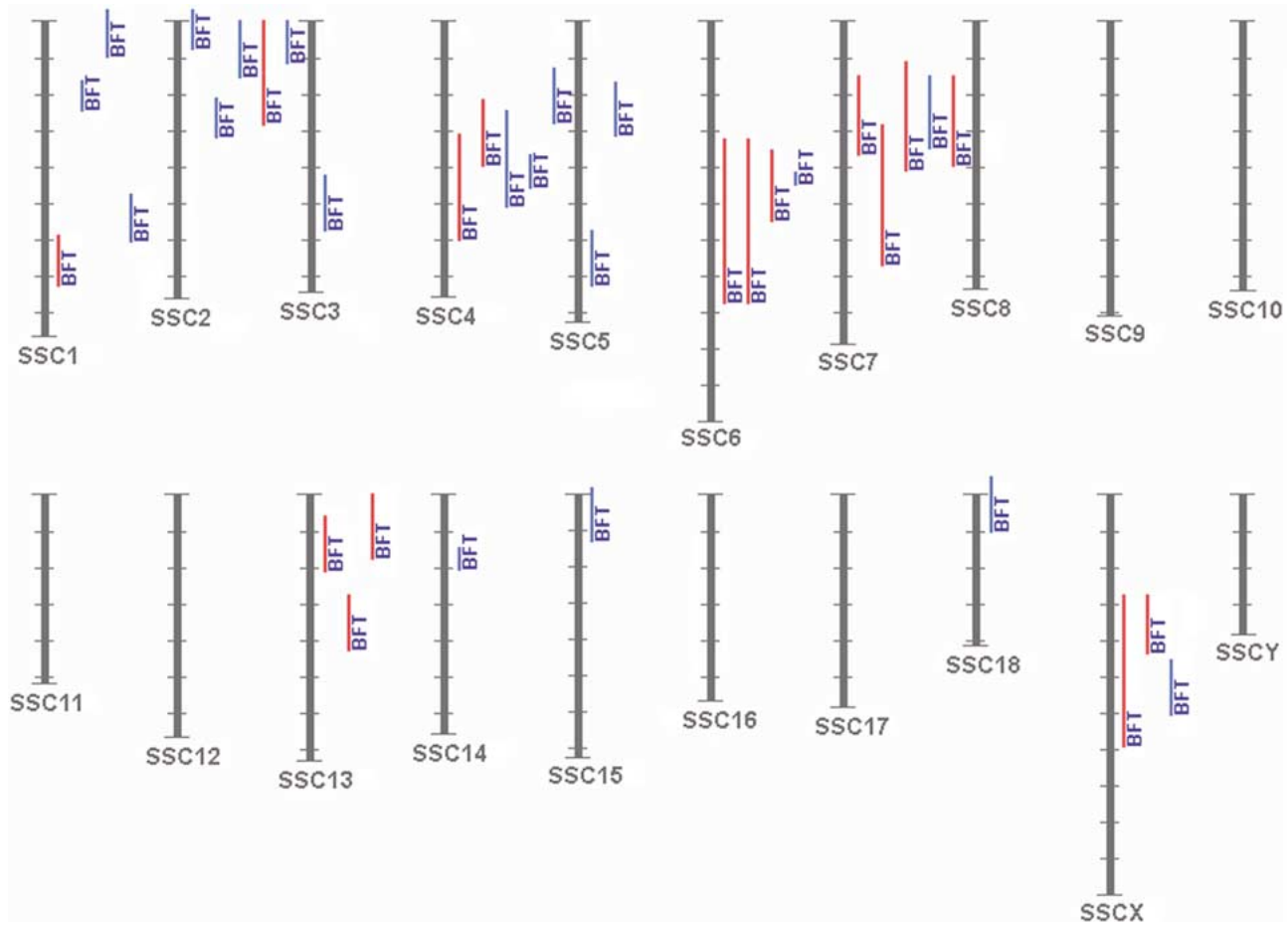
**Software.** We used MySQL (version 12.22) as the underlining relational database and Apache 1.3.31 as the worldwide web server. Perl (5.8.5) was used to program the common gateway interface (CGI) to present and interpret data, synthesize maps, and make dynamic links to various data resources. Lincoln Stein's Perl GD library (Lincoln 2000) was used to draw QTL map graphs "on the fly." All data and tools are hosted on a RedHat Linux server located at Iowa State University.

