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Genetic technologies for deer breeding

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ABSTRACT

The deer industry has made significant progress in developing and applying genetic tools to accelerate genetic gain. This paper briefly outlines the application of current tools (DNA parentage, DNA breed composition and genetic evaluation for growth and velvet), and then suggests a range of other tools which might be used in deer breeding in the future and makes brief comment as to their application. These tools include: genetic evaluation of a wider range of traits; economic indices, mate allocation software, breeding program diagnostic software, enhanced breed composition tests, single gene tests and whole genome selection.

Keywords: red deer; Wapiti; genetics; selection; DNA; breeding values.

INTRODUCTION

The deer industry has made significant progress in developing objective methods for breeding deer over the past decade. However, significant potential still exists to increase genetic gain in profit-related traits through further implementation of genetic technologies. This paper briefly describes the current situation, and then suggests a range of further developments which might be implemented in deer breeding in the future. The paper is restricted to genetic technologies and will not cover reproductive technologies, although the significant contribution of reproductive technologies and their synergies with genetic technologies is acknowledged.

GENETIC TECHNOLOGIES CURRENTLY USED

The major genetic technologies currently available and used by the deer industry include DNA-based parentage verification, DNA-based genotype prediction, and Breeding Values based on phenotype measurement and pedigree information. DNA parentage tests, currently based on micro-satellite markers, have been widely adopted by New Zealand deer breeders with approximately 30% of sire breeding herds using the technology (Anderson *et al.*, 2007). A DNA genotype prediction which distinguishes Elk/Wapiti (*Cervus elaphus* subspecies *canedensis*, *manitobensis*, *roosevelti* and *nelsoni*) from other subspecies of red deer (*i.e.* *Cervus elaphus* subspecies *scoticus* and *hippelaphus*) and provided an estimate of "breed proportion" for individual deer has also been available for approximately a decade, and was used widely by several Elk/Wapiti breeders when first available. However, usage of

this test has declined as breeders established for themselves the desired base level of Elk/Wapiti genes in their herds.

Breeding value analysis has also been available to the deer industry for almost a decade, initially as a pilot service, but more recently as the DEERSelect program (Archer *et al.*, 2005). This program currently offers analysis of growth traits and velvet production for "red" deer. As yet it does not include Elk/Wapiti subspecies, although this is currently under development. Approximately 50% of New Zealand herds known to be selling "red" stags or semen use the DEERSelect growth BVs, with most of the top tier herds involved. However, uptake of the velvet BVs has been significantly lower, due to the penalties involved with measuring the trait and that breeders perceive little additional benefit from objective description over and above visual evaluation and un-analysed phenotype measurements. This perception is no doubt largely due to the fact that velvet production is highly heritable, and systematic management effects are generally small, meaning that phenotype is a reasonable predictor of genotype for velvet.

OPPORTUNITIES TO APPLY CURRENT AND FUTURE TECHNOLOGIES

Genetic evaluation of other profit-related traits

It is recognised that many traits other than growth and velvet are related to profit in deer farming, but at present there are no objectively based tools to improve these traits. The first step in developing such tools is to find practical ways of measuring or predicting these traits (this primarily refers to phenotypic measurement, although future roles for DNA-based tests will be covered later). Secondly, scientific understanding of the genetic

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variability as encapsulated in estimates of heritabilities, phenotypic variances and correlations of these traits is required. Finally, standardised measurement protocols must be devised and implemented by breeders intending to use these tools in their selection programs. A non-exhaustive list of additional traits that might usefully be objectively evaluated in breeding value analyses would include:

1. Reproductive success/failure,
2. Reproductive seasonality (early calving),
3. Carcase traits (lean yield, meat colour stability),
4. Disease resistance (to Tuberculosis, Johnes disease, parasites),
5. Trophy score,
6. Temperament.

Of these, current research effort has directed towards 2, 3, and 6.

Economic indices

Indices which combine trait breeding values to predict profit for a given production system have two distinct roles. Firstly, they calculate the optimum balance between multiple traits, enabling selection candidates with strengths in different traits to be compared and ranked. Secondly the index provides a means of calculating the return on investment from using a particular animal in a breeding program at the commercial level, and so can potentially be used as a guide for commercial breeders purchasing stags as to what an animal might be worth.

The deer industry has three distinct products (venison, velvet and trophy), and economic indices will be useful in identifying the most profitable deer for different production systems. For example, the balance between growth and velvet traits will be markedly different for specialist venison self-replacing herds versus dual purpose herds producing velvet and venison. Economic indices to balance growth and velvet are under development and will be available soon. As further traits are added to the genetic evaluation system indices will need to be extended to include these traits.

