

# Constraints for re-establishing a meta-population of the European bison in Ukraine

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## Abstract

The European bison *Bison bonasus* had been extirpated from the present territory of Ukraine by late 18th century. Since its restitution initiated in mid-sixties of the 20th century, seven bison herds occur in lowlands, and four along the Ukrainian Carpathians. Initial genetic structure of a herd has been evaluated on the basis of pedigree records on founder animals available for seven herds. Low bison numbers in particular herds, and considerable distances among their home ranges, do not create favourable conditions for further development of the population and natural gene exchange. Due to limited natural linkage among present bison ranges, and impenetrable barriers fragmenting lowland Ukraine, the establishment of a viable meta-population would require an active population management including the monitoring of its genetic structure, enrichment of gene pool through exchange of animals among herds, and facilitation of contacts with free ranging bison in neighbouring countries – Byelorussia, Poland and Romania.

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## 1. Introduction

According to historical sources, the European bison *Bison bonasus* was a common game species in Ukraine until the 16th century, but from the late 17th century onwards its numbers dwindled as a result of over-hunting and agricultural development. The last records on the bison presence in the Ukrainian Carpathians come from 1762 and 1814. First attempts at its restitution were undertaken in the beginning of 20th century at Askania Nova Reserve and the Crimean Peninsula but failed because of acts of warfare (Turjanin, 1975; Nac'hlyk, 1992).

Recent reintroduction of the bison to Ukraine, initiated in 1965 in two sites had been continued until 1986, by establishing herds in seven other localities. Two other

herds were formed in 1992 and 1994 by spontaneous migrations. So far, Ukrainian reintroduction program has resulted in establishment of 11 scattered herds, which size in most cases fluctuates below 50 animals (Akimov et al., 2001) (Table 1).

Considerable distances among particular herds, their long time isolation, and very low effective reproductive numbers impel doubts about the future of that population.

In this study, the spatial distribution and genetic structure of present Ukrainian herds were analysed, in order to assess the chances of restoring a viable population of the European bison over its former natural range in Ukraine.

Discussed are the potentials for transboundary co-operation in conservation of the species on eco-regional scale and possibilities to maintain viable populations of rare large mammals in anthropogenically transformed environment.

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Table 1  
Basic data on origin and current numbers of the European bison in Ukrainian herds

Herd name in brackets location on map (Fig. 1)	Origin	Year of foundation	Number of founders (M/F)	Notes	Current number in herd (2001)	Pedigree available for founders
Bukovinskié/ Zubrovica (4)	Byelorussia/Russia	1970	23 (9/14)		148	✓
Cumanskié (6)	Byelorussia	1965	15 (6/9)		95	✓
Danivskié (10)	Russia	1980	12 (5/7)		70	✓
Konotopskié (11)	Zaliskié herd	1986	14 (4/10)	Additional 11 animals brought in 1993 from Zaliskié herd	31	✓
Lopatinskié (5)	Lithuania	1980	12 (7/5)		9	✓
Majdan	Byelorussia	1965	10 (4/6)	Split in 1992 into Rozlucz and Skole herds	0	✓
Nadvirnianskié (3)	Russia	1976	7 (??)		4	X
Podilskié (7)	Uladiivskié herd	1994	16 (??)	Migration	3	X
Rozlucz (1)	Majdan herd	1992	8 (??)	Migration from Majdan	14	X
Skole (2)	Majdan herd	1992	17 (??)	Migration from Majdan	16	X
Uladiivskié (8)	Cumanskié herd	1976	6 (??)	Migration from Cumanskié	85	X
Zaliskié (9)	Byelorussia	1967	8 (4/4)		12	✓

2. Study area, materials, methods

Ukraine with its area of over 600 thousand square km is the largest European country after Russia. Its population of over 51 million people is unevenly distributed, with only less than 30% of rural inhabitants and an average density of about 85 people per square km. The majority of the country consists of lowlands (former

steppe, below 300 m above sea level) with rich soils. These lowlands are therefore dominated by agriculture, with relatively low (about 18%) percentage of forests. The Carpathians – the only continuous, considerable mountain range in the country – cover just 37 thousand square km along its south-western border. Transportation routes (railroads, highways) connected with several major cities exceeding 1 million inhabitants (Kiev,



Fig. 1. Spatial distribution of free-ranging Ukrainian herds of the European bison and location of free ranging bison herds in neighbouring countries. See Table 1 for key.

Dnipropetrovs'k, Donetsk, Kharkiv, Odessa), and large rivers like Dniiper, Dnister, Boh, Donetsk or Desna make effective barriers for wildlife (Fig. 1).

