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PODOLIC CATTLE IN THE UKRAINE AND EASTERN TERRITORIES

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Introduction

Industrialization of cattle breeding inevitably leads to a decrease in animal variability. The sizes of herds of local cattle continuously decrease. This is induced by wide use of specialized breeds of cattle that are adapted to industrial technologies. Nevertheless, it is well known that development of new breeds, types, and lines of animals is impossible without hereditary diversity. Unique genes and gene complexes of populations of local breeds increase efficacy of breeding. Most local breeds are characterized by valuable hereditary traits developed in them in the course of evolution. These unique complexes of genetic systems are necessary in modern breeding. This is why the preservation and utilization of local breeds in breeding is an up to date problem. Due to special biological features, the rate of reconstruction and perfection of gene pools of breeds via the methods of breeding is low, and such gene pools are used for a long time. This is why genes that were eliminated in the course of selection could be lost forever (Glazko 1994). Of 19 local breeds of cattle that were bred on the territory of the former USSR, herds of 13 breeds are quite small. Ukrainian Gray cattle is one such unique aboriginal breed, whose numbers have declined to a critical level.

The major problem of gene pool preservation in local breeds of limited stocks is the preservation of the set of genes that determine their specific features. For the Ukrainian Gray cattle, it is important to avoid a decrease in genetic variability and to preserve qualitative and quantitative traits that are characteristic of this breed. It is also important to preserve high genetic diversity in the herd.

The comparative analysis of phenotypic characteristics, polymorphism of blood groups, and genetic-biochemical systems was conducted for some years

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for groups of Ukrainian Gray cattle that were bred both in the Ukraine and Russia. The data on special features in the genetic structure of this breed and intrabreed differences in space and time are considered. The comparative analysis of genetic differentiations between three species of Bovinae, domestic cattle, European bison and American bison using different types of molecular genetic markers. Studies of genetical-biochemical (35 loci) and DNA markers (RAPD-PCR, ISSR-PCR) were carried out. It was shown that the evaluation of interspecific genetic relations was connected more with the identified molecular-genetic markers (loci) included in the analysis, than with the markers characteristic of a certain type (protein polymorphism, variability of DNA repeat distributions).

Material and Methods

We conducted an investigation of the genetic structure of the remaining population of Gray cattle in the Ukraine and Russia. Cattle of the Ukrainian Gray type were represented by several groups. The first one involved animals bred in the experimental farm of Polivanovka (680 animals in 1975 and 197 animals in 1985). The second group involved animals bred in Askaniya-Nova (1990, 1994, 1999). The third group involved animals that were delivered to Cherga (Altayskii Kray) in 1982 from Askaniya-Nova (125 animals) and their progeny (32 animals).

Forty samples were collected from two groups of European bison (*Bison bonasus* L. 1758) were analyzed from the reservation of Askania-Nova (Ukraine) and Prioksky's reserve (Russia). Ten additional samples were taken from American bison (*Bison bison* L. 1758) in Askania-Nova.

Blood for the investigation was taken from the jugular vein of animals into tubes containing heparin (25 MU per 1 ml of blood). Erythrocytes were separated from the plasma by centrifuging: They were washed three times with physiological solution and destroyed with sawing-melting. Electrophoresis in vertical slabs of polyacrylamide gel and horizontal slabs of 13% starch gel with subsequent staining according to the commonly used procedures was used for analysis of polymorphism of loci (Glazko 1988; Gahne, Juneja and Crolmus 1977). We analyzed the polymorphism of 35 loci encoding the following serum proteins:

ceruloplasmine (CP), amylase-1 (AM-1),
transferrin (TF), post-transferrin-1 (pTF-1),
post-transferrin-2 (pTF-2),
post-transferrin-3 (pTF-3),

D-vitamin receptor (GC),
hemoglobin (HB).

We also analyzed polymorphisms of isozymes of erythrocytes and tissues:

carboanhydrase (CA), (E. C. 4:2. 1. 1)
phosphoglucomutase 1(PGM i), (E. C. 2. 7. 5. 1)
catalase (CAT), (E. C. 1. 11. 1. 6)
peptidase A, B, S (PEP A, B, S), (E. C. 3. 4. 11. or 13)
peptidase D (PEP D), (E. C. 3. 4. 13. 9)
purin nucleoside phosphorylase (NP), (E. C. 2. 4. 2. 1)
aspartate-aminotransferase-1 (GOTI), (E. C. 2. 6. 1. 1)
6-phospho-gluconate-dehydrogenase (6PGD), (E. C. 1. 1. 1. 44)
hexokinase (HK), (E. C. 2. 7. 1. 1)
creatinkinase (CK), (E. C. 2. 7. 3. 2)
adenylate kinase (AC), (E. C. 2. 7. 4. 3)
glucoso-6-phosphate-dehydrogenase (G6PD), (E. C 1. 1. 1. 49)
glucosophosphate-isomerase (HPI), (E. C. 5. 3. 1. 9)
syperoxide dismutase (SOD), (E. C. 1. 15. 1. 1)
malate dehydrogenase (MDH), (E. C. 1. 1. 1. 37)
malic-enzyme (ME), (E. C. 1. 1. 1. 40)
lactate dehydrogenase (LDH), (E. C. 1. 1. 1. 27)

To detect the electrophoretic variants, different buffer solutions or their combinations described in the literature (Glazko 1988; Gahne, Juneja and Crolmus 1977) as well as our modifications of these buffers were used. Data were mathematically processed (genetic distances were calculated according to Nei, gene equilibrium was calculated according to the Hardy-Weinberg law, cluster analyses were also conducted). The calculations were performed using the standard computer software, BIOSYS-1.

Antigens of erythrocytes were tested using hemolytic methods based on 62 antiserum reagents, unified in international comparative tests.

Nuclear DNA extraction from blood cells was based on a standard technique (Ausubel et al. 1997; Zietkiewicz, Rafalski and Labude 1994).

The RAPD-PCR method was applied using two primers. This primary sequence was published by E. Bailey and T. Lear (1994): UBC-85: 5'-GTGCTCGTGC-3' and UBC-126: 5'CTTTCGTGCT-3'. It was amplified in the DNA region included between direct and inverted sequences, complementary to the primer.

The reactive mix of the volume 20 mkl contained: 50 MM KC1, 10 mM TRIS-HC1 (pH 9.0), 0.01% triton X-100, 0.3 mM everyone of dNTP, 2 mM MgC12 (Promega), 0.2 mM primers, 1 ed. act. polymerase Thermus aquaticus ("Dialat LTD", Moscow), 20-50 ng DNA.

PCR was carried out on a "Master Cycler Gradient" (Germany) thermocycler. During the application of the RAPD-PCR method, the temperature cycles included the following: 5 cycles - 1 mun at 92°C, 1 min at 35°C, 2. 5 min at 72°C; 35 cycles - 1 min at 92°C, 1 min at 42°C, 2. 5 min at 72°C (in summary 40 cycles).

The ISSR-PCR reaction (Zietkiewicz, Rafalski and Labude 1994) was carried out by the following temperature regime: initial denaturation - 2 min at 94°C; 30 cycles: 30 sec at 94°C, 30 sec at 55°C, 2 mines at 72°C; terminal elongation - 10 min at 72°C; cooling down to 4°C.

The amplification's products were divided by electrophoresis on 1.5% agarose gels. Visualization of amplification products in gels was carried out under ultra-violet radiation on a transilluminator, after having colored the gels by ethidium bromide. Only those amplificatiom products were considered which had reproduced in 3-5 during the independently repeated PCR-procedures and represented DNA from the same animals. The sizes of amplification products were defined using the marker molecular weight 0.1-kb DNA Ladder (Gibco BRL) on each of the gels used.

Results and Discussion

The origins of the breed

The Ukrainian Gray cattle is a result of a long evolution and folk selection. It originates from the wild cattle, aurochs (*Bos primigenius* Bojanus 1827) which became extinct in the 17th century. The Ukrainian Gray breed is characterized by a unique genetic complex. During the course of evolution it was not crossed with other breeds. The Ukrainian Gray cattle is thus a plentiful source of valuable genetic material for breed development.

