

# 1992 Gather Genetics Summar

Genetic Marker Analysis of the Feral  
Horse Herd from the McCullough Peak  
Herd Management Area, Wyoming

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Genetic marker analysis can provide information about both the past and the future of a population. Because gene markers are passed from one generation to the next, they can tell us something about the ancestry of a population. Also, because demographics can affect the distribution of genetic markers within a population, these markers can often be used to interpret past populational characteristics. In the same way, current demographic conditions can be used to make predictions about the future level of variability of gene markers.

The Wild and Free-Roaming Horse and Burro Act of 1971 mandates that feral horses on public lands be managed in a manner that maintains a viable, healthy horse population and achieves an ecological balance. Maintenance of such a balance frequently requires that wild horse populations be kept small. Unfortunately, from the standpoint of management of the horses, small population size inevitably leads to loss of genetic variation and inbreeding. However, it is possible to manage small populations in a manner that minimizes loss of variation and inbreeding. The first step in this process is an assessment of the current status of the population. In this report I present the results of genetic marker analysis of the McCullough Peaks, WY, management area wild horse herd.

#### METHODS

Blood samples from a total of 47 horses from the McCullough Peaks management area were received at the Equine Blood Typing

Research Laboratory of the University of Kentucky in September of 1992 from recently rounded-up horses. Each sample was tested for 17 genetic marker systems (loci). Seven of these systems were red blood cell antigen loci (known and 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; alpha 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.

Genetic variability was measured in several ways. The first and simplest was simply the total number of variants (alleles) present. A more informative measure is the effective number of alleles (Ea). Ea is a measure of genic diversity that takes into account both the number of variants and the frequency of the variants. Individual variability was measured by heterozygosity (H). A locus is heterozygous when the two copies of the genes at the locus are different. H is the average number of systems that are heterozygous. H was calculated in two ways. Observed heterozygosity (Ho) was calculated by counting the number of heterozygous loci per individual horse. Ho was only calculated for

biochemical systems due to the possibility of recessive genes at the blood group loci. Expected heterozygosity ( $H_e$ ) is an estimate of heterozygosity based upon gene frequencies and the laws of random mating.

Genetic markers also can provide some information about ancestry in some cases. Genetic resemblance was calculated using Roger's 1972 genetic similarity coefficient  $S$ . Genetic relationships also were estimated by construction of a genetic tree diagram (dendrogram) by use of a restricted maximum likelihood procedure.

## RESULTS

The range of genetic variants per population seen in 102 samples of domestic breeds and feral herds was 27 to 96 (out of 125 recognized variants). We observed 61 total variants in the McCullough Peaks herd. This ranks the herd 47th out of 102 populations. Average number of variants for the 102 populations was 62.5. Most of the breeds with below average numbers of variants were rare breeds or those that either now or in the past have had very small population size. There also were several breeds that have not yet been well sampled and thus we likely have not observed all variants present in those breeds. Many of the other populations with a total number of observed genetic markers less than 61 were small feral populations. Overall, the number of variants observed in the McCullough Peaks herd were in the middle of the range for horses.

Measures of genetic variability for the McCullough Peaks herd and other feral populations are given in Table 1 and data for selected horse breeds are shown in Table 2. The domestic breeds were selected to cover the range of variation seen in domestic horses. The domestic horse mean values were based upon 55 horse breeds. Overall, genetic variability of the McCullough Peaks herd was near the average for horses. With the exception of the number of alleles, all measures were slightly higher than the domestic means. Expected heterozygosity for the 10 biochemical loci was 0.394 which is not significantly different from the observed heterozygosity.

Values of  $H_o$  also were compared among the age classes of horses sampled to see whether variability levels had changed through time. Six age classes were considered; less than one year, yearlings, two year olds, three and four year olds, five and six year olds, and seven years or older. Mean  $H_o$  for the six age classes were 0.382, 0.400, 0.370, 0.320, 0.425 and 0.457, respectively. Although the highest values of the  $H_o$  were for the oldest and next to oldest horses, there was no significant trend for  $H_o$  to be associated with age.

Genetic similarity of the McCullough Peaks herd with a number of selected breeds is shown in Table 3. Mean  $S$  with groups of breeds with similar ancestry and use also are shown. Overall,  $S$  for the McCullough Peaks herd with domestic breeds was low. The highest individual  $S$  was with the Percheron and highest mean similarity was with the Draft breeds. Second highest mean  $S$  was

with the Spanish breeds and the difference was only 0.001. If only New World breeds of Iberian Peninsula ancestry are considered, mean  $S$  was 0.793 and the individual  $S$  values only range from 0.779 to 0.807.

