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Genic Variation in White-tailed Deer From Arkansas

PHYLLIS K. PRICE[1], MICHAEL CARTWRIGHT[2], and MITCHELL J. ROGERS[2]

ABSTRACT

Liver and kidney samples of 33 white-tailed deer *(Odocoileus virginianus)* representing three populations in Arkansas were examined with horizontal starch gel electrophoresis. Of 17 loci examined, only PGM-1 and ES-2 exhibited polymorphism. Average individual heterozygosity, ranging from 2.3% to 4.7% with a mean of 3.1%, was much lower than that reported for white-tailed deer in other parts of its range. The three populations examined in this study were highly similar based on Rogers' genetic similarity coefficient.

INTRODUCTION

Several investigators have used electrophoretic techniques to study the genetics of white-tailed deer, *Odocoileus virginianus*. Cowan and Johnston (1962), Weisberger (1964), Miller et al. (1965), Harris et al. (1973), and others have examined blood proteins with a major emphasis on hemoglobin. Manlove et al. (1975), Baccus et al. (1977), Johns et al. (1977), and Ramsey et al. (1979) studied liver and kidney proteins in addition to blood proteins and extensibly examined relationships between heterogeneity and age, sex, and/or reproductive rate; spatial subdivisions of populations based on single locus gene frequencies were also examined.

Harris et al. (1973) included deer from two Arkansas counties (Stone and Desha) in an analysis of hemoglobin variation over the southeastern United States. However, at this time, there is still relatively no published genic information concerning white-tailed deer from Arkansas. Smith et al. (1976) have noted the use of such data in wildlife management practices. Since genic information may have important management application, the purpose of our study was to: (1) examine the genic composition of deer from Arkansas and (2) compare enclosed and non-enclosed populations.

MATERIALS AND METHODS

Two populations occupied Caney and Big Springs enclosures which encompass 243 and 273 hectares, respectively. The enclosures, located within the Sylamore District of the Ozark National Forest in north-central Arkansas, are separated by approximately 402 meters and have been maintained since 1962. Background information on the enclosures has been given by Segelquist and Green (1968) and Segelquist et al. (1969). A non-enclosed population was represented by deer in the Sylamore Wildlife Management Area (Sylamore WMA) surrounding the enclosures.

Liver and kidney samples of 33 white-tailed deer were obtained from the enclosures and the surrounding Sylamore WMA between January and March 1978. Information as to age and sex was available for 29 of 33 animals. Ages ranged from 0.5 to 15.5 years, with the majority of animals between 1.5 and 5.5 years. Number of known males and females for each sample are given in Table 1.

Tissues were subjected to horizontal starch gel electrophoresis. Apparatus, tissue preparation, buffer systems, and staining procedures were similar to those of Selander et al. (1971) and Manlove et al. (1975). The following 14 protein systems encoded by 19 loci were examined: albumin (ALB), esterases (ES-2, ES-4), glutamate dehydrogenase (GDH), glutamate oxalate transaminase (GOT-1, GOT-2), α-glycerophosphate dehydrogenase (α-GPD), indophenol oxidase (IPO), isocitrate dehydrogenase (IDH-1, IDH-2), lactate dehydrogenase (LDH-1, LDH-2), malate dehydrogenase (MDH-1, MDH-2), malic enzyme (ME), 6-phosphogluconate dehydrogenase (6-PGD), phosphoglucomutase (PGM-1), phosphoglucose isomerase (PGI), and sorbitol dehydrogenase (SDH). PGI was scored as a single locus although Manlove et al. (1975) has hypothesized the presence of two loci for this protein in white-tailed deer. Scoring of the remaining systems followed the method of Manlove et al. (1975). ME and SDH were not consistently scorable and, thus, not included in subsequent analysis. Allele frequencies and average individual heterozygosity ($\overline{H}$ = number of individuals x number of loci) were determined from genotype counts. Comparisons of paired combinations of populations were based on allele frequencies analyzed by Rogers' (1972) coefficient of genetic similarity. The resulting matrix was subjected to the unweighted pair-group method using arithmetic averages of cluster analysis from NT-SYS programs (Rohlf et al., 1969).

RESULTS AND DISCUSSION

Of 17 scorable loci, only ES-2 and PGM-1 exhibited polymorphism (Table 1). Two alleles were present at the ES-2 locus. The homozygous state of the fast allele (designated a) appeared as a fast-migrating band, while the homozygous state of the slow allele (designated b) appeared as a slow-migrating band. The heterozygote was expressed as a triple-banded pattern. Manlove et al. (1975) noted three alleles at ES-2. In their study, cathodal subbanding for homozygotes of two alleles and anodal subbanding for homozygotes of their slowest allele gave the appearance of an intense band and a light subband for homozygotes. Heterozygotes were expressed as two intense bands and one or two light subbands depending on allelic composition. In the present study, two ES-2 alleles were expressed at equal frequencies in the sample from Sylamore WMA and at near equal frequencies in the sample from Caney enclosure. Animals from Big Springs enclosure showed a predominance for the slower allele.

Variation at the PGM-1 locus was limited to a single heterozygote in the Sylamore WMA sample. The heterozygote, expressed as two bands, indicated the presence of a slow allele (designated b in Table 1). Homozygotes of the fast allele appeared as single fast-migrating bands. This locus is probably the same as the PGM-2 locus of Manlove et al. (1975). They noted the presence of three alleles at PGM-2 in homozygous and heterozygous states.