The influence of soil, climatic, and other conditions of the South of Ukraine, on the one hand, and the folk selection on the other, have resulted in the exclusive endurance, good meat productivity characteristics and low milk yields. When provided with fodder, the Ukrainian Gray cattle can withstand the hot steppe summer as well as the cold winter. They are kept outdoors throughout the year. This is why these animals were indispensable in small peasant farms and were the most frequent breed in the Ukraine up to the beginning of the 20th century (Rode and Acebain 1886; Pahornov 1909; Leopol'dov 1924; Zorin 1951; Shnirelman 1980; Aisner 1986; Godonanets 1986; Stolpovskii et al.1999).

The Ukrainian Gray breed derived from the Gray Steppe cattle known as the Podol breed. It was common in the Southern part of the European continent, the steppe zone of the Mediterranean region and the Black Sea region. The replacement of the Ukrainian Gray breed with productive breeds started during the 19th century. The development of horse breeding has led to the replacement of the bullock with the horse. This is the period when the crisis for the breed started.

The Ukrainian Gray cattle, developed by folk selection, was well consolidated. The direction for productivity towards an improvement in milking features took a long time to change. This was the basis for the development of productive native breeds such as: Simmentals, Brown Carpathian, Red Steppe, and Lebedinskaya breeds. This has resulted in a decline in the number of cattle.

External traits

The color of the cattle is gray with variations ranging from almost white or silver, through gray-yellow to dark-gray and black (Figure 1). Bulls are significantly darker than cows. Dark almost black "spectacles" around the eyes and the dark "belt" (or light one if the color of the animals is black) along the back are chacacteristic. Dark patterns could be observed on the breast, the neck, shoulders, forelimbs, the belly, and in the groin region (especially in bulls). The hair in the ears is gray, dark-gray, and red-yellow. The ear's margin is black. The tail brush is dark, sometimes turning gray. The color of newborn calves is mostly red. However red-gray animals could be observed: A gray color in the young is infrequent (Table 1, Figure 2). After the first molting at the age 4-6 months, the color gradually turns into th color of sexually mature animals. The color of the Ukrainian Gray breed is recessive or of an intermediary type of inheritance regarding other cattle colors (crossings with the Red Steppe, Kostroma, Brown Swiss, and Blonde d'Aquitaine breeds).

The skin of the Ukrainian Gray breed is dark or black. The color of the muzzle, eyelid mucosa, tongue, palate, anus, the sexual loop of cows, the low margin of testes, and the tips of the horns is the same. Unpigmented skin is characteristic of the space between thighs, on the scrotum, on the udder, the ears, and under the lips.

Figure 1. - HEAD COLOR

Light gray hair on the frontalpart, botton part dark (B8), mask around the eyes, black "spectacles" (C3), black edging on the ears (D1), curl on the forehead (-,F2)

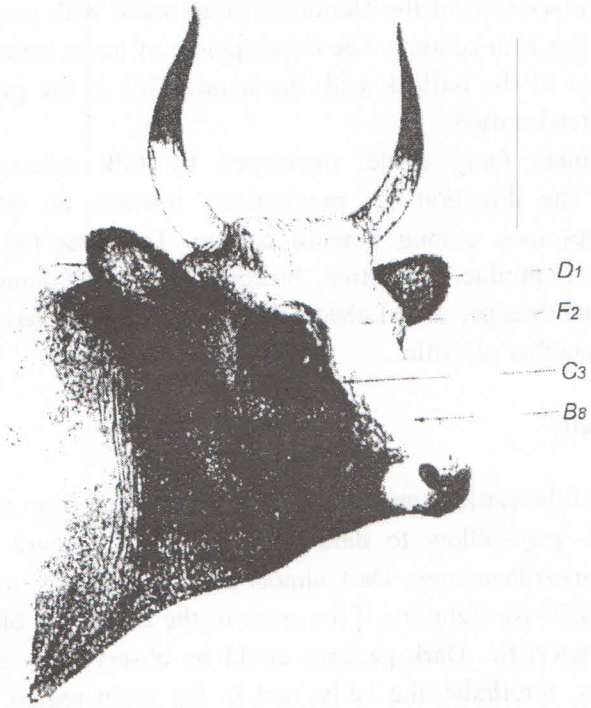


Table 1. - FREQUENCY OF MORPHOLOGICAL PHENS IN UKRAINIAN GRAY CATTLE (%)

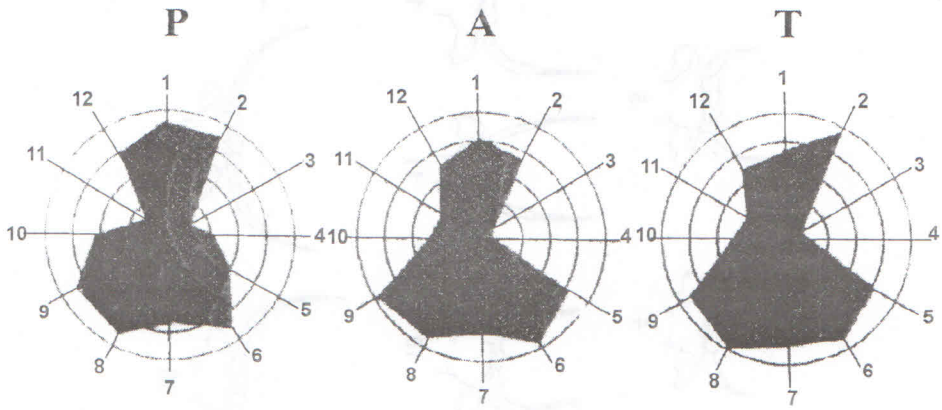
Phen	Phen code	Cattle population			On breed in whole	
		Polivanovka n=320	Askaniya Nova n=117	Altay Tcherga n=95	cows n=95-532	bulls n=44
Coat:	A					
Grey	A_1	65.3	75.2	73.6	69.0	68.2
Light grey	A_2	12.5	12.8	14.7	13.0	2.3
Dark grey	A_3	7.8	6.8	3.2	6.8	20.6
Pale-yellow grey	A_4	8.0	5.2	7.4	7.1	0
Red grey	A_5	0.9	0	0	0.6	0
Black	A_6	1.2	0	1.1	0.9	4.5
Mouse	A_7	3.7	0	0	2.3	4.5
White	A_8	0.6	0	0	0.3	0

Phen	Phen code	Cattle population			On breed in whole	
		Polivanovka n=320	Askaniya Nova n=117	Altay Tcherga n=95	cows n=95-532	bulls n=44
Head colour:	B					
Completely grey	B_1	44.0	-	2.2	33.0	52.3
-"- Light grey	B_2	13.8	-	9.5	12.8	2.3
-"- Dark grey	B_3	11.6	-	3.1	9.6	22.7
-"- Pale-yellow grey	B_4	2.5	-	3.1	2.7	0
-"- Black	B_5	1.5	-	1.1	1.4	9.1
-"- Mouse	B_6	1.1	-	0	0.8	0
-"- White	B_7	0.7	-	0	0.5	0
Light grey hair on the fore part, dark grey lower part	B_8	17.5	-	66.3	30.0	11.3
Red grey hair on the fore part, light grey lower part	B_8	4.0	-	14.7	6.8	0
Dark grey hair on the fore part, light grey lower part	B_{10}	3.3	-	0	2.4	2.3
Mask (black. light "spectacles" around eyes)	C					
(+) light "spectacles"	C_1	86.5	73.5	90.5	84.4	36.4
(-) light "spectacles"	C_2	13.5	26.5	9.5	15.6	63.6
(+) black "spectacles" around eyes	C_3	13.1	6.8	7.4	10.7	79.5
(+) -"- under eyes	C_4	34.1	9.4	16.8	25.6	18.2
(+) -"- over eyes	C_5	0.9	0	0	0.6	0
(-) -"-	C_6	51.9	83.8	75.8	63.1	2.3
Black edging on the ears	D					
(+)	D_1	93.7	97.4	92.6	94.4	97.7
(-)	D_2	6.3	2.6	7.4	5.6	2.3
Black strip on testicles						
(+)	D_3	-	-	-	-	100
(-)	D_4	-	-	-	-	0
Color of fringe between horns	E					
Pale-yellow	E_1	27.6	-	22.1	26.3	9.1
Red (chestnut)	E_2	30.9	-	22.1	28.8	0
White	E_3	18.3	-	40.0	23.4	20.5
Grey	E_4	3.9	-	11.6	5.7	38.6
Combined	E_5	19.3	-	4.2	15.8	31.8
Curl of hair on the forehead	F					
(+)	F_1	44.9	-	42.1	43.5	50.0
(-)	F_2	55.1	-	57.9	56.5	50.0

