

Persistent selection for fecundity increases milk production in inbred Quackenbush (IQS5) mice: a potential model for the discovery of genes regulating lactation

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The biosynthetic capacity of the mammary gland is all-important in determining production efficiency in the dairy industry. This trait is responsive to quantitative genetic selection, but we have been unable to elucidate the pool of important genes responsible for improved milk output. We are using two lines of mice to assist with this process.

We report here on the characterization of the lactational performance of 2 inbred strains of mice that differ greatly in fertility. Dams of the 2 strains, the IQS5^A and CBA^A, were mated and upon pupping, litters were normalised to a maximum of 12 pups (range 9–12) and 6 (range 3–6) pups for the two lines respectively. Dams were offered *ad libitum* a soluble high energy glucose-based diet (high glycaemic index: Higgins *et al.* 1996) and housed at 21°C in a 12:12 (light:dark) lighting regimen. Milk production was assessed using a weigh-suckle-weigh technique in which differences in pup bodyweight over a suckling period (2 h) following a 4 h separation of pups and dams was estimated over 24 h (commencing at 0000, 0600, 1200 and 2400h daily) for 18 days *post-partum*. Litters were left undisturbed for the first day so as not to disrupt colostrum intake. Litter liveweight gain in each 2 h suckling period was corrected for metabolic loss assessed during the 4 h period of separation.

Dam weight (W), feed intake and total litter liveweight were recorded daily in addition to estimates of milk synthesis (Table 1). Lactation curves were

constructed for each strain and the mean (\pm SD) data analysed by unpaired t test.

Peak milk yield was reached on days 10 and 14 for IQS5 and CBA mice respectively. The significantly greater milk output from IQS5 mice is associated with an earlier peak in the lactation curve with a greater efficiency of partitioning of nutrients into milk in this genotype. This latter observation is based on the similar feed intake per unit of dam W in the two strains. Despite the highly variable demands of lactation dam, liveweight was conserved in both strains over the course of the lactation (W for IQS5 and CBA dams respectively at day 1 were 40.8 ± 1.5 g and 23.5 ± 1.8 g, and at day 18 were 39.8 ± 1.2 g and 26.7 ± 2.3 g).

The lactational performance of these mouse strains diverges sufficiently to provide a basis for studies of differential gene expression between key metabolic tissues to elucidate mechanisms associated with the superior lactational performance of the IQS5 strain. Elucidation of these genes will provide the scope for the identification of polymorphisms potentially useful in quantitative genetic selection programs used in the dairy industry.

IQS5 and CBA mice were provided by Associate Professor Chris Moran and Dr Ian Martin.

Higgins, J.A., Brand Miller, J.C. and Denyer, G.S. (1996). *Journal of Nutrition* 126, 596–602.

Table 1 Milk production and feed efficiency in the two mouse genotypes (* $P < 0.05$).

Strain	Total milk production (g) *	Total feed consumption (g) *	Total growth (g) *	Milk production (g/d) /g dam W *	Milk production (g/d) /g feed *	Feed intake (g)/d per g dam W
IQS5	83.5 \pm 5.14	272.7 \pm 23.4	5.17 \pm 0.20	0.114 \pm 0.005	0.308 \pm 0.040	0.368 \pm 0.030
CBA	29.8 \pm 6.68	158.0 \pm 14.9	4.46 \pm 0.97	0.064 \pm 0.018	0.179 \pm 0.055	0.334 \pm 0.073