Although SDH was not consistently scorable, this locus did indicate polymorphism. Manlove et al. (1975), Baccus et al. (1977), Johns et al. (1977), and Ramsey et al. (1979) also noted variation at GOT-2, LDH-2, and MDH-1 which were monomorphic in our samples from Arkansas.

Cowan and Johnston (1962), Miller et al. (1965), Tets and Cowans (1966), and Seal and Erickson (1969) have noted very limited significant differences between sexes, age classes, or seasons in mobility of blood proteins. Ramsey et al. (1979) have observed significant differences between herds, sexes, or age classes for gene frequencies at the hemoglobin and ES-2 loci using large samples of white-tailed deer. Also using large sample sizes, Johns et al. (1977) noted a positive correlation between reproduction and $\overline{H}$. $\overline{H}$ tended to be higher for females with two fetuses than for females with one fetus. Of 17 known females in the present study, 11 had two fetuses, and three

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were not pregnant. No trend was apparent for the reproductive data as well as the age and sex data.

Values of $\bar{H}$ obtained in the present examination of white-tailed deer were quite low in comparison to those from other areas. As seen in Table 1, $\bar{H}$ ranged from 2.3% for the Caney sample to 4.7% for the Sylamore WMA sample with a mean of 3.1%. The low $\bar{H}$ values may be partially accounted for by the kind of loci examined. Harris et al. (1973) observed beta-hemoglobin polymorphism in their samples of white-tailed deer from Arkansas. Hemoglobin and SDH loci may be additional sources of variation. Studies including kidney, liver, and blood proteins yielded $\bar{H}$ values averaging 12.1% (Smith et al., 1976), 9.1% (Johns et al., 1977), and 12.7% (Ramsey et al., 1979) with SDH, hemoglobin, and ES-2 as major contributors.

The two enclosed population samples had similar $\bar{H}$ values which were lower than those for the non-enclosed population sample (Table 1). The lower values could be indicative of inbreeding within the enclosures which reduces genetic variability (Smith et al., 1976). The Caney sample represents that entire population which has been terminated. Within such a small population, inbreeding would be expected, Smith et al. (1976) have noted that the effects of inbreeding in natural populations are not really known; however, unfavorable consequences of inbreeding have been well illustrated in laboratory and domestic animals. Genic variability may also be reduced due to genetic drift which would occur when only a few animals are introduced into a small population (Smith et al., 1976). After the cessation of restocking, Caney enclosure had very limited change in population size; such conditions would favor genetic drift (Smith et al., 1976). A similar situation was probably present for Big Springs enclosure.

The biochemical matrix obtained from Rogers' genetic similarity coefficient shows all samples to be highly similar (Table 2). These relationships are depicted in the resulting dendrogram (Figure 1). The high degree of similarity for the three population samples may be due to the initial stocking of the enclosures and subsequent restocking of the enclosures until approximately 1969 from the surrounding Sylamore WMA. Each enclosure may have had similar genetic input. Caney enclosure has suffered high fawn mortality at least in recent years with a similar situation probably present at Big Springs enclosure. Thus, similarity between the three population samples could be partially explained by the lack of opportunity for new combinations of genes to occur. Since few fawns were reaching an age to become part of the effective breeding population and since the deer being stocked into the enclosures were probably genetically similar to those already present, little new genetic input into the population was occurring.

The current study has shown a reduction in genetic variability in deer probably due to inbreeding, genetic drift, and/or lack of change in the effective breeding structure of the populations. Since there was little new genetic input into the enclosed populations, opportunity for genetic change was limited. Smith et al. (1976) pointed out that mutation is the only way new genetic material may be developed from within a population but is an insignificant source of variation during time intervals that are meaningful in a management context. Selection and emigration will alter gene frequencies of population but do not add new material. New genetic information must come from additional introductions or immigrations. Therefore, in the reintroduction of species into areas, the investigator should introduce the maximum number from a variety of sources to found new populations (Smith et al., 1976). The significant genetic considerations for stocking of species is discussed by Smith et al. (1976).

Additional work is needed to better understand the genic structure of Arkansas deer. Future works may well show how genic studies can be of use in discriminating breeding units, assessing degree of inbreeding, and increasing herd productivity in deer.

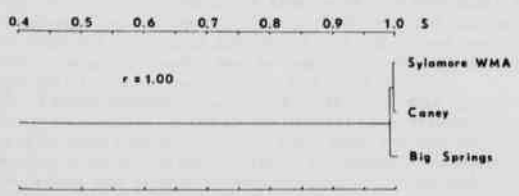

Figure 1. Genic similarity dendrogram based on Rogers' genetic similarity coefficient.

Table 1.--Sample size (n=total;known males;known females), allele frequencies of the polymorphic loci, and average individual heterozygosity ($\bar{H}$) in *Odocoileus virginianus*.

Locality (Sample Size)	Polymorphic Loci				$\bar{H}$ (%)
	ES-2		PGM-1		
	a	b	a	b	
Big Springs (n=10;4;5)	0.30	0.70	1.00	0.00	2.4
Sylamore WMA (n=5;2;3)	0.50	0.50	0.90	0.10	4.7
Caney (n=18;6;10)	0.53	0.47	1.00	0.00	2.3
					3.1 = mean

Table 2.--Similarity matrix based on Rogers' genetic similarity coefficient for *Odocoileus virginianus*.

	Sylamore WMA	Big Springs	Caney
Sylamore WMA	1.000		
Big Springs	0.982	1.000	
Caney	0.992	0.986	1.000

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