**Implementation.** The PigQTLdb is implemented at both the National Center for Biotechnology Information (NCBI) and at Iowa State University (ISU). The QTL pipeline developed for other model organisms at NCBI was applied to managing the pig QTL data. The newly developed web tools for QTL data organization and graphic display are implemented at the ISU site. Implementation at ISU emphasizes links with pig phenotypic and other pig information, while implementation at NCBI emphasizes links with sequences and other genomic information. Data are crosslinked between the two implementations at related fields.

#### Results

To date, 791 QTL from 73 publications have been curated into the PigQTLdb. Those QTL represent 219 different traits. The PigQTLdb is implemented as a stand-alone database on the NAGRP Animal Genome server at Iowa State University (ISU implementation; URL: <http://www.animalgenome.org/QTLdb/>), and as part of NCBI Gene database (NCBI implementation), each with some unique features to facilitate easy user access to and efficient use of the data.

**ISU implementation.** The PigQTLdb web interface is designed for general users to easily search, browse, and download QTL information stored in the PigQTLdb. The database is designed in such a



**Fig. 2.** A snapshot of QTL map view showing QTL for “back-fat thickness” mapped to multiple chromosomes in the pig genome. The QTL names are hyperlinked to detailed QTL information. Each chromosome name is also linked to a graph with all QTL mapped to that chromosome, as shown in Fig. 3. The red lines represent QTL that passed significant testing threshold, and the blue lines represent that of suggestive threshold.

way that each searched or browsed result is dynamically linked to further results. In this way users can quickly traverse through the information on the PigQTLdb and related databases.

**Phenotype data organization.** All pig phenotypes (traits) are organized into different trait classes by their “categories” and “types.” We define *trait category* to describe very general aspects of pork products or the processes by which the product is made, e.g., meat quality, health, reproduction. *Trait type* describes physical or chemical properties of the pork products or features that can influence the process by which a pork product is made, or it describes types of measurements within each *trait category*, e.g., average daily gain, muscle pH, feed intake. *Trait names* are then defined within each trait type with more detailed specifics. Trait description and measurement criteria are recorded in order to correctly list, compare, and index the trait

names. In this way, QTL from different studies, derived using different populations and methods, can be organized by the traits they represent.

**Graphical display of QTL for a trait mapped to multiple chromosomes in the pig genome.** A QTL region on a chromosome is depicted by a parallel bar with the QTL abbreviation along the side and the peak position indicated with a green dot. From the *Trait details* page, a link is provided to show all QTL mapped in the pig genome for the trait under examination. Figure 2 shows a total of 35 back-fat thickness (BFT) QTL that are mapped to multiple chromosomes. The marker names and QTL names on all graphs in the PigQTLdb are hyperlinked to details in respective databases. Users can follow up QTL on each chromosome to find more supporting evidence for a particular QTL or to get an overview of all QTL mapped to that chromosome.



