

Genetic analysis of the
Barcus Creek wild horse
population

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In August of 1992, 12 blood samples from horses identified as Barcus Creek mustangs were sent to the Equine Blood Typing Research Laboratory of the University of Kentucky for genetic marker analysis. These horses were from the White River Resource Area of the Bureau of Land Management in Meeker, Colorado. The blood was tested for 17 genetic marker systems. Seven of these systems were red blood cell antigen loci (known as the A, C, D, K, P, Q and U equine blood groups) which were examined by standard immunological techniques involving hemagglutination and complement mediated hemolysis. The remaining systems (albumin, Al; a-1-B glycoprotein, AlB; serum cholinesterase, Es; vitamin D binding protein, Gc; glucosephosphate isomerase, GPI; hemoglobin, Hb; phosphoglucomutase, PGM; phosphogluconate dehydrogenase, PGD, protease inhibitor, Pi; and transferrin, Tf) were typed by standard starch and polyacrylamide gel electrophoresis and isoelectric focusing. The genetic data were analyzed to determine levels and patterns of genetic variation within the group and also to attempt to determine the possible ancestry of the herd.

Results

Genetic variability

Genetic variation can be estimated at both the level of the population and the individual. At the population level, genetic variation or diversity gives an estimate of the genetic health of the population and its potential for adaptability. The two measures of populational variability estimated here are the

effective number of alleles (ENA) and genotypic diversity (GD). ENA is a measure of allelic (genetic variant) diversity which takes into account both the number of variants and their frequency. GD is similar to ENA except that it is based upon the number of genotypes (or gene combinations) which are possible in the population. Because it is difficult to accurately determine genotypes at the blood group loci, GD is estimated from the 10 biochemical systems only.

At the individual level, we can estimate the average amount of genetic variation present in an individual. The measure of individual variation is heterozygosity. An individual is heterozygous at a gene locus if the genetic variant it inherited from one parent is different from the one from the other parent and heterozygosity (H) is the average number of heterozygous loci per individual. Observed heterozygosity (H_o) is the average H actually observed and could be calculated accurately for biochemical loci only. Expected heterozygosity (H_e) is that H predicted by Hardy-Weinberg equilibrium theory from gene frequencies within the population. H_e was calculated for all 17 loci and the 10 biochemical systems.

Values of ENA, GD, H_e , and H_o for the Barcus Creek horses are given in Table 1 as well as the same measures for a variety of domestic breeds and other feral populations. Among the populations shown in Table 1, only the feral Chloride Utah herd has lower levels of populational genetic diversity (ENA and GD). This is a small herd in southwestern Utah that has shown possible signs of

inbreeding depression. Heterozygosity levels of the Barcus Creek population also are quite low. H_e for all loci was the third lowest in the table while H_e for the biochemical systems was fourth lowest. However, H_o was higher in the Barcus Creek sample than it was for five other populations. These results clearly show that the genetic variability of this sample of Barcus Creek horses is among the lowest observed for a horse population. Although only the Chloride herd, among the populations with comparable low genic diversity, has shown deleterious conditions that are likely to be due to reduced genetic variation, the genetic variability level of the Barcus Creek herd is a potential concern. One point should be made here. The sample size of the Barcus Creek population is small for a horse population. Thus, the values obtained for genetic diversity measures may not be representative of the herd as a whole. However, heterozygosity estimates are not usually effected by sample size. Unless these 12 horses are not at all representative of the whole population, the H_o and H_e values probably are valid.

Low genetic variation is usually a result of small population size and isolation, and these two conditions inevitably lead to inbreeding (which reduces heterozygosity). The low variability and conformity of gene marker types suggests that inbreeding and isolation are factors for at least this sample of the Barcus Creek population. Additional samples would be required to confirm this observation.

Genetic Origins

Because the markers that we examine are genetic characteristics that are passed from ancestor to descendent, it is possible to use these markers to deduce something about the ancestry of a population. One method is simply to examine the genetic markers present in a population and compare them to what are found in other breeds or populations. Genetic resemblance can also be calculated across all genetic systems using a genetic similarity coefficient (in this case Rogers' S coefficient). Genetic similarity is not actually a measure of relatedness but because these are genetic characters being analyzed, high genetic similarity usually can be taken as an indication of relationship. Table 2 shows the genetic similarity coefficient S for the Barcus Creek herd with a number of different horse breeds and the average S with groups of related breeds.

