

The John M. Airy Beef Cattle Symposium Visions for Genetics and Breeding

Edited by: JAMES M. REECY

Technical Support:

ANN SHUEY
DONNA WATSON

IOWA STATE UNIVERSITY
Department of Animal Science
Iowa Beef Center
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6 Relationship Between Mitochondrial DNA Polymorphism and Postnatal Growth of Japanese Black Beef Cattle

MASANORI KOMATSU¹, ADULI E. O. MALAU-ADULI¹, ATSUKO NISHIMURA-ABE², TOMOMI NIIBAYASHI¹, YASUAKI YASUDA², TAKATOSHI KOJIMA¹, SHIGEKI ABE², KASUNAGA OSHIMA¹ AND KIYOTOSHI HASEGAWA²

¹National Agricultural Research Center for Western Regions, Oda, Shimane 694-0013, Japan. ²Shimane Prefectural Institute of Animal Industry, Izumo, Shimane, Japan

Correlation coefficients (r) between mitochondrial DNA (mtDNA) haplotypes, maternal lineage (ML), birth weight (BWT), preweaning average daily gain (PREADG), weaning weight (WT6), post weaning average daily gain (POSTADG) and yearling weight (WT12) were computed in Japanese Black beef cattle within the same herd and management. The objective was to study the relationship between maternal and postnatal growth traits and to investigate if postnatal growth of calves to yearling age could be accurately predicted from mtDNA genotype at an early age. Blood samples and phenotypic records from 129 cattle which were part of a QTL mapping herd were utilized. mtDNA from the displacement-loop (D-loop) region (496 bp) was genotyped and classified into sub-groups 2 and 3 haplotypes and sequenced. General linear models procedure was utilized to adjust for genetic and non-genetic effects on postnatal growth traits. Simple and multiple linear regressions were fitted to predict postnatal growth traits from mtDNA haplotypes and the coefficients of determination (R^2) were computed. Results revealed 19 maternal lineages and four mtDNA types (1, 11, 73 and a new hitherto unreported one). There were strong, positive and highly significant ($P < 0.001$) r among mtDNA, ML, Sub-groups 2 and 3 haplotypes, ranging from 0.52 to 0.98. Similarly, among postnatal growth traits, most of the r were also strong, positive and highly significant ($P < 0.001$), the highest ($r = 0.94$) was between PREADG and WT6. However the r between WT6 and POSTADG and PREADG and POSTADG were medium and antagonistic ($r = -0.30$ and -0.29 , respectively). Most importantly, r between mtDNA haplotypes and postnatal growth traits were very low, mostly negative and non-significant ($P > 0.05$) ranging from -0.05 to 0.1 . Prediction of postnatal growth from mtDNA yielded very low R^2 values ranging from 0.002 for BWT to 0.019 for WT6. The addition of ML, sub-group 2 and sub-group 3 haplotype information did not lead to any appreciable improvement in prediction accuracy. It was concluded that mtDNA polymorphism has no significant association with postnatal growth from birth to yearling age, and by implication, nuclear rather than cytoplasmic DNA, is most likely responsible for genetic variation observed in postnatal growth of Japanese Black cattle. Therefore, mtDNA genotyping at an early age has no bearing on future growth performance of calves.