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6-PHOSPHOCLUCONATE DEHYDROGENASE POLYMORPHISM AND GENETIC DIFFERENTIATION IN RED DEER *(Cervus elaphus)* AND SIKA DEER *(Cervus nippon)*

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Abstract

Previous studies on the 6-phosphogluconate dehydrogenase (6-PGD) enzyme system in the genus *Cervus* have revealed a lack of 6-PGD polymorphism in wapiti *(Cervus canadensis,* CAMERON and VYSE, 1978), red deer *(Cervus elaphus,* GYLLENSTEN et al., 1983; HARTL, 1986) and fallow deer *(Cervus dama,* PEMBERTON and SMITH, 1985; HARTL et al., 1986).

The present investigation of 161 red deer from different populations in Deutschland as well as 56 animals from an Irish red deer x sika deer hybrid population has revealed a phenotypic variation of this enzyme system only in the hybrid population. Three different phenotypes, designated "a", "ab", and "b" have been found, leading to the hypothesis of one biallelic gene locus coding for a dimeric enzyme.

This hypothesis is supported by the results of genetic analysis of the pedigrees shown in figure 1. In order to increase the number of offspring, all offspring of mating types with the same phenotypes have been pooled.

Isozyme analysis in connection with the morphology of the animals in question reveals that morphologically pure sika (HARRINGTON, personal communication) are fixed for the allele $6\text{-}PGD^{b}$ (showing the slower migrating band) whereas pure red deer in the Irish population as well as in the populations from Deutschland exhibit only the faster migrating band of the $6\text{-}PGD^{a}$ allele. In red x sika hybrids, both alleles are present in the homozygous as well as in the heterozygous condition.

The genotypic structure of the polymorphic Irish sample shows a significant deviation from the Hardy-Weinberg structure ($\hat{G}=4.755^{*}$, $\alpha=0.05$, df=1; see WEBER, 1978).

A probable explanation for the observed excess of homozygotes is a Wahlund effect due to an assumed influence of hybridisation on the population subdivision.

The present findings in connection with the previously published data allow the conclusion that the 6-PGD polymorphism is, like karyotype polymorphisms, caused by the hybridisation between so called "species", representing in fact members from different populations of one and the same biological species.

The actual amount of heterozygosity in the hybrid populations $\bar{H}_A$=0,161, the conditional heterozygosity ($\bar{H}_C$), that avoids one fundamental disadvantage of H_A, namely the dependence on the underlying gene frequencies (MÜLLER-STARCK and GREGORIUS, 1986), is equal to 0.525.

The genetic distance d_O (p,q) between two populations p and q (GREGORIUS, 1974), which is a more suitable measure than NEI's (1972) distance *D*, to equal 0.745 was caluclated between the hybrid population and the pure red deer populations at the 6-PGD locus. The genetic distance between the groups "pure sika deer" and "red deer" is equal to 1, since the populations are fixed on different alleles.

The genetic differentation δ (GREGORIUS and ROBERDS, 1986), which for the case of two demes is equal to the distance d_O, can be used also as a measure for introgression. Therefore the 6-PGD polymorphism offers us a powerful tool for studies on hybridisation in natural as well as park or zoo populations.

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Fig.1: Pedigrees and corresponding 6-PGD phenotypes analyzed in the present study.