The relationships based upon genetic similarity can be summarized by the dendrograms of figures 1 and 2. Figure 1 compares the McCullough Peaks herd with mean frequencies for major breed groupings. The McCullough Peaks population clusters with the cold blood breeds (draft horses and ponies). In figure 2, the McCullough Peaks herd was compared to 51 breeds. Again, the herd is clustered within the draft horse grouping, however, the pairing with the Exmoor pony at the outside of the cluster indicates the relationship is not a close one.

In trying to access ancestry of feral horse populations it also is important to look at the specific genetic variants present. The variants found for the McCullough Peaks herd and their frequency are given in Table 4. Several variants with some diagnostic value were present. The Tf-D2, Pi-H, and A-bc variants are most common in draft horse breeds. The Es-R and Tf-H1 markers are most strongly associated with Spanish horses. The total array of variants present in the McCullough Peaks herd indicate a mixed composition of the current herd.

#### DISCUSSION

From the standpoint of genetics, the major concern for management of feral horse populations is loss of genetic variation.

Loss of genic variation can reduce the long term adaptability of a population and if population size is small, inbreeding, which can reduce viability and fertility, also becomes a potential problem. Levels of genetic variability within the McCullough Peaks herd were essentially average for horse populations and fairly high for a feral herd (Tables 1 and 2). Current genetic variation levels of this herd probably are a reflection of a diverse ancestry of the herd. Population size of the herd over the last 15 years has been high enough to maintain genic variation. The comparison of H values among age classes of the herd supports the stability of genetic variation within the herd, at least over the last 10 years. However, the population size in the early 1970s was small enough for loss of genetic diversity to occur. This is probably why the genic variation levels are not as high as might be expected with mixed populations.

Genetic variability should not be a problem for the McCullough Peaks herd for many generations based upon the current management plan for the herd size. Maintaining an average herd size of 100 adult horses within a range of 60 to 140 adult horses should keep effective population size high enough to minimize loss of genic variation. Returning animals 10 years of age or older to the population after round ups for population control, also helps insure that most of the current genetic variation will be maintained. Another consideration is that because the McCullough Peaks herd appears to be of mixed origins, introduction of animals from other management areas could be used as a means of increasing

genetic diversity if needed.

The genetic variability data for the McCullough Peaks herd is consistent with a mixed ancestry for the herd. The genetic similarity results also support mixed ancestry. Genetic similarity for all comparisons with domestic breeds were low (Table 3). This is what is commonly seen for mixed populations. All the data clearly point to at least some draft horse ancestry for the herd with the Percheron being the breed most like the herd in terms of genetic markers. There also is clearly some Spanish contribution to the genetic makeup of the herd. The high genetic similarity with New World Spanish breeds is perhaps most significant. These breeds, primarily from South America, are probably more like the horses the Spanish brought to the Americas during conquest and colonization than are modern breeds such as the Andalusian.

It is, unfortunately, difficult to quantify the contributions of the various types of breeds to the current herd. From a qualitative standpoint, the draft horse input appears to be the strongest with the Spanish contribution second. However, this is complicated by the history of the domestic breeds. The native horses of the Iberian peninsula were from the same northern European stock that were the ancestors of the draft horses. Thus, these two groups share a number of genetic markers that are not common in other breeds. Both prior to domestication and after domestication the Iberian horses received genetic input from the Arab type horses through Northern Africa. After domestication, the Iberian stock and the draft stock developed markers that were

unique to each group. The only such unique marker observed in the McCullough Peaks herd was the Tf-D2 variant seen in only one individual. For this reason it also is important to consider the physical characteristics of the horses. Although horses under natural selection appear to converge upon a common, primitive like appearance that much resembles the Spanish type, any draft horse influence upon this herd is likely of recent enough origins to be detectable in body conformation.

In conclusion, both genetic variability estimates and genetic similarity values indicate that the McCullough Peaks feral horse herd is of mixed ancestry. This is consistent with the known history of the herd. Genetic variation within the herd is at a high enough level that there should be no immediate concerns about problems associated with low genetic variation (i.e., inbreeding depression). As long as the population size is not drastically reduced, current management plans should be adequate for maintenance of satisfactory levels of genic variation for many generations.

TABLE 1. GENETIC VARIABILITY ESTIMATES FOR FERAL HORSE POPULATIONS

LOCATION	NUMBER OF ALLELES	EFFECTIVE NUMBER OF ALLELES	Ho	He	POP. SIZE
MCCULLOUGH PEAKS (WY)	61	2.48	.391	.438	L
15 MILE HERD AREA (WY)	59	2.28	.379	.411	L
KIGER RANGE (OR)	77	2.72	.406	.463	L
PRYOR MOUNTAINS (MT)	71	2.52	.419	.459	M
CEDAR CITY AREA (UT)	49	2.63	.389	.424	M
T. ROOSEVELT NP (ND)	62	2.15	.369	.389	M
GRAND JUNCTION (CO)	59	2.32	.300	.389	M
CERBAT MTNS 1970 (AZ)	39	1.92	.357	.335	S
CERBAT MTNS 1990 (AZ)	27	1.41	.267	.128	S
CHLORIDE HERD (UT)	38	1.81	.267	.318	S
SOCORRO AREA (NM)	42	2.03	.342	.352	S

L Population size greater than 150 individuals.

