

Genomics of Feed Efficiency for Livestock



Presented By

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The work presented in this thesis was undertaken to identify regions of the mouse and cattle genomes' containing quantitative trait loci (QTL) and candidate genes for net feed intake (NFI). Prior to mapping QTL in mice, a number of experiments were performed on mice from the eleventh generation of selection for divergent NFI to quantify the effects of selection for NFI on growth, body composition, protein turnover, metabolic rate, activity, and gastric emptying. Eleven generations of selection for and against NFI did not significantly alter body weight or growth rate. Mice from the high NFI selection line contained 32% less body fat, were 85% more active with no significant difference in body weight, growth rate or protein synthesis. There was a significant difference in gastric emptying of solid food between the mice lines with the high NFI mice grinding (25%) and emptying (21%) their gastric contents faster than the low NFI mice. This difference indicates the potential for gut hormones that regulate gastric emptying such as cholecystokinin, gastrin, motilin, secretin, and peptide YY as candidate genes for NFI.

Cattle that were more efficient (lower NFI) had lower maintenance requirements, and consumed less feed per day. The eye muscle area, peak force of the L⁴ muscle and meat, fat and bone weight significantly influenced NFI. However, only 17% of the variation in NFI was accounted for by these traits. Also, eating rate, number of feeding sessions per day and time spent feeding influenced NFI, accounting for 15% of the variation in NFI. Low NFI cattle ate slower, spent less time feeding and had fewer trips to the feeder than those animals with higher NFI suggesting a possible action of the serotonin and/or dopamine systems as candidate genes for NFI.

Multiple interval mapping revealed nine NFI QTL in F₂ mice from the eighth generation of selection for divergent NFI. Interval mapping, a simpler method for QTL mapping was used in Limousin-Jersey backcross cattle and detected four QTL for NFI on BTA 1, 8, 9, and 20. The comparative gene maps between cattle and mice revealed that NFI QTL located on BTA 1 and 20 were comparative with the NFI QTL detected on MMU 16 and 13 respectively. A further two QTL that were almost significant in cattle on BTA 6 and 16 were also comparative with two of the mouse NFI QTL (MMU 1 and MMU 5 respectively). Based on these cattle QTL results and certain assumptions regarding NFI, selection for NFI in stud bulls would appear to be profitable for a producer. Validation of

these QTL in other beef cattle breeds is required before commercialisation of any DNA based test.

There were 19 genes in these four regions that could act as candidates for NFI located in these regions. Overall, the neurotransmitters appear to be the most promising candidate genes making up 11 of the potential 19 candidate genes identified. However, further biochemical and gene expression studies are required in cattle to confirm or contradict this.