

# Whole genome single nucleotide polymorphism associations with feed intake and feed efficiency in beef cattle

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**Abstract :**

Feed intake and efficiency are economically important traits because feed is the greatest variable cost in beef production. Feed efficiency can be measured as residual feed intake (RFI), which is the difference between actual DMI of an animal and the expected DMI based on its BW and growth rate. Feed conversion ratio (FCR) is the inverse of gross feed efficiency and is the ratio of DMI to ADG. A total of 2,633 SNP across the 29 bovine autosomes were analyzed in 464 steers sired by Angus, Charolais, or Alberta Hybrid bulls for associations with RFI. A total of 150 SNP were associated with RFI at  $P < 0.05$  of which 23 were significant at  $P < 0.01$ . Nine of the SNP pairs show high linkage disequilibrium ( $r^2 > 0.80$ ), so only 1 of the SNP pairs was used in further multiple-marker analyses. Two methods were used to create a panel of SNP that were maximally informative for RFI based on the data. In the first method, 141 unique SNP were combined in a single multivariate model and a backward elimination model was used to drop SNP until all SNP left in the model were significant at  $P < 0.05$ . The SNP had greater effects when combined in the multivariate model than when tested individually. In the second method, the estimates from the 141 SNP were used to create a sequential molecular breeding value (MBV) according to the compound covariate prediction (CCP) procedure. The sequential MBV was built by adding the estimated effects one at a time, but only keeping SNP effects in the sequential MBV if the test statistic and the proportion of variance explained were improved. Predictabilities of the 2 methods were compared by regressing RFI on a final MBV created from SNP that remained in each analytical model. The MBV from the compound covariate prediction model produced an  $r^2$  of 0.497, whereas the multivariate model MBV had a decreased  $r^2$  of 0.416. The significant SNP were also tested for associations with DMI and FCR. The SNP showed different combinations of associations with the 4 traits, including some that were only associated with RFI. About 9.5% of the SNP from the 2 models were within 5 cM of previously identified RFI QTL and pinpoint areas to further explore for positional candidate genes. In conclusion, this study has identified a panel of SNP with significant effects on RFI that need to be validated in an independent population and provides continued progress toward selecting markers for use in marker-assisted selection for feed efficiency in beef cattle.

**Key Word :**

beef cattle, residual feed intake, single nucleotide polymorphism, whole genome association

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