Expanding the Utility of the Animal QTLdb

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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 contributes to 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.

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References


Figure 1. A GBrowse web view showing the chromosomal 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 linked 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 be added to animal genetics/genomics research.