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An interspecies hybrid in deer

By Gideon J.C. Goosen

B.Rural Science (Hons) University of New England

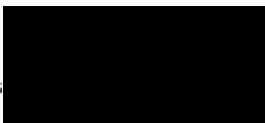
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Declaration

I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree or qualification.

I certify that any help received in preparing this thesis, and all sources used, have been acknowledged in this thesis.



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Abstract

Interspecies hybridisation between Père David's (*Elaphurus davidianus*, PD) and red (*Cervus elaphus*, red) deer, generating fertile F₁ offspring of both sexes, presents a unique opportunity for the evaluation of backcross hybrids in the New Zealand deer industry and for the investigation of the genetic control of quantitative traits. Backcross hybrids (¼ Père David's / ¾ red deer) were used for both comparative studies with reds and in the search for quantitative trait loci (QTL) in deer. Comparative aspects of growth and of physiology and the genetic control of gestation length, growth and seasonality traits were examined.

Evolution, speciation and the classification of species with particular reference to the deer family (Cervidae) are reviewed. The ability of Père David's and red deer to hybridise is discussed with reference to their taxonomic classification and genetic divergence. The uses of several mammalian hybrids are discussed including in particular the interspecies mouse hybrids which have been used extensively in the development of genome mapping and in genetic linkage studies.

Patterns of food intake, growth, carcass composition and seasonality in backcross hybrids and red deer were examined and compared. Feed intake patterns and growth of hybrids and reds (both sexes) were recorded in a controlled environment; all genotype/sex groups displayed a sinusoidal fluctuation in feed intake similar to that in other seasonal species of deer. Marked differences in patterns of voluntary food intake were evident between hybrids and red deer with the differences between genotypes being more evident in males than in females. Based on the published performance of the pure bred species on a high quality diet, the growth rate of hybrid genotypes was below expectation while the reds performed very well. In addition the reds performed well compared with growth rates on pasture.

The carcass characteristics of hybrids appear favourable for venison production with a greater proportion of total muscle in the hind quarter; several individual hind quarter muscle groups were also larger when compared with reds at both 15 and 28 months of age. Sex comparisons indicated males had proportionately more carcass muscle and bone with less fat and are thus consistent with gender studies in sheep and cattle.

The comparative patterns of growth in reds and hybrids on pasture from birth to 16 months of age indicated hybrids had significantly higher live weights from six months of age to their peak live weight at around 16 months in mid March. There were no significant differences in growth rates between hybrids and reds during their first winter (7 to 10 months of age) or the early autumn period of mid-January to mid-March (13 to 15 months). For all other growth periods hybrids grew significantly faster than reds in both sexes. Hybrids initiated their pedicles at a later date and a higher live weight than reds, indicating genotype differences in this pubertal trait. In addition to this, hybrids cleaned their antlers and cast their hard antler buttons earlier than reds indicating an earlier pattern of seasonal response to changing daylength.

The studies to search for putative QTL in the backcross hybrids made use of a genetic map with up to 250 segregating genetic markers 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. The linkage relationships of the markers were analysed using MAPMAKER/EXP and the Kosambi mapping function for all autosomal chromosomes. The map was 1240 cM long with the average spacing between markers of 7.3 cM. A total of 339 backcross animals were generated. An animal is described as “informative” if genotype data at a particular locus can be used to identify the parental origin of gametes (i.e. which allele was inherited from the sire and which from the dam). Informativeness is a prerequisite for linkage analysis, which examines the co-inheritance of gametes at any one marker loci. The species specific variants used were close to fully informative and on average were 96% informative in backcross offspring in the mapping panels thus providing a powerful resource for QTL detection.

The large number of single point tests conducted across the genome using ANOVA of trait against marker brings to light the importance of determining the true or trait-wise significance

thresholds. The type I error, where the sample suggests rejecting the null hypothesis where in fact it is true, is not considered as erroneous (for the purposes of detecting QTL) as the type II error where the hypothesis is accepted when in fact it is not true. Thus thresholds which ensure the type II error is no greater than would be expected (5%) with a one off test of significance were simulated. Simulations used normally distributed populations with residual degrees of freedom representative of the traits examined and using 1000 iterations, estimated the trait-wise 5% thresholds. These thresholds were then converted to LOD scores to determine significance. However, because the ANOVA thresholds are more conservative than those for maximum likelihood, the putative QTL reported here have been identified using a conservative significance test.

The control of gestation length in this interspecies hybrid is clearly very complex although there was evidence for four QTL of which three were on the same linkage group. Similar analyses also provided evidence for the segregation of QTL for birth weight, live weights and growth rates in backcross hybrids. These included two linkage groups for 6 month live weight and growth rate from 3 months to 6 months and linkage groups for growth rates and live weights from 9 months to 16 months of age. The search for QTL for pubertal (date and live weight at pedicle initiation) and seasonality (date of antler cleaning and casting) traits provided evidence, on separate linkage groups, for both date and live weight at pedicle initiation. Interestingly allele substitution with a Père David allele had both positive and negative effects on many traits including live weights, growth rates, pubertal and seasonality traits.

In conclusion red deer and the backcross interspecies hybrids between Père David's and red deer show marked differences in food intake patterns, carcass characteristics, growth patterns and seasonality, while the interspecies hybrids provide a powerful and unique platform for the detection of QTL in deer.

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