The Barcus Creek sample had the highest mean S with the saddle and harness light horses and the arab type horses were a close second. However, all the S values are relatively low. This likely is due primarily to the low genic variation in this sample but also may simply be related to sample size. In such a case it is necessary to go to the actual variants present and analyze them on a one by one basis.

Table 3 gives the genetic marker types for the 12 horses examined. I will not go into the details of the variant (marker) names in this report. The relatively high S with the arab type horses was mainly due to the relatively high frequency of the Hb-

AII and Qabc variants. The Pi-U, Tf-D and Ddk variants largely account for the high S with the saddle and harness light horses. The Pi-V variant also is at a relatively high frequency in this herd and this is a strong Spanish marker. The Ddek marker is also a good Spanish marker but it is present in no more than two of the Barcus Creek horses. The overall picture presented by the specific variants is that the herd is of mixed origins, which is probably not unexpected.

Conclusions

The genetic marker data from the Barcus Creek horses indicate that the founding population was of mixed genetic origins. Genetic diversity measures suggest that, at least for this sample, the population has been isolated for a number of generations and that some inbreeding may be taking place. It should be understood that inbreeding in this case is not necessarily close inbreeding such as father/daughter or brother/sister matings. It is a genetic term that indicates that there is mating among relatives due to no non-related mates being available. The main point is that inbreeding reduces heterozygosity and heterozygosity within the Barcus Creek horse sample is relatively low.

Due to the small sample size available for this analysis, it would not be prudent to make specific recommendations about genetic management. However, some general principles can be presented which will be relevant in any case. Culling of horses to reduce population size for the protection of the local environment should

concentrate on removal of the very young and the very old individuals. Leaving the breeding individuals on the range will preserve the present levels of genetic variation. When these individuals are post reproductive or die they can be replaced by their offspring. It also would be possible to bring in horses from other areas to increase genetic diversity within the herd. The wild horse herd near Grand Junction CO is a good genetic match based upon gene marker studies. Future work in this lab may identify additional source populations. Physical characteristics of the horses within the Barcus Creek herd also should be considered when making management decisions.

TABLE 1. Genetic variability measures for the Barcus Creek herd, selected breeds, and some other feral herds.

BREED NAME	EFFECTIVE NUMBER OF ALLELES ALL LOCI	GENOTYPIC DIVERSITY BIOCHEMICAL LOCI	EXPECTED HETEROZYGOSITY ALL LOCI	EXPECTED HETEROZYGOSITY BIOCHEMICAL LOCI	OBSERVED HETEROZYGOSITY BIOCHEMICAL LOCI
Barcus Creek	1.92	2.53	.344	.334	.367
Thoroughbred	1.99	3.06	.319	.279	.294
Quarter Horse	2.76	5.67	.439	.391	.398
Morgan Horse	2.37	3.32	.421	.391	.380
American Saddlebred	2.49	5.53	.432	.406	.404
Arabian	2.20	3.29	.393	.354	.317
Percheron	2.66	4.95	.450	.400	.404
Clydesdale	2.22	2.95	.358	.329	.334
Welsh Pony	2.72	3.47	.435	.377	.381
Miniature Horse	2.71	4.43	.488	.404	.411
Andalusian	2.50	3.83	.428	.362	.353
Peruvian Paso	2.68	4.97	.469	.460	.486
Pryor Mountains Herd	2.51	4.66	.456	.433	.419
Chloride Utah Herd	1.82	1.84	.293	.237	.267
T. Roosevelt N.P.	2.17	2.78	.395	.360	.369

TABLE 2. Rogers' 1972 genetic similarity coefficient for the Barcus Creek herd compared to 41 modern horse breeds.

Saddle and harness light horses		TB	QH	PA	TR	MH	TW	MP	RM	SB	MEAN
Barcus Creek		.757	.796	.759	.790	.807	.781	.790	.756	.808	.783
Arabian breeds		AR	BS	SA	MB	AT	KU	PE	CS	MEAN	
Barcus Creek		.810	.734	.824	.776	.765	.813	.740	.769	.779	
Heavy draft horses		CD	BE	BR	PC	SH	SU	CL	HF	MEAN	
Barcus Creek		.677	.710	.701	.713	.704	.624	.671	.716	.690	
Pony breeds		WP	HP	SP	MN	DT	GT	EX	MEAN		
Barcus Creek		.769	.757	.715	.744	.751	.718	.651	.729		
Iberian peninsula derived breeds (Spanish breeds)		PR	AN	LU	PP	CP	CC	RP	PF	MM	MEAN
Barcus Creek		.745	.722	.748	.735	.760	.729	.768	.761	.752	.747

