Extension of Animal QTLdb (II): Alignment of New Microsatellite Markers, SNPs and Microarray Elements to cattle, chicken and pig QTL maps and Comparative Mapping Tools for Positional Genome Information Mining

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Abstract

The Animal QTL database (QTLdb) and its ability to link structural genomic information has provided a powerful tool for QTL map based, structural genome information mining. Previously, we reported on the alignment of pig BAC finger print maps and pig-human RH maps to pig QTL map. The QTLdb has extended its utility for cattle and chicken QTL data. Additional progress has been made to align SNPs, new microsatellites, and microarray elements to cattle, chicken and pig QTL maps within the QTLdb. Here we report the alignments of 18,183 SNPs, 14,728 affy-microarray elements, 15,627 oligo-microarray elements to the bovine genome, 4,528 new microsatellites, 435 gene-based SNPs, 18,487 affy-microarray elements, 16,700 oligo-microarray elements to swine genome, and 2,978 SNPs to chicken genome. Web interfaces have been developed for users to easily access this information, and link the interested information to other public databases for additional details. The alignments of the new information are publicly available on-line. One application of these alignments is demonstrated through the utility of the web tools we developed to easily locate the differentially expressed genes of interests on the pig genome map to which hundreds of QTL locations are aligned.

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). Continued improvements to the Animal QTLdb were made within the past year. Here are some preliminary reports.

Results

The new improvements include:

1. Joint by 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.

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

♦ <u>1.8 million cattle SNP data</u> from Baylor and <u>2,978 chicken SNPs from dbSNP</u> 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 SNP data and pig oligo data, respectively.
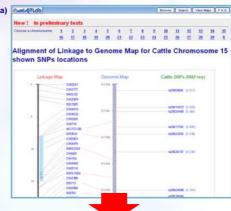
Table 1
Current Animal QTLdb data summary.

Species	Number of QTL	Number of traits	Number of publications the data is collected from
Cattle	1125	106	71
Chicken	657	112	45
Pigs	1675	281	110
Sheep *	51	27	13

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

Figure 1
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 quickly select SNPs for screening in his / her population.
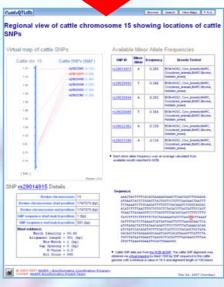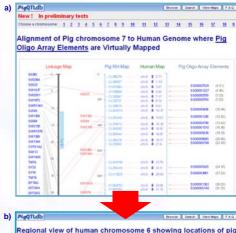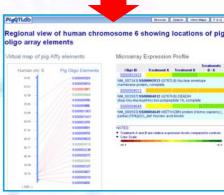

Figure 2
Pig oligo microarray elements were aligned with pig genome / QTL map (a). This made it possible that the microarray expression data may be aligned with QTL locations which would potentially enhance the power of QTL data mining. The microarray expression levels are displayed in colour, and the colour code is displayed below as a reference (b).

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.

♦ Available minor allele frequencies (MAF) were added to aligned SNP information (Figure 1b). 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.

♦ Attempts were made to display expression data on microarray elements (Figure 2b). 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.

Table 2
Status of structural genomics information being aligned with QTL maps.

Species	Genome	RH map	BAC FPC	SNPs	New microsatellites	Microarray Elements Affy	Microarray Elements Oligo	Human map
Pigs	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Cattle	Yes	Yes	Yes	Yes	n/a	Yes	Yes	Yes
Chicken	Yes	Planned	Planned	Yes	n/a	Planned	Planned	Planned
Sheep	Planned	Planned	Planned	Planned	Planned	Planned	Planned	Planned

References

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