Phen	Phen code	Cattle population			On breed in whole	
		Polivanovka n=320	Askaniya Nova n=117	Altay Tcherga n=95	cows n=95-532	bulls n=44
Hook-nosed ("saiga muzzle")	G					
(+)	G_1	26.6	21.4	15.8	23.5	68.2
(-)	G_2	73.4	78.6	84.2	76.5	31.8
Light coloured ring around nose-labial mirrow	H					
(+)	H_1	95.0	97.4	100	96.4	97.7
(-)	H_2	5.0	2.6	0	3.6	2.3
Belt alon the spine	I					
Red grey						
(+)	I_1	25.6	-	22.1	24.8	11.4
(-)	I_2	74.4	-	77.9	75.2	88.6
Light						
(+)	I_3	7. 5	-	6.3	7.2	38.6
(-)	I_4	92.5	-	93.7	92.7	61.4
Pigmentation of vulva	J					
(-) rosy	J_1	10.3	0	6.3	7.3	-
(+) black	J_2	89.7	100	93.7	92.7	-
Dark grey, red grey places of hair on the body, neck, breast and legs	K					
(+)	K_1	54.6	40.1	43.1	49.4	100
(-)	K_2	45.4	59.9	56.9	50.6	0
Location of light and dark places of skin cover	L					
"Badger colour type - light top, dark bottom"	L_1	8.1	0	1.0	5.1	56.8
The fore part of one third of body (head, neck, breast. fore legs) - dark	L_2	18.7	30.7	32.6	23.8	43.2
Even coloring	L_3	73.2	69.3	66.4	71.1	0
Horn shapes (see fig. 7)	1. 2. 6. 7. 8. 12. 14. 16	-	-	1.2	-	-
	3	-	-	12.1	-	-
	4	-	-	41.9	-	-
	5	-	-	26.8	-	-
	10	-	-	4.8	-	-
	6, 13	-	-	2.4	-	-

The hide of the Ukrainian Gray cattle is superior to that of other breeds in terms of thickness, density and elasticity. The thickness of the skin fold on the last rib is 12.3 mm, and 5-7 mm under the lock, displaying considerable variability (13.1-14.7%). Available information shows that bull calves of 15-16 months had heavy hides: 41-42 kg, or 8-10% of the pre-slaughter mass, and sufficiently long: 244 cm and 173 cm wide.

Figure 2. - COMPARISONS OF THE 12 MORPHOLOGICAL PHENS IN THE THREE GROUPS OF UKRAINIAN GRAY COWS KEPT AT DIFFERENT FARMS

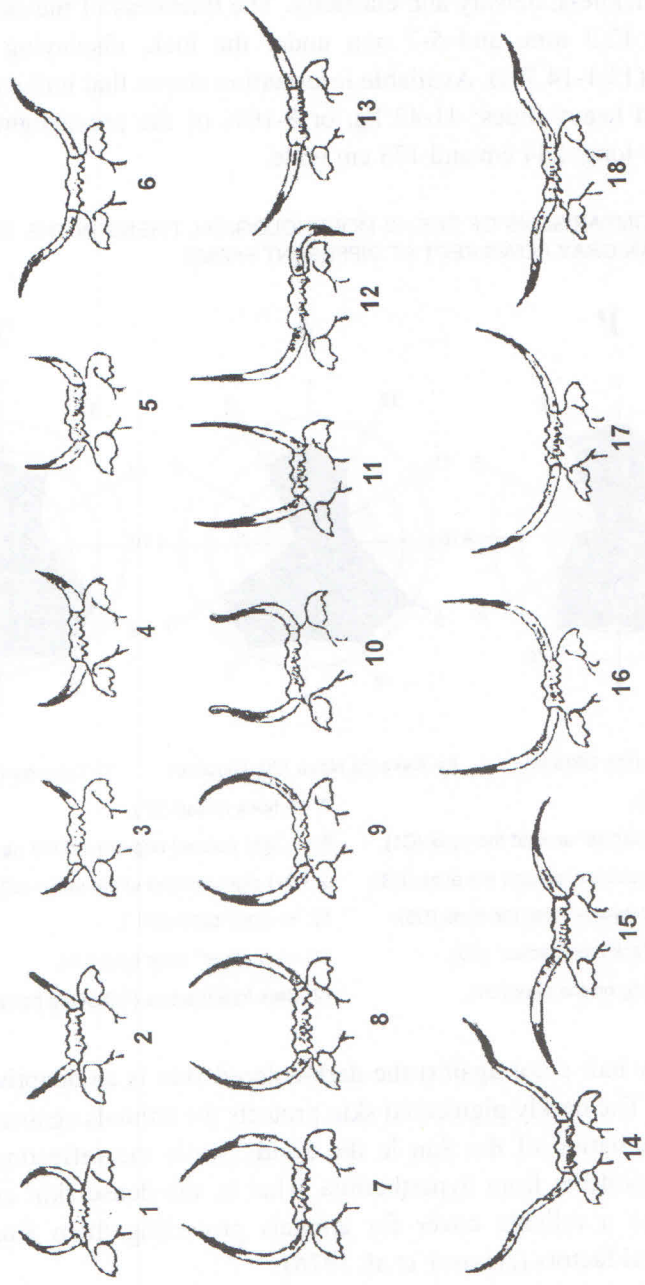


P= Polianovka (the Ukraine) A= Askania Nova (the Ukraine) T=Tcherga (Altay, Siberia)

1: grey color (Al),
2: +/- light „spectacles" around the eyes (C1),
3: +/- black „spectacles" around the eyes (C3),
4: +/- black „spectacles" over the eyes (C5),
5: absence of black „spectacles" (C6),
6: +/- black edging on the ears (D1),
7: +/- hook nosed (G"),
8: +/- light colored ring around the nose-labial mirrow,
9: + (+) pigmentation of the vulva (V2),
10: +/- color patch (K1),
11: +/- „badger" color type (L1),
12: Dark forequarters (1/3 of the body, L2).

The gray hair color against the dark-colored skin is an adaptive feature in hot climate. The darkly pigmented skin protects the animals against burns from ultraviolet radiation of the Sun in the South, while the reflecting surface of white hairs protects from hyperthermia. That is, the dense skin and the thick hair serve as a reliable cover for animals protecting them from injurious environmental factors (Aisner et al. 1976).

