

August 28, 1995

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Dear Valerie,

Here is the report on my analysis of the genetic data from the White River Area horses. Please look it over and contact me with questions or comments. Also, please let me know if there are any aspects of the genetics of the herd that you or your colleagues think were not covered in sufficient detail. Thanks for your patience.

Sincerely yours,



E. Gus Cothran, Ph.D.
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EGC/jp

enclosure

Genetic analysis of the feral horses of the White River Resource Area of Colorado

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Maintaining populations of feral horses on public lands frequently requires that the populations be kept small to ensure preservation of the habitat. Unfortunately, small population size can frequently lead to the loss of genetic variability and inbreeding. Loss of genetic variation threatens long term adaptability while inbreeding can result in reduced viability or fertility. It is possible to manage populations so that the effects of small population size upon genetic variability can be minimized. The first step in building an effective management plan is the assessment of current levels of genetic variation in the population. In this report I present the genetic analysis of the feral horse population of the White River Resource Area (WRRRA) Wild Horse Herd Area of the Bureau of Land Management.

METHODS

In August of 1992, 12 samples from the Barcus Creek area were obtained. In July of 1993, 14 samples from Barcus Creek and 18 samples from 84 Mesa area were obtained. An additional 11 samples from Barcus Creek plus 16 samples from the Square S Well Area were obtained in August of 1993. In October of 1993, 15 samples from the West Fork of Spring Creek were collected. In August of 1994, samples were obtained from additional areas as follows: 9 from Hammond, 11 from Greasewood, 15 from Little Duck Creek, and five from Spring Creek. The total number of horses sampled was 126. Seventeen genetic marker systems were analyzed. Seven systems were red blood cell alloantigen loci (the A, C, D, K, P, Q and U horse blood groups) tested by standard serological methods of agglutination and complement mediated hemolysis. The other 10 systems were biochemical polymorphisms detected by electrophoretic techniques. These systems were Albumin (Al), Alpha-1-beta Glycoprotein (A1B), serum Cholinesterase (Es), Vitamin D Binding Protein (Gc), Glucose Phosphate Isomerase (GPI), alpha

Hemoglobin (Hb), Phosphoglucomutase (PGM), Phosphogluconate Dehydrogenase (PGD), Protease Inhibitor (Pi), and Transferrin (Tf).

A variety of genetic variability measures were calculated from the gene marker data. The measures were observed heterozygosity (H_o) which is the actual number of loci heterozygous per individual and is based upon biochemical loci only; expected heterozygosity (H_e) which is the predicted number of heterozygous loci based upon gene frequencies, it was calculated for biochemical and all marker systems; unbiased H_e (H_u) which is H_e corrected for sample size; effective number of alleles (ENA) which is a measure of marker system diversity; total number of variants (TNV); and estimated inbreeding level (F_{is}) which is calculated as $1-H_o/H_e$. Genetic structure of the total population was examined by analysis of F-statistics.

Genetic markers also can provide some information about ancestry in some cases. Genetic resemblance to domestic horse breeds 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 (RML) procedure.

RESULTS AND DISCUSSION

The primary genetic variability measures of the sampling areas of the WRRRA are given in Table 1. The mean values for these same measures for domestic horse breeds also are shown in the Table. In most cases (not considering F_{is}), values of genetic variation of the WRRRA horses were less than that for domestic horse breeds. The exceptions were the expected heterozygosity measures (H_e and H_u) for the 84 Mesa and West Fork populations.

The most basic measure of genetic diversity is the total number of genetic variants (TNV). TNV for the WRRRA horses was quite low compared to the average for domestic horses. Even

the largest value (Barcus Creek) is considerably lower than the domestic mean. However, this is somewhat misleading. TNV is strongly influenced by sample size in horse populations and this trend is evident for the WRRRA sampling areas. Also, if the entire WRRRA is considered as a single population, TNV would be higher than the domestic mean as 73 variants were observed overall.

A more informative measure of genic diversity of a population than TNV is ENA. ENA measures the number of alleles per gene locus that actually contribute to overall genetic variation. It is not inflated by rare variants that may occur only once or twice in a population as TNV is. ENA is influenced by sample size but not to the degree that TNV is. ENA for the WRRRA samples also was well below that for domestic breeds. The highest values were for the West Fork and 84 Mesa samples. Note that the West Fork sample had one of the lowest values for TNV. The main observation is that ENA for the WRRRA herds is low for horses and that this is not due to small sample size of the separate populations.

Expected heterozygosity measures (H_e and H_u) gave similar results to ENA. The unbiased measure (H_u) is probably better as a comparative measure as most of the sample sizes were small. Again, these measures indicated a lower level of populational genetic variability than that found in domestic breeds. However, the West Fork and 84 Mesa populations did have H_e and H_u measures that were greater than the mean for horse breeds. Overall, all populational measures of genetic diversity of the WRRRA populations were low compared to genetic diversity of domestic horse breeds. However, these measures for the WRRRA horses were greater than the means for feral horse populations.

Individual genetic variation (H_o) also was lower for the WRRRA populations than for the domestic horse mean. Only the West Fork population had an H_o value near the domestic breed

mean while the Little Duck Creek population had an extremely low value of H_o . H_o in horses is not statistically associated with sample size. Thus the H_o values of the WRRR populations support the relatively low values of genetic variation indicated by the other measures.

The ratio of observed and expected heterozygosities (H_o/H_e) theoretically is related to inbreeding level and the statistic F_{is} uses this relationship to provide a relative measure of inbreeding level in a population. The F_{is} values for the WRRR populations give mixed results. Four of the values were positive indicating some inbreeding while four were negative indicating an absence of inbreeding. The populations with the positive inbreeding values were those with the highest expected heterozygosities. The F_{is} values for the Square S and West Fork populations essentially were not different from zero. The other six populations had F_{is} values, both positive and negative, that were fairly high. There is a statistically significant trend for values of F_{is} of feral horse populations to be positively associated with both sample size and population size. This means the largest values of F_{is} (positive values) tend to be associated with the larger sample or population sizes. There is no such pattern shown by the WRRR samples.