Mate allocation tools

Software to allocate mates so as to maximise genetic gain in a desired objective, while minimising long-term inbreeding, is available to other industries and is readily adaptable for deer (Amer *et al.*, 2001). At this point in time, no deer breeders to our knowledge have used this tool. However, some imported strains of deer appear to have a small effective population sizes (based on

observations of pedigrees and founder animals, rather than explicit calculations), and mate allocation tools can play a valuable role in minimising long-term inbreeding in these populations.

Breeding program diagnostic tools

Recent tools developed for cattle breeding provide a diagnostic analysis of genetic gain at a breed level and in individual herds (Johnston & Moore, 2005). These tools can highlight areas in which breeders could potentially make more genetic progress, by calculating key determinants of genetic progress (*e.g.* selection differentials and generation intervals) and comparing across herds to determine which factors are influencing genetic progress. By providing confidential reports to individual breeders on areas in which genetic gain can be increased in their individual herds, the overall level of genetic gain across the industry can potentially be accelerated. While this type of approach is not currently a priority for the deer industry, it may prove useful in the future, particularly if it were to include advice around constructing optimal programs for breeding structure (*e.g.* progeny-testing a proportion of young stags) and measurement of phenotype and DNA-tests on animals.

DNA-based breed composition tests

Recently the technology to produce a DNA-based prediction of breed composition has been enhanced, providing the ability to differentiate between strains of deer from Europe and Britain as well as North America (Hall, R. pers. comm.). This test extends the currently available “elkometer” test which only differentiates North American Elk/Wapiti from European and British red deer. Such a test has useful research and practical applications. The practical applications include providing the ability to account for breed proportion in genetic evaluation, thereby increasing the accuracy of evaluations both within European and British red deer, and also extending the evaluations to deal with composites of European, British and North American origin. Much of the deer population in New Zealand are composites and in many instances pedigree information back to pure strains is missing (or contains errors), so the new DNA-based breed composition test will likely prove a useful tool in improving genetic evaluation. It may also have a role in verifying composition and origin of deer and deer products. This will be valuable in many scenarios but has practical and immediate application in velvet.

Single gene tests

Single gene tests for economically relevant traits have been the focus of significant research in other livestock species for the past two decades. Where no information from other species exists, this research is currently expensive, with a long period to payback. The scale of the New Zealand deer industry is too small to justify large programs of this nature. However, knowledge of individual genes influencing key traits in other species (and their location in the genome) provides an immediate avenue for development of specific gene tests in deer at a greatly reduced cost. This is best utilised where known gene variants controlling traits in cattle or sheep are examined to see if there are variants in the same genes controlling equivalent traits in deer. The limitations of this strategy include the fact that deer have unique traits with no equivalents in other species, and the possibility that variation in a trait in deer is due to gene variants which are fixed in cattle or sheep. Currently there are no single gene tests available in deer, but current research is using this strategy in several cases where a trait is sufficiently important in deer to warrant investigation.

Whole genome selection

Whole genome selection (WGS) is an emerging technology beginning to be applied in dairy cattle breeding. Essentially it relies on SNP (single nucleotide polymorphism) chips containing many thousands of DNA markers which enable a dense marker coverage across an individual's genome at a relatively low cost. This provides ability to identify potentially elite animals from a very young age based on DNA results without measurement of phenotypes. Genetic merit is predicted using a "black box" statistical analysis based on marker results in the absence of knowledge of individual genes (Meuwissen *et al.*, 2001). WGS is likely to have marked impact on genetic gain in dairy cattle (Schaeffer, 2006) and other species (Dodds *et al.*, 2007). The potential of WGS to advance genetic gain in deer has not been quantified, but intuitively it would appear to have potentially large impact. Its benefits are most marked in difficult to measure, or sex linked traits and traits only available at older ages. In deer, these include host disease resistance and reproductive traits including seasonality. Development of a SNP chip for deer would require an investment of approximately \$NZ2 million in partially sequencing the deer genome (McEwan, J.C. pers. comm.), plus a subsequent cost of approximately \$NZ700 per animal for genotyping at existing prices. These costs are declining rapidly

as the technology develops and is implemented on larger scales in other species, notably humans, but also cattle. Given historical trends prices will have declined 10 fold in another decade. We expect the benefit to the deer industry will outweigh the development and implementation cost within that timeframe. Availability of SNP chips in deer would likely have significant benefits to research in addition to its direct role in accelerating genetic gain. An example of this would be the ability to identify candidate genes responsible for disease resistance that differ between deer strains.

SUMMARY

There are several opportunities to further accelerate genetic gain in deer breeding, ranging from simple enhancement of existing technologies through to implementing latest developments in breeding tools from other livestock industries. The deer industry's best strategy is likely to adapt and apply technologies developed in other livestock industries as they become cost effective, but this need not involve a long time lag in application. As deer breeding technologies become increasingly sophisticated and a large quantity of information is generated, it will be important that application of genetic improvement remains straight forward at the commercial level, and must not become removed from simple practical realities such as the requirement for functionally sound animals.

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