M Population size greater than 60 individuals but less than 150.

S Population size less than 60 individuals.

TABLE 2. GENETIC VARIABILITY ESTIMATES FOR DOMESTIC BREEDS

BREED	NUMBER OF ALLELES	EFFECTIVE NUMBER OF ALLELES	Ho	He
SHAGYA ARABIAN	48	2.30	.416	.357
FRIESIAN	49	1.88	.300	.343
BLUE STAR ARABIAN	52	1.89	.203	.303
BRETON	54	2.25	.387	.413
HACKNEY PONY	59	2.36	.311	.421
ARABIAN	63	2.15	.308	.370
THOROUGHBRED	64	2.01	.294	.326
STANDARBRED TROTTER	68	2.10	.398	.414
PERCHERON	68	2.68	.404	.450
ANDALUSIAN	75	2.50	.349	.426
MINIATURE HORSE	82	2.58	.411	.477
CAMPOLINO	83	2.81	.410	.457
CHILEAN CRIOLLO	86	2.96	.374	.457
MOUNTAIN PLEASURE HORSE	89	2.66	.389	.439
QUARTER HORSE	93	2.75	.398	.453
AMERICAN SADDLEBRED	96	2.51	.404	.433
DOMESTIC HORSE MEANS	65.5	2.39	.381	.412

TABLE 3. Rogers' 1972 genetic similarity coefficient for the Tullough Peaks horses compared to 39 modern horse breeds.

Saddle and harness light horses								
TB	QH	PA	TR	MH	TW	RM	SB	MEAN
.736	.804	.784	.776	.802	.758	.744	.788	.774
Arabian breeds								
AR	BS	SA	MB	AT	KU	PE	CS	MEAN
.782	.758	.764	.795	.753	.780	.736	.770	.767
Heavy draft horses								
CD	BE	BR	PC	SH	SU	CL	HF	MEAN
.780	.780	.781	.829	.767	.757	.751	.801	.781
Ponies								
WP	HP	SP	MN	GT	EX	DT	MEAN	
.819	.765	.774	.778	.764	.745	.769	.772	
Iberian peninsula derived breeds								
AN	LU	PP	CP	CC	RP	PF	MM	MEAN
.758	.720	.782	.804	.795	.793	.807	.779	.780

TB-THOROUGHBRED, QH-QUARTER HORSE, PA-STANDARD BRED PACER, TR-STANDARD BRED TROTTER, MH-MORGAN HORSE, TW-TENNESSEE WALKING HORSE, RM-ROCKY MOUNTAIN 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, GT-GOTLAND HORSE, EX-EXMOOR PONY, DT-DARTMOOR PONY, AN-ANDALUSIAN, LU-LUSITANO, PP-PERUVIAN PASO, CP-CAMPOLINA, CC-CHILIAN CRIOLLO, RP-PUERTO RICAN PASO FINO, PF-AMERICAN PASO FINO, MM-MANGALARGA MARCHADOR

Table 4. Allele frequencies for the McCullough Peaks herd.

BIOCHEMICAL SYSTEMS			BLOOD GROUP SYSTEMS		
SYSTEM	ALLELE	FREQUENCY	SYSTEM	ALLELE	FREQUENCY
Tf	D	.425	A	adf	.461
	D2	.011		b	.133
	F2	.222		bc	.370
	G	.011	-	.036	
	H1	.011	C	a	.256
	H2	.064		-	.744
	O	.043			
	R	.213			
Xk	K	1.000	D	ad	.185
Es	F	.064		dn	.250
	G	.564		dk	.095
	I	.212		dghm	.043
	R	.160		de	.062
Al	A	.638		deo	.216
	B	.362		bcm	.095
Gc	F	.831		cgm	.043
	S	.169	cegimn	.011	
PGD	F	.532	K	a	.055
	S	.468		-	.945
PGM	S	1.000	P	ac	.279
PHI	F	.021		ad	.026
	I	.979		acd	.284
Hb	BI	.521	-	.411	
	BII	.479	Q	abc	.011
Pi	F	.032		b	.136
	H	.085		c	.173
	I	.276		-	.680
	L	.096	U	a	.271
	L2	.106		-	.729
	P	.011			
	R	.011			
S	.181				
T	.053				
U	.149				

### Figure Legends

- Figure 1. Dendrogram of genetic resemblance of the McCullough Peaks herd to major domestic horse groups. The Przewalski horse was included as an outgroup in order to root the tree.
- Figure 2. Dendrogram of genetic resemblance of the McCullough Peaks herd to 51 domestic horse breeds.



