Expanding the Utility of the Animal QTLdb

Zhi-Liang Hu [1], Carissa Park [1], Eric Fritz [1], Mindy Dwindell [2], Mary Shimoyama [2] and James M. Reecy [1]

1. Department of Animal Science and Center for Integrated Animal Genomics, Iowa State University, 2255 Kildee Hall, Ames, IA 50011
2. Rat Genome Database, Human and Molecular Genetics Center, Medical College of Wisconsin, Milwaukee, WI 53226

Abstract

Whole genome sequencing and genome-wide association analysis technologies have generated tremendous opportunities and challenges for animal genome researchers. While genome-wide association studies provide a mechanism to detect genes whose biological function controls traits of interest, assembled genome sequences make it possible to link genetics and biological information. Therefore, mining genome information to facilitate genetics study becomes possible via structural alignments and standardized terminology. To facilitate the analysis of QTL and whole genome association data, we have been working to curate all published studies in cattle, chickens, sheep and swine. In collaboration with the Rat Genome Database, Mouse Genome Informatics, SABRE and EADGENE, we are developing the Vertebrate Trait (VT) Ontology to standardize phenotype nomenclature across species, which will facilitate across species comparison. To meet the community needs for analysis of QTL and gene association studies in connection with their research data, we have developed a GBrowse-based genomics information hub through which all QTL and gene association data can be readily aligned, and raw and dissected data sets be downloaded for further analysis. This GBrowse-based information hub is part of our plan to incorporate related functionality of distributed annotation system (DAS), BioMart and NCBI Powertools, to build a seamless information integration system across platforms.

Introduction

The AnimalQTLdb was designed to house all publicly available QTL data on livestock animal species for easily locating and making comparisons within and between species. The functions of the database were subsequently expanded by adding tools to link the QTL data to other types of structural genomic information, allowing comparative viewing of RH maps, physical maps, SNPs, microarray elements and human genome maps (Hu et al., 2007). This has greatly facilitated the community research activity on positional mining of QTL information as our QTLdb has been cited in more than 50 journal papers during the past 4 years.

As more genome assemblies for livestock species become available, the need is growing for the ability to mine genome annotation information for candidate gene search via structural alignments, and to facilitate genetic study through standardized trait terminologies. Here we present our work towards making the QTLdb a more useful tool for the researchers by further expanding its functions.

Results

1. To meet the community needs for QTL analysis and gene association studies, we have developed a GBrowse-based genomics information viewer through which all QTL and gene association data can be readily aligned for cattle and chicken. **Figure 1** shows how cattle QTL #1491 is aligned with annotated genes and transcripts in the overlapping genomic region through Gbrowse, and that QTL details can be briefly viewed by mouse-over, and further details are available by clicking on the QTL line in the Gbrowse view. Users also have the option to upload their own genome features for alignment (red oval). All these information is available at the user's finger tips.
2. We are adding animal "breed" information to the QTLdb, so that QTL can be linked to the breeds it is associated with. This will help in future QTL meta-analysis where it will be possible to dissect QTL information by breed origins. Shown in **Figure 2** is a QTLdb Curator window where breed information can be linked in a database-controlled manner. It is also our intention that an animal breed ontology be developed to effectively manage, use and share the breed information among researchers. A "breed ontology" will also be useful in the animal germplasm management.

Figure 1.

A GBrowse web view showing the chromosome track of BTA 1, where QTL are aligned to other genome features such as annotated genes and transcripts. The details of each QTL are shown in a pop-up balloon upon mouse-over, and in QTLdb upon clicking on the QTL line which are embedded with hyper links.

