The role of parentage bloodtyping in genetic improvement

B. Kyle
Invermay Agricultural Centre, Private Bag 50034, Mosgiel, New Zealand

Bruce is the Deer Bloodtyping Consultant at AgResearch, Invermay. He has been largely involved in the development of the pedigree certification service and the Wapiti Society's Elk Registration Scheme.

Introduction

Greater emphasis on performance breeding means that accurate pedigree records are essential for deer breeders who wish to identify, sell or purchase superior animals. Many breeders have found that recording accurate pedigrees in deer is considerably more difficult than in other farm animals such as sheep and cattle. Furthermore, while modern animal breeding technologies such as artificial insemination can facilitate large genetic gains, they often produce an increase in pedigree errors which can reduce much of that genetic gain.

In New Zealand, deer breeders who have previously paid high prices for elite bloodlines now require proof of parentage before buying breeding stock. Parentage blood testing provides a means of (a) checking pedigree records and (b) solving cases of unknown parentage. This paper outlines the use of the test to improve genetic gain and explains how the test is performed.

Pedigree Errors and Genetic Gain

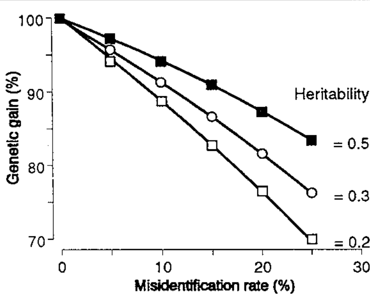
For breeding purposes it is important to know how pedigree errors influence the accuracy of progeny tests and reduce selection response. In the literature, most studies have involved cattle. However, the results of these are equally applicable to deer.

For example, Geldermann *et al.* (1986) examined the estimation of breeding values, heritabilities and correlations for milk performance traits among 1221 German dairy cows. They found that at a misidentification rate of 15%, the genetic gain for milk fat yield dropped between 9% (h^2=0.5) and 17% (h^2=0.2) below values attained without pedigree errors.

They conclude that a reduction in pedigree errors allows breeders to achieve the following:

- The number of progeny per test sire can be reduced for a constant genetic gain.
- Test sires can be ranked more precisely according to their "true" breeding values.
- More test sires can be used over the same number of females and with the same precision of ranking.

Parentage bloodtyping now enables deer breeders to maximise genetic gain by eliminating pedigree errors. The following diagram illustrates that as the pedigree error rate increases, genetic gain is reduced. This is particularly so among traits with low to moderate heritability:



Causes of Pedigree Errors

Both research and commercial bloodtyping has shown that several factors are linked to the occurrence of parentage errors. Tate *et al.* (1990) tested pedigrees from eight South Island breeding herds and found first calving hinds to have error rates of 25%, 32% and 61%. Six groups of mixed age hinds had error rates ranging from nil to 13%. Tate and others (pers. comm.) have found that synchronised calving following artificial insemination (AI) or embryo transfer (ET) programmes encourages mismothering and crossfostering - particularly among maiden hinds. Further, it is generally recognised that mismothering and crossfostering rates are increased at calving by human disturbance, high stocking rates and by providing inadequate vegetative cover.

Semen and embryo mix-ups during AI or ET programmes have been identified through bloodtyping, and a (supposedly) vasectomised stag has even been identified as the sire of several calves in an ET programme. Another cause of pedigree error is mixed sire mating - a result of stags jumping fences or gates being left open, or in some cases, because the breeder may want to cover a low libido stag with other stags to ensure the hinds are mated. Yet another factor is the difficulty in correctly matching calves with hinds at weaning time - usually because of cross suckling behaviour.

Another major problem is the wide variation in gestation length found among red deer. For example, Fennessy *et al.* (1991) reported a range of 224 to 242 days, with a mean of 234 days and a standard deviation of 3.4 days. The standard deviation indicates that about two-thirds of the calves would have a gestation length between about 230 and 238 days, effectively merging the calving dates of first cycle and second cycle mating groups. As a result, paternity is often in doubt where chaser stags are used. Finally, pedigree mistakes also occur through bad record keeping, often in combination with poor memory ("I'll correct that record when I get back to the house")!

