BRIEF COMMUNICATION: Genetic parameters for growth in Wapiti deer farmed in New Zealand

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INTRODUCTION

The New Zealand deer industry commonly uses "Wapiti" type deer as terminal sires mated to "red" hinds in venison production systems. The terms "Elk" and "Wapiti" are commonly used almost inter-changeably in the New Zealand deer industry to describe subspecies of red deer originating in North America (*Cervus elaphus* subspecies *manitobensis*, *roosevelti* and *nelsoni*). These subspecies are approximately twice the mature body size of "red" deer subspecies originating in Britain and Europe (Cervus elaphus subspecies scoticus and hippelaphus). The term "Elk" is often used to describe recent importations of these genotypes, while "Wapiti" commonly describes deer descended from a historical (wild) importation into Fiordland National Park, New Zealand which has naturally introgressed with "red" deer subspecies as a consequence of overlapping home geographical boundaries. For this paper the term Wapiti will be used to cover both terms, as the populations are not distinct. In reality the deer in Wapiti herds providing terminal sires to "red" herds are usually a hybridised mixture between North American genotypes and the British and European genotypes, with North American genotypes making up from 40% to 100%, in the case of pure importations, of the breed composition.

As Wapiti are commonly used as venison terminal sires, it is desirable to describe genetic merit of individual animals in terms of breeding values (BV) for growth traits. Creating a BV estimation system requires estimates of genetic parameters (heritabilities and genetic correlations) for Wapiti. Moreover, as the population being described is a composite of genotypes with widely different growth characteristics, accounting for breed composition in a BV analysis is potentially useful. Techniques for estimating breed composition from DNA markers are now available and this information can potentially be used in breeding value analyses to assist in BV estimation. This paper describes an analysis of Wapiti live weight data incorporating breed composition information to estimate genetic parameters.

MATERIALS AND METHODS

Data from five New Zealand Wapiti herds were obtained. Traits were defined as live weight at approximately 3 months of age (W3 - February to April), 12 months of age (W12 – September to December), 15 months of age (W15 – January to March) and mature live weight (MWT – weights from 24 months of age onwards). Table 1 gives numbers of records for each trait, along with unadjusted means. In all a total of 4,201 animals had records on at least one trait and 6,979 animals were included in the analysis based on pedigree.

Information on up to 14 micro-satellite markers on a subset of 3,026 animals was used to predict breed composition using the *Structure*[TM] software package (Pritchard *et al.*, 2000). Pure-bred animals imported directly from North America were used as the reference population for Wapiti when assigning breed. The breed composition estimates obtained from *Structure*[TM] were used to infer breed throughout the pedigree for animals without direct genotype information using the method described by (Gengler *et al.*, 2007).

Data analysis was performed using ASReml 2.0 (Gilmour *et al.*, 2006) to fit an animal model. The model fitted for W3, W12 and W15 included fixed effects for age of dam and contemporary group, and birth date deviation from mean birth date within herd-year-sex subclasses as a covariate when available for all traits. For MWT where the records were repeated across years, the fixed effects fitted were age in years, age of dam and management group. Breed composition in terms of the proportion of Wapiti blood was fitted as a covariate for all traits. Random effects fitted included a direct additive genetic effect for all traits, maternal additive genetic effect for W3 and a permanent environmental effect for MWT.

RESULTS AND DISCUSSION

A summary of genetic parameter estimates is given in Table 1. Estimates of phenotypic variance, variance ratios, and regression coefficients on breed are from uni-variate analyses. All growth traits were moderately heritable, indicating that responses to selection could be achieved for these traits. There was a small but significant effect of additive maternal genetics on W3, but no significant maternal variation was present for the weights taken at older ages. Mature live weight had a large permanent environmental variance associated with it.

All traits showed a positive regression on breed, although the coefficients appear to markedly

TABLE 1: Genetic parameters for live weight traits, including phenotypic variance (V_p), proportion of phenotypic variance (± standard error) explained by direct additive genetic, maternal additive genetic and permanent environmental effects, regression coefficient on proportion of Elk/Wapiti genes and phenotypic (above diagonal) and genetic (below diagonal) correlations (± standard error). Traits are live weight at 3 (W3), 12 (W12), and 15 (W15) months of age, and mature live weight (MWT).

Parameter	Traits			
	W3	W12	W15	MWT
Number of records	2586	2678	925	1638
Mean (kg)	70.0	115.3	179.2	180.4
V_p (kg^2)	99.0	163.5	254.7	488.7
Direct genetic effect	0.29 ± 0.05	0.40 ± 0.05	0.33 ± 0.10	0.36 ± 0.07
Maternal genetic effect	0.05 ± 0.02			
Permanent environmental effect				0.45 ± 0.07
Breed regression co-efficient	3.11	10.83	18.88	23.75
Correlations				
W3		0.71 ±0 .01	0.71 ± 0.03	0.62 ± 0.02
W12	0.76 ±0 .05		0.75 ±0 .03	0.76 ±0 .01
W15	0.82 ±0 .12	0.92 ±0 .08		0.79 ±0 .02
MWT	0.77 ±0 .07	0.95 ±0 .03	0.97 ±0 .04	

underestimate the true differences between Wapiti and red deer. In this data set the average proportion of Wapiti genes across all genotyped animals was 0.69, with a standard deviation of 0.13. There are several possible explanations for the lower than expected regression coefficients. The most likely explanation is that error in the breed percentage prediction leads to underestimated regression coefficients as the assumption of the independent variable being measured without error is violated. This violation generally biases regression coefficients downwards (Robinson, 2005). In this situation, prediction of breed based on only 14 micro-satellite markers has reasonably wide confidence intervals which were typically ± 0.18. Furthermore, breed then needs to be inferred for animals with missing genotypes. An alternative explanation is that heterosis in crossbred and composite animals raises performance in animals which have breed mixtures around 50%, and this, together with the fact that animals which are predominantly red deer, being less than 30% Wapiti, were not present in the data set, lowers the regression slope.

However, although the regression coefficients were lower than expected, utilising breed information in breeding value predictions by adding individual solutions to breed solutions will result in an improved prediction, as any underestimate in the breed solution will be at least partially compensated for by the individual solution. This improvement might be particularly useful where an animal has breed composition estimates available but little performance information. In this situation, knowing the breed composition will provide a better starting point than simply assuming the animal's BV is the population average. The utility of breed composition estimates in genetic evaluation is likely to improve as a result of improved genotyping technologies giving better coverage of the genome and hence more accurate breed predictions. With time it is likely that a greater number of animals in the pedigree will have DNA samples analysed to obtain breed composition estimates, and so ability to infer breed for animals without genotypes will also be improved.

Genetic and phenotypic correlations estimated from pair-wise bivariate analyses are also presented in Table 1. Genetic correlations tended to be slightly higher than the equivalent phenotypic correlation. All traits were strongly positively correlated; indicating that selection for live weight at any age will produce responses in weight at other ages. The genetic parameters estimated in this study form the basis of a commercial breeding value estimation service now available to Wapiti breeders through DEERSelect (Archer *et al*., 2005).

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