Figure 3. - SOME HORN SHAPES IN THE UKRAINIAN GRAY CATTLE (AFTER BODO ED. 1991)



The exterior of the Ukrainian Gray breed has been determined by one-sided selection for working capacity for many centuries. The head is characterized by an elongated face but an average size. Frequently it is heavy, with an aquiline nose. The forelock is thick and light. The eyes are small. The orbits are pronounced. The animal has a healthy looking gaze. The horns are long, lyre-shaped, slightly sloping, with black ends (Figure 3). The neck is somewhat short, with pronounced musculature under the breast. The withers are high, well developed, and muscled. The back is straight and strong, the loins are long, while the sacrum is slightly upraised. The chest is well-developed, especially in its depth. This measurement comprises 53% of withers height. The belly is deep but not hanging down. The hindquarters are moderately developed with straight thighs, curving slightly downward and forward. Limbs are of average length, strong, thin and dry, with well-developed conjunctions, and strong claws. The udder is small and shallow (23-29 cm) and satisfactory regarding its length (31-36 cm). The front lobules are well developed, and those in the rear are less well developed. The teats up front are widely spaced and those at the back are closely pitched. Mature animals are tall, with a strong skeletal makeup. Bullocks work up to 12 hours a day and can transport loads up to 2 tons. Measurements and indices of body conformation are used to complement the characteristics of the cows' exterior features in grading.

The breeding practice in the herd has resulted in changes in the type of body build. Comparisons between measurements and indices of cows from herds before World War II and populations of modern cows revealed a significant increase in the width measurements, heart girth and the circumference of the metacarpal region. Nevertheless, measurements indicate that the herd is uniform regarding the type of the body coriformation. This is the beef purpose form of the Ukrainian Gray cattle, whose body conformation indices are also used to complement the evaluation of external traits (Table 2, Figure 4).

Immunogenetic characteristics

In 1981, special features of blood groups as well as inherited versions of proteins and enzymes were evaluated starting with the results of previous investigations. Conclusions were drawn during the complex expedition entitled "Gene Pool 1979-1981" set up to investigate the Ukrainian Gray breed. Similarity of this breed with other varieties of Gray cattle as well as some special features of the polymorphous systems were registered.

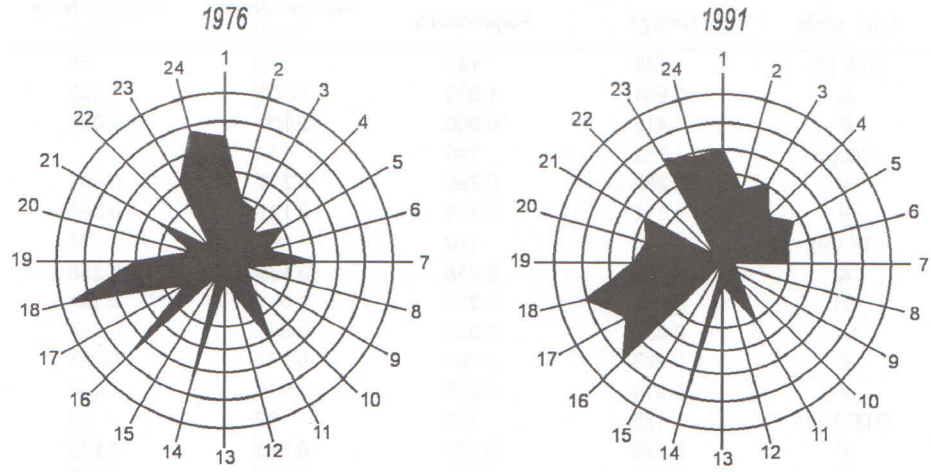
Table 2. - MEASUREMENTS (CM) AND INDICES OF BODY BUILD OF COWS OF THE UKRAINIAN GRAY BREED (STOLPOVSKII ET AL. 1998)

Measurements and indices	Data of S. Kromin, 1973	UPF Polivanovka, 1986		AEF SO RAS Cherga, 1990	
		M	m	M	m
Height at					
withers	135.6	133	0.4	137.1	1.13
back	134.4	134	0.5	135.9	1.06
sacrum	140.5	139	0.4	139.2	1.21
Chest					
width	41.8	49	0.4	43.1	0.2
depth	71.6	70	0.3	70	0.64
Body length with					
ribbon	170.2	160	0.7	161.8	1.6
stick	158.4	171	0.6		
Oblique rump length	53.6	54	0.3	48.9	0.68
Rump width at					
ileum	53.3	50	0.2	51.7	0.67
hip joints	45.2	46	0.3		
Hearth girth	188.2	200	0.8	192	1.5
Metacarpus circumference	18.1	19	0.1	19.3	0.25
Indices of:					
compactness	118.8	125	118.9		
length of limbs	47.2	47.4	48.7		
length	116.9	120.3	118.3		

The investigation of pools of alleles involved in polymorphous systems (erythrocyte antigens, blood group alleles) could be used as an objective criterion in assessing genetic variability. Such analysis was conducted for the herd of Ukrainian Gray cattle at the Polivanovka experimental farm. In particular, herd structures between 1975 (680 animals) and 1985 (197 animals) were compared.

No significant changes in the structure of this breed were detected within the studied period. However, the frequency of the following antigens increased II, 03, T2, A' 1, Q', P', R' 1, W, X1, X2, J, S, U, H", while the frequency of the following antigens decreased: Y2, D', I' M', H', U". A narrowing in the range of alleles was detected (Table 3).

Figure 4. DIACHRONIC CHANGES IN THE GENETICAL STRUCTURE OF THE UKRAINIAN GRAY CATTLE KEPT AT THE POLYANOVKA EXPERIMENTAL FARM, ACCORDING TO RED CELL ANTIGENES.



System A: 1 = A^2,
System B: 2 = B^2, 3 = G^3, 4 = i^1, 5 = Q, 6 = T^2,
7 = Y^2, 8 = B", 9 = D", 10 = G", 11 = I", 12 = O", 13 = P",
System C: 14 = C^2, 15 = R', 16 = W, 17 = X^1,
System F: 18 = F, 9 = V,
System J: 20 = J,
System L: 21 = L,
System M: 22 = M,
System S: 23 = S,
System Z: 24 = Z

Animals close to extinction were characterized by the alleles B BPQA'D', B A'E'K'p'Y', B QTY2A'B'D'C', B BGKQY2B'D'E'I'O'. At the same time, the herd retained its high genetic variability, since the coefficient of homozygosity increased only insignificantly (from 0. 0511 to 0. 0776).

In servicing bulls, the variation of alleles is limited. Among the cattle type close to extinction, only the bull Probnyi 2653 was characterized by the allele B OA'D'G' that is characteristic of the breed. Of 30 alleles almost half (14 alleles) are represented by B BIIQTI' and Bb in 15 bulls.

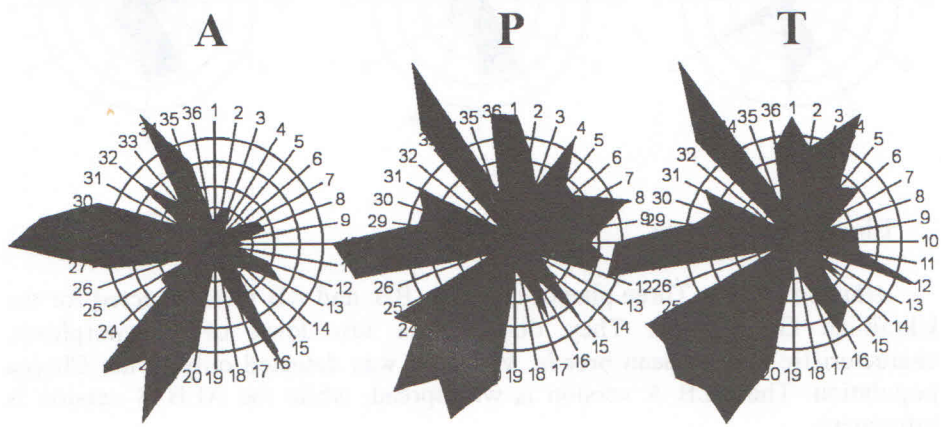
Data from the immunogenetic analysis indicate a certain narrowing of genetic variation in the herd. This can be explained by two factors. The first is the decrease in the number of animals in the herd. The second is violation of pairing plans. The latter is indicated by an increase in the number of animals characterized by the phenotypes BI1QTI', BGRE'G'O'G', I1OGI'. Therefore, 48 of 49 antigens were detected in the Ukrainian Gray cattle. Factor Z', on the other hand, was not detected for the breed. The high (45-92%) frequency of antigens A, G3, C1, C2, R2,.W, X1, X2, E, F; Y, J, H' Z was detected, while the frequency of the following antigens is significantly lower (2-10%): P1, P2, B', J2, P' Y', R, C', L', M, H".

