

Red Deer in Bavaria – Identifying Populations for Conservation



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Abstract

Subsequent habitat fragmentation has presumably changed the genetic structure of the Bavarian red deer population. Understanding the process and patterns of gene flow requires a detailed knowledge of how landscape characteristics and anthropogenic influences structure populations. This understanding is crucial for managing properly the genetic diversity of threatened and endangered populations. New approaches, defined as “Landscape genetics”, were used to facilitate the understanding of how geographical, anthropogenic and environmental features influence genetic variation of the red deer in Bavaria. In addition, genetic criteria were used to select candidate subpopulations to be given priority for conservation. Conventional diversity measures such as expected heterozygosity H_e , number of polymorphic alleles n_p , or allelic richness A_R have been considered. For conservation purpose priority should be given to additional measures like probability of allelic co-ancestry F_{IS} and effective population size N_e under the drift or drift-migration model. Additionally, the contribution of the genetic variability of each population to total diversity C_T , subdivided into a diversity and a differentiation component as a measure of the uniqueness of a population, was used to identify populations for conservation.

Introduction

The red deer (*Cervus elaphus*) population of Bavaria in Southern Germany was severely reduced during the 19th century due to over-hunting. The species has since recovered within designated areas influenced by habitat and population fragmentation. Wildlife authorities and hunting organisations have recently become concerned about the effects of isolation, small population size, and loss of genetic variability. Regulations that take into consideration demographic fluctuations and habitat fragmentation are planned by the government. The aim of conservation genetics is to use the information of range-wide genetic surveys to implement conservation policies for given species or populations and, in particular, to identify areas for conservation. Knowledge of genetic structure, allowing an understanding of the demographic processes which have led to the current situation and the identification of populations for conservation are essential for sound and sustainable wildlife management.

Methods

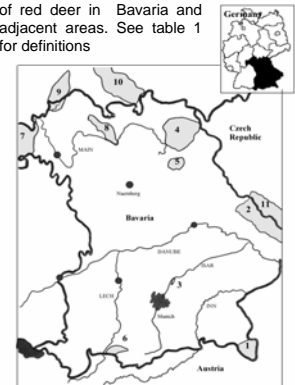
Material: 395 samples of different sex and age obtained from nine Bavarian and two adjacent (Thuringen and Czech-Republic) red deer populations (Fig. 1) were genotyped by 19 microsatellite loci¹.

Statistical Analysis: The program *fstat*² was used to calculate the classical population parameters n_p , A_R , H_e , and H_o . F_{IS} and N_e values were estimated based on the comparison of the likelihood for the equilibrium between gene flow and drift (gene flow model) versus an ancestral population fragmentation into independent units diverging purely by drift (drift model)^{3,4}(Tab1). The contribution of genetic variability of a particular population to the total population was analyzed based on the C_T - and C_{TR} -parameters⁵ (Fig. 3). Populations were spatially clustered according to genetic similarity using principle component (PC) analysis⁶. Interpolating the hypothetical PC1 scores by kriging-procedure from the actual sampling points at the 'nodes' of a regular grid that encompasses the entire sampling area allow to delineate any barriers to gene flow among the study populations (Fig. 2)⁷.

Results and conclusion

The classical intrapopulation indices revealed a slightly but significantly lower variability in the populations in Hassberge and Isarau compared to the other Bavarian red deer populations. The significant high F_{IS} (Tab. 1) and the low N_e values support the effect of random drift on the genetic structure of these populations and are useful for identifying populations for conservation. The PC1 contour plots as “Landscape genetic” methods revealed an isolated genetic structure of the populations Isarau and Hassberge and a considerable differentiation between north-western and southern populations. However, the population genetic indices as well as the contour plot did not indicate the genetic value of a particular population to the total population. Based on the C_T - and C_{TR} -values no population showed significant contribution of genetic variability to the total population variability. The population Isarau shows in both parameters some of the highest values of the contributions. This is due to its divergence as well as to its level of diversity from the other populations (differentiation component). The generally low levels, of C_T and C_{TR} are caused by the normally very high variability of microsatellites. Kimura and Crow (1963)⁸ have shown that although drift in subdivided populations could lead to inbreeding and local loss of alleles, total diversity will nevertheless be higher than in a single population of equal total size. Frankel (1974)⁹, however, was reluctant to conclude that many small reserves or populations are more efficient than few large ones. The discussion - referred to as SLOSS (single large or several small) - is still going on. It appears from our results that isolated populations of the Bavarian red deer may contribute more to total diversity than other populations, however, Millar and Libby (1991)¹⁰ suggest that it may not be the genetically distinct outlier populations that should rank highest but the core population from the centre of the species range, and that within-stand diversity may be qualitatively more important than the uniqueness of a population. The extraordinary genetic structure of the Bavarian red deer population mainly influenced by drift leads to the conclusion that each of the subpopulations are worth to be conserved. However, the population Isarau should be given top priority with respect to conservation.

