

AnimalQTLdb: A Livestock QTL Database Tool Set for Positional QTL Information Mining and Beyond

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Abstract

QTL (Quantitative Trait Loci) information may be linked to various genomics information such as linkage maps, comparative physical maps, radiation hybrid maps, BAC finger printed contig maps, SNP maps, etc. We have further developed the formerly known "PigQTLdb" into an "Animal QTLdb" (Animal QTL database) to accommodate multiple species and comparative map alignments within each species. The design of the database was modified to house all publicly available as well as private QTL data on livestock animal species from which researchers can easily locate and compare QTL within and between species. New database tools are also added to link the QTL data to other types of genomic information, such as radiation hybrid (RH) maps, finger printed contig (FPC) physical maps, linkage maps, single nucleotide polymorphism (SNP) locations, and comparative maps to the human genome, etc. Currently, this database contains data on 1,287 pig, 630 cattle and 657 chicken QTL, which are dynamically linked to respective RH, FPC and human comparative maps. QTL from more animal species and more structural genome information for alignment may be added to aid comparative structural genome studies. As the QTLdb can house both public and private/experimental data, privileged users may find it useful, not only as a QTL information resource but also as a powerful research tool (URL: <http://www.animalgenome.org/QTLdb>).

Introduction

The PigQTLdb has provided a useful tool to visualize genomic regions that harbor QTL (Hu et al., 2005). The further dissection of the QTL region for useful candidate gene analysis requires the use of comparative and sequence information. We have extended the database into an Animal QTLdb (Figure 1), which has been expanded to also include cattle and chicken QTL data (Hu et al., 2006, 2007), and included new data types for map alignment, such as the RH-human map data, the BAC FPC map data, new microsatellite markers and SNP information.

Results

The new improvements to the Animal QTLdb were made in three fronts:

- With a long term goal of providing a platform for comparative QTL analysis, the database has been modified to accommodate data from multiple species. To date, cattle and chicken QTL data have been added to the database besides the pig data (Table 1).
- Significant progress has been made to align new structural genomics data types with respective QTL maps when data is available (Table 2). These include RH/human comparative maps, BAC FPC clones, new markers and SNPs, etc (Figure 2).
- 1,308 pig SNPs from dbSNP were virtually assigned human genome locations, thereby aligned to pig QTL locations via human-pig RH comparative maps (Figures 3, 4; BLAST identities > 80%; E-value < 1E-5).
- 60,375 cattle SNP data from dbSNP were virtually assigned human genome locations, thus aligned to bovine QTL locations via human-cattle RH comparative maps (Displayed in a similar way for pig SNPs; E-value < 1E-5; Identities > 80%; alignment length > 100 bases).
- 4,528 new microsatellites from Sino-Danish Pig Genome Sequencing Consortium were virtually assigned human genome locations, thus aligned with pig QTL maps via pig-human comparative maps (BLAST cut-off threshold = 1E-5; Displayed in a similar way for pig SNPs).

Table 1
Data summary on Animal QTLdb.

Species	Number of QTL	Number of traits	Number of publications the data is collected from
Cattle	832	91	52
Chicken	657	112	45
Pigs	1675	281	110

Table 2
Status of structural genomics information are being added to align with QTL maps.

Species	RH map	BAC FPC map	SNP locations	New microsatellites	Expression data	Human map
Pigs	Yes	Yes	In progress	Yes	Planned	Yes
Cattle	Yes	Yes	In progress	Yes	Planned	Yes
Chicken				n/a	Planned	Planned

Figure 1.

The front page view of the Animal QTLdb, showing data summary from three species: pigs, cattle and chicken.



Figure 2.

A snap shot of the QTLdb showing that the QTL maps are aligned to various types of other structural genome information, and the alignment information is within the reach of a computer mouse-click.

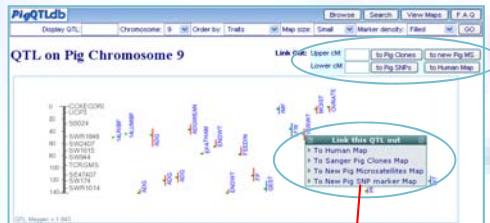


Figure 3.

Alignment of Pig SNPs to Pig chromosome 2 via Virtual Mapping to Human Genome

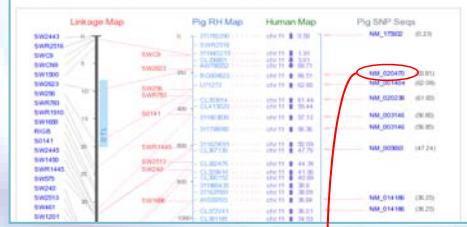
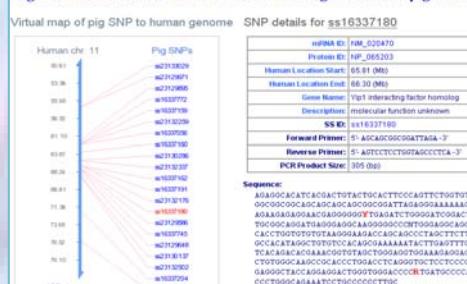


Figure 4.

Regional view of human chromosome 11 showing locations of pig SNPs



A notable feature of this tool is that when you click on other markers in the map, the map window re-centers on the new marker, therefore users can move along the chromosome to look for desired markers.

Figure 5.

The curator / editor login portal. Researchers are encouraged to apply to be a data curator to enter his / her own data.

This figure shows the login portal for the Animal QTLdb. It has fields for 'Login name' and 'Password', and a 'Login' button. Below the login form, there is a section titled 'Curators / Editors: Your starting point' with a list of benefits for becoming a data curator. At the bottom, there is a note about data submission and a 'Submit' button.

Figure 6.

This figure shows the 'Data Management Tools for editor' section of the Animal QTLdb. It includes sections for 'Manual for Curators' (with a 'Download Instructions in PDF format' link), 'Curator / Editor Tools' (with links for Reference data, Experiment Description, QTL details, Traits Data, and Map data), and a 'Logout' button. A red arrow points from the 'Logout' button to the right side of the interface.

Results (cont'd)

- Now the QTLdb tool set are open to public for new data input (Figure 5). To make the QTLdb a common platform to harvest, store and compare animal QTL data, a set of data curation tool were developed within the QTLdb (Figure 6) for multiple users to work together from different locations. The curator / editor tools are made such that the QTLdb can be used either as a data curation tool, or as a research platform to examine, review and compare user's own data. The data owners can decide when their data may be released into public data pool or kept as private data, per their wish.

- Linking of QTL locations to respective genome tracks: Markers underlining a QTL on the cattle QTLmap can now be linked to Ensembl cattle genome sequence track or NCBI STS database. This feature will apply to pig and chicken QTLdb once their genome sequences become available.

References

- Hu, Zhi-Liang, S. Dracheva, W. Jang, D. Maglott, J. Bastiaansen, M.F. Rothschild and J.M. Reecy (2005). A QTL resource and comparison tool for pigs: PigQTLDB. *Mammalian Genome*. Volume 16(10):792-800.
- Hu, Zhi-Liang, Eric Ryan Fritz and James M. Reecy (2006). AnimalQTLdb: a livestock QTL database tool set for positional QTL information mining and beyond. *Nucleic Acids Research*, doi:10.1093/nar/gkl946.
- Hu, Zhi-Liang and James M. Reecy (2007). Animal QTLdb: Beyond a Repository - A Public Platform for QTL Comparisons and Integration with Diverse Types of Structural Genomic Information. Accepted for publication by *Mammalian Genome*.