Table 3. - GENETICAL STRUCTURE OF UKRAINIAN GRAY BREED ON GENETIC-BIOCHEMICAL SYSTEMS

Loci. allele	Cherga	Polyvanovka	Askania-Nova 1992	Askania-Nova 1999
ALB (n)	125	140	90	34
A	0.984	1.000	1.000	1.000
B	0.416	0.000	0.000	0.000
GC (n)	125	140	34	
A	0.288	0.296	0.278	0.603
B	0.712	0.704	0.722	0.397
TF (n)	125	140	90	34
A	0.122	0.218	0.106	0.250
D1	0.220	0.275	0.011	0.191
D2	0.396	0.336	0.661	0.294
E	0.268	0.164	0.178	0.221
F	0.004	0.007	0.044	0.044
PTF-1 (n)	125	140	90	34
F	0.720	0.696	0.828	0.850
S	0.280	0.304	0.172	0.150
PTF-2 (n)	125	140	90	-
F	0.724	0.745	0.511	-
S	0.276	0.255	0.489	-
PTF-3 (n)	49	112	80	
F	0.092	0.089	0.000	-
S	0.908	0.911	1.000	
CA (n)			50	34
F	-	-	0.360	0.177
S	-	-	0.640	0.823
PGM-1 (n)	76	-	-	-
A	0.375	-	-	-
B	0.579	-	-	-
X	0.046	-	-	-
NP (n)	20		30	34
L	0.700	-	0.800	0.559
H	0.300	-	0.200	0.441
CP (n)	31	9	30	34
A	0.823	0.740	0.733	0.824
B	0.177	0.260	0.267	0.176
AMY-1 (n)	29	9	30	34
B	0.897	0.840	0.933	0.721
C	0.103	0.160	0.067	0.279
HB (n)	25	9	30	34
A	1.000	1.000	1.000	1.000
B	0.000	0.000	0.000	0.000

We analyzed changes that took place in the genetic structure of group of animals at the Polivanovka Breeding Farm (UPF) for 14 years. Whereas the frequency of antigens P1, Q, T1, Y2, B', D', 0', P', F, V, L, H', U", H" remains the same (or insignificant changes took place), the frequency of antigens I', U', Z significantly decreased. On the other hand, the frequency of antigens I1, X1, X2, J significantly increased. Investigations of blood groups in the Ukrainian Gray breed conducted by Mesheryakov et al. (1971) are indicative of 41 alleles of the most informative system B in the Ukrainian Gray breed. Now their numbers have decreased to 24 alleles in the group of animals kept at Polivanovka. We detected only 14 alleles in the Cherga herd. Of these, alleles B B2 G3 I1 Q T1 F; B B2 G2 K Q Y2 E'2 G' O' G" are breed specific. Noteworthy is the saturation of this breed with alleles of comparatively high numbers (5-10) of antigens (Figure 5).

Figure 5. - COMPARISONS BETWEEN THE ERYTHROCYTE ANTIGENE FREQUENCIES IN UKRAINIAN GRAY CATTLE KEPT AT DIFFERENT FARMS



A = Askania Nova (the Ukraine) P = Polianovka (the Ukraine) T = Tcherga (Altay, Siberia)

System A: 1 = A^2,

System B: '2 = B^2, 3 = G^2, 4 = G^3, 5 = I^1, 6 = I^2, 7 = O^1, 8 = O^2,
9 = Q, 10 = T^1, 11 = T^2, 12 = Y^2, 13 = D', 14 = E2,
15 = Q', 16 = G', 17 = I, 18 = O', 19 = P',

System C: 21 = C^2, 22 = R", 23 = W, 24 = X1, 25 = X^2, 26 = C', 27 = E,

System F: 28 = F, 29 = V,

System J: 30 = J,

System L: 31 = L,

System M: 32 = M,

System S: 33 = S, 34 = H', 35 = U,

System Z .

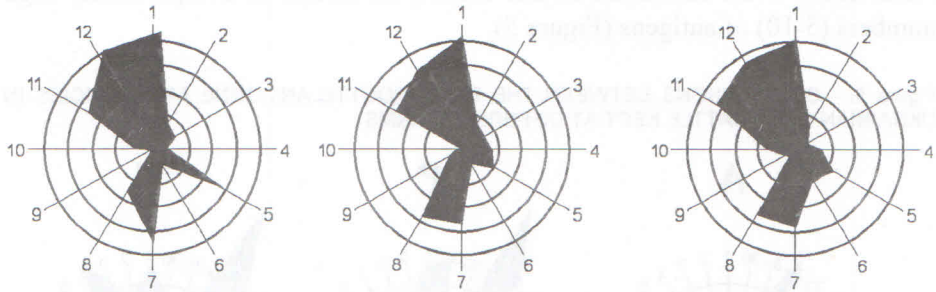
The homozygosity coefficient (Ca) for system B comprises 0.14. This indicates sufficient genetic diversity. Nevertheless, the narrowing pools of

alleles down to this low margin indicate that the Ukrainian Gray breed is close to extinction.

Biochemical markers

We investigated 35 loci encoding serum proteins as well as erythrocyte and tissue isozymes (Figure 6).

Figure 6. - THE GENETICAL STRUCTURE OF THE UKRAINIAN GRAY CATTLE KEPT AT P= POLIANOVKA (THE UKRAINE), A= ASKANIA NOVA (THE UKRAINE), T=TCHERGA (ALTAY, SIBERIA). ACCORDING TO GENETIC-BIOCHEMICAL SYSTEMS: 1=ALB A, 2=GC A, 3=TF A, 4=TF D', 5= TF D^2, 6=TF F, 7=PTF-1 F, 8=PTF-2 F, 9=PTF-3 F, 10=NP H, 11=CP A, 12=AM B



Blood serum protein

Albumin (ALB). Three phenotypes AA, BB, and AB were detected for the Ukrainian Gray breed. They displayed a low level of polymorphism, characteristic of European breeds. Variation was detected only in the Cherga population. The ALB A version is widespread, while the ALB B version is infrequent.

The vitamin D receptor (GC). Three phenotypes AA, BB, and AB were detected for the Ukrainian Gray breed. The frequency of the GC A allele was the same in herds of the Ukrainian Gray breed. The GC B allele is predominant. The same results were detected for the Simmental and Friesian breeds (Stolpovskaja and Stolpovskii 1990). However, a sharp increase in the frequency of theGC A allele (q = 0.406) was registered in the Cherga population (32 animals), which are the progeny of cattle delivered into Askaniya-Nova in 1982 (4-5th generations; Table 4).

Posttransferrin-1 (PTF-1). We detected three genotypes FF, FS, and SS. Predominance of the PTF F allele was detected in the Ukrainian Gray breed,

whereas the frequency of this allele is slightly higher than 0.5 in most European breeds of cattle (Thinnes, Gelderman and Wens 1976).

Posttransferrin-2 (PTF-2). The analysis of electrophoregrams revealed three phenotypes: FF, FS, SS. PTF2 F is predominant. This agrees with data concerning other European breeds (Agergaard and Larsen 1979; Van de Weghe et al. 1982). The differences between the herds from Askaniya-Nova and Polivanovka in the frequencies of PTFI and PTF2 are significant ($P<0.05$).

