HYBRIDISATION BETWEEN RED DEER (Cervus elaphus) AND OTHER DEER SPECIES

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SUMMARY

Red deer (R) are the predominant species of farmed deer in New Zealand. There is considerable interest in hybridisation with other deer species to improve growth rate and possibly alter the breeding season of the progeny. Analysis of gestation lengths indicates that the progeny of Canadian wapiti (CW) or CW x R deer have gestation lengths intermediate between the parental strains but the progeny of Pere David's deer (PD) x R have highly variable gestation lengths (mean ± SD of 252 ± 5.0 days). Analysis of the three species for electrophoretic protein variation has located fixed protein polymorphic differences between R and CW (haemoglobin and a post-transferrin) and between R and PD (transferrin and albumin). The segregation of the protein variants in the backcross hybrids followed the expected Mendelian pattern for codominant inheritance at a single locus.

INTRODUCTION

Red deer (mainly of Cervus elaphus scoticus origin) are the predominant species of farmed deer in New Zealand. Typically the adult hinds have mature bodyweights of around 100 kg with mature stags being about twice this weight. The breeding season starts in late March with calving in November-December after a 234 day gestation. There is interest in hybridisation of the local red deer with larger subspecies imported from Europe (European red deer such as C.e. elaphus and C.e. hippelaphus) and from North America (wapiti such as C.e. nelsoni and C.e. rooseveltii) principally to increase growth rates, mature weight and antler weight. There is also the prospect of hybridisation with other less closely related species such as the tropical rusa deer (C. timorensis) or the Pere David's deer (Elaphurus davidianus). Hybrids with these species offer the prospect of deer with an altered breeding season, as the tropical species are essentially aseasonal while the Pere David's deer is a summer breeder, albeit with a longer gestation (about 283 days; Wemmer et al. 1989) which means that a December breeding results in an October calving. At Invermay, artificial insemination (AI) and synchronised natural breeding have been used to produce hybrids of Canadian wapiti (CW) and red deer (R) and Pere David's (PD) and red deer (Fennessy et al. 1991). Hybridisation was confirmed by visual characters and biochemical genetic markers (Dratch 1986; Asher et al. 1988). This paper presents data on the birth weight and gestation length of various hybrids, and on the segregation of electrophoretic protein variation in hybrids backcrossed to red deer.

EXPERIMENTAL

Animals and biometrical analysis

Oestrus was synchronised in adult red deer hinds (>3 years) using progesterone and pregnant mares serum gonadotrophin (PMSG) and the hinds inseminated (Fennessy et al. 1991), or alternatively run with a male for natural breeding. Hinds were ultrasonically scanned to assess pregnancy status to AI at 35-40 days after insemination, having been run with entire red stags from 10-12 days after AI. The calves were weighed and tagged within 24 hours of birth, and the dam identified. In the case of calves born to AI or to a synchronised natural oestrus, the gestation length was calculated. The calves born were of the following strains: R, (CWxR)xR, CWxR or (PDxR)xR. The data were analysed for birth weight and gestation length within strain using REML implemented in GENSTAT with sires as a random effect and various fixed effects as indicated in the data. There were no significant interactions among any of the fixed effects (sex of calf, mating weight of dam, birthdate).

Protein polymorphisms

Two fixed protein polymorphic differences have been identified which distinguish CW from red deer, with two further differences which distinguish PD deer from red deer (Table 1). The electrophoretic variation in haemoglobin (Hb) and post-transferrin (Ptf) was examined in CW hybrids using starch gel electrophoresis (Dratch 1986) and alkaline polyacrylamide gel electrophoresis (alkaline PAGE; Gahne et al. 1977) respectively. Variation in transferrin (Trf) and albumin (Alb) was examined in PD hybrids using alkaline PAGE and isoelectric focusing (pH 4-8) in the presence of 8M urea.

