

## **INTEGRATED AND COMPARATIVE MAPS IN LIVESTOCK GENOMICS\***

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### **SUMMARY**

The creation of a single integrated map, incorporating all available mapping information for an unsequenced species, provides the best possible resource for meta analyses of QTL, for a backbone for assembly of sequence, and for comparative mapping. Using a strategy encapsulated in the Location DataBase (LDB), integrated maps for cattle, sheep and pigs have been produced from all publicly available mapping information for these livestock species, and are freely available at <http://medvet.angis.org.au/ldb/>. A very useful tool for comparative mapping is the Oxford grid. Of particular interest are grids comparing an integrated map from an unsequenced species with the annotated sequence map from a sequenced species. Web-based examples can be viewed at (<http://oxgrid.angis.org.au/>). By an additional iteration of the LDB approach or a variant of the Oxford-grid software, it is possible to create a virtual genome of the unsequenced species, i.e. a map comprising predicted locations for all loci identified in the sequenced species.

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