Abstract
One application of genetic linkage maps in livestock species is mapping traits underlying the genetic differences of economically important traits. As a result of active mapping of quantitative trait loci (QTL) in pigs during the past decade, hundreds of QTL in pig genome have been reported for growth, meat quality, reproduction, disease resistance and other traits. We are developing a pig QTL database to allow easy search and comparison of publically available QTL data. A few approaches have been taken to accommodate the complex need for QTL information: QTL database integration, database management, and software development. QTL database is designed to include data representing both major genes and markers having large effect on economically important traits. Our purpose is to make this database a public tool to use. Also, we try to present the QTL/mapping data in an integrated way. In Figure 3 is shown how shall the QTL data may be presented along with linkade data and physical mapping data. The pig QTL database is designed to include data representing both major genes and markers having large effect on economically important traits. It is our intention to make this "QTL database" merge functional genomic data with the mapping data, therefore serve the purpose of database integration. This will be largely achieved through making use of existing pig QDB databases and other publicly available databases resources. In Figure 2 is shown a conceptual database model in which the pig QTL database is linked with other existing public databases. It also shows that similar works may be done for other livestock species.

4. Platform, interface, and other considerations
In order to enable the utility of public databases, we designed the database to be interfaced with World Wide Web for both database curators/editors and the users. In this way we make the database a public tool to use. Also, we try to present the QTL/mapping data in an integrated way. In Figure 3 is shown how shall the QTL data may be presented along with linkade data and physical mapping data. On these mapping representations, hyper-links will be embedded in the graph so that dynamic links are built under each feature on the map. The database system is web based on an UNIX platform. Standard DBMS/DB with CGI developed in Perl will make it easy to transferable or adapted into similar environment.

Material and Methods
1. Platform: Digital UNIX 4.0D running on a Compaq 522u work station.
2. Approach: We plan to program the web interface in generic DBI/DBD with Perl/CGI. The graphic tool to present QTL will also be embedded in CGI. Image manipulation techniques is to be used for presenting hyper-links from attributes on the graph to various database locations. The purpose for this approach is for easy transfer or add from the current database schema and to other available ones when needed.

Results
Several approaches have been taken to accommodate the complex need for QTL information organization and presentation.

1. "Trait ontology" – a standardized way to describe traits
In the farm animal industry, it is not uncommon to encounter different names to describe the same production trait. In animal science, physiologists, geneticists and nutritionists often have their own terms within their specialty for the same trait. We have therefore introduced a "trait ontology" concept to standardize the way animal traits are named and to simplify the way that the traits may be organized, in order for comparisons of QTL data to be possible, and the trait data to be manageable with a relational database.

Table 1. A snapshot of a trait ontology table showing classification of 169 pig production traits in 5 trait classes and 26 trait types.

<table>
<thead>
<tr>
<th>Level 1 Trait</th>
<th>Level 2 Trait</th>
<th>Level 3 trait</th>
<th>Level 4 trait</th>
<th>Level 5 trait</th>
</tr>
</thead>
<tbody>
<tr>
<td>Traits</td>
<td>Classes</td>
<td>Types</td>
<td>Sub-types</td>
<td>Attributes</td>
</tr>
<tr>
<td>PERFORMANCE</td>
<td>Growth</td>
<td>Protein</td>
<td>20</td>
<td>5</td>
</tr>
<tr>
<td>HEALTH</td>
<td>Reproduction</td>
<td>Coat</td>
<td>10</td>
<td>8</td>
</tr>
<tr>
<td>QUALITY</td>
<td>Meat Quality</td>
<td>Hair</td>
<td>15</td>
<td>10</td>
</tr>
<tr>
<td>OTHERS</td>
<td>Other</td>
<td>Other</td>
<td>5</td>
<td>2</td>
</tr>
</tbody>
</table>

Figure 1A relational database schema showing how the QTL related information are managed

Discussion
1. There are already some public databases that have QTL data components, such as the mouse QTL for animal models of obesity (http://www.obesity.ch/). Mammalian Genome database (http://www.agron.missouri.edu/bob/qtl.html), Barley genome database (http://www.barleydb.org), etc. However the QTL database is still intended to be used as a "universal" tool for everybody, we also realize that not everyone makes their QTL database available for use. In building our pig QTL database, we are also trying to provide a generic tool for continuing QTL data update, analysis, and comparison, in pigs. As for a long term goal, our continued efforts will be made to make it part of the integrated functional genomics resources for pigs in the future.

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References
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