Table 1 Protein polymorphic variants which exhibit fixed differences between red deer (n=400) and Canadian wapiti (n=200) or Pere David's deer (n=35)

	Red deer[1,2]	Canadian wapiti[1,2]	Pere David's deer[1,3]
Haemoglobin (Hb)	AA	BB	*
Post-transferrin (Ptf)	22	11	*
Transferrin (Tf)	AA, AB, BB	*	EE
Albumin (Alb)	SS	*	FF

[1] Tate et al. (1988); [2] Dratch (1986); [3] Asher et al. (1988)

RESULTS AND DISCUSSION

Birth weight

Mean birth weights derived from the REML models (which included dam mating weight and sex of the calf) for the four strains are presented in Table 2. In all cases, male calves were heavier than females ranging from about 9% for the progeny of the PDxR male to 19% for those of the CWxR males. The relationship between calf birth weight and dam mating weight was positive for all strains being significant for the R and the (PDxR)xR calves. While the difference in birth weight between the sexes was higher than those generally reported (see Table 3), the R calves, particularly the males were heavier than other studies with NZ red deer (Asher and Adam 1985; Moore et al. 1988a,b) while the regression coefficient for birth weight on dam mating weight was lower (see Table 3). It is possible that the R male calves were approaching their genetic weight limit, particularly when the coefficients for birth weight on dam weight for the two sexes are considered. Although not significantly different, the regression coefficient for the R females was markedly higher than that for the males (0.039 and 0.018, SED = 0.018, respectively). There was no significant relationship between birth date and birth weight in the progeny (n=61) of three stags born over a two month period (sire was fitted as a fixed effect).

Table 2 Mean birth weights (BW, kg) for male and female calves and the regression coefficient for birth weight on dam mating weight for the four strains of calves

Strain of calf[1]	N	Birth weight (kg)[2] Male	Female	SED	BW ratio M/F	Regression coefficient ± SE: BW on dam weight (kg/kg)
Red	195	9.93	8.96	0.16**	1.10	$0.018 \pm 0.0097^{(*)}$
(CWxR)xR	40	12.17	10.25	0.57**	1.19	0.016 ± 0.034^{NS}
CWxR	35	13.83	11.96	0.56**	1.16	0.022 ± 0.035^{NS}
(PDxR)xR	17	10.93	10.05	1.01^{NS}	1.09	0.120 ± 0.055*

[1] CW, Canadian wapiti; R, red deer; PD, Pere David's deer; [2] BW adjusted for dam mating weight

At birth the CWxR calves were about 36% heavier than the R calves with the (CWxR)xR being intermediate between the two parental strains. Such differences are slightly smaller than those expected based on other Invermay data (Fennessy and Pearse 1990) but, for managerial reasons relating to hind nutrition in late pregnancy, hinds carrying CW hybrid calves are not run with hinds carrying R calves. The (PDxR)xR hybrid calves were about 11% heavier than the R calves at birth. There are very few data available for pure PD so that comparisons are difficult.

Table 3 Comparison of published estimates for the ratio of male to female birth weight and the regression coefficient of birth weight on dam mating weight

Strain of calf	Birth weight ratio M/F	Regression coefficient BW on dam weight	Reference
R	1.07	0.041 to 0.079	Blaxter and Hamilton 1980
R	1.06	0.036	Asher and Adam 1985
R	1.10	0.033	Moore et al. 1988a
R	1.05	-	Moore et al. 1988b
R	1.05	0.045	Fennessy et al. 1990
R	1.10	0.018	This study
CWxR	1.06	0.081	Moore and Littlejohn 1989
CWxR	1.15	0.022	This study