**Table 1. Some overlapping QTL found on various chromosomal regions with the PigQTLdb tool**

<i>Chromosomes</i>	<i>Number of QTL found</i>	<i>Traits</i>	<i>Flanking markers</i>	<i>Evidenced by</i>
1	18	Back-fat thickness	S0354 and TPS6871	Bidanel et al. (2001) de Koning et al. (1999) Milan et al. (2002) Rohrer and Keele (1998) Rohrer (2000) Su et al. (2002b)
1	6	Average daily gain	SW745 and SW1301	Bidanel et al. (2001) Casas-Carrillo et al. (1997) Paszek et al. (1999) Quintanilla et al. (2002)
1	11	Body weight	S0354 and TPS6871	Bidanel et al. (2001) Quintanilla et al. (2002) Rohrer (2000) Su et al. (2002a, 2004) Wada et al. (2000)
2	10	Back-fat thickness	SW2443 and FSHBHAЕ	Bidanel et al. (2001) de Koning et al. (1999, 2000, 2001b) Jeon et al. (1999) Knott et al. (1998) Milan et al. (2002) Nezer et al. (1999) Rattink et al. (2000)
4	13	Average daily gain	SWR73 and SW524	Bidanel et al. (2001) Knott et al. (1998, 2002) Malek et al. (2001a) Marklund et al. (1999) Walling et al. (2000) Wang et al. (1998)
4	18	Back-fat thickness	SW752 and SW524	Bidanel et al. (2001) de Koning et al. (2001b) Grindflek et al. (2001) Knott et al. (1998) Malek et al. (2001a) Marklund et al. (1999) Milan et al. (2002) Perez-Enciso et al. (2000) Varona et al. (2002) Walling et al. (1998, 2000)
4	3	Intramuscular fat	SW752 and SW589	Gerbens et al. (2001) Rattink et al. (2000) de Koning et al. (1999)
4	6	Body weight	SW839 and SW524	Bidanel et al. (2001) Knott et al. (2002) Walling et al. (2000)
6	9	Intramuscular Fat	S0294 and EAH	de Koning et al. (1999, 2000) Gerbens et al. (2000) Grindflek et al. (2001) Ovilo et al. (2002a, 2002b) Szyda et al. (2002, 2003)
6	5	Average daily gain	S0294 and EAH	Bidanel et al. (2001) Sato et al. (2003) Su et al. (2002a)
6	12	Back-fat thickness	S0087 and A1BG	Bidanel et al. (2001) de Koning et al. (2001b) Ovilo et al. (2002b) Rohrer (2000) Sato et al. (2003) Szyda et al. (2003) Varona et al. (2002)
6	4	Body weight	S0560 and EAH	Bidanel et al. (2001)

Continued

**Table 1. Continued**

<i>Chromosomes</i>	<i>Number of QTL found</i>	<i>Traits</i>	<i>Flanking markers</i>	<i>Evidenced by</i>
7	33	Back-fat thickness	SWR1078 and S0102	Sato et al. (2003) Su et al. (2002) Bidanel et al. (2001) de Koning et al. (1999, 2000, 2001b) Malek et al. (2001a) Milan et al. (2002) Rattink et al. (2000) Rohrer and Keele (1998) Rohrer (2000) Sato et al. (2003) Su et al. (2002b) Wada et al. (2000) Wang et al. (1998)
8	3	Average daily gain	SW2521 and SE47610	Casas-Carrillo et al. (1997) Malek et al. (2001a) Quintanilla et al., <i>Genet Sel Evol.</i> 34(2):193–210.
9	2	Average daily gain	SE47407 and SWR1014	Malek et al., <i>Mamm Genome.</i> 12(8):630–6.
10	2	Teat number	S0070 and SW951	Quintanilla et al. (2002) Hirooka et al. (2001)
13	5	Back-fat thickness	S0282 and SW344	Rohrer (2000) Malek et al. (2001a) Nezer et al. (2002)
14	4	Back-fat thickness	SWC26 and SWR1042	Rohrer and Keele (1998) de Koning et al. (2001b) Malek et al. (2001a)
15	6	Meat color	SW1217 and SW1262	Rohrer and Keele (1998) Bertram et al. (2000) de Koning et al. (2001a)
15	6	Muscle pH	SW159 and SW1983	Malek et al. (2001b) Bertram et al. (2000) Ciobanu et al. (2001)
15	2	Ovulation rate	SW1401 and SW1983	Malek et al. (2001 b) Rathje et al. (1997) Rohrer et al. (1999)
X	21	Back-fat thickness	KS149 and S0022	Bidanel et al. (2001) de Koning et al. (2001b) Harlizius et al. (2000) Knott et al. (1998) Milan et al. (2002) Rohrer and Keele (1998) Rohrer (2000)

error checks. In addition, a two-layer (curator layer and editor layer) quality control mechanism is built in, which helps to minimize the errors, including those of grammar, wording, or data formatting. The tool also helps keep track of which curator is responsible for which entry, and so on. This tool set uses a server-client model so that it is possible for multiple curators and/or editors from different locations to work together.

