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# Lack of biochemical-genetic variation in native Sika deer (*Cervus nippon hortulorum*) from the far east of the Asian continent

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In contrast to various other deer species (see Hartl et al. 1990, for review), Sika deer (*Cervus nippon*) has only poorly been investigated for biochemical-genetic variation. Population genetic data are available only from representatives of the Japanese subspecies *Cervus nippon nippon*, introduced into Great Britain and Ireland, and from hybrids of this subspecies with the Red deer (*Cervus elaphus scoticus;* see Harrington 1973). A multilocus investigation including 11 RBC/plasma enzyme systems was performed by Herzog (1988) without detecting polymorphism or differences from the Red deer except for 6-phosphogluconate dehydrogenase, where the occurrence of genetic polymorphism is indicative for hybrid populations of Red and Sika deer.

In order to examine genetic variation in native Sika deer from the easternmost point of Asia, possibly belonging to the subspecies *C. n. hortulorum* (Ratcliffe 1987), whole blood samples of 43 individuals from a population in Primor'e (USSR) were collected during the hunting season of 1989/1990. The blood was fractioned into plasma and erythrocytes and stored frozen at −20 °C. Horizontal starch gel and agarose gel electrophoresis, blood protein and enzyme staining as well as the interpretation of band-patterns were done as summarized by Hartl and Höger (1986), Hartl et al. (1986) and Hartl and Ferrand (1991). The following blood proteins and enzymes were screened (abbreviation, E.C. number and gene loci scored are given in parentheses): hemoglobin (Hb, alpha and beta chain, *Hb-α, Hb-β*), transferrin (Tf, *Tf*), lactate dehydrogenase (LDH, E.C. 1.1.1.27, *Ldh-2*), NADH-diaphorase (DIA, E.C. 1.6.2.2, *Dia*), catalase (CAT, E.C. 1.11.1.6, *Cat*), aminoacylase-1 (ACY-1, E.C. 3.5.1.14, *Acy-1*), and glucose phosphate isomerase (GPI, E.C. 5.3.1.9, *Gpi-1*).

None of the gene loci investigated was polymorphic in the Sika deer. When compared to band-patterns in the Red deer (*C. e. hippelaphus*), allelic differences were observed at the *Hb-β* and the *Cat* locus. Whereas the lack of genetic variation in introduced Sika deer (*C. n. nippon;* Herzog 1988) can be explained by genetic drift and inbreeding, which are frequently associated with the artificial foundation of populations (comp. Hartl et al. 1986; Hartl 1989), this result was not to be expected in our native Sika deer population. As far as the evolutionary rate of proteins is concerned, some of the blood proteins and enzymes investigated showed considerable genetic variation in other deer species (see Hartl et al. 1990, and references therein). Further studies are required to elucidate the population history and distribution of Sika deer in our study area as well as its genetic structure to detect a possible threatening by genetic pauperization. Concerning the genetic differences from the Red deer, the fixation of alternative alleles at two out of eight loci is in accordance with allozyme differentiation at the species level.

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