Table 4. - TEMPORAL DYNAMICS OF GENETICAL STRUCTURE OF TWO HERDS OF UKRAINIAN GRAY CATTLE BREED WHICH REPRODUCE IN DIFFERENT ECOGEOGRAPHICAL CONDITIONS (ASKANIYA-NOVA IN THE SOUTH OF UKRAINE AND TCHERGA IN THE ALTAYSKY REGION, RUSSIA)

Locis, alleles	Allelic frequencies in investigated groups of animals				
	Askaniya-Nova, 1992	Askaniya-Nova, 1994	Askaniya-Nova, 1999	Tcherga, 1992	Tchega, 1997
Number of animals studied	90	30	34	125*	32
Transferrin (Tf)					
A	0.117	0.167	0.182	0.116	0.156
D1	0.006	0.011	0.017	0.212	0.141
D2	0.661	0.667	0.520	0.400	0.609
E	0.172	0.117	0.234	0.004	0.00
F	0.044	0.050	0.047	0.268	0.094
Vitamin D receptor (GC)					
A	0.278	0.183	0.266	0.294	0.311
B	0.722	0.817	0.734	0.716	0.688
Post-transferrin-2 (Ptf -2)					
F	0.506	0.617	0.588	0.782	0.719
S	0.494	0.383	0.412	0.272	0.281
Purine-nucleoside hos horilase (EC 2.4.2.1)					
L	0.800	0.824	0.700	0.667	
H	0.200	0.176	0.300	0.323	
Ferroxidase (EC1.16.3.1)					
?	0.733	0.765	0.823	0.828	
?	0.267	0.235	0.177	0.172	
Amylase -1 (??-1)					
?	0.000	0.000	0.000	0.000	
?	0.933	0.926	0.897	0.844	
?	0.067	0.074	0.103	0.156	

Posttransferrin-3 (PTF-3). Despite five well-known polymorphous proteins in the blood plasma of cattle, we detected another polymorphous protein that has not been described in the literature previously. The analysis of families showed that all three are phenotypes of posttransferrin-3 (PTF-3) and are controlled by two codominant alleles, F and S. The PTF-S allele is the most widespread in this breed.

Transferrin (TF). As opposed to previously published data concerning the Ukrainian Gray breed (Mesheryakov, Mesheryakov and Dasyuk 1974; Zubarena, Mashurov and Uhanov 1986) we detected five alleles in this breed (TF A, TF D1, TFD2, TFF, TFE; Stolpovskaja and Stolpovskii 1990) and all 15 possible phenotypes. The Cherga population of the Ukrainian Gray breed was described for the first time. This population is characterized by an elevated level of the TF F allele. This version is characteristic of zebu and was not detected in most European breeds. In 1972, Kovacs et al. (1972) detected the TF F allele in the Hungarian Gray breed that deviated from the same group of the Gray Steppe cattle. However, while the TF F allele of the Hungarian Gray cattle is characterized by a 0.0273 frequency. This version is more frequent in the Ukrainian Gray breed: 0.044 in Askaniya-Nova and 0.268 in Cherga. The frequency of the TF F allele in the Cherga population is determined by the high concentration of this allele in a group of ancestor-cows that were initially delivered to Cherga in 1982. In these cows (n=28), the frequency of this allele comprises 0.33. The TF D2 allele is predominant in the TF system in all three investigated groups. On the other hand, TF E is the most infrequent allele. Significant differences ($P<0.001$) were detected in the frequencies of all five TF alleles between the two major herds (Askaniya-Nova and Polivanovka).

Amylase-1 (AM-1). Electrophoretic analysis revealed three phenotypes: BB, BC, and CC. The AM-1 B allele is predominant in the Ukrainian Gray breed.

Ceruloplasmin (CP). Three phenotypes were detected for this locus: AA, AB, and BB. The allelic version CP A was detected previously.

Hemoglobin (HB). All investigated breeds were characterized by the A type.

Erythrocyte and tissue isozymes

The following isozymes were investigated: carboanhydrase (CA), (E. C. 4. 2. 1. 1); phosphoglucomutase 1 (PGMI), (E. C. 2. 7. 5. 1); catalase (CAT), (E. C. 1. 11. 1. 6); peptidases A, B, S (PEP A, B, S), (E. C. 3. 4. 11. or 13); peptidase D (PEP D), (E. C. 3. 4. 13. 9); purinenucleoside phosphorylase (NP), (E. C. 2. 4. 2. 1.); aspartate aminotransferase 1 (GOTI), (E. C. 2. 6. 1. 1); 6-phosphogluconate dehydrogenase (6PGD), (E. C. 1. 1. 1. 44.). Of these,

polymorphisms were detected for pGM1 and CA. The mos infrequent versions were detected for NP. PEP B, PGM 1 (Table 5).

Phosphoglucomutase 1 (PGM 1). In addition to the two versions of PGM 1 described for cattle, we detected a new allele that was designated as X (Stolpovskii and Stolpovskaya 1991). Five of six possible phenotypes were detected: AA, AB, BB, AX, and BX. Ukrainian Gray cattle is characterized by higher frequency of PGM1 A in comparison to the German Hochblecvich breed (Ananthakrishanan and Scheider 1976), and it significantly differs from the Danish Jersey breed (Karadjole et al. 1972) Our data well agree with those for the Japanese Nogiishi breed (Abe et al. 1980).

Table 5. – POLIMORPHOUS MARKER ALLELE FREQUENCIES IN THREE BOVINAE SPECIES

Loci and allele	Ukrainian Gray Cattle	Brown Carpatian Cattle	Pinzgau	White-Haeded Ukrainian Cattle	Bison bonasus	Bison bison
TF						
A	0.250	0.381	0.552	0.465	1.000	1.000
D1	0.191	0.238	0.186	0.293	0.000	0.000
D2	0.294	0.357	0.252	0.103	0.000	0.000
E	0.221	0.024	0.010	0.035	0.000	0.000
F	0.044	0.000	0.000	0.014	0.000	0.000
PTF						
A	0.850	0.515	0.767	0.568	1.000	1.000
B	0.150	0.485	0.233	0.432	0.000	0.000
AMY-1						
A	0.000	0.000	0.000	0.000	0.440	0.250
B	0.721	0.737	0.737	0.482	0.560	0.750
C	0.279	0.263	0.263	0.518	0.000	0.000
CP						
A	0.824	0.553	0.633	0.517	0.712	0.700
B	0.176	0.447	0.367	0.483	0.288	0.300
GC						
A	0.603	0.152	0.138	0.397	1.000	1.000
B	0.397	0.848	0.862	0.603	0.000	0.000
PGM						
F	1.000	1.000	1.000	1.000	0.400	0.650
S	0.000	0.000	0.000	0.000	0.600	0.350

Loci and allele	Ukrainian Gray Cattle	Brown Carpatian Cattle	Pinzgau	White-Haeded Ukrainian Cattle	Bison bonasus	Bison bison
GPI						
F	1.000	1.000	1.000	1.000	1.000	0.650
S	0.000	0.000	1.000	0.000	0.000	0.350
PEP B						
F	1.000	1.000	1.000	0.743	0.850	0.500
S	0.000	0.000	0.000	0.267	0.150	0.500
ME						
F	1.000	1.000	1.000	1.000	0.650	1.000
S	0.000	0.000	0.000	0.000	0.350	0.000
ICD						
F	1.000	1.000	1.000	1.000	0.900	1.000
S	0.000	0.000	0.000	0.000	0.100	0.000
NP						
F(H)	0.000	0.000	0.000	0.000	1.000	1.000
H	0.559	0.330	0.280	0.069	0.000	0.000
L	0.441	0.670	0.720	0.931	0.000	0.000
DP-1						
F	1.000	1.000	1.000	1.000	1.000	0.400
S	0.000	0.000	0.000	0.000	0.000	0.600
MPI						
F	0.647	1.000	1.000	0.776	1.000	1.000
S	0.353	0.000	0.000	0.224	0.000	0.000
CA						
F	0.177	-	-	0.190	1.000	1.000
S	0.823	-	-	0.810	0.000	0.000
AP						
F	0.177	-	-	0.190	1.000	1.000
S	0.706	0.810	0.000	0.000		
D	0.117	0.000	0.000	0.000		
P	0.300	0.300	0.300	0.333	0.200	0.167
H	0.108	0.102	0.091	0.105	0.065	0.068

Carboanhydrase (CA). We detected three phenotypes: FF, FS, and SS. CA S is a predominant phenotype for the Gray cattle. The same data were detected for the Jersey and Hereford breeds (Stormon, Morris and Suwki 1970) as well as for Texas long-horn cattle (Morris, Stormont and Suzuki 1980).

