Genetics of Growth and Development in Cattle

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Abstract

Growth and development is a good description of animal for size and shape as opposed to the conventional measurements of weight and changes in weight over time for the determination of growth across ages. The inclusion of body dimensions (e.g. height), muscularity (defined as ratio of stifle over hip-width), fat depth measurements with weight in multi-variate analysis would be appropriate for body composition evaluation in the Australian beef industry. It is expected that these component traits would predict beef carcasses for yield and possibly for quality.

Genetic variation in growth and development was examined in 12 different cattle breeds generated from two major projects (Southern Crossbreeding Project (SXB) and Davies Gene Mapping Project (DGM)) to enhance genetic improvement tools for carcass value through production traits. The SXB comprises 1215 progeny of 97 sires from seven breeds (Jersey, Wagyu, Hereford, Angus, South Devon, Limousin and Belgian Blue) mated to 766 mature Hereford cows with calves born across four years (1994-1997). The 591 DGM progeny were from 7 sires (2 Jersey, 2 Limousin and 3 F1 crosses) mated to 280 cows (Jersey and Limousin) to produce purebred Jersey, purebred Limousin, Jersey x Limousin crosses, Jersey backcross and Limousin backcross with calves born across five years (1994-1998). Significant breed differences were obtained across ages for growth and development traits. Differences in cohorts (year of birth & sex of calf) were high across ages while the significance due to day or month of birth decreased as age advanced.

As a preliminary study, live animal measurements of weight, height, length, girth, P8 fat depth, stifle- and hip-width of 241 steers (second calf drop) from 10 breed combinations in both projects were used to predict seven carcass traits. A complete bone-out was carried out on all 1995-drop steers to allow for the stepwise regression of carcass traits on live measurement traits. The results of the first study demonstrated with reasonable precision that there could be value gained in defining carcass composition using the objective live animal measurements herein as an alternative to most commonly used subjective measurements.

Southern crossbreeding progeny were used to determine the heritability and genetic correlations between the measure of growth (weight and body dimensions) and muscular development (defined as ratio of stifle to hip width) plus P8 fat depth. Across ages (birth to 600-day), height was highly heritable (0.34-0.57). However, weight, length and girth were
low to moderately heritable (0.12-0.40) at the same ages. From weaning to 600 days, muscularity measurement was low to high (0.20-0.44) while measure of fatness was moderate to high (0.31-0.41). At the average age of 400 days, moderate and positive genetic correlations (rG) existed between weight and height (0.47) but strong and positive rG were between weight and other body dimensions of length (0.59) and girth (0.62). While the rG between weight and muscularity was low, weight and P8 fat depth had zero relationship at this age.

An experiment was also conducted using 591 progeny from DGM to separate the additive from non-additive genetic effects on growth and development traits not possible in earlier studies because of the single dam used in the SXB. Direct effects were the most significant for most of the traits across ages, an indication of the importance of individual gene composition on growth regardless of age. There were significant maternal effects on some early postnatal growth traits. At weaning, heterosis was large and positive for fatness and moderate for weight and muscularity. There was also indication of the significance of epistasis on muscularity at older age.

The location and size of QTL effects on growth and developmental traits were tested on 370 backcross progeny of three F1 sires from DGM. Chromosome-wide significance QTL for individual traits was observed on 17 of the 29 autosomes. However, the number of autosomes with significant QTL was reduced to eight using the first principal components of six genetically related trait groups that represent over 50% of the total phenotypic variance per group. Significant QTL for prenatal growth (size) had no effect on late growth. Interestingly, QTL for postnatal muscularity (BTA 2) and fatness (BTA 21) were mapped to different regions of the genome. This is an indication that the genetic improvement for beef cattle body composition should be possible in very early life before measurements.

The thesis concludes that strong evidence of separate associations between markers and QTL on pre-natal and postnatal growth and development exist. Thus, the problem of genetic antagonism between calf survival and growth (development) could be solved using new techniques in genetics in very early life. Furthermore, the size of estimates for breed and genetic effects in conjunction with the genetic parameter estimates herein suggests that selection indices for desired carcass composition through multi-trait prediction of live-measurements is feasible.