Although F_{is} is considered as an estimate of inbreeding, this does depend upon a number of assumptions about the populations which frequently may not be met. This is most likely the case for the WRRR horses because of the wide variation in F_{is} values in horses likely derived from the same founding population and in the same geographic area. In this case, F_{is} is simply a comparison of H_o to H_e , where positive values of F_{is} represent cases where H_e is greater than H_o and vice versa. The three populations with the highest F_{is} values all show some evidence of recent introductions into the population (this will be discussed in more detail below). If individuals from a population with different gene frequencies are introduced into another

population, this will inflate values of H_e . This could be the case for the Barcus Creek, Little Duck Creek and 84 Mesa populations. For the three populations with high negative values of F_{is} , Greasewood, Hammond and Spring Creek, a recent reduction in breeding population size could be the cause of the excess of H_o relative to H_e .

As indicated above, although these samples are from populations that are very close to each other geographically, each population is genetically distinctive. By this I mean that each population has a characteristic set of gene markers that is different from each other sample. For example, the Square S sample has a very high frequency of the Es-L variant seen elsewhere in only two individuals of the 84 Mesa herd. The West Fork herd has a very high frequency of the Es-F marker, only seen in three other individuals not in that sample. The patterns of marker distribution suggest genetic subdivision of the total population. The marker distributions also potentially could be used to track movements between populations, although this would not be simple. Also, there were several markers, for example the Hb-A2 variant, that occurred in several of the sample populations but only as a single copy. Such variants may represent markers in the original population from which the entire herd is derived. These markers are now widely distributed but at low frequency and may be examples of genetic variants that will eventually be lost.

Genetic subdivision of populations can be measured by use of F-statistics, primarily F_{st} (the standardized variance in allele frequency). F_{st} was calculated for all pairwise comparisons of WRRRA samples (Table 2). F_{st} for all populations also were calculated as was a comparison the WRRRA herd to the Little Bookcliffs population from near Grand Junction, CO. All comparisons yielded statistically significant F_{st} values. The overall F_{st} value was 0.131. This indicates that

approximately 13% of the total variability in gene frequencies was accounted for by among sample variation, which does indicate genetic substructuring of the total herd. Surprisingly, the within WRRR F_{st} was greater than the WRRR/Little Bookcliffs F_{st} (0.125). This indicates that there was greater differentiation among the WRRR subpopulations than between the WRRR and Little Bookcliffs herds.

Genetic association among the WRRR samples also was assessed by genetic similarity (Table 3) and cluster analysis using the RLM procedure (Figure 1). The genetic similarity matrix clearly shows the within group similarity (the diagonal) is much greater than among groups similarity. Mean within group similarity was 0.840 compared to among group similarity of 0.793. Among group similarity is fairly accurately depicted in Figure 1. The tree reveals that there is not a strict geographic basis to relationship. One major cluster consisted of the eastern most populations (Greasewood, Barcus Creek, Square S, and Little Duck Creek). The other two clusters contained the South Western most populations (West Fork and 84 Mesa) and the two most northwestern populations (Spring Creek and Hammond). Based upon geographic distance, it would be expected that populations such as 84 Mesa, Little Duck Creek and Square S or Spring Creek, Hammond and Greasewood would have clustered together. The observed cluster may be due to ecological or physical barriers to dispersal that I have no information about or could perhaps be due to sampling biases.

The primary conclusions from the analysis of genetic variability of the WRRR horse herd are that significant genetic subdivision of the herd exists and that, in general, genetic variation within subdivisions is relatively low. However, within the entire WRRR genetic diversity is fairly high. From a management standpoint, this is an almost ideal situation. Population subdivision

with limited inbreeding within subdivisions and occasional exchange of individual among subdivisions is one of the best strategies for the long term maintenance of genetic variability. The subdivision of the WRRRA population with the levels of dispersal that now appear to exist should be sufficient to maintain genetic variation within the area for many generations even if relatively small numbers of individuals are maintained within subdivisions. If additional interchange of individuals appears to be needed in the future, transfer of one or two two-year old females every three to five years would be the most efficient strategy. Patterns of exchange between populations should be randomized to minimize the rate of homogenization of the gene pool.

Analysis of gene markers also can provide some information about the origins or ancestry of populations. Qualitative appraisal of the variants present indicate some evidence of Spanish ancestry, however, only a small number of animals carry markers indicative of Spanish ancestry with the exception of the Pi-V allele. This allele is primarily found in New World horses of Iberian descent and may have been a marker for the type of horse brought over by the early Spanish explorers, conquerors and colonists. There also is some suggestion of draft horse influence but this is much less clear. Other specific breed affiliations cannot be determined at this point.

Quantitative measures of resemblance are given by genetic similarity coefficient (Table 4) and cluster analysis (Figure 2). Mean values of genetic similarity of the WRRRA populations to the major groupings of domestic breeds shows that four of the populations have their highest S with the gaited North American breeds and one each with Thoroughbred type, Arabian type and Draft horse groups. The high similarity to the gaited North American breeds is difficult to interpret. These breeds have an important, old Spanish component to their ancestry, probably the Spanish

Jennet. However, these breeds also were the types of breeds that could have contributed to the feral populations within the last century. The high frequency of the Pi-V marker is more likely from old Spanish type horses as it is rarely seen in the gaited North American breeds. There also were two individuals with clear cut Spanish markers not found in the gaited North American breeds.