Figure 1. Sampling locations of red deer in Bavaria and adjacent areas. See table 1 for definitions



Population	n	n _p	A _R	H _e	H _o	F _{IS}	N _e under drift model
1 NP Berchtesgaden (BG)	46	6,6	4,01	0,654	0,558	0,1205 ± 0,0203	218,2 ± 34,7
2 NP Bayerischer Wald (BW)	43	6,8	4,14	0,640	0,610	0,0871 ± 0,0144	301,0 ± 50,2
3 Isarau (FS)	34	4,3	3,06	0,527	0,497	0,3052 ± 0,0433	80,6 ± 11,6
4 Fichtelgebirge (SK)	75	6,2	3,84	0,636	0,599	0,1481 ± 0,0216	186,7 ± 27,7
5 Grafenwoehr (GW)	73	5,8	3,76	0,610	0,580	0,1500 ± 0,0242	176,8 ± 28,0
6 Armmengebirge (DA)	44	6,4	3,96	0,641	0,551	0,0936 ± 0,0182	281,8 ± 59,7
7 Spessart (SP)	16	5,2	3,94	0,648	0,502	0,1443 ± 0,0327	174,2 ± 40,5
8 Hassberge (HB)	12	4,2	3,57	0,581	0,503	0,2778 ± 0,0505	82,8 ± 18,0
9 Rhoen (RH)	10	4,2	3,66	0,645	0,574	0,2062 ± 0,0464	107,9 ± 23,9
10 Thuringer Wald (TC)	26	6,4	4,25	0,666	0,586	0,0938 ± 0,0180	242,9 ± 50,6
11 Böhmerwald (TS)	16	5,3	4,04	0,641	0,500	0,1451 ± 0,0265	163,7 ± 30,6

Table 1 Number of sampled animals (n) and alleles per locus (n_p), expected (H_e) and observed (H_o) heterozygosities, allelic richness (A_R), mean F_{IS} values (probability of allelic co-ancestry) calculated by 2MOD program³ and mean N_e values under the drift model based on diik1.2⁴ in studied Bavarian red deer populations over all loci.

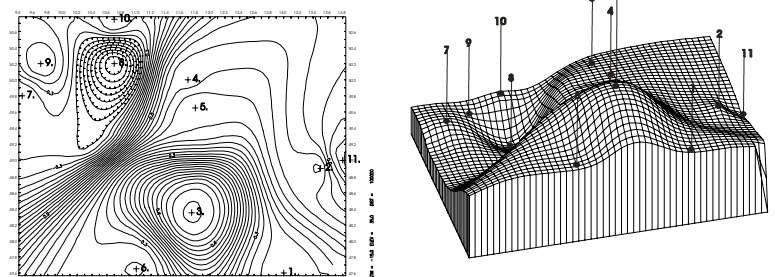


Figure 2 Contour plot showing the hypothetical first-axis principal-Component (PC1 scores derived from the kriging procedure) in A) two dimensions, and B) three dimensions for the area delimitating the sampled population given in Fig. 1. The lines connect points of equal PC1 score, and the actual sampling points are highlighted. The “genetic maps” indicate the populations Isarau (3) and Hassberge (8) as isolates. Considerable differentiation is detected between north-western and southern populations

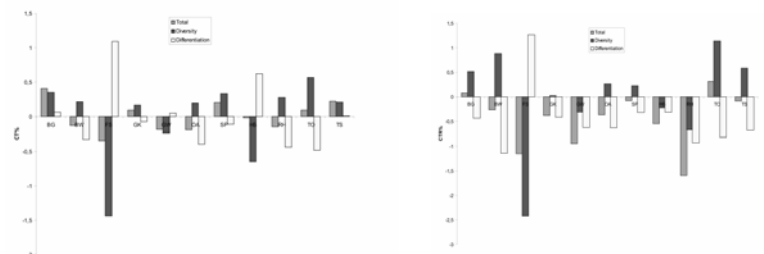


Figure 3 Contribution (CT%) to total diversity H_T and contribution (CTR%) to allelic richness A_R of each population of the Bavarian red deer, subdivided into a diversity and a differentiation component. See Table 1 for definitions of population abbreviations.

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