

**640 Genome scan of BTA1 for QTL affecting weaning weight, yearling weight and postweaning growth in Japanese Black cattle.** A. E. O. Malau-Aduli\*<sup>1</sup>, T. Niibayashi<sup>1</sup>, T. Kojima<sup>1</sup>, K. Oshima<sup>1</sup>, Y. Mizoguchi<sup>2</sup>, Y. Sugimoto<sup>2</sup>, and M. Komatsu<sup>1</sup>, <sup>1</sup>*Dept of Livestock & Grassland Science, National Agric Res Center for W/Region, Oda, Shimane, Japan.*, <sup>2</sup>*Shirakawa Institute of Animal Genetics, Fukushima, Japan.*

A genome scan for chromosomal regions of bovine chromosome one (BTA1) influencing weaning weight (WT6), yearling weight (WT12) and postweaning average daily gain (PWADG) was performed using 112 half-sib progeny of 4 Japanese Black (Wagyu) sires and 98 microsatellite DNA markers. Identity-By-Descent (IBD) probabilities at specific chromosomal locations from multiple marker data were determined and a linear model containing the fixed effects of sex, parity and season of birth as well as age as a covariate, was fitted to the IBD coefficients and phenotypic data. Data were analysed by generating an F-statistic by the regression of phenotype on the IBD probabilities of inheriting an allele from the sire. Permutation tests at chromosome-wide significance thresholds were carried out over 1, 000 iterations at 1cM intervals while the bootstrap with resampling procedure was followed to estimate confidence intervals and average QTL locations. All these procedures were implemented in the QTL Express Computer programme with a web-based user interface (available at: <http://qtl.cap.ed.ac.uk/>). A significant QTL (P chromosome-wise threshold = 0.05) for PWADG was identified in Sires 2 and 3 located at 27cM and 29cM (95% confidence intervals of the QTL locations being 0-132cM and 0-125cM) respectively. Another QTL for WT12 was identified at 113cM in Sire 2. No significant effect on WT6 was detected in any of the sires. Selection indices that include QTL with accurately estimated effects on carcass characteristics could reduce the amount of lengthy and costly data collection by providing a means of genetic evaluation early in the life cycle. Since PWADG is positively correlated with WT6 and WT12 in beef cattle, the identification of these QTL in Japanese Black Cattle holds a high prospect for the implementation of marker-assisted selection for the early attainment of slaughter weight in this breed .

**Key Words:** QTL, Japanese Black, Growth