The RML cluster analysis also gave ambiguous results. Six of the eight WRRA populations grouped essentially together within the cluster that contained most of the Arabian type breeds. These in turn grouped with the Morgan horse and Standardbreds. The remaining two populations grouped with Turkoman (an oriental breed which is closely related to the Arabian types) but the cluster is within the grouping that contains the remaining gaited North American breeds. The Turkoman and the Akhal-Teke (another oriental breed with Arabian affinities) show a high similarity to the gaited North American breeds, thus the overall pattern supports the high similarity of the WRRA herd to these breeds. Overall the results of the analysis suggest that the WRRA horses certainly have a component of Spanish ancestry that probably is not recent. However, the WRRA horses appear to be primarily derived from North American breeds. One final point is that the WRRA horses appear to have a close relationship to the Little Bookcliffs population although they do not cluster close to each other in Figure 2.

Table 1. Measures of genetic variation of the WRRR feral horse populations and the mean of these measures for domestic horse breeds.

SAMPLE	N	Ho	He	Hu	TNV	ENA	Fis
BARCUS CREEK	37	0.311	0.348	0.353	56	1.972	0.107
GREASEWOOD	11	0.345	0.287	0.301	41	1.752	-0.202
HAMMOND	9	0.322	0.286	0.303	38	1.817	-0.127
LITTLE DUCK CREEK	15	0.287	0.327	0.338	47	1.873	0.123
84 MESA	18	0.340	0.383	0.395	54	2.046	0.112
SPRING CREEK	5	0.300	0.248	0.276	30	1.664	-0.210
SQUARE SWELL	16	0.313	0.304	0.313	44	1.917	-0.029
WEST FORK SPRING CREEK	15	0.371	0.392	0.405	43	2.127	0.053
DOMESTIC HORSE MEAN	87	0.373	0.364	0.371	64	2.391	-0.025

Table 2. Measure of standardized variance of allele frequencies (F_{st}) between each population from the WRRRA (above the diagonal) and the chi-square with 84 degrees of freedom for each F_{st} (below the diagonal).

	BC	MS	SS	WF	HA	GS	LD	SC
BARCUS CREEK - BC	-	.0621	.0358	.0926	.0629	.0163	.0176	.0395
84 MESA - MS	1038	-	.0855	.0173	.0995	.0695	.0783	.0526
SQUARE'S WELL - SS	643	813	-	.111	.1075	.0820	.0855	.0859
WEST FORK - WF	1189	837	903	-	.0934	.1265	.1208	.1289
HAMMOND - HA	1113	919	1038	818	-	.0917	.0722	.1330
GREASEWOOD - GS	218	669	792	904	717	-	.0172	.1189
LITTLE DUCK CREEK - LD	279	1049	851	1109	814	215	-	.1096
SPRING CREEK - SC	944	609	889	806	702	906	1037	-

Table 4. Mean Rogers genetic similarity for each WRRRA population compared to major groups of domestic horse breeds.

	BC	GS	HA	LD	MS	SC	SS	WF
Thoroughbred type breeds	.747	.782	.731	.786	.752	.701	.780	.751
Arabian type breeds	.797	.785	.739	.792	.776	.728	.788	.734
Old World Iberian breeds	.786	.770	.738	.772	.776	.734	.780	.717
New World Iberian breeds	.755	.740	.731	.748	.749	.721	.701	.705
Gaited North American breeds	.808	.783	.738	.804	.786	.711	.789	.744
Heavy Draft Horse breeds	.729	.702	.752	.727	.758	.713	.718	.724
Pony breeds	.761	.734	.738	.754	.754	.704	.747	.712

Figure 1.