Purinenucleqside phosphorylase (NP). We detected two alleles: NP L and NP H. Of these, NP L is the predominant allele.

Peptidase B (PEPB). In the spleen of a Ukrainian Gray cattle, we detected a version of peptidase. We have not found data concerning the polymorphism of this enzyme in the literature.

We did not detect polymorphism for the following forms: hexokinase (HK), (E. C. 2. 7. 1. 1); creatinkinase (CK), (E. C. 2. 7. 3. 2); adenylate kinase (AK), (E. C. 2. 7. 4. 3); glucoso-6-phosphate dehydrogenase (G6PD), (E. C. 1. 1. 1. 49); glucose phosphate isomerase (HPI), (E. C. 5. 3. 1. 9); superoxide dismutase (SOD), (E. C. 1. 15. 1. 1); malate dehydrogenase (MDH), (E. C. 1. 1. 1. 37); malic-enzyme (ME), (E. C. 1. 1. 1. 40); and lactate dehydrogenase (LDH), (E. C. 1. 1. 1. 27).

Restriction analysis of mitochondrial DNA

Our investigations of lengths of restriction fragments for 13 restrictases (among them are 12 which "recognize" six pairs of nucleotides and one which "recognizes" five nucleotides) revealed polymorphism only for endonuclease Eco471, the recognition site is GG (A/T CC; Watanabe et al. 1989). This enzyme produces two restriction patterns: A, with five fragments and B, with six fragments. In all, we detected 41 sites (Table 6). The comparison of our results with the results of restriction analysis of mtDNA in other breeds of cattle (Khrisafonova and Kalashnikova 1991) indicates that analogous restriction patterns (regarding the number of sites) of EcoR1 and PnuII restrictase are characteristic of the Holmogorskaya and Alatauskaya breeds respectively. Only one site for KpnI restrictase was detected, whereas three sites were described for the Holmogorskaya breed and two for Holstein cattle.

Analysis of marker polymorphism RAPD-PCR: This study included comparisons between the polymorphisms of three Bovine species: domestic cattle and European as well as American bison.

Amplicon sizes were determined within the 2.4-0.4 kb range using the UBC-85 marker. Fragments of 0.5 and 0.6 kb lengths were characteristic only for European bison, while fragments measuring 0.8 and 1.1 kb only for cattle. Fragment lengths of 0.7 and 1.3 occurred exclusively in American bison.

Using this primer, 14 amplicons were revealed in the three species studied. They included only four (lengths: 1 .7, 1.8, 1.9 and 2.0 kb) common to all three of them. Three occurred both in cattle and American bison (0.4, 1.5, 1.6 kb), one for both cattle and for European bison (2.4 kb). Six amplicons representing this spectrum were found only in one of the three researched species (in pairs within each species). There is a noteworthy similarity of species differentiation

by the polymorphism of protein markers and by the presence of amplicons in the UBC-85 spectrum. All three species offered a similar picture of polymorphisms in 4 out of 15 polymorphic protein systems. European and American bison were distinguished from one another by the polymorphism of four other systems. UBC-126 primer fragments of 0.5 and 1.8 kb lengths were encountered only in cattle, while a length of 0.7 kb occurred only in European bison. Only one of the nine amplicons was revealed in all three species (1.9 kb). Four amplicons (0.9, 1.0, 1.3, 1.4 kb) were shared by European bison and cattle. Only one amplicon (2.3 kb) was common to American and European bison.

Table 6. - THE NUMBER OF SITES IN MITOCHONDRIAL DNA FOR 13 RESTRICTASES AND MOLECULAR MASS OF THE FRAGMENTS (THE UKRAINIAN GRAY BREED; STOLPOVSKII ET AL. 1998)

Restrictase	Recognition site	Type	Number of site	Sizes of fragments (kb)	Number of investigated animals
BamHI	GIGATCC	A*	3	11.2; 3.2; 1.9	5
BglII	AIGATCT	A*	2	9.7; 6.6	7
EcoRI	GIAATTC	4	6.7; 4.3; 4.0; 1.3	6	
Eco52I	CIGGCCG	2	13.1; 3.2	4	
Eco105I	TACIGTA	2	9.3; 7.0	3	
Eco47I	GIG(A/T)CC	A* *	6	6.3; 4.5; 2.8; 1.3: 1.0:0.4	2
B	5	6.3; 4.5; 2.8; 1.6; 1.1	3		
HindIII	AIAGCTT	A*	3	10.2; 4.5; 1.7	7
KpnI	GGTACIC	1	16.3	3	
PvvII	CAGICTG	2	13.3; 3.1	4	
PstI	CTGCAIG	A*	2	9.4; 7.0	4
SalI	GITCGAC	1	16.4	3	
XbaI	TICTAGA	6	5.1; 3.1; 2.9: 2.5; 1.7; 1.0	3	
XhoI	CTCIGAG	1	16.3	3	

Thus, according to protein markers, European and American bison were more similar to each other. But according to a primer of one decanucleotide (UBC-85), all three species were differentiated approximately equally by the spectra of amplicons. Using another primer (UBC-126) cattle and European bison had a spectrum of amplicons more similar to one another than those of European and American bison.

Analysis of marker polymorphism ISSR-PCR. Spectrum analysis of the amplification products of zones between inverted repeats of microsatellite loci revealed interspecific differences in this type of molecular-genetic markers. On electrophoregrammes of amplification products, 21 and 24 lines for primers $(GA)_9C$ and $(AG)_9C$ corresponding were identified. The size of amplicons analysed was within the 2.2-0.5 kb range. Each amplification product was examined as a separate locus. Using the primer $(AG)_9C$, common amplification products were observed in sizes 1.0; 1.7 and 2.0 kb in all three studied Bovine species. Fragment lengts of 0.6, 0.8 and 0.9 kb were specific for American bison. No species markers could be revealed for European bison and cattle, owing to the poor spectra of amplicons (Table 7).

Table 7. - FREQUENCES OF AMPLIFICATION PRODUCTS IN BOVINAE SPECIES USING ISSR-PCR MARKERS

	$(GA)_9C$			$(AG)_9C$			$(AC)_9T$		
Amplicons, kb	Ukrainian Gray Cattle	Bison bonasus	Bison Bison	Ukrainian Gray Cattle	Bison bonasus	Bison Bison	Ukrainian Gray Cattle	Bison bonasus	Bison Bison
0.4	-	-	-		-		-	-	-
0.5	+	+	+	+	-	+	-	-	-
0.6	+	+	-	-	-	+	-	-	-
0.7	+	-	-	-	-	-	-	-	-
0.8	-	-	-	-	-	-	+	+	+
0.9	-	-	-	-	+	+	-	-	-
1.0	-	-	-	+	-	+	-	+	-
1.1	+	+	+	+	-	+	-	+	+
1.2	+	-	-	-	-	-	-	-	-
1.3	-	-	-	-	+	-	+	+	+
1.4	-	-	-	+	-	+	+	+	+
1.5	+	-	+	-	-	-	-	+	+
1.6	+	+		-	+	-	-		+
1.7	-	-	-	+	+	+	-	+	-
1.8	-	-	-	-	-	-	-	-	-
2.0	-	-	-	-	-	-	-	+	+
2.1	-	-	-	+	-	+	-	-	-
2.2	-	-	-	-	-	+	-	-	+
2.3	-	-	-	-	-	-	-	-	-
2.4	-	-	-	-	-	-	-	-	-
2.5	+	-	-	-	-	-	-	-	-

The fullest spectrum of amplicons was revealed in American bison (10 fragments of lengths ranging from 2.2 to 0.5 kb) by use of primer $(AG)_9C$ among the studied species of the Bovinae subfamily.

