Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Generation of a preliminary bovine gene atlas, using expression clustering to annotate gene function

O.M. Keane[1,3], N. Maqbool[2], A.F. McCulloch[2], J.C. McEwan[2] and K.G. Dodds[2]

[1]Department of Biochemistry, University of Otago, AgResearch, Molecular Biology Unit, Dunedin, New Zealand
[2]AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand
[3]Animal Bioscience Centre, Teagasc, Grange, Dunsany, Co. Meath, Ireland

Corresponding author: O.M. Keane
E-mail: orla.keane@teagasc.ie

Genet. Mol. Res. 8 (3): 1013-1027 (2009)
Received February 3, 2009
Accepted June 10, 2009
Published August 25, 2009

ABSTRACT. Genes whose products function in a common biological process are often co-regulated. When regulation occurs at the transcriptional level, co-expressed genes can be detected globally by expression arrays or by sequencing non-normalized cDNA libraries. We examined bovine gene expression in 27 tissues using non-normalized cDNA library sequencing. Contigs were generated from expressed sequence tags whose sequences overlapped. Contigs containing a minimum of five expressed sequence tags were ordered via a hierarchical clustering process, where the distance between the contigs represents their expression pattern similarity across tissues. Gene ontology terms associated with the genes in each cluster showed that co-clustered genes encoded proteins involved in a common biological process. This process can be used to annotate genes of unknown function in the cluster. Gene expression was compared between bovine and human tissues; there were significant correlations between species for each tissue, with the exception of thyroid and placenta. Tissues were also clustered based on the genes they express; tissues with similar physiological functions clustered

closely. Based on this information, we generated the first preliminary gene atlas of the bovine genome. Genes with similar expression patterns were clustered, and genes with a common function co-clustered. This method can be used to annotate genes of unknown function in the bovine genome.

Key words: Bovine; Expressed sequence tag; Contig; Cluster; Transcriptional profiling; Gene atlas