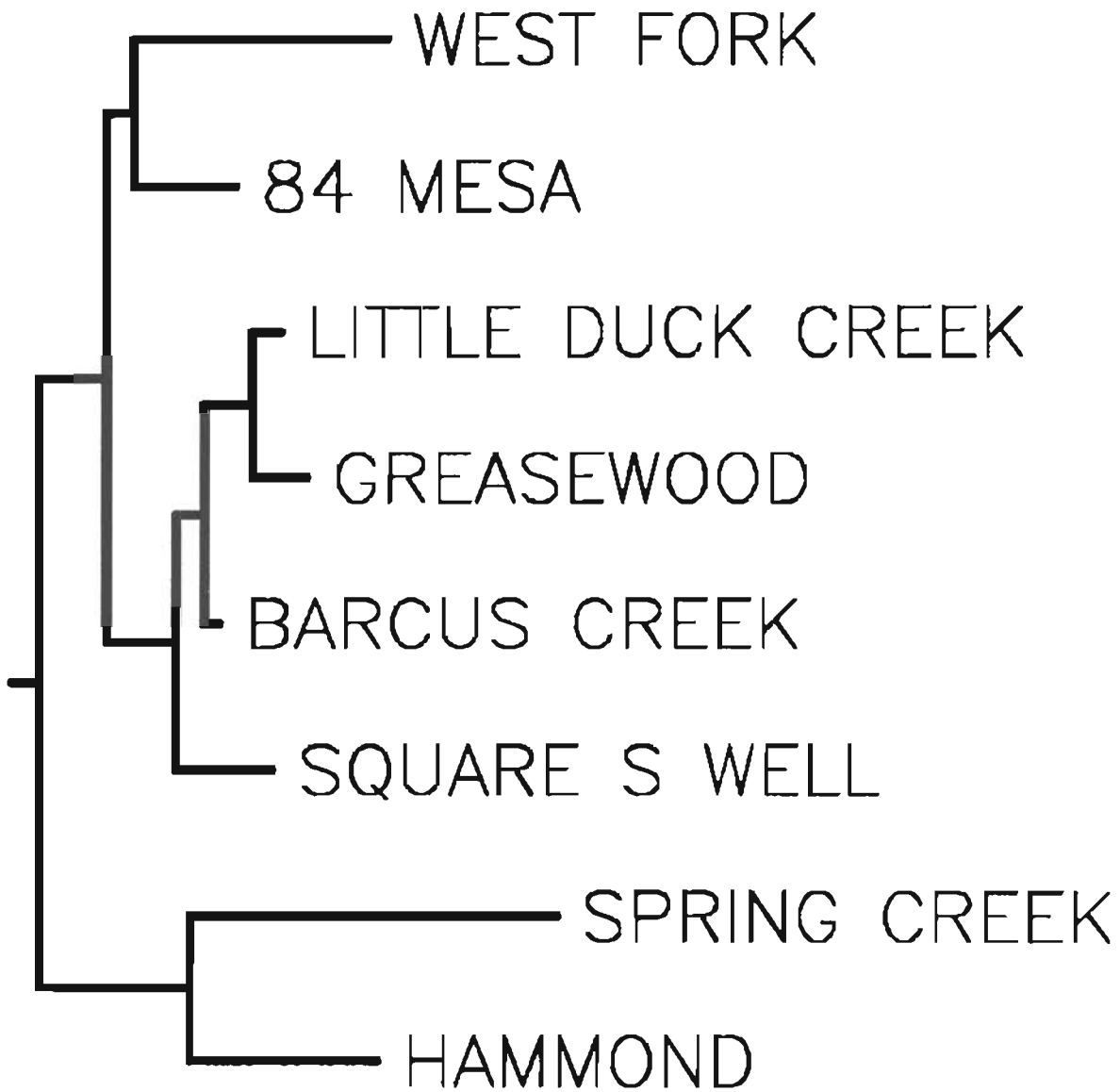
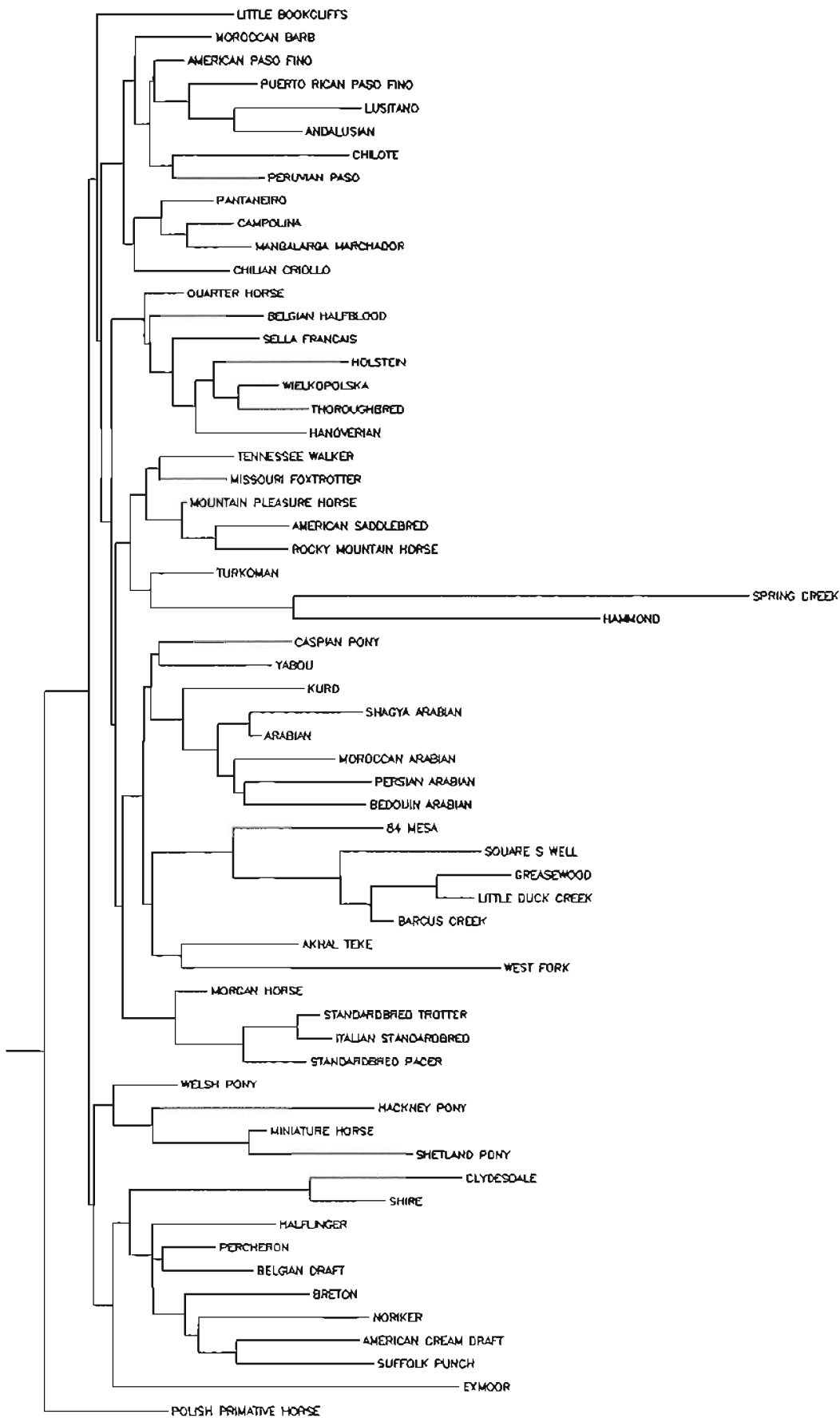


Figure 2.



APPENDIX 1. Genetic types for the WRRRA horses by sampling locality.

