Uterine involution in Holstein-Friesian cows genetically selected for high or low mature body weights

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Abstract

The main objective in dairy herds is to produce milk as economically and efficiently as possible. To achieve maximum production, cows must calve regularly; hence the fertility of the herd affects the productivity of the farm dramatically. High fertility requires early uterine involution, early onset of oestrous cycles postpartum and optimal oestrus detection and conception rates (Pelssier 1976). The modern high producing, lactating dairy cow in North America is subfertile (Thatcher et al., 2006) as managed under current production systems. However, whether such subfertility occurs in high-producing cows under our pastoral system in New Zealand is not fully known. However, recent movement of genetic material across the globe, in the form of semen or frozen embryos might suggest that New Zealand herds could be drifting in a similar direction in subfertility.

The main objective of the present study was to investigate the effect of genetics on uterine involution in the context of a pastoral system by comparing two strains Holstein/Friesian cows that had been genetically selected for high (H) or low (L) mature body weight. Involution was studied through the following measurements: (i) cervical diameter, as assessed by measurement *per rectum*, (ii) plasma concentrations of the prostaglandin $F_{2\alpha}$ metabolite, 15-keto-13,14-dihydro-prostaglandin F2α (PGFM), (iii) urinary concentrations of the collagen breakdown product pyridinoline and (iv) bacteriology of the cervical canal.

From the results, it was concluded that, whilst H cows exhibited similar physical involution characteristics to those of L cows ($P>0.5$), they had higher levels of post-calving bacterial contamination ($P<0.05$). On Days 4, 7 and 10 post partum, the anaerobic bacterial load was significantly ($P<0.05$) greater in H than L cows. On Day 10, both strains peaked with mean

anaerobic bacterial counts of 23.4 x 10^5 cfu and 0.41 x 10^5 in H and L cows, respectively. Similarly, on Days 7 and 10, the total bacterial load (aerobic plus anaerobic) was also greater ($P<0.05$) in H than L cows. On Day 7 mean total bacterial counts were 2.27 x 10^6 cfu in H cows. Peak numbers of bacteria in H cows were attained on Day 10 (3.39 x 10^6 cfu). Values in L cows were maximal on Day 7 (1.18 x 10^6 cfu).

PGFM Concentrations in L cows were significantly ($P<0.05$) higher than in H cows on Days 17, 28 and 35. Although total pyridoline and deoxypyridoline /creatinine ratio concentrations differed between strains and times, the strain.time interaction term was not significant. However, on Day 11, values in L cows tended ($P=0.07$) to be higher than in H cows.

Simple correlations established that different parameters e.g cervical diameter; PGFM, PYD and bacterial contamination are highly correlated and moving simultaneously together and are not independent of each other. Accordingly, the relationships between actual and predicted intervals between calving and; first oestrus, first insemination and conception, were calculated based on principle component and partial regression analyses of parameters of uterine involution. Indices calculated from these parameters as predictors of reproductive outcomes, were significantly correlated with intervals between calving and first oestrus ($P<0.05$) and calving and first insemination ($P<0.01$), but not significant with conception rate ($P>0.5$).

Taken together, these data show that uterine involution is impaired in H compared to L strain cows, inasmuch as there is a greater degree of bacterial contamination and a more sluggish pattern of PFGM secretion in H cows. Collagen remodelling may also be

attenuated in H than L cows, although differences between strains only tended towards significance.

More work need to be carried out to further investigate the reason for these differences whether it is genetically based or higher production is negatively affecting the above mentioned traits at a cellular level.

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