Home ranges of the European bison in lowland Ukraine are dominated by oak and mixed oak-pine forests. In the Carpathians, prevail fir and beech stands with considerable admixture of spruce. In all lowland ranges, as well as in three Carpathian sites: Nadvirna, Skole and Rozlucz, damages to agricultural crops are recorded. That is connected with fairly low percentage of forests in Ukraine, and their relatively low carrying capacity for large herbivores, due to high percentage of coniferous stands, especially spruce monocultures.

In Europe, the *Bison bonasus* was completely extirpated from nature by the 20-ties of 20th century. Only 54 animals were left in zoological gardens or reserves and all of them can be derived from 12 founders. The species went through extreme bottleneck in the beginning of its restitution, and at present it is divided into two genetic lines; the Lowland line with seven founders and the Lowland–Caucasian line with all 12 founders' genotypes represented in gene pool (Slatis, 1960; Pucek, 1991; Olech, 1999).

Pedigree data for mutually related animals, were obtained from the European Bison Pedigree Book (EBPB), and from Ukrainian agencies. The gene dropping method (Lacy, 1989, 1995) was used to determine founder representation parameters. Inbreeding coefficients were calculated, and the relationship among groups deduced from the average kinship coefficient for every pair of herds (Olech, 1999).

Effective population size of each related group was calculated, corrected for mean inbreeding, and mean loss of heterozygosity in the first generation (Frankham et al., 2002). For comparison, founder representation parameters were calculated for the fully pedigreed captive European bison in the EBPB for 2000.

### 3. Results

#### 3.1. Distance and barriers among herds

The analysis of spatial distribution of European bison herds in Ukraine shows, that only in few cases, mutual

contacts are possible there through spontaneous migrations. That is the case of herds at Skole and Rozlucz formed by the division of Majdan herd, Uladivskie and Podilskie herds where such migration had occurred already leading to the creation of Podilskie herd, and finally among Danivskie and Zaliskie herds, however the latter is at the moment confined by fencing. In all those cases a minimal distance, measured along the straight line between neighbouring herds is about 50 km, and no impenetrable barriers preventing their movements occur. Cumanskie and Lopatinskie herds although situated only about 100 km apart are separated by densely inhabited and intensively used agricultural area, a major railway and a highway. Nearest distances among other herds in lowlands (Konotopskie–Danivskie, Zaliskie–Uladivskie, Podilskie–Lopatinskie), as well as between Carpathian herds and the most proximate Podilskie and Lopatinskie herds from lowlands, are longer than 100 km. Migrating animals would have to cross mostly open agricultural areas with many settlements, major communication routes and large rivers. The only theoretically possible open migration route remains for Carpathian herds, along mostly forested, south-western border of Ukraine (Fig. 1).

#### 3.2. Genetic structure

Due to the lack of pedigree information some animals were excluded from genetic calculations. This is a case of two males (numbers 4303 and 4383) of Lithuanian origin, released to Lopatinskie herd. Some animals used to create the Bukovinskie, Cumanskie and Majdan herds, not having complete pedigree data, were included in genetic analysis, but the true relation between them and any other animal could be underestimated because of those gaps in pedigree information. The values of inbreeding and kinship coefficients presented in Table 2, were computed after exclusion of those not fully pedigreed animals.

The genetic structure of herds, measured as founder contribution, in comparison with the structure of living contemporary in captivity Lowland–Caucasian animals, is presented in Table 3. Two founder Nos. 35 and 46 are not represented in any of Ukrainian herds. Animals released in all except one Ukrainian herd (Lopatinskie)

Table 2

The genetic relation measured by average kinship values between all European bison released to Ukrainian herds, except animals with incomplete pedigree data (C – Cumanskie, D – Danivskie, L – Lopatinskie, M – Majdan, B – Bukovinskie/Zubrovica, Z – Zaliskie herd)

Herd	C	D	L	M	B	Z
Cumanskie	0.263	0.230	0.220	0.240	0.220	0.241
Danivskie		0.290	0.277	0.221	0.293	0.253
Lopatinskie			0.449	0.217	0.267	0.254
Majdan				0.219	0.217	0.220
Bukovinskie/Zubrovica					0.301	0.238
Zaliskie						0.274

Values on the diagonal reflect the level of inbred in the first generation after release of a herd.