Accno	Loc	Tf	A1B	Es	A1	Gc	PGD	PGM	GPI	Hb	Pl	A	C	D	K	P	Q	U		
HAMMOND																				
94-14556	ha71	F2H2	K K K	I I I	B B	S S S	F F F	S S S	I I I	B1B2	K P	-bc-----	-	---de---	k	---	-	a-c-	---	
94-14566	ha71	H2R	K K K	G I I	A B	F S S	F F F	S S S	I I I	B1B2	L P	-----	-	-bcd----	k	m--	-	-----	abc	a
94-14567	ha71	R R R	K K K	I I I	A B	F S S	F F F	S S S	I I I	B1B2	K P	-----	-	-bcd----	k	m--	-	-----	-c	a
94-14568	ha71	D R R	K K K	M M M	B B	F F F	F F F	S S S	I I I	B1B2	U V	a--d-f-	a	---de---	k	---o	-	---d	abc	-
94-14580	ha71	F2F2	K K K	I I I	A B	F F S	F F F	S S S	I I I	B2B2	K P	-----	a	---de-gh	k	m--	-	a--d	-b-	a
94-14581	ha71	F2F2	K K K	I I I	A A	F F F	F F F	S S S	I I I	B2B2	L P	-----	a	---d-gh	k	m--	-	a--d	-b-	a
94-14582	ha71	H2R	K K K	I I I	A B	F F S	F F F	S S S	I I I	B1B2	L P	-bc-----	a	-bcd----	k	m--	-	a-c-	---c	a
94-14583	ha71	H2O	K K K	I I I	A A	F F F	F F F	S S S	I I I	B2B2	K K	-----	a	---d-gh	k	m--	-	a-c-	---a	
94-14579	ha71	H2R	K K K	I I I	A B	F F S	F F F	S S S	I I I	B1B1	P P	-----	-	---cde-g-	k	m--	-	a-c-	abc	a
94-14595	ha71	F2H2	K K K	I I I	A B	F F F	F F F	S S S	I I I	B2B2	K L	a--d-f-	-	---d-gh	k	m--	-	-----	-b-	a

GREASEWOOD																				
94-14557	gs72	D R	F K K	M M M	A A	F F F	F F F	S S S	I I I	B1B2	U V	a--d-f-	a	---cd--g-	k	m--	a	---d	abc	-
94-14558	gs72	D D	F K K	M M M	A A	F F F	F F F	S S S	I I I	B1B1	S V	-b-----	a	---de---	k	---o	-	a--d	---c	-
94-14559	gs72	D H2	K K K	M M M	A A	F F F	F F F	S S S	I I I	A2B1	U V	a--d-f-	a	---cd--g-	k	m--	-	-----	---	-
94-14560	gs72	D D	K K K	M M M	A B	F F F	F F F	S S S	I I I	B1B2	S S	a--d-f-	a	---cd--g-	k	m--	-	---	-c	-
94-14561	gs72	D D	K K K	M M M	A B	F F F	F F F	S S S	I I I	B1B2	U V	a--d-f-	a	---cd--g-	k	m--	-	---d	adc	-
94-14562	gs72	D R	K K K	M M M	A A	F F F	F F F	S S S	I I I	B1B2	S U	a--d-f-	a	---cd--g-	k	m--	-	---	---	-
94-14574	gs72	D H2	K K K	I M	A A	F F S	F F S	S S S	I I I	B1B1	L2U	a--d-f-	a	---de---	k	---o	-	a-c-	---	-
94-14575	gs72	D D	F K K	I I I	A A	F F F	F F F	S S S	I I I	B1B2	U U	a--d-f-	a	---d-gh	k	m--	-	a--d	---	-
94-14586	gs72	D H2	K K K	I I I	A A	F F F	F F F	S S S	I I I	B1B1	R S	a--d-f-	a	---d-gh	k	m--	-	---	abc	-
94-14587	gs72	D H2	K K K	M M	A A	F F F	F F F	S S S	I I I	B1B2	S V	a--d-f-	a	---cd--g-	k	m--	-	---	abc	-

LITTLE DUCK CREEK																				
94-14563	1d73	D H2	K K K	M M M	A A	F S S	F S S	S S S	I I I	B1B1	U V	a--d-f-	a	---cd--g-	k	m--	a	---c-	abc	-
94-14564	1d73	D D	K K K	I I I	A B	F F F	F F F	S S S	I I I	A2B1	U V	a--d-f-	a	---c--g-	k	m--	-	---d	---	-
94-14565	1d73	H2R	F K K	M M M	A B	F S S	F F F	S S S	I I I	B1B1	U U	-----	a	---cd--g-	k	m--	-	a-cd	---	-
94-14569	1d73	D D	K K K	I M	B B	F F F	F F F	S S S	I I I	B1B2	L U	a--d-f-	a	---cd--g-	k	m--	-	---	-c	-
94-14570	1d73	H2R	K K K	I M	A B	F F F	F F F	S S S	I I I	B1B1	U U	-----	a	---de---	k	---o	-	---	-c	-
94-14571	1d73	D R	F K K	I I I	A B	F F F	F F F	S S S	I I I	B1B1	U U	a--d-f-	a	---cde-g-	k	m--	a	a-cd	---	-
94-14572	1d73	R R R	K K K	I I I	A A	F F F	F F F	S S S	I I I	B1B1	S S	a--d-f-	a	---cd--gh	k	---	-	---	-c	-
94-14573	1d73	D D	F F F	I I I	A A	F F F	F F F	S S S	I I I	B2B2	U U	a--d-f-	a	---d----	k	---	-	a-cd	---	-
94-14576	1d73	H2O	K K K	I I I	A B	F F F	F F F	S S S	I I I	B1B2	U U	a--d-f-	a	---d----	k	m--	-	a-c-	---	-
94-14577	1d73	F2H2	K K K	F I I	A A	F F F	F F F	S S S	I I I	B1B2	L T	a--d-f-	a	-bcd----	k	m--	-	a-c-	---	-
94-14578	1d73	D D	K K K	I M	A A	F S S	F S S	S S S	I I I	B2B2	U U	a--d-f-	a	---d----	k	---	-	a--d	---	-
94-14584	1d73	D H2	K K K	I M	A B	F S S	F S S	S S S	I I I	B1B2	U U	ab--d-f-	a	---de---	k	---o	-	a-c-	abc	-
94-14585	1d73	D H2	K K K	M M	A A	F F F	F F F	S S S	I I I	B1B1	R S	a--d-f-	a	---d----	k	---	-	---	-c	-
94-14588	1d73	D D	K K K	I M	A B	F S S	F S S	S S S	I I I	B1B1	U U	-----	a	---d----	k	---	-	---	-c	-
94-14589	1d73	D D	F F F	M M	A A	F S S	F S S	S S S	I I I	B2B2	U U	a--d-f-	a	---d----	k	---	-	a--d	---	-