Gestation length

The means, ranges and standard deviations for gestation length are presented in Table 4. In no cases were there significant differences between males and females. The gestation length and its SD for red deer are within the normal published range (Asher et al. 1988; Kelly and Moore 1977; Moore and Littlejohn 1989; Fennessy et al. 1990), while the gestation length for the CWxR calves was about 2 days longer than that reported by Moore and Littlejohn (1989), whereas those for the CWxR calves were about midway between the two parental strains, with a value of about 253 days being recorded for purebred CW at Invermay (Moore and Littlejohn 1989). Similarly the (CWxR)xR calves were also about midway between the two parents. The intriguing feature of the gestation length data relates to the (PDxR)xR hybrids with the comparatively high SD of ± 5.0 days (compared with the red deer SD of 3.4 days), reflecting a very wide spread without any obvious peak. Such a wide spread of gestation length has also been seen with the PDxR hybrids (produced by AI) where a mean of 266 ± 6.9 (n=17) has been observed (Asher et al. 1988; P.F. Fennessy, C.G. Mackintosh and G.W. Asher, unpublished data). Such variability in gestation length raises questions about the control of foetal growth and/or the nature of the signals for parturition in the PD hybrid deer. A mean gestation length of 283 days with a high SD of 6.1 days has been reported for pure PD deer (Wemmer et al. 1989). It appears therefore that a high SD is a feature of the PD gestation length. The regression coefficients of gestation length on birth weight are also presented in Table 4. In no case was the coefficient significant in contrast to previous studies at Invermay, where a significant negative relationship has been reported (Moore and Littlejohn 1989; Fennessy et al. 1990).

Table 4 Mean gestation lengths for male and female calves, the range and standard deviation (SD) of gestation length (within calf sex) and the regression coefficient for gestation length on birth weight for the four strains of calves

Strain of calf	N	Gestation length (days) Male	Female	SED	Range	SD	Regression coefficient ± SE: Gestation length on BW (days/kg)
Red	86	234.6	234.1	0.76^{NS}	224-242	3.41	0.10 ± 0.35^{NS}
(CWxR)xR	41	238.1	237.9	1.19^{NS}	233-247	3.79	0.33 ± 0.36^{NS}
CWxR	35	242.2	242.4	1.23^{NS}	233-248	3.64	-0.23 ± 0.41^{NS}
(PDxR)xR	17	252.4	251.9	2.41^{NS}	240-262	4.97	-0.61 ± 0.52^{NS}

Protein variation

The generation of backcross hybrids provides the opportunity to examine the reported electrophoretic variation (Table 1) for Mendelian segregation. Trf and Alb are usually coded for by single genes (eg: cattle, Jamieson 1965; sheep, Tucker 1968), and therefore Mendelian segregation is expected in the backcross. However, other modes of inheritance are possible for Hb (which is the product of two unlinked genes, α globin and β globin) and Ptf, a protein which has not yet been identified and characterised. The results, presented in Table 5, compare the observed segregation of each protein variant in the two

backcross hybrids to that expected for codominant inheritance at a single locus. For each of the four proteins, the expectation that one-half of the backcross hybrids will exhibit the homozygous red deer type and one-half the heterozygous hybrid type is fulfilled. These results strongly support the hypothesis that each protein is coded for by a single gene.

Table 5 Comparative segregation of protein variants with that expected in the two backcross hybrids, assuming codominant inheritance at a single locus for each protein (proportion observed, expected)

	Sire	Dam		
	CWxR	R	n progeny	Progeny
Haemoglobin (Hb)	AB	AA	39	AA (.44, .50); AB (.56, .50)
Post-transferrin (Ptf)	12	22	39	22 (.60, .50); 12 (.40, .50)
	PDxR	R		
Transferrin (Tf)	AE/BE	AA/AB	15	AA/AB (.60, .50); AE/BE (.40, .50)
Albumin (Alb)	FS	SS	15	SS (.53, .50); FS (.47, .50)

The existence of single gene marker loci provides a useful tool for the identification of hybrids in farmed red deer (Tate et al. 1988) particularly as phenotypic characters used to identify hybrids such as gestation length and growth rate show wide variation and considerable overlap between the different hybrid classes. Genetic analysis of backcross hybrids, including investigation of segregation of both quantitative traits and chromosomal regions offers the opportunity to identify regions influencing quantitative traits (eg. Paterson et al. 1988 for the tomato). Deer hybrids, particularly those between red deer and Pere David's deer, where a large number of fixed protein polymorphic differences between the two species have now been identified (Tate et al. 1988; M. Tate and B. Emerson, unpublished data), may be a particularly useful resource for this type of experiment.

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