Table 3

The contribution of founders (%) in Ukrainian herds compared to contemporary captive herds of Lowland–Caucasian line (EBPB – European Bison Pedigree Book)

Herd	Founder number in EBPB											
	45	42	89	87	16	15	147	100	35	46	95	96
Cumanskie	31.30	23.59	10.39	10.34	6.07	6.08		3.04			3.10	6.09
Danivskie	38.88	26.75	9.20	9.14	4.01	4.04	0.06	1.98			1.96	3.97
Lopatinskie	43.11	35.27	8.51	8.43	2.35	1.14	1.20					
Majdan	29.66	23.64	10.35	10.41	6.52	6.40		3.28			3.30	6.44
Bukovinskie/ Zubrovica	35.78	26.92	9.04	9.04	4.92	4.82	0.08	2.35			2.35	4.69
Zaliskie	39.23	26.08	8.03	8.18	5.41	4.63	0.82	1.89			1.93	3.80
Captive animals of LC line (EBPB 2000)	23.07	18.09	11.77	8.98	8.20	7.55	0.52	7.10	3.24	1.26	3.80	6.41

originate from two Russian reserves (Prioksko-Terrasnyj and Okskij) and Byelorussia (Table 1). Those reserves were isolated for years from all foreign breeding centres. This one-way isolation of herds was very characteristic for European bison breeding in all countries of the region. This isolation has led to the present status quo – a great difference in genetic structure between Ukrainian herds and animals kept in captivity, mainly in Western Europe.

The structure of Ukrainian herds is strongly skewed with overrepresentation of two founders Nos. 42 and 45; in almost all herds the genes of this pair contribute to more than 60% of their genetic pool. This overrepresentation caused higher genetic similarity between herds as well as higher inbreeding and relationship within a herd. The contribution of one Caucasian subspecies founder No. 100 is generally very low compared to what is seen in captive herds. In the herd from Bukovina/Zubrovica the participation of the founder No. 100 is 2.35%, which is less than 35% of the value in captive herds. Only the representation of two founders Nos. 87 and 89 remain at the level very similar to that in the captive part of the world population (Table 3).

The herd Lopatinskie is of Lithuanian origin and those animals are of Lowland line having only seven founders (Slatis, 1960). Since, it would not be reasonable to keep this particular herd in isolation within the

country, it is included in our analysis. Therefore, despite the fact that the region has been declared as exclusive for Lowland–Caucasian line of European bison, this herd will be treated as an integral part of the Ukrainian population.

Two herds: Cumanskie and Majdan originating from Byelorussia, have relatively the best structure: the highest among all herds values of participation of founders characteristic only for Lowland–Caucasian line (Nos. 95, 96 and 100), however in both those herds the lack of founder 147 is observed.

Table 4 compares the values of retention of founders' genes in all herds in Ukraine and animals living now in captivity. Less than 10% of founders' genes (Nos. 95 and 100) are saved in Ukrainian herds, for founder No. 147 that value is even twice smaller. The retention of founder No. 100 genes in captivity exceeds 60%, i.e., a value 7–10 times higher than the average for Ukraine. In comparison with captive herds only a part, for some founders very small, of genetic pool is saved in Ukrainian herds. However, due to different origin of those herds the total value of retention of founders' genes in Ukrainian population is higher than in particular herds.

Table 5 presents the summarised genetic characteristics for all Ukrainian herds. The mean value of retention of founders' genes in every Ukrainian herd is very low,

Table 4

The retention of founders' genes (%) in Ukrainian herds compared to captive herds of Lowland–Caucasian line (EBPB – European Bison Pedigree Book)

Herd	Founder number in EBPB											
	45	42	89	87	16	15	147	100	35	46	95	96
Cumanskie	70.0	50.6	34.7	34.7	17.9	17.9		8.9			9.2	17.9
Danivskie	77.6	53.4	32.2	31.9	14.0	13.6	0.8	6.4			6.5	12.8
Lopatinskie	65.6	47.6	19.6	19.3	7.9	3.9	4.0					
Majdan	63.6	49.2	34.6	34.9	18.4	18.1		9.2			9.3	18.1
Bukovinskie/ Zubrovica	75.8	54.4	39.3	39.4	20.4	18.8	1.1	8.6			8.8	17.4
Zaliskie	69.4	48.5	25.2	25.7	19.8	15.7	4.6	5.8			5.9	11.7
Captive animals of LC line (EBPB 2000)	92.2	66.3	81.2	66.2	78.5	71.0	25.3	62.6	43.4	26.2	33.8	56.8

Table 5

Genetic characteristic of Ukrainian herds compared to captive Lowland–Caucasian line (C – Cumanskie, D – Danivskie, L – Lopatinskie, M – Majdan, B – Bukovinskie/Zubrovica, Z – Zaliskie herd)

