BRIEF COMMUNICATION

The use of protein polymorphism and DNA fingerprinting to solve complex pedigree problems in deer

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ABSTRACT

We examined the practicality of using a combination of protein polymorphism and DNA fingerprinting to match up hinds and calves in nine separate mating groups of red deer with between 8 and 21 progeny each. Variation in 10 polymorphic proteins excluded 0.61 to 0.89 of the possible dam-calf combinations in each sire group, leaving between 2 and 200 pedigree combinations per group to be solved by DNA fingerprinting. Of the 44 sire-dam-calf combinations tested by DNA fingerprinting, 22 were excluded, while four calves matched the parents at all bands. However, 16 pedigrees were equivocal, due to the fact that one or both parents were not in a lane directly adjacent to the calf on the fingerprinting gel. The low probability of exclusion of protein testing in some sire groups, combined with the practical limitation of having to run each possible pedigree combination side by side on DNA fingerprinting gels, mean that the present techniques do not provide a routine method for identifying the dam-calf pairings in red deer mating groups on farms.

Keywords Deer, pedigree, parentage, protein polymorphism, DNA fingerprinting.

INTRODUCTION

Pedigree recording in farmed red deer is more difficult than in other farmed ruminants, such as sheep and cattle, because of the behaviour of farmed red deer and their sensitivity to disturbance during calving. The use of biochemical genetic variation to test of the accuracy of deer farm pedigree records has identified a high level (>10%) of incorrectly recorded pedigrees in some red deer herds (Tate *et al.*, 1990). Pedigree tests conducted by the Invermay Blood Typing Laboratory, to certify the accuracy of deer farm pedigrees, support this view. For example, in 1991, 19% of the 302 calves tested had one or both of their parents incorrectly assigned. In this study, we examined the practicality of using a combination of the two biochemical testing systems, protein polymorphism and DNA fingerprinting (Tate *et al.*, 1990), not just to detect pedigree errors but to match up the correct pedigrees in deer mating groups.

METHODS

We evaluated these techniques by attempting to match the progeny and dams in nine sire groups, calved separately, with 8 to 21 progeny each (9 to 32 dams). Farm pedigree records were available for 75% of the 159 calves involved. All the animals were scored for polymorphism in isocitrate dehydrogenase, plasminogen, transferrin, vitamin-D-binding protein (Tate *et al.*, 1992; Tate and Dratch, 1988), glucose phosphate isomerase, mannose phosphate isomerase, phosphoglucomutase (Tate *et al.*, 1990) haemoglobin, post-transferrin (Fennessy *et al.*, 1991) and superoxide dismutase (Herzog, 1990). The data were analysed to provide a list of all combinations of dams and calves in a sire group which had compatible protein types. The use of DNA fingerprinting to identify the correct pedigree among the possible combinations remaining after protein testing was evaluated by testing 44 pedigrees. DNA fingerprinting involved the techniques and probes (pV4, cHa-ras HVR, pUCJ, and (AC)n) described by Crawford and Buchanan (1990).

RESULTS

The total number of possible pedigree combinations in each sire group (no. of dams x no. of calves) ranged from 72 to 588. The proportion of these possible pedigrees excluded using protein testing varied from 0.61 to 0.89 in different sire groups, leaving between 2 and 200 pedigree combinations per sire group to be analysed by DNA fingerprinting.

The use of DNA fingerprinting to identify the correct pedigrees among those not excluded by protein testing was evaluated by DNA fingerprinting 44 sire-dam-calf pedigree combinations, from three sire groups. Of these, 22 were clearly excluded, while four calves matched the parents at all bands. The results for 16 pedigrees were equivocal for one or more probes. This was due to the fact that one or both parents were not in a lane directly adjacent to the calf. We concluded that for unequivocal results it was necessary to run the sire and dam either side of a putative calf.

All the dams and calves were uniquely matched using the biochemical methods in only one mating group with 72 possible pedigree combinations. The results were identical to farm pedigree records. Overall only five of the 119 calves with farm pedigree records had protein or DNA types incompatible with their putative pedigree. Of the unrecorded calves, 25% (10) were successfully matched to a single dam.

DISCUSSION

Protein parentage testing methods were efficient in that each animal was typed only once and the recorded blood type was then used for all subsequent pedigree analysis. However, the tech-

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niques could not uniquely identify the pedigree of most calves. In theory DNA fingerprinting could be used to "tidy up" the remaining combinations after protein testing. However the usefulness of the technique was severely constrained by the practicality, and cost of having to run animals many times, side by side in each of their possible pedigree combinations. These practical limitations are also noted by Pemberton *et al.,* (1992).

We conclude that while the present techniques are very useful for checking existing pedigree records, and can solve complex pedigree problems, they do not provide a practical means of identifying the dam-calf pairings in red deer mating groups. This will require a reliable system of computer-based storage and comparison of DNA fingerprinting band patterns or alternatively, a much larger number of individually scored polymorphic loci. Methods for pursuing the latter approach have been described in sheep and may be applicable to deer (Crawford *et al.*, 1991).

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