# Animal QTLdb: A Tool Set to Warehouse and Compare Cattle, Pigs, Chicken and Sheep QTL Within and Between Species

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### Abstract

The Animal QTL database (QTLdb; http://www.animalgenome.org/ QTLdb/) was developed to aid with identifying causal mutations responsible for economically important traits by allowing comparative viewing of all published porcine OTL data. The capability of AnimalOTLdb has since been expanded by: (1) modifying the database so that OTL from multiple species can be warehoused and comparisons made within and across species; and (2) extending QTL map alignments to a greater range of structural genomic features, such as radiation hybrid markers, microsatellites, finger printed contig BAC clones, SNPs, and microarray elements. AnimalQTLdb now contains QTL data for cattle, swine, chicken and sheep; serves as both a data warehouse and search tool; and a powerful OTL oriented, map based data mining tool through easy-to-use and user-friendly web interfaces. Animal Trait Ontology (ATO) was introduced to improve consistency of trait nomenclature and organise traits for database management. Current initiatives include extending the utility of AnimalOTL db by integrating mouse, rat and human OTL information and by working with livestock, rat and mouse communities to extend the ATO to facilitate cross-species trait comparisons. As new types of data (e.g. copy number variation and metabolomics) become available these will be incorporated into AnimalOTLdb to further enhance data mining.

# Introduction

The Animal QTLdb has provided a powerful tool to visualize genomic regions that harbor multiple QTL. The further dissection of each QTL region for candidate gene analysis requires the use of comparative and sequence information and included new data types for map alignments. such as the RH-human map data, the BAC FPC map data, new markers such as microsatellites and SNPs information (Hu et al., 2005, 2006, 2007). Since its inception in 2004, continued improvements to the Animal QTLdb were made in the the past few years to meet this challenge. This helps to make the QTLdb a more useful tool for reseachers. Here we present some preliminary reports.

# Results

#### The new improvements include:

1. With the addition of sheep, the Animal QTLdb now contains QTL information from four species: pigs, cattle, chicken and sheep. In the mean time, the new release of the database contains more QTL data (Table 1). This effort is for a long term goal of providing a platform for comparative QTL analysis.

2. The QTLdb is modified to include a new data type, marker-phenotype association data. The inclusion of the association data is useful in terms of QTL regional data mining for underlining genes.

3. Significant progress has been made to align new structural genomics data types with respective QTL maps based on availability of data (Table 2, new data addition indicated in red). The new data includes map location information of SNPs for cattle, pigs and chicken, microarray elements for cattle and pigs, genome locations for cattle and chicken, etc.

 14,728 cattle and 18,487 pigs Affy microarray elements, 15,627 cattle and 21,269 pigs oligo microarray elements, were virtually aligned with respective genome locations by BLAST (identities > 80%; E-value < 1E-5) thus to the OTL locations

1.8 million cattle SNP data from Baylor and 2,978 chicken SNPs from dbSNP were virtually aligned to respective genome thus indirectly to respective QTL locations by BLAST (E-value < 1E10-5; Identities > 80%; alignment length > 100 bases).

Figure 1a and 2a show examples of alignments of cattle pig oligo data and SNP data, respectively.

#### Table 1 Current Animal OTI db data summary

Species	Number of QTL	Number of traits	Number of publications the data is collected from
Cattle	1123	101	71
Chicken	657	112	45
Pigs	1831	316	113
Sheep *	53	28	14

\* In progress. Data entry is being carried out by Jill Maddox's group at the University of Melbourne, Australia

## Discussions

Besides adding structural genomics data to the QTL maps, we also attempted to extend its capability by including more informative information to facilitate users using tools for QTL data mining. A couple of examples are presented in the Figures 1 and 2 on the right.

 Available minor allele frequencies (MAF) were added to aligned SNP information (Figure 2b). While this is an useful addition, one draw-back might be that the MAF data were volunteered by those who wish to share their data. Therefore the use of the data may only be a reference before we may more of such data from users.

Attempts were made to display expression data on microarray elements (Figure 1b). This tool can be a powerful tool to aid QTL information mining once a candidate gene expression profile is recognized by simple map location match.

While the above tools appear useful, further successful experimental data mining may be necessary to further ratify its utility. Users are encouraged to explore new functions via tools built in its user-friendly web interface.

### 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.
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#### Figure 1

Pig oligo microarray elements were aligned with pig genome / QTL map (a). This made it possible that the microarray expression data may be aligned with OTL locations which would potentially enhance the power of OTI data mining. The microarray expression levels are displayed in colour, and the colour code is displayed below as a reference (b).







### Figure 2

Cattle SNP data alignments with the cattle genome / QTL map (a). Additional attempts were made to include the minor allele frequency data where available (b). This is aimed to help users who wish to guickly select SNPs for screening in his / her population.



### Table 2



Status of structural genomics information, such as SNP, Oligo, Array elements, BAC FPC clones, etc., included in the alignment with QTL maps within each respective species

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