Genetic parameters of a herd	C	D	L	M	B	Z	Captive LC line
Number of founders	9	10	7	9	10	10	12
Mean retention of founders' genes	0.291	0.249	0.240	0.284	0.284	0.232	0.586
Founder genome equivalents	1.743	1.552	1.049	1.768	1.645	1.522	3.102
Retained fraction of source gene diversity	0.713	0.678	0.523	0.717	0.696	0.671	0.839
Mean inbreeding coefficient	0.172	0.298	0.427	0.243	0.219	0.251	0.214
Effective size of released group ( $N'_e$ )	12.3	9.0	8.2	7.7	18.0	6.4	–
Loss of diversity in first generation for above $N'_e$ (%)	4.1	5.5	6.1	6.5	2.8	7.8	–

being at least twice smaller than the average value for captive herds in year 2000. In a consequence, also the fraction of diversity retained is lower, ranging between 52.3% in Lopatinskie and 71.7% in Majdan herd. The effective size of released group was rather small, only in Bukovinskie herd its value was above 20. The consequence of such bottleneck in the moment of herd creation is a very rapid decrease of diversity. In a majority of herds, predicted values of heterozygosity loss in the first generation are around 5.5%.

The highest value of inbreeding was for animals that created the Lopatinskie herd, all coming from Lithuania and belonging to Lowland line, that originated from seven founders only, comparing to 12 founders of the Lowland–Caucasian line.

The lowest value of inbreeding was for animals released in Cumanskie herd. The source of those animals was Byelorussia the same as for Majdan herd. Probably only by chance those two groups of animals have different values of inbreeding coefficient. The other genetic parameters for those two herds are very similar. In both herds, the fraction of diversity retained is above 70%, and the founders' contribution is less skewed than in other herds (Table 4).

## 4. Discussion

### 4.1. Population dynamics

According to Akimov et al. (2001), numbers of bison in newly established herds were low, between 6–19 animals (12 on average). Herds grew up until the mid-nineties when they started to decrease. This tendency was especially well visible in largest herds, so in an effect the whole bison population in Ukraine has decreased considerably in last several years.

Present bison population in Ukraine now being below 500 animals, is divided into 11 herds counting between 3 and 148 individuals (Table 1). Only in Cumanskie, Danivskie, Uladivskie and Bukovinskie herds the number of animals in a herd exceeds 50. Podilskie and Nadvir-

nianskie herds have dwindled to a critical level (respectively, 3 and 4 individuals) threatening their further existence. At present population, male:female ratio is 1:1.4 with only 9% of calves, and 40% of animals older than 10 years. Comparing to long term data obtained for free ranging populations in north-eastern Poland (Biaerrorowicza: 14.2–16.1% of calves, and 22% of animals older than 10 years, and Borecka Forest: 12.1% of calves), those data are quite alarming, however in bison reserves no direct evidence on age related decrease in fecundity of females has been found so far (Kraśiński and Raczyński, 1967; Kraśiński, 1978; Kraśiński and Kraśińska, 1992; Akimov et al., 2001).

Unfavourable age structure in contemporary Ukrainian population of the European bison, may contribute to further decline of bison numbers (mainly resulting from poor management), and considerably increase the degree of inbred, especially in smaller herds. Ageing of the population and decreasing numbers reduce also chances for natural migrations, allowing for contacts among herds and mutual gene exchange. Additionally, fairly common poaching can minimise chances for a successful migration and negatively influences the survival of calves. Population structure appears then an important factor to consider while assessing chances for successful restitution of an endangered species. Apart from using for introduction optimally composed groups of animals, a continuous monitoring of population structure and its subsequent active corrections are necessary.

### 4.2. Spatial distribution

The assessment of distances among existing bison herds in Ukraine, and an importance of barriers (large rivers, major railroads and highways, densely populated areas) has proved that only few herds have a chance for an exchange of individuals through natural migrations. Occasionally however, as it has happened in case of Polish herds, in favourable conditions some solitary males could migrate up to distances longer than 100 km (Leszczyńska, 2003). Such possibility exists mostly in the

Carpathians, which appear to be the major potential migrating route for all species of large mammals in Central and Eastern Europe (Webster et al., 2001). Some chances for preventing further inbred and genetic isolation in a natural way are there for two small herds situated close to Polish border (at Skole and Rozlucz), and one herd living at the border with Romania (Bukovina), where in a near future planned is a major reintroduction program. Recent extension of the Eastern Carpathian Biosphere Reserve and subsequent international agreements have created a real potential for establishing a linkage between Polish herds, western Ukrainian herds and a free ranging herd being established in Slovakia, which would produce a spatially continuous bison sub-population over 200–300 km along the Carpathians. Further reintroduction in Ukrainian Carpathians could be planned towards east, to establish a linkage with already existing herds at Nadvirna and Bukovina (Fig. 1).