SPRING CREEK

94-14590 sc74 F2H2 K K G G A B F F F F S S I I B1B1 I I a--d-f- a -bcde----- m-o - a-c- --- a
94-14591 sc74 H2H2 K K I I B B F F F F S S I I B1B2 I I2 a--d-f- a -bc----- m- - - - - -b- a
94-14592 sc74 H2O K K G I A B F F F F S S I I B1B1 I I - - - - - a -bcde- - - - - -b- a
94-14593 sc74 F2O K S K S A B F F F F S S I I B1B1 I I a--d-f- a -bc----- m- - - - - -a-c- -b- a
94-14594 sc74 F2O K K K K A B F F F F S S I I B1B1 I I2 a--d-f- a -bcde- - - - - m-o - a-c- a-c a

BARCUS CREEK

92-16013 bc30 D R K K I I A B F F F F S S I I A2B1 S U a--d f a --cd--g--k m-- - --d abc -
92-16014 bc30 D H2 F K S S A B F F F F S S I I B1B1 L U a--d f a --cd--g--k m-- - a-cd --c -
92-16015 bc30 D R K K I O A A F F F F S S I I B1B1 U U a--d f a --cd--gh-- m-- - a-cd --- -
92-16016 bc30 D R K K I I A B F F F F S S I I B1B1 L U a--d f a --c--g-- m-- - - - - -
92-16017 bc30 D O K K I I A B F F F F S S I I B1B2 K L2 a--d f a -bcde--k m-- - a-c- --- -
92-16018 bc30 D R F K I I B B F F F F S S I I B2B2 V V a--d f a --cd--g--k m-- a --d --- -
92-16019 bc30 D D F K I I A B F F F F S S I I B1B2 S V a--d f a --cde--g-- m-o a --- -c a
92-16020 bc30 D D K K I I A B F F F F S S I I A2B2 U V a--d f a --de--k --o a --- -c -
92-16021 bc30 D D F K I I A A F F F F S S I I B1B2 V V a--d f a --de--k -- - a-cd --c -
92-16022 bc30 D H2 F K I I A A F F F F S S I I B1B1 V V a--d f a --d-----k --- a-cd abc a
92-16023 bc30 D D K K I I A B F F F F S S I I B1B2 U U a--d f a --d-----k --- a-cd abc -
92-16024 bc30 D D F K I S A A F F F F S S I I B1B1 U U a--d f a --de----- --o a a-cd --- -
93-12062 bc30 D H2 K K I I A A F F F F S S I I B1B1 L U a--d-f- a --de--k --o a-c- --- -
93-12063 bc30 D H2 F K I I A A F F F F S S I I B1B1 U U a--d-f- a --cd--g--k m-- - a-c- --- -
93-12064 bc30 F2H2 K K I S B B F F F F S S I I B1B1 U U a--d-f- a --cd--g--k m-- - a-c- --- -
93-12065 bc30 D D K K I I A B F F F F S S I I B1B1 U V ----- a --cd--g--k m-- - a-c- --- -
93-12066 bc30 R R F K H I A B F F F F S S I I B1B2 L U a-b-d-f- a --d--gh--k m-- - a-c- --- -
93-12067 bc30 D F2 K K I I A A F F F F S S I I B1B1 U U a-b-d-f- a --d--gh--k m-- - a-c- --- -
93-12068 bc30 D D K K H S B B F F F F S S I I B2B2 L U a-b-d-f- a --d--gh--k m-- - a-c- --- -
93-12069 bc30 D D K K I I A B F F F F S S I I B2B2 S V a--d-f- a --d--gh--k m-- - a-c- --- -
93-12070 bc30 D R K K I M A B F F F F S S I I B2B2 L L2 a-b-d-f- a --d--gh--k m-- - a-c- --- -
93-12071 bc30 D R K K I S A B F F F F S S I I B2B2 S V a-b-d-f- a --d--gh--k m-- - a-c- --- -
93-12072 bc30 D H2 K K I I A A F F F F S S I I B1B1 U U a--d-f- a --de--gh-- m-- - -b- --- a
93-12073 bc30 D D F F L S A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12074 bc30 D R K K I I A B F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12075 bc30 D R K K I M A B F F F F S S I I B2B2 U U a--d-f- a --d--gh--k m-- - a-cd --- a
93-12076 bc30 D R K K I S A B F F F F S S I I B1B1 I I a--d-f- a --cd--gh-- m-- - -b- --- -
93-12077 bc30 D R K K I I A B F F F F S S I I B1B1 S S a--d-f- a --de--gh-- m-- - -b- --- -
93-12078 bc30 D R K K I I A B F F F F S S I I B1B1 S S a--d-f- a --de--gh-- m-- - -b- --- -
93-12079 bc30 D R K K I S A B F F F F S S I I B1B2 U U a--d-f- a --d--gh--k m-- - a-cd --- a
93-12080 bc30 D R K K I I A B F F F F S S I I B1B2 U U a--d-f- a --d--gh--k m-- - a-cd --- a
93-12081 bc30 D H2 K K I I A A F F F F S S I I B1B1 S S a--d-f- a --d--gh--k m-- - a-cd --- a
93-12082 bc30 D H2 K K I I A A F F F F S S I I B1B1 S S a--d-f- a --d--gh--k m-- - a-cd --- a
93-12083 bc30 D H2 K K I I A A F F F F S S I I B1B1 S S a--d-f- a --d--gh--k m-- - a-cd --- a
93-12084 bc30 D H2 K K I I A A F F F F S S I I B1B1 S S a--d-f- a --d--gh--k m-- - a-cd --- a
93-12085 bc30 D H2 K K I I A A F F F F S S I I B1B1 S S a--d-f- a --d--gh--k m-- - a-cd --- a
93-12086 bc30 D H2 K K I I A A F F F F S S I I B1B1 S S a--d-f- a --d--gh--k m-- - a-cd --- a
93-12087 bc30 D D K K H S B B F F F F S S I I B2B2 L U a-b-d-f- a --d--gh--k m-- - a-c- --- -
93-12088 bc30 D D K K I I A B F F F F S S I I B2B2 S V a-b-d-f- a --d--gh--k m-- - a-c- --- -
93-12089 bc30 D R K K I S A B F F F F S S I I B1B1 I I a--d-f- a --cd--gh-- m-- - -b- --- -
93-12090 bc30 D R K K I I A B F F F F S S I I B1B2 U U a--d-f- a --d--gh--k m-- - a-cd --- a
93-12091 bc30 H2O K K I I A A F F F F S S I I B1B1 S S a--d-f- a --de--gh-- m-- - -b- --- -
93-12092 bc30 D H2 K K I I A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12093 bc30 D D F F L S A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12094 bc30 D D F F I I A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12095 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12096 bc30 D R K K O O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12097 bc30 D R K K I O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12098 bc30 D R K K I S A A F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a
93-12099 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12100 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12101 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12102 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12103 bc30 D R K K O O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12104 bc30 D R K K I O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12105 bc30 D D F F L L A B F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a
93-12106 bc30 D D F F L L A B F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a
93-12107 bc30 D R K K I I A B F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12108 bc30 D R K K I I A B F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12109 bc30 D R K K I I A B F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12110 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12111 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12112 bc30 D R K K O O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12113 bc30 D R K K I O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12114 bc30 D D F F L L A B F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a
93-12115 bc30 D D F F L L A B F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a
93-12116 bc30 D R K K I S A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12117 bc30 D R K K I I A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12118 bc30 D R K K I I A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12119 bc30 D R K K I I A A F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12120 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12121 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12122 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12123 bc30 D R K K O O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12124 bc30 D R K K I O A B F F F F S S I I B1B2 S S a--d-f- a --cd--g--k m-- a --- -c a
93-12125 bc30 D D F F L L A B F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a
93-12126 bc30 D D F F L L A B F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a
93-12127 bc30 D R K K I I A B F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12128 bc30 D R K K I I A B F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12129 bc30 D R K K I I A B F F F F S S I I B1B2 U V a--d-f- a --d--gh--k m-- - a-cd --- a
93-12130 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12131 bc30 D D F F L L A B F F F F S S I I B1B1 L U a--d-f- a --cde--g-- m-o - a-cd --- -
93-12132 bc30 D R K K I I A B F F F F S S I I B1B2 U V a-b-d-f- a --d-----k --- a-cd --c a