In 1991, 19% of the 302 calves pedigree tested had one or both of their parents incorrectly assigned (Tate *et al.* 1992). The tests were routine pedigree checks to provide certificates for either naturally mated herds or ET herds, and as such were typical of most herds within the elite deer breeding industry. Obviously, such a high misidentification rate should be of major concern to all farmers and breeders.

The Parentage Profile

Deer parentage testing uses a technique called gel electrophoresis to separate and identify various proteins from a blood sample. Each protein has two components (alleles), one of which is inherited from each parent. Thirteen proteins, or markers, are currently used to create a blood profile which looks like a supermarket barcode and is easily compared with the profiles of other individuals to check pedigrees.

The process is simple, effective and currently cheaper than DNA fingerprinting. Most importantly, the genetic information contained in the blood profile is easily stored on computer, enabling the bloodtyping laboratory to instantly access a profile out of the thousands so far recorded from blood samples.

Pedigrees are tested by aligning the blood markers of an animal against those of its putative parents and checking that the blood types are compatible:

	Protein		
	GC	PLG	HBB
Calf	BC	BD	BB
Sire	BB	AC	BB
Dam	AC	AB	BB

In the above example, just three out of the total thirteen blood markers have been shown for simplicity. In this case, the sire has a blood type at the PLG marker which is incompatible with that of the calf. The sire therefore can be excluded as a possible parent of the calf. Where all of a parent's markers are compatible with those of the calf, it is said to qualify as a possible parent.

It should be noted that parentage testing works by a process of exclusion. That means identifying and discarding animals that clearly have wrong blood type(s) in a pedigree test. The Invermay parentage test normally identifies over 90% of incorrect pedigrees.

Pedigree Verification

Parentage blood typing is most commonly used to check pedigrees so that deer breeders can sell certified breeding stock, the benefit being a premium price for the vendor and known genetic background for the buyer. The system works most effectively when the breeder submits a putative pedigree to the laboratory for verification; if either or both parents are found not to qualify, the breeder is asked for an alternative pedigree. The laboratory is usually unwilling to provide a pedigree certificate after two alternatives have been excluded.

Solving Pedigree Problems

The blood test is frequently used to solve pedigree mix-ups by crossmatching the blood profiles of calves with several dams and sires. The result is a list of matings that qualify for each calf; using this process it is possible to solve the correct pedigree of most calves.

Parentage certificates are not normally provided in these circumstances as there is a small but real possibility of "false positive" errors occurring.

DNA Testing

AgResearch is developing new DNA techniques for deer parentage testing. They are being evaluated for their usefulness and cost effectiveness compared to protein bloodtyping, and it is hoped that they will lead to cheaper and even stronger tests.

Breed Registration

Parentage testing is useful in breed registration schemes where accurate pedigree information is required (eg the New Zealand Wapiti Society's imported Canadian Elk register). Furthermore, the blood profile belonging to each animal is a useful means of permanent identification.

Conclusion

Parentage bloodtyping enables deer breeders to maximise genetic gain by eliminating pedigree errors. The cost involved should be recovered through a combination of genetic improvement, reduced workload and, when pedigrees are certified, through sale premiums.

References

Fennessy, P.F.; Tate, M.L. and Johnstone, P.D. 1991. Hybridisation between red deer (Cervus elaphus) and other deer species. *Proc. 9th Conference AAABG (1991)* p469-472.

Geldermann, H.; Pieper, U. and Weber, W.E. 1986. Effect of misidentification on the estimation of breeding value and heritability in cattle. *J. Anim. Sci. 63:* 1759-1768.

Tate, M.L.; Buchanan, F.C. and Crawford, A.M. 1990. Parentage testing in farmed red deer. *Proceedings of Deer Course for Veterinarians (Deer Branch NZVA):* 7:177

Tate, M.L.; Dodds, K.G.; McEwan, K.M.; Buchanan, F.C. and Swarbrick, P.A. 1992. The use of protein polymorphism and DNA fingerprinting to solve complex pedigree problems in deer. *Proc. NZ Soc.Anim.Prod.1992, Vol 52:* 43-144.