Bison herds in lowland Ukraine though, are spatially separated by hundreds of kilometres of densely populated, agricultural and industrialised area. Only Cumanian herd in north-western part of the country is close enough to ranges occupied by free ranging bison in Byelorussia, to design a possible migration corridor, allowing for their mutual contact through forested in over 50% Polesje region. Therefore, chances to plan a continuous population of the European bison in Ukrainian lowlands are minimal. The best solution there seems the maintenance of bison numbers at the level preventing an imminent threat of an inbred and genetic drift.

In general then, for lowland Ukrainian herds seems to be no other future, but their further physical isolation, due to impenetrable barriers like large rivers, dam reservoirs (e.g., river Dniper), major highways or railroads, and vast areas of intensive agriculture or dense settlements. The only prospective management measure, preventing further inbred and loss of genetic variability is the periodic supplementing of those herds with animals selected towards an improvement and enrichment of gene pool, allowing them to maintain genetic diversity, and assure their viability in the long term perspective. The present, low retention of founders' genes results from the isolation of herds, and could be improved through the reintroduction of animals of other origin. Fortunately, animals living in zoos and reserves throughout the Europe, retain much higher proportion of founders' genetic pool.

The case of the European bison in Ukraine can be then a good example of a threatened large mammal in contemporary Europe, where due to the fragmentation and loss of natural habitats, small scattered sub-populations have no chances for a natural exchange of genes. Therefore the viability of such populations depends on active conservation including the monitoring of genetic

structure and subsequent supplementation of lacking or underrepresented genomes.

#### 4.3. Genetic structure

A comparison of the founder parameters of the animals which initially formed the Ukrainian herds with animals actually living in captivity is very interesting. In captive population, the value of founder genome equivalent is almost than twice higher, and the fraction of diversity retained is at least by 12% higher than in the best Ukrainian herd. A similar situation was already shown by Belousova (1999) for Russian herds of the European bison.

Those figures indicate a critical genetic condition of Ukrainian herds and need for their substantial enrichment. Fortunately an adequate source for improvement of genetic stock are bison kept in European breeding centres.

Table 2 shows, how the average inbreeding coefficients of the population in the first generation after release, are higher than the average kinship coefficients between the different populations. This reflects the relatively close pedigree relationships within each released group. Despite the high kinships among the released groups, an exchange of animals among today's herds is recommended. Those herds being isolated geographically and genetically for 3–5 generations, are now much less related than at the moment of herd creation. The genetic status of present herds could be checked using genetic markers like DNA or protein analysis. This methodology is very useful for the estimate of genetic variation within and between groups (Scribner, 1993). Moreover, the results of DNA analysis could be combined with pedigree data, to improve the ability to determine animal's relationship (Jones et al., 2002).

The number of herd founders in Ukraine, lower than the average value for world population, could have resulted in demographic stochasticity, and additional effects of inbreeding depression. This may increase the probability of group extinction either due to lowered fitness, or higher mortality of calves being the progeny of related parents – the latter has been already proved in Lowland–Caucasian line of the European bison (Ballou and Lacy, 1995; Keller and Waller, 2003; Olech, 1998).

Improvement of Ukrainian herd network can be done through an enrichment of their gene pool by introduction of animals from captivity. Such procedure has been recommended in many management programs (Ralls and Ballou, 1992; Kleiman, 1996). In the United States 64% of 314 recovery plans included this approach (Tear et al., 1993). Bouman (2000) has demonstrated that in the reintroduction project of Przewalski horses *Equus przewalskii* released groups were carefully chosen towards equalizing the contribution of all founders. As an example also the Alpine ibex *Capra ibex*, which popu-

lations were created via translocation, could be given, as well as a reintroduction into wild the Guam rails *Rallus owstoni*, as a part of their conservation program (Haig et al., 1990; Scribner and Stüwe, 1994). The captive-reared animals were used for augmenting endangered bighorn sheep *Ovis canadensis* in California (Ostermann et al., 2001). Similar pedigree analysis was also performed for reintroduction programs of California condor *Gymnogyps californianus* and golden lion tamarin *Leontopithecus rosalia* (Ballou and Lacy, 1995). The European bison is among few species, including Arabian oryx *Oryx leucoryx* or American bison *Bison bison*, where such approach was successful (Kraśniński, 1967; Snyder et al., 1996; Perzanowski and Paszkiewicz, 2000). The situation of European bison is however exceptional, because the species has been restored from known founders, and all free-living herds are of captive origin.