TB-THOROUGHBRED, QH-QUARTER HORSE, PA-STANDARDBRED PACER, TR-STANDARDBRED TROTTER, MH-MORGAN HORSE, TW-TENNESSEE WALKING HORSE, RM-ROCKY MOUNTAIN HORSE, MP-MOUNTAIN PLEASURE HORSE, SB-AMERICAN SADDLEBRED, AR-ARABIAN, BS-ARABIAN (BLUE STAR), SA-SHAGYA ARABIAN, MB-MOROCCAN BARB, AT-AKHAL TEKE, KU-KURD, PE-PERSIAN ARAB, CS-CASPIAN PONY, CD-AMERICAN CREAM DRAFT, BE-BELGIAN DRAFT, BR-BRETON, PC-PERCHERON, SH-SHIRE, SU-SUFFOLK PUNCH, CL-CLYDESDALE, HF-HALFLINGER, WP-WELSH PONY, HP-HACKNEY PONY, SP-SHETLAND PONY, MN-MINIATURE HORSE, DT-DARTMOOR PONY, GT-GOTLAND HORSE, EX-EXMOOR PONY, PR-SPANISH PURE BLOOD, AN-ANDALUSIAN, LU-LUSITANO, PP-PERUVIAN PASO, CP-CAMPOLINA, CC-CHILLIAN CRIOLLO, RP-PUERTO RICAN PASO FINO, PF-AMERICAN PASO FINO, MM-MANGALARGA MARCHADOR

TABLE 3. Genetic marker types for the Barcus Creek horses. Biochemical marker systems show the observed genotype for each horse. Blood group systems show only the factors found and do not indicate genotype. The lower case letters under the capital letters of the blood group system names are the antigenic factors that are known to occur at the systems. A matching letter under each such column indicates that the factor was tested for and was present, a - indicates it was tested for and not present, and a blank means it was not tested for.

ID	Biochemical Systems											Blood Group Systems																
	Tf	A1B	Es	A1	Gc	PGD	PGM	GPI	Hb	Pi	A	C	D	K	P	Q	U											
245101	D	R	K	K	I	I	A	B	F	F	F	S	S	I	I	A2B1	S	U	a--d	f	a	--cd--g-	K	m--	-	---d	abc	-
245103	D	H2	F	K	S	S	A	B	F	F	F	S	S	I	I	B1B1	L	U	a--d	f	a	--cd--g-	K	m--	-	a-cd	---c	-
245106	D	R	K	K	I	O	A	A	F	F	F	S	S	I	I	B1B1	U	U	a--d	f	a	--cd--gh	-	m--	-	a-cd	---	-
245108	D	R	K	K	I	I	A	B	F	F	F	S	S	I	I	B1B1	L	U	a--d	f	a	--c--g-	-	m--	-	---	---	-
245110	D	O	K	K	I	I	A	B	F	F	F	S	S	I	I	B1B2	K	L2	a--d	f	a	-bcde--	K	m--	-	a-c-	---c	-
245112	D	R	F	K	I	I	B	B	F	F	F	S	S	I	I	B2B2	V	V	a--d	f	a	--cd--g-	K	m--	a	---d	---	-
245115	D	D	F	K	I	I	A	B	F	F	F	S	S	I	I	B1B2	S	V	a--d	f	a	--cde-g-	-	m-o	a	---d	---c	a
245117	D	D	K	K	I	I	A	B	F	S	F	S	S	I	I	A2B2	U	V	a--d	f	a	--de--	K	-o	a	---	---c	-
245122	D	D	F	K	I	I	A	B	F	F	F	S	S	I	I	B1B2	U	V	a--d	f	a	--d--	K	---	-	a-cd	---c	-
245125	D	H2	F	K	I	I	A	A	F	F	F	S	S	I	I	B1B1	V	V	a--d	f	a	--d--	K	---	-	a-cd	abc	a
245127	D	D	K	K	I	I	A	B	F	S	F	S	S	I	I	B1B2	U	U	a--d	f	a	--d--	K	---	-	a-cd	abc	-
245129	D	D	F	K	I	S	A	B	F	F	F	S	S	I	I	B1B1	U	U	a--d	f	a	---de--	-	-o	a	a-cd	---	-