84-MESA

93-12070 ms53 D F2 K K K G I I A A S S F F F S S I I B1B1 L2S a--d-f- a --cde-g--- m-o - abc-
93-12071 ms53 H2O K S I I I A B F F F S S I I B1B1 S S a--d-f- a --c--fg--k m-- -
93-12072 ms53 D F2 K K K G G * A B F F F S S I I B1B1 * a--d-f- a --cdefg--- m-o -
93-12073 ms53 F20 K K K F G F A B F F F S S I I B1B1 F G abcd-f- a --cde-g--- m-o - a-c-
93-12074 ms53 F20 K K K G I G A A F F F S S I I B1B1 F S a--d-f- a --cde-g--- m-o - a-c-
93-12075 ms53 F2H1 K K K I S A A S S S F F F S S I I B1B1 G S a--d-f- a abcd----- m-- - a-c-
93-12076 ms53 D D K K K I I I A A S S S F F F S S I I B1B2 G S ab-d-f- a -bcd-----k m-- -
93-12077 ms53 D F2 K K K G I I A A S S S F F F S S I I B1B1 F S ab-d-f- a -bcde----- m-o - a-c-
93-12081 ms53 H2R K K K M S B B F F F S S I I B1B1 L2T a--d-f- a --c--g--- m-- -
93-12082 ms53 D H2 K K K S S A B F F F S S I I B1B2 L L2 a--d-f- a --cd--g--k m-- - a-c-
93-12083 ms53 D R K K K L L A B F F F S S I I B1B2 L U a--d-f- a --cd--g--k m-- -
93-12084 ms53 D R K K K G M A B F F F S S I I B1B1 U U a--d-f- a --c--g--- m-- - a-c-
93-12085 ms53 D R K K K G S A B F F F S S I I B1B1 S S a--d-f- a --cd--gh-- m-- -
93-12086 ms53 D F2 K K K G S A B F F F S S I I B1B1 S S a--d-f- a -bc--g--- m-- - a-c-
93-12087 ms53 F2H2 K K K F G A B F F F S S I I B1B1 S S a--d-f- a --cde-g--- m-o - abc-
93-12088 ms53 F2F2 K K K G I A A S S S F F F S S I I B1B1 S S a--d-f- a -bc--g--- m-- -
93-12090 ms53 D H2 K K K G G A B F F F S S I I B1B1 S S a--d-f- a --cd--gh-- m-- - b-b-
93-12093 ms53 D F2 K K K G I A B F F F S S I I B1B1 S S abcd-f- a --c--g--- m-- - b-b-