In Ukraine, in most cases natural exchange among herds is impossible because of geographic distance and barriers. Therefore a solution would be to create a meta-population there, through facilitating spontaneous migrations where conditions are favourable, while otherwise by arranging for a periodical exchange of individuals (Hanski and Gilpin, 1996).

Selection of optimal strategy for introduction programs depends mostly on available source of suitable animals (viable wild populations or captive stock) and the diversity of existing genetic pool (Ballou and Lacy, 1995). In case of the European bison, introductions so far are based only on animals bred in captivity, and since their genetic diversity is among the lowest reported for large mammals, the choice of selection pattern and subsequent genetic management is extremely limited (Olech, 1987; Hartl and Pucek, 1994; Tiedeman et al., 1998).

All Ukrainian herds require careful management regarding their level of genetic variability, which can be assessed now only upon an information from European Bison Pedigree Book. However, because mating patterns in free ranging herds could not be precisely followed, and therefore the actual level of genetic variation and contemporarily dominating genotypes are not known, a study on a present degree of genetic variability should be performed for making a better decisions on supplementing those herds with a “fresh blood”. The most important general rule seems to be at the moment the principle adopted and carefully observed in Poland, to keep separately the bison of pure Białowieża lowland line from those with an admixture of Caucasian blood. In practice, it is done by restricting the Lowland–Caucasian line to sites in the Carpathians, while leaving all suitable lowland sites for descendants of Białowieża bison, as it is proposed in species Action Plan (Pucek, 2002).

Difficulties encountered by the restitution program for European bison in Ukraine are typical for any effort to re-establish a large mammal over a part of its former

natural range in contemporary Europe. Apart from habitat transformation and fragmentation, making impossible the reconstruction of a continuous home range of the species, irreversible reduction of gene pool makes necessary a precise monitoring of a genetic structure of introduced population. That is indispensable for the maintenance of possibly the highest genetic diversity and planning for an improvement of gene pool. Since a natural way, to maintain such populations above the minimal viable numbers is rather impossible due to the lack of adequate space, the only realistic approach seems to be to design a meta-population of a species, composed of family groups occupying optimal habitat patches with sufficient carrying capacity. To assure functionality of such meta-population an exchange pattern of individuals should be prescribed in order to prevent the loss of genetic diversity and inbred related effects. According to recommendations of Mills and Allendorf (1996), that ought to be done with rate of at least one animal per generation.

#### 4.4. Recommendations for the management of European bison in Ukraine

The management plan aimed towards saving or increasing genetic diversity should be performed in two stages. The first one, that can be implemented on the basis of present knowledge, would be to enrich Ukrainian herds with animals bearing genes of lacking (Nos. 35, 46) and considerably underrepresented founders (Nos. 95, 100, and 147), to retain possibly the highest degree the original genetic composition of the population just after the bottleneck. To design such enrichment necessary is information about the structure of Ukrainian herds at the moment of their creation and pedigree data about animals from present captive herds. Possible source of animals with desired ancestry are zoos and bison reservations in western European countries, mainly the Germany.

The second stage of genetic management should be based on possibly precise information about the present genetic status of particular herds. Our knowledge on genetic structure is limited to the moment of introduction, whereas we have no data on further mating patterns, or individual reproduction success. Therefore there is an urgent need for a study (most likely based on DNA analyses of randomly collected hair samples from each locality) to determine a genetic structure of all herds and genetic distance among them. That should allow for identification both the allelic diversity and heterozygosity within herds. Subsequently, the more precise exchange of animals between herds, and the proper choice from the captive stock could be made.

Because especially lowland bison herds in Ukraine are effectively isolated from each other, they should be considered as components of a metapopulation that requires

active management. This ought to include a periodic monitoring and subsequent improvement of genetic structure through prescribed introductions from captivity and in future an exchange of 1–3 animals in every 6–8 years between herds, to prevent the loss of genetic variability and an increase of inbred within every herd.

On the one hand then, important is to supplement present herds with genetic material of lacking founders, and after the analysis of DNA structure – precise enrichment of the genome with still lacking or underrepresented alleles, because in that way increased will be the allelic variability. The other way of action is to minimise the rate of inbred by creating a metapopulation where an exchange of individuals could happen either in a natural way or through facilitated migrations and transfer of animals. Such metapopulation with maintained gene flow should have much slower loss of heterogeneity (Lacy and Lindenmayer, 1995; Lindenmayer and Lacy, 1995; Hedrick and Gilpin, 1997).

