



## Hybridisation using Père David's (*Elaphurus davidianus*) and red deer (*Cervus elaphus*)

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### Introduction

Hybrids between Père David's and red deer have been used as a tool for the rapid and relatively easy identification of genome regions (quantitative trait loci - QTL) associated with production traits in deer. The vast genetic differences between Père David's and red deer form the basis for such a strong comparison and identification process. Future research is aimed at verifying these results using commercially viable Wapiti hybrids. The ultimate objective being to develop a simple DNA test (e.g. blood) which is capable of ranking animals on genetic merit for a specific trait. This work has been conducted in parallel with a strong international research effort to identify the molecular genetic basis for superior production performance in many domesticated species.

### Hybrid generation & genotyping

Male hybrid F<sub>1</sub> progeny were generated by artificial insemination (PD x R) and subsequently used to generate backcrosses ((PD x R) x R). The hybrid status of all backcrosses was confirmed by DNA typing and that of F<sub>1</sub> hybrids by DNA and/or protein testing (Tate *et al.* 1995). The segregations of up to 250 genetic markers were analysed in the backcross herd including restriction fragment length variants (RFLV), protein variants and microsatellites. The term "variant" has been used for the fixed differences observed between the species whereas the word "polymorphism" has been reserved for variation within a species.

### Management & measurements

The sexes were managed as separate groups after weaning along with a cohort of red deer and treated using standard animal health protocols. Live weights were recorded at birth, weaning (c. 3 months of age) and thereafter at least once per month (every second week through the spring period) until 15 to 16 months of age (16m).

### Statistical analyses

#### Comparative growth

All data were analysed using REML analysis (SAS 1989). Live weights and live weight gains were modelled fitting genotype, sex, birth day, year, sire within genotype and a sex by year interaction. Dam live weight was also included in birth weight and weaning weight / growth rate to weaning analyses while calf fate was also included in the former analysis.

## Linkage analysis

This analysis effectively tests for point associations or correlations between individual genetic markers and traits within the backcross hybrids. Linkage analyses were carried out testing within sires and investigated differences in backcrosses which inherited either PD or R alleles from the hybrid parent.

## Results & Discussion

### Comparative growth

Live weights were recorded at similar dates over the four years and subsequently adjusted to a common date using covariance procedures. Adjusted live weights are presented in Table 1.

Hybrid males had significantly greater body weights at all seven defined points from birth

**Table 1. Adjusted<sup>1</sup> live weights (kg) at seven points on the growth curve up to 16 months of age for hybrids (1/4 Père David / 3/4 red) and red deer**

	Birth	Weaning (26 Feb)	Early winter (28 May)	Early spring (26 Aug)	Early summer (19 Nov)	Mid summer (14 Jan)	Peak autumn (12 Mar)
Male							
Hybrid	9.37 * <sup>2</sup>	52.3 **	66.8 ***	75.2 ***	99.7 ***	118.0 ***	122.9 * * *
Red	8.85	48.8	61.4	69.2	89.9	104.7	108.4
Female							
Hybrid	8.74 NS	47.2 NS	60.3 **	64.6 **	82.7 ***	93.7 ***	99.7 * * *
Red	8.28	45.0	55.5	59.5	74.3	84.7	89.2
SED <sup>3</sup> within sex	0.239	1.26	1.52	1.63	2.03	2.28	2.21
between genotypes							
SED between sexes	0.207 *	0.71 ***	0.94 ***	0.99 ***	1.26 ***	1.57 ***	1.60 * * *

<sup>1</sup> adjusted for environmental effects and sire

<sup>2</sup> P < 0.05 \* . P < 0.01 \*\* P < 0.001 \*\*\*

<sup>3</sup> standard error of difference

through to 16m (8-13%). Hybrid male growth rates were higher than their red contemporaries by 13, 10, 6, 19, 23 and 21% for the six growth intervals (all except winter and early autumn were significant). Hybrid females averaged 8% heavier at the seven points through the growth period although the differences were not significant at birth and weaning. Hybrid female growth rates were superior to their red counterparts by 10, 21, 4, 23, 20 and 23% for the six growth intervals (again differences for the winter and early autumn periods were not significant). Hybrids had significantly (P<0.01) higher live weight than reds from around six months of age in late May to their peak live weight at around 16 months in mid March. Hybrid males were also significantly heavier than reds at birth (9.37 vs 8.85kg, P<0.05) and at weaning (52.3 vs 48.8kg, P<0.01) approximately three months later. There were no significant

differences in growth rates between hybrids and reds during the winter period of late May to late August and the early autumn period of mid January to mid March. For all other growth periods including birth to weaning, weaning to early winter and spring to peak summer, hybrids grew significantly faster than reds in both sexes.

### Linkage analysis

In addition, analysis within the backcross hybrids revealed several regions of the genome had significant effects on live weight and growth rates. These include 2 putative QTL for six month weight (LOD 3.90  $P < 0.01$  and 2.74  $P < 0.05$ ) on linkage groups 12 and 5, 3 putative QTL for growth rate from 3 to 6 months (LOD 4.19  $P < 0.01$ , 3.92  $P < 0.01$  and 3.34  $P < 0.05$ ) on the same linkage groups and linkage groups 20 and 1 for growth rates and live weights between 9 and 16 months. The variance in traits explained by these QTL ranged between 5.3% and 11.2% and interestingly allele substitution with Père David's alleles at different loci had both positive and negative effects on live weights and growth rates. Linkage group 5 contained putative QTL with effects on 6 and 9m live weights; this region of the genome includes the growth hormone gene thus providing a candidate gene for these effects. This type of analysis has also been conducted for a large number of other traits measured in the backcross hybrids including, gestation length (Goosen *et al.* 1997), birth weight (Goosen *et al.* 1998) and antler seasonality traits.

Future deer breeding developments are likely to include advanced molecular genetic findings including QTL and marker assisted selection techniques (MAS) in the drive to improve the genetic basis of deer in the industry. These may be particularly useful for traits which are difficult to quantify such as resistance to disease (e.g. Tuberculosis) and for late maturing traits such as mature antler weights and grades.

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