The numbers of amplification products in cattle and European bison were 6 and 4 respectively: All amplicons revealed in European bison were found also in the spectra of the two other species.

A different picture was observed in the case of another dinucleotide primer with the $(GA)_9C$ sequence. The most complete amplicon spectrum was present in cattle (8 fragments in lengths from 2.3 to 0.4 kb). Amplification product of 1.2 kb length was revealed only in cattle and while it was absent in other species.

Amplicon of a length of 0.8 kb was present only in American bison. As has been shown by electrophoregrammes, there were equal quantities of amplification products in European and American bison, although they differed in terms of their lengths. Two common amplicons were observed for cattle and European bison: 1.7 and 0.5 kb. A common amplicon of 1.6 kb length was found in both cattle and American bison. As for the amplification product RAPDPCR, the value of interspecific differentiation is essentially variable depending on the primer used in analyzing certain lengths of amplicon. It is evident that using high levels of the polymorphism markers RAPD-PCR, ISSR-PCR is convenient and irreplaceable in solving genetic problems in the intraspecific certification of animals. However, there is a possibility of making mistakes in interspecific comparisons.

Finally, comparions between the genetic structures of cattle, European and American bison were carried out through the distribution of amplification products obtained using the primers $(GA)_9C$ and $(AG)_9C$. Analysing genetic interrelations between the Ukrainian Gray cattle and European as well as American bison using ISSR-PCR markers, European bison turned out to be closer to cattle. The analysis of protein polymorphism displayed a greater degree of genetic propinquity between European and American bison, than between either of them and domestic cattle. The main reason for this is that some loci (e. g. transferrin, purinnucleoside phosphorylase) of allele variants in the European bison, differ from the electrophoretic characteristics typical for cattle.

Using varied primers resulted in different, "anonymous" amplification products, high levels of polymorphism, and qualitatively different values of interspecific relations.

Thus, it did not seem likely that in genetic-taxonomic research, DNA markers based on repeated nucleotide sequences can be applied to solve traditional problems (interspecific relations, rates of evolution etc.) more

successfully than through the use of protein polymorphism analysis. Apparently, for DNA markers studied in genetic-biochemical systems it is necessary to individually estimate the information and efficiency that can be expected from the use of some markers in the solving concrete tasks.

Thus, the data obtained lead to the conclusion, that differences in the estimations of genetic differentiation between three species - European bison, American bison and domestic cattle vary qualitatively from marker to marker, independently of their type, but depending on the way they are identified.

It in necessary to note, however, that in the species of Bovinae studied here, mechanisms apparently exist that promote intraspecific genetic variability, in spite of the limited number of parents (European and American bison) and artificial crossings (breeds of cattle).

Conclusions

Initiatives taken by some governments and associations promote measures directed towards preservation of local cattle breeds all over the world. In many countries, reserves and parks have been created, where various breeds are preserved as living exhibits. This is why methods and approaches of gene pool preservation should be developed. The minimal number of the gene pool herd should be no less than 500 animals. Such a herd permits the preservation of genetic specificity of breeds and helps maintain genetic variability within a system of enclosed breeding using 5-6 major lines of bulls and 5-6 genealogical groups of cows, based on rotation and hybrid selection. The regions of distribution of local breeds should be chosen as well as farms that would preserve the animals. Some state institutions should supervise these measures. Small groups of animals are preserved in the Polivanovka experimental farm (Dnepropetrovskaya Oblast), the National Park Askaniya-Nova (Khersonskaya Oblast), and Cherga (Altayskii Kray). There are altogether 600 purebred individuals.

The following traits of the Ukrainian Gray breed should be used in selection: unique adaptation to local conditions, a strong constitution, the high content of milk protein and butterfat, good beef features, the high stature of animals, their ability to digest fodder efficiently, the high quality of hide, etc. A special feature of the Ukrainian Gray breed is its small birthweight.

To preserve the gene pool of the Ukrainian Gray breed, a greater number of purebred bulls should be introduced into the herd. They should be used for a short period for crosses with cows and heifers, or for the preservation of their semen. After 1-2 years they should be replaced by new sires. The following special features should be preserved in the Ukrainian Gray breed: special constitution and external features, adaptation to local conditions, small

birthweight, high indices of fertility, universal productivity (high milk fat, pronounced beef features, and hide quality), the long productivity life of animals, and the wide range of erythrocyte antigens. Obtaining purebred animals should be a major goal of breeding. It should provide for preservation of diversity of the special features of the breed via controlled selection and pairing.

The major type of pairing is intragroup homogeneous pairing directed towards the preservation of related groups as structural units. Then crossings and rotation of the related groups are expected. The pairing should be individual, but involve related groups (small circle, a group of females), which may be followed by the rotative selection of bulls (large circle, a group of bulls).

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PODOLSKO GOVEDO U UKRAJINI I ISTOČNIM PODRUČJIMA

Sažetak

Inicijative što su ih pokrenule neke vlade i udruženja potiču mjere za očuvanje lokalnih pasmina goveda po čitavom svijetu. U mnogim zemljama stvoreni su rezervati i parkovi gdje se čuvaju razne pasmine kao živi eksponati. Zbog toga bi trebalo razviti metode i pristupe za čuvanje pula gena. Najmanji broj krda pula gena ne bi smio biti manji od 500 životinja. Takvo krdo omogućuje očuvanje genetske specifičnosti pasmina i pomaže održavanje genetske varijabilnosti unutar sustava obuhvaćenog uzgojem, upotrebom 5-6 važnijih linija bikova i 5-6 genealoških skupina krava na temelju rotacije i hibridske selekcije. Trebalo bi izabrati područja razdiobe lokalnih pasmina kao i farme koje će očuvati životinje. Državne bi ustanove morale nadzirati ove mjere. Male skupine životinja očuvane su na pokusnoj farmi Polivanovka (Dnjepropetrovska oblast), Nacionalnom parku/Askaniya-Nova (Khersonska oblast) i Chergi (Altajski kraj). Ukupno ima 600 čistokrvnih jedinki.

Sljedeće osobine Ukrajinske sive pasmine trebalo bi upotrijebiti u selekciji: jedinstvena prilagođenost lokalnim uvjetima, jaka konstitucija, visoki sadržaj bjelančevina i masnoće u mlijeku, dobra svojstva govedine, visok rast životinja, njihova sposobnost djelotvornog probavljanja krme, visoka kakvoća kože, itd. Posebna značajka ukrajinske sive pasmine je malena porođajna težina.

Da bi se očuvao pul gena Ukrajinske sive pasmine u krdo bi trebalo uvesti veći broj čistokrvnih bikova. Njih bi trebalo upotrijebiti u kratkom razdoblju za križanje s kravama i junicama ili za očuvanje njihova sjemena. Nakon 1-2 godine njih bi trebalo nadomjestiti novim bikovima. Sljedeće posebne značajke trebalo bi očuvati u Ukrajinskoj sivoj pasmini: posebna konstitucija i značajke eksterijera, prilagođenost lokalnim uvjetima, mala porođajna težina, visok indeks plodnosti, univerzalna produktivnost (visoka masnoća mlijeka, izražene značajke govedine i kakvoća kože), dug proizvodni vijek životinje te široki raspon antigena eritrocita. Dobivanje čistokrvnih životinja trebao bi biti glavni cilj uzgoja. Trebao bi poslužiti za očuvanje raznolikosti posebnih značajki pasmine putem kontrolirane selekcije i parenja.

Glavni tip parenja je homogeno parenje unutar skupine usmjereno očuvanju srodnih skupina kao strukturalnih jedinica. Zatim se očekuju križanja i rotacija srodnih skupina. Parenje bi trebalo biti individualno ali uključivati srodne skupine (mali krug, skupina ženki) nakon čega može slijediti kružna selekcija bikova (veliki krug, skupina bikova).

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