Herds inhabiting mountains still have a chance to become linked to pan-Carpathian free-ranging population. This is most likely under the umbrella of international program for the restitution of the European bison population in the Carpathians that includes also Poland, Romania, and Slovakia. Especially important is close co-operation on this issue with a Romanian program initiated fairly close to the largest Ukrainian herd at Bukovina (Olech and Perzanowski, 2002).

In all cases, appropriate measures should be undertaken to minimise possible conflicts with forestry and agriculture, including the assessment of maximal carrying capacity for the bison within every home range of a herd, to be able to set a limit for an acceptable number of animals. Present management of herds should be improved especially towards elimination of excessive mortality.

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## References

- Akimov, I., Kozak, I., Kryzanovskij, V., Perzanowski, K., 2001. Long-term population records – a crucial factor for the success of the re-establishment of European bison (*Bison bonasus*) population in Ukraine. *Ekologia – Bratislava* 20 (Suppl. 2), 57–62.
- Ballou, J.D., Lacy, R.C., 1995. Identifying genetically important individuals for management of genetic variation in pedigreed populations. In: Ballou, J.D., Gilpin, M., Foose, T.J. (Eds.), *Population Management for Survival and Recovery: Analytical Methods and Strategies in Small Population Conservation*. Columbia University Press, New York, pp. 76–111.
- Belousova, I.P., 1999. Znachenie i otsenka pokazatelej geneticheskogo raznoobrazija dlja reshenija problemy sokhraneniya evropejskogo zubra. Prioksko-Terrasnyj gosudarstviennyj biosfernyj zapovednik. Pushchino, 1–104 (in Russian).
- Bouman, I., 2000. The reintroduction of Przewalski horses in the Hustain Nuruu mountain forest steppe reserve in Mongolia an integrated conservation development project. *Gazella (Zoo Praha)* 27, 27–51.
- European Bison Pedigree Book. 1947–1973. Żabiński, J. (Ed.); 1974. Krysiak, K. (Ed.); 1975–1984. Pilarski, W. (Ed.); 1992–1998. Raczyński, J. (Ed.); 1947–1971. PWN Warsaw; 1972–1991. PWRiL Warsaw; 1992–1998. BPN Białowieża.
- Frankham, R., Ballou, J.D., Briscoe, D.A., 2002. *Introduction to Conservation Genetics*. University Press, Cambridge.
- Haig, S.M., Ballou, J.D., Derricksen, S.R., 1990. Management options for preserving genetic diversity: reintroduction of Guam rails to the wild. *Conservation Biology* 4, 290–300.
- Hanski, I., Gilpin, M.E. (Eds.), 1996. *Metapopulation Biology: Ecology, Genetics and Evolution*. Academic Press, London.
- Hartl, G.B., Pucek, Z., 1994. Genetic depletion in the European bison (*Bison bonasus*) and the significance of electrophoretic heterozygosity for conservation. *Conservation Biology* 8, 167–174.
- Hedrick, P.W., Gilpin, M.E., 1997. Genetic effective size of a metapopulation. In: Hanski, I., Gilpin, M.E. (Eds.), *Metapopulation Biology, Ecology, Genetics and Evolution*. Academic Press, San Diego, pp. 65–180.
- Jones, K.L., Glenn, T.C., Lacy, R.C., Pierce, J.R., Unruh, N., Mirande, C.M., Cavez-Ramirez, F., 2002. Refining the Whooping Crane studbook by incorporating microsatellite DNA and leg-banding analyses. *Conservation Biology* 16, 789–799.
- Keller, L.F., Waller, D.M., 2003. Inbreeding effects in wild populations. *Trends in Ecology and Evolution* 5, 230–241.
- Kleiman, D.G., 1996. Reintroduction programs. In: Kleiman, D.G., Allen, M.E., Thompson, K.V., Lumpkin, S. (Eds.), *Wild Mammals in Captivity: Principles and Techniques*. The University of Chicago Press, Chicago and London, pp. 297–305.
- Krasiński, Z., 1967. Free-living European bison. *Acta Theriologica* 12, 391–405.
- Krasiński, Z., 1978. Dynamics and structure of the European bison population in the Białowieża Primeval forest. *Acta Theriologica* 23, 3–48.
- Krasiński, Z., Krasińska, M., 1992. Free ranging European bison in Borecka forest. *Acta Theriologica* 37, 301–317.
- Krasiński, Z., Raczyński, J., 1967. The reproduction biology of European bison living in reserves and in freedom. *Acta Theriologica* 12, 407–444.
- Lacy, R.C., 1989. Analysis of founder representation in pedigrees: founder equivalents and founder genome equivalents. *Zoo Biology* 8, 111–123.
- Lacy, R.C., 1995. Clarification of genetic terms and their use in the management of captive populations. *Zoo Biology* 14, 565–578.
- Lacy, R.C., Lindenmayer, D.B., 1995. A simulation study of the impacts of population subdivision on the mountain brushtail possum *Trichosurus caninus ogilby* in south-eastern Australia. II. Loss of genetic variation within and between subpopulations. *Biological Conservation* 73, 131–142.
- Leszczyńska, A., 2003. Perspektywy hodowli żubrów w Puszczy Boreckiej. Master Thesis, Agricultural University of Warsaw, pp. 1–57 (in Polish).
- Lindenmayer, D.B., Lacy, R.C., 1995. A simulation study of the impacts of population subdivision on the mountain brushtail possum *Trichosurus caninus ogilby* (phalangeridae: marsupialia) in south-eastern Australia. I. Demographic stability and population persistence. *Biological Conservation* 73, 119–129.



