Assessment Of Genetic Variability In Mink By DNA Fingerprinting

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ABSTRACT

Genomic DNA was extracted from 87 dark mink from two farms in Nova Scotia. Genetic variability was assessed by DNA fingerprints generated using Hae III restriction endonuclease and Jeffreys' 33.15 probe. The results showed a high degree of DNA polymorphism in both farms. All but one of the 22 bands scored in the range of 4 to 7.2 kb were polymorphic. The two farms were comparable for the mean number of bands per individual (6.2 and 6.8), average band frequency (0.33 in both farms), locus heterozygosity (0.51 and 0.53) and index of band sharing among individuals within each farm (0.53 and 0.54). The results suggest a higher genetic variability than expected based on the population number and the historic prevalence of inbreeding of mink in the region. Similarity between the two farms could be due to gene flow from common sources.

INTRODUCTION

Despite advancements in nutrition and management practices during the past decade, reproductive performance, particularly litter size, has declined in mink farms in Nova Scotia. The inbreeding resulting from intense selection on fur quality traits could have reduced genetic variability and increased inbreeding and may have caused the observed reduction in fertility. Absence of long-term pedigree information impeded estimation of inbreeding and genetic variability by conventional methods, and DNA fingerprinting seems to be the only logical method of obtaining baseline genetic information on the mink herds. Hypervariable minisatellite DNA sequences are excellent tools for generating DNA fingerprints that have multiple applications in population genetic studies (Jeffreys et al., 1985). We are currently using hypervariable minisatellite DNA sequences to investigate several genetic properties of mink populations in the region. This report deals with genetic variability within two mink herds.

MATERIALS AND METHODS

Source of DNA: Liver tissue was taken from dark mink (*Mustela vison*) in two breeding farms in Nova Scotia during spring pelting of 1993. Both farms have been breeding mink for more than 15 years. Fur quality traits have been the major selection criteria in both farms with some emphasis on litter size during the recent years.

Flow of genetic material between the two farms has been very limited during the recent years, but both have imported some individuals for breeding from few common sources in the U.S.A. One farm (A) has been keeping approximately 1200 breeding females, and has been following assortive mating with avoidance of parent-offspring and brother-sister matings. The number of breeding females in the other farm (B) has not been less than 2000 over the past 15 years. Several lines have been established in this farm. Lines originated from one full-sib family with distinguished fur characteristics. Lines are not closed, as males from each line are mated to females from other lines, and the progeny that possess the desirable characteristics are added to the line.

Laboratory procedures: Genomic DNA samples were digested with Hae III restriction endonuclease and subjected to fingerprinting following previously reported procedure (Sabour et al., 1992). Southern blot hybridization was performed using labelled single-stranded Jeffreys' 33.15 probe (Jeffreys et al., 1985). Membranes were autoradiographed at -80°C. Four exposures for 10, 20, 36 and 72 h were made of each membrane to accurately score bands of differing intensity. The DNA from each individual was run on more than one gel in various combinations with other samples for cross-referencing. Only bands greater than 4 kb molecular weight were scored. Data on 26 and 61 individuals from farm A and B, respectively (out of more than 130) could be unambiguously scored and are used in this report.

Locus heterozygosity (H) and band sharing (BS) were estimated using the following equations:

$$H=[\Sigma^{N}_{k=1}S_k/[N-\Sigma^{N}_{k=1}\sqrt{1-S_k}]-1 \qquad BS=2N_{ab}/(N_a+N_b)$$

where N is the total number of bands scored (polymorphic or monomorphic) and S_k is the frequency of band k in the population (Gilbert et. al., 1991), N_{ab} is the number of bands shared between individuals A and B, and N_a and N_b are the total number of bands scored in individuals A and B (Jeffreys and Morton, 1987). A FORTRAN program was written for analysis of band information.

RESULTS

A high degree of DNA polymorphism was observed in the range of 4 to 7.2 kb. No band with a molecular weight higher than 7.2 kb was observed. All but one of the 22 bands scored in this range were polymorphic. The number of bands per individual ranged from 4 to 9 in farm A and from 5 to 10 in farm B with means of 6.2±1.4 and 6.8±1.3 in farms A and B, respectively. Average band frequency in farms A and B was 0.33±0.27 and 0.33±0.28, respectively. The average locus heterozygosity was estimated to be 0.51 and 0.53 in farms A and B, respectively. Mean of band sharing among individuals within each farm was 0.53±0.16 in farm A and 0.54±0.16 in farm B. Index of band sharing among all possible combinations of

individuals from the two farms was 0.54±0.16.

DISCUSSION

Breeding for high quality fur characteristics has been the predominant selection criteria in the region for many years. Some farmers chose to capitalize on elite individuals with notable fur characteristics using a line-breeding program. The inbreeding resulting from intense selection and line-breeding would reduce genetic variability and might have caused the observed reduction in reproductive performance. The observed degree of DNA polymorphism in both farms was, however, higher than expected based on the population number and the historic prevalence of inbreeding of mink in the region. This could be the result of continuous infusion of new stock from the U.S.A.. The same process could be responsible for the observed similarity between the two farms with regard to the parameters studied, and high index band sharing index among mink in the two farms. In addition, indiscriminate infusion of jet black (an allele that causes intense darkness of coat color in mink that was discovered in Nova Scotia in 1960's (Mullen, 1991)) into many breeding herds could have resulted in a high degree of relatedness among mink herds in the region.

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