**NCBI implementation.** Data supplied from PigQTLdb were processed to create records in Entrez Gene. These data included the unique ID assigned by

PigQTLdb, the names of the defining markers, and publications. Connections between Entrez Gene and PigQTLdb are based on the unique identifier (QTL\_number) from PigQTLdb. Connections between Entrez Gene and the markers on the MARC Genetic Map (Rohrer et al. 1996) were computed based on shared marker symbol. Connections between Entrez Gene and PubMed were based on the common PubMed id. These interconnections make it easier for a user to start at any point (PigQTLdb, Entrez Gene, PubMed, UniSTS, Map Viewer) and navigate to any of the others to extract related information.



The ISU and NCBI implementations are cross-referenced to each other at the level of each QTL. This allows all unique information on each site to appear to be "integrated" via the worldwide web.

### Discussion

PigQTLdb is the first and largest comprehensive pig QTL data collection to date. Our emphasis has been on developing infrastructure to support the update, analysis, and comparison of data. Users can develop new hypotheses for QTL with this tool. Our database tools allow continued addition or and corrections to QTL data online. Thus, the database is kept up-to-date and allows for the inclusion of new data for future comparisons.

The PigQTLdb has features not seen in other QTL databases or genome databases with QTL components. Such databases include mouse and human obesity (web site <http://www.obesity.chair.ulaval.ca/ctl.html>; web site <http://obesitygene.pbr.c.edu>), human and mouse bone density (web site <http://132.192.64.52/ctl/>), rat (web site <http://ratmap.org/ctlr/>; web site <http://rgd.mcg.edu/qtl/>), mouse WebQTL (Williams et al. 2001; web site <http://www.genenetwork.org/cgi-bin/WebQTL>), maize (web site <http://www.agron.missouri.edu/body/ctl.html>), gramene (web site <http://www.gramene.org>), and grain (web site <http://wheat.pw.usda.gov/ggpages/maps.shtml>). These QTL database tools are either unavailable to the general public or are built as a component to the specific database thus making it difficult to be used as a stand-alone database tool. The feasibility of further developing them to include specific functionality that we needed was limited. While we realize there has been a lack of a "universal" tool, we also realize that not everyone makes his/her database design, database schema, and codes easily accessible by the public. One of our key goals was to minimize redundant work by sharing the tool with the public. The database structure, data presentation, and curation tools of PigQTLdb can be readily used for other species.

While developing this database, we quickly came to the realization that there is a great need to standardize terminology when describing traits. For example, average back fat, 12th rib back fat, and lumbar back fat may or may not represent the same trait. Therefore, we would like to introduce the concept of trait ontology to manage diverse pig production traits for a controlled trait vocabulary management and cross-experiment QTL comparison. We envision patterning this hierarchical terminology after that used for gene ontology. We realize that our efforts are only a first step toward a

fully expanded trait ontology. We plan to continue our work on making it a more generally acceptable resource/tool for the community.

As genome research progresses, so do various genome databases. Increasing amounts of genomics data and new data types will become available. Therefore, it will become more of a challenge to combine various mapping and sequence data to facilitate comprehensive genome analysis. Integration of QTL data and phenotype information with genome data is extremely important in bringing together the maps, sequences, and expression results from microarray studies (Fischer et al. 2003). Our efforts to make the pig QTL data available through two implementations (located at ISU and at NCBI) by cross-referencing and linking them to other sequence and map data were successful in developing a database capable of dynamic information integration. This effort is a good example of genome information integration with distributed databases. Our long-term goal is to make the PigQTLdb part of the integrated functional genomic information resources for pigs and for other species at large.

### Acknowledgments

The authors thank Drs. Jack Dekkers from Iowa State University, Gary Rohrer from USDA Meat and Animal Research Center (MARC), Andy Law from the Roslin Institute (UK), and Lizhen Wang from Sygen International for their useful discussions in the process of the database design. Thanks also go to Drs. David Adelson from Texas A&M University and Per Johnson from Göteborg University (Sweden) for sharing their materials on cattle and rat QTL database design, respectively. The data for the template chromosome maps are made possible with data mainly from the USDA-MARC comprehensive pig genome map. This work was supported in part by USDA-NAGRP Pig Genome and Bioinformatics Coordination Programs, the Iowa Agriculture and Home Economics Experiment Station, and State of Iowa Hatch funds.

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