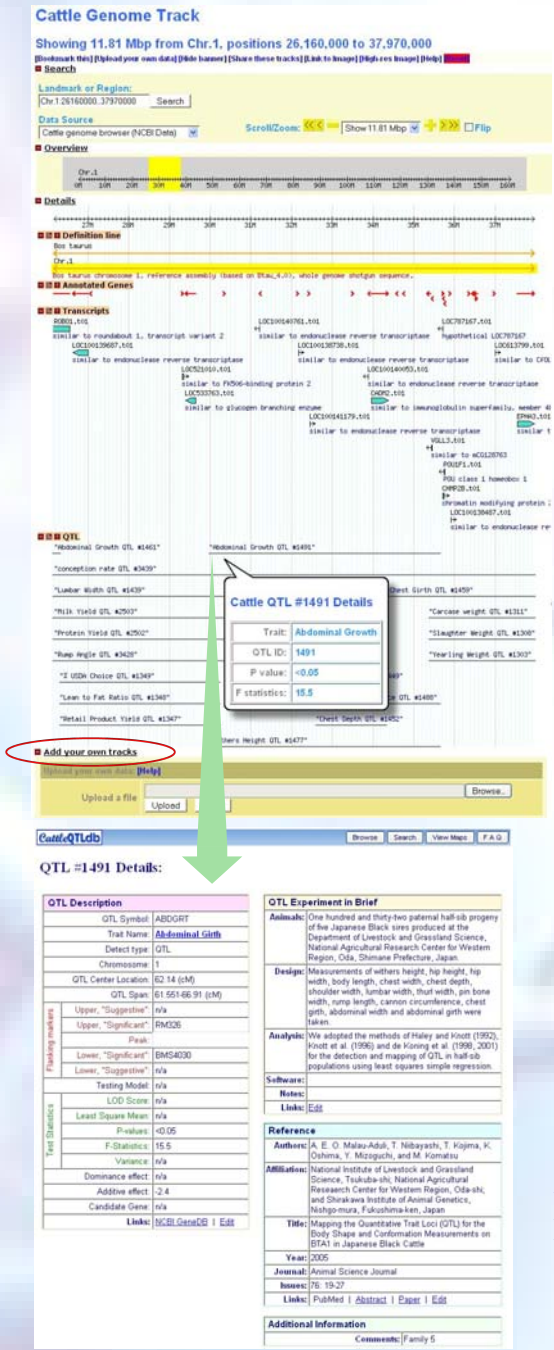


Figure 2.

Animal breed information is being added to the QTLdb. The purpose of this is to make it possible to include breed information for the meta QTL analysis .

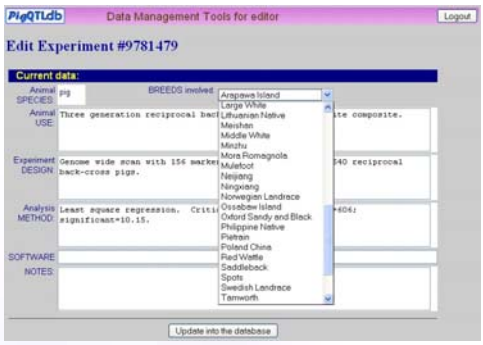
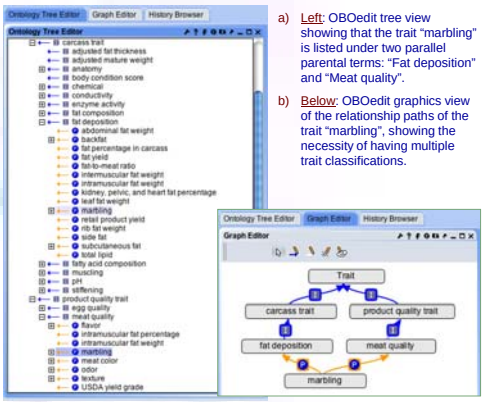


Figure 3.

An OBO-Edit window showing one hierarchy of the ATO where multiple parental terms are found for some of the trait terms. This is one of the new features we are adding to the ATO, to make it more useful across diverse types of fields in animal science, as well as in general genome sciences where comparative studies may add strength to animal genetics/genomics research.



a) Left: OBOedit tree view showing that the trait "marbling" is listed under two parallel parental terms: "Fat deposition" and "Meat quality".

b) Below: OBOedit graphics view of the relationship paths of the trait "marbling", showing the necessity of having multiple trait classifications.

Results (continued)

3. Animal Trait Ontology (ATO) was developed as part of Animal QTLdb to help with managing and organizing trait information (Hu et al., 2005, 2007) and was introduced to the community (Hughes et al., 2008). To make the ATO more useful, we have started to further develop a Vertebrate Trait (VT) Ontology in collaboration with the Rat Genome Database, Mouse Genome Informatics, SABRE and EADGENE. This is aimed at enhancing the ability to standardize phenotype nomenclature, and facilitate across species QTL comparisons. Shown in **Figure 3** are two OBO-Edit views of the trait hierarchy in which the trait "marbling" is shown to have two parental classes. This demonstrates that multiple trait classifications by different research communities are possible, and that the ATO will be made more widely useful to the general animal genomics community.

In summary, our work on extending the utility of the QTLdb will improve its functionality as a community research tool (Hu and Reecy, 2007). The Animal QTLdb is available at *http://www.animalgenome.org/QTLdb/;* The ATO project site is at *http://www.animalgenome.org/bioinfo/projects/ATO/*

Acknowledgements

This research is supported by the USDA-NRI Grant number 2007-04187 and the USDA NAGRP Bioinformatics Coordination Project. Kind helps from Burcu Bakir of *Human and Molecular Genetics Center, Medical College of Wisconsin*, Scott Cain from *Ontario Institute for Cancer Research*, and Justin Reese from *Georgetown University* for setting up the GBrowse are greatly appreciated. We also thank Animal Breed Committee of the *Oklahoma State University* for their generous agreement on the use of their livestock breed information collections.

References

Hu, Zhi-Liang, Svetlana Dracheva, Wonhee Jang, Donna Maglott, John Bastiaansen, Max F. Rothschild and James M. Reecy (2005). **A QTL resource and comparison tool for pigs: PigQTLDB.** Mammalian Genome. 16(10):792-800.

Hu, Zhi-Liang, Eric Ryan Fritz and James M. Reecy (2007). **AnimalQTLdb: a livestock QTL database tTool set for positional QTL iInformation mining and beyond**. *Nucleic Acids Research, 35(Database issue):D604-D609.*

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.** *Mammalian Genome, 18: 1-4.*

Hughes, LaRon M., Jie Bao, Zhi-Liang Hu, Vasant G. Honavar, James M. Reecy (2008). Animal Trait Ontology (ATO): The importance and usefulness of a unified trait vocabulary for animal species. *Journal of Animal Science, 86(6):1485-1491.*