

Animals with willpower: Genes controlling feed intake in cattle

Dr Cindy Bottema
Phone: 8303 7641
Office: Room G15, Davies Bldg, Roseworthy

Assoc Prof Wayne Pitchford
Phone: 8303 7642 Email: wayne.pitchford@adelaide.edu.au
Office: Room G16, Davies Bldg, Roseworthy

Aims:

The purpose of this project will be to investigate the observed metabolic differences between high and low net feed intake cattle by using real-time PCR to examine the expression of key genes. Differences in gene expression will be correlated with DNA sequence variants in an effort to develop a DNA test for selection of feed efficiency in cattle

Background:

Genome mapping in livestock is utilised to determine which genes control which production traits. First, the trait is mapped to regions of the genome known as quantitative trait loci (QTLs). Secondly, the gene within the chromosome region controlling that trait is identified. By identifying the gene, DNA tests can be developed and applied in breeding programs to select for the trait. Feed is the single largest cost for cattle producers. Therefore, the highest priority for a DNA test is one that can be used by the beef and dairy industries to select for efficient cattle with low feed intakes.

The Davies Cattle Gene Mapping Project was established to map the genetic loci controlling cattle production traits. The mapping herd was designed using backcrosses between the Jersey dairy breed and the Limousin beef breed in order to study such traits as fatty acid composition, marbling, meat yield, growth rate, age of puberty, etc and net feed intake. Thus, during the course of this cattle genome mapping project, 4 specific chromosomal regions (QTL) were identified that are likely to control net feed intake.

In an effort to discover the actual genes underlying these QTL, a series of experiments have been initiated to examine the physiological differences between animals with high feed intake and animals with low feed intake. Proteomic and biochemical differences have been discerned, however, these observations need to be confirmed using molecular approaches so the genes themselves can be identified.

Key words: cattle, feed intake, feed efficiency, genetics, quantitative trait loci

Other information: A Beef CRC honours scholarship may be available for this project

References:

Dekkers JCM and Hospital F (2002). The use of molecular genetics in the improvement of agricultural populations. *Nature Rev. Genet.* 3:22-32
Arthur PF and Herd RM (2005). Efficiency of feed utilisation by livestock: Implications and benefits of genetic improvement. *Can. J. An. Sci.* 85:281-209.