- Mills, L.S., Allendorf, F.W., 1996. The one-migrant-per-generation rule in conservation and management. *Conservation Biology* 10, 1509–1518.
- Nachlyk, A., 1992. Pro transilwanskjho zuba. *Lisove gospodarstvo, lisowa, papirowa i derewoobrobna promyslowist' 2*, 22–27 (in Ukrainian).
- Olech, W., 1987. Analysis of inbreeding in European bison. *Acta Theriologica* 32, 373–387.
- Olech, W., 1998. The inbreeding of European bison (*Bison bonasus* L.) population and its influence on viability. In: Proceedings of the 49th Meeting of the EAAP, Warsaw, p. 26.
- Olech, W., 1999. The number of ancestors and their contribution to European bison (*Bison bonasus* L.) population. *Annales of Warsaw Agriculture University, Animal Science* 35, 111–117.
- Olech, W., Perzanowski, K., 2002. A genetic background for reintroduction program of the European bison (*Bison bonasus*) in the Carpathians. *Biological Conservation* 108, 221–228.
- Ostermann, S.D., Deforge, J.R., Edge, W.D., 2001. Captive breeding and reintroduction evaluation criteria: a case study of peninsular bighorn sheep. *Conservation Biology* 15, 749–760.
- Perzanowski, K., Paszkiewicz, R., 2000. Restytucja i współczesny stan populacji żubrów w Bieszczadach. *Monografie Bieszczadzkie* 9, 219–229 (in Polish).
- Pucek, Z., 1991. History of the European bison and problems of its protection and management. In: Bobek, B., Perzanowski, K., Regelin, W. (Eds.), *Global Trends in Wildlife Management*. Świat Press, Kraków–Warszawa, pp. 19–39.
- Pucek, Z. (Ed.), 2002. European bison: current state of the species and an action plan for its conservation. *Species Action Plan, LHI – WWF*, p. 59.
- Ralls, K., Ballou, J.D., 1992. Managing genetic diversity in captive breeding and reintroduction programs. In: *Transactions of 57th North American Wildlife and Natural Resources Conference*, pp. 263–282.
- Scribner, K.T., 1993. Conservation genetics of managed ungulate populations. *Acta Theriologica* 38 (Suppl. 2), 89–101.
- Scribner, K.T., Stuwe, M., 1994. Genetic relationships among Alpine ibex *Capra ibex* populations re-established from a common ancestral source. *Biological Conservation* 69, 137–143.
- Slatis, M.A., 1960. An analysis of inbreeding in the European bison. *Genetics* 45, 275–287.
- Snyder, N.F., Derrickson, S.R., Beissinger, S.R., Wiley, J.W., Smith, T.B., Toone, W.D., Miller, B., 1996. Limitations of captive breeding in endangered species recovery. *Conservation Biology* 10, 338–348.
- Tear, T.H., Scott, J.M., Hayward, P.H., Griffith, B., 1993. Status and prospects for success of the Endangered Species Act: a look at recovery plans. *Science* 262, 976–977.
- Tiedemann, R., Nadlinger, K., Pucek, Z., 1998. Mitochondrial DNA-RFLP analysis reveals low levels of genetic variation in European bison *Bison bonasus*. *Acta Theriologica* 30 (Suppl. 5), 83–87.
- Turjanin, I.I., 1975. Ungulates of USSR fauna. *Ekologiczesknei osobennosci i sowremennoe sostojanie karpatskich populacij dikich parnokopytnych. Kopytnyje fauny SSSR, Moscov*, pp. 26–27. (in Russian).
- Webster, R., Holt, S., Avis, C. (Eds.), 2001. *The status of the Carpathians. WWF – The Carpathian Ecoregion Initiative Report*, 67pp+CD.