SQUARE-S WELL

93-17388 ss57 D R K K K I I B B F F F S S I I B1B2 L T a--d-f- a --c--g--- m-- -
93-17391 ss57 D D K K K I L A B F F F S S I I B1B2 S U a--d-f- a --d--gh-k m-- -
93-17393 ss57 D R K K K L L A B F F F S S I I B1B2 S U a--d-f- a --cd--g--k m-- -
93-17394 ss57 D R K K K L L A B F F F S S I I B1B1 U U a--d-f- a --cde-g--- m-o -
93-17395 ss57 D R K K K L L A B F F F S S I I B2B2 L T a--d-f- a --d--gh-k m-- -
93-17396 ss57 D R K K K L L A B F F F S S I I B2B2 L T a--d--g a ----d-----k ---
93-17397 ss57 R R K K K L L A B F F F S S I I B1B2 L L S
93-17398 ss57 D F2 K K K L L A B F F F S S I I B1B2 T U
93-17399 ss57 D H2 K K K L L A A F F F S S I I B1B2 P S a--d-f- a --de-gh-k m-- -
93-17400 ss57 D D K K K L L A B F F F S S I I B1B2 L U a--d-f- a --d--gh-k m-- -
93-17401 ss57 D F2 K K K L L A A F F F S S I I B1B1 L U ab-d-f- a ----d-----k --- a-cd
93-17402 ss57 D D K K K L L A A F F F S S I I B1B1 L U ----- a --d-----k ---
93-17403 ss57 D R K K K I I A A F F F S S I I B2B2 L U a--d-f- a --cd--gh-- m-- -
93-17404 ss57 D F2 K K K L L A B F F F S S I I B1B2 S U ab-d-f- a --cd--gh-- m-- -
93-17405 ss57 F2F2 K K K L L A B F F F S S I I A2B1 S U a--d-f- a --c--g--- m-- - a-c-
93-17406 ss57 D D F F F L L A A F F F S S I I B1B2 U U a--d-f- a ----d-----k --- a-cd

WEST FORK

93-21588	WF60	D	D	K	K	G	O	B	B	F	F	F	F	F	F	S	S	I	I	B2B2	K	U	a--d-f-	a	-bcd--gh--	m--	-	a-c-	-b-
93-21589	WF60	D	D	K	K	F	F	A	B	F	F	F	F	F	F	S	S	I	I	B2B2	K	N	a--d-f-	a	---de-gh--	m-o	-	a-c-	-c-
93-21590	WF60	D	O	K	K	F	F	B	B	F	F	F	F	F	F	S	S	I	I	B2B2	K	K	a--d-f-	a	---d--gh--	m--	-	---	-bc-
93-21591	WF60	D	O	K	S	I	I	B	B	F	F	F	F	F	F	S	S	I	I	B2B2	S	U	a--d-f-	a	-bcde-----	m-o	-	a-cd	-b-
93-21592	WF60	O	O	S	S	O	O	A	B	F	F	F	F	F	F	S	S	I	I	B2B2	S	Z*	a--d-f-	a	-bcd--gh--	m--	-	a-c-	---
93-21593	WF60	D	O	K	S	F	I	A	B	F	F	F	F	F	F	S	S	I	I	B2B2	U	*	a--d-f-	a	-bcd--gh--	m--	-	a-cd	-b-
93-21594	WF60	D	O	K	S	F	F	A	B	F	F	F	F	F	F	S	S	I	I	B1B2	L	S	a--d-f-	a	-bcd--gh--	m--	-	a-cd	-b-
93-21595	WF60	D	O	K	K	F	F	A	A	S	S	S	S	S	S	S	S	I	I	B1B2	L	U	a--d-f-	a	---cd--gh--	m--	-	a-cd	-b-
93-21596	WF60	O	O	S	S	F	I	B	B	F	F	F	F	F	F	S	S	I	I	B2B2	S	U	a--d-f-	a	---c---g---	m--	-	a-c-	---
93-21597	WF60	D	O	K	S	F	I	A	B	F	F	F	F	F	F	S	S	I	I	B2B2	K	U	a--d-f-	a	---cde-g---	m-o	-	a-cd	-b-
93-21598	WF60	O	O	K	S	F	I	B	B	F	F	F	F	F	F	S	S	I	I	B2B2	K	U*	a--d-f-	a	-bc-----g---	m--	-	a-cd	---
93-21599	WF60	F20		K	K	I	I	A	A	S	S	S	S	S	S	S	S	I	I	B1B2	L	S	a--d-f-	a	---cde-g---	m-o	-	a-c-	---
93-21600	WF60	O	O	K	K	I	I	A	B	F	F	F	F	F	F	S	S	I	I	B2B2	L	S	a--d-f-	a	-bcde-----	m-o	-	a-c-	---
93-21601	WF60	D	D	K	K	F	G	A	B	F	F	F	F	F	F	S	S	I	I	B2B2	K	S	a--d-f-	a	---de-gh--	m-o	-	a-c-	-c-
93-21602	WF60	D	F2	K	S	F	F	B	B	F	F	F	F	F	F	S	S	I	I	B1B2	R	T	ab--d-f-	a	-bcd--gh--	m--	-	a-c	---

Appendix 2. Summaries of complete genetic variability measures for each population of WRRR horses.

BARCUS CREEK

LOCUS #ALS	HO	VAR	He	N	X	ENA	FIS	X2	df	Heub	X3	VAR	Fisub
Tf	5	.595	.0067	.530	37.	.291	2.127	-.122	10	.537	.421	.0032	-.107
AlB	2	.351	.0063	.324	37.	.085	1.478	-.084	1	.328	.180	.0030	-.070
Es	6	.243	.0051	.531	37.	5.770*	2.131	.542	15	.538	11.116	.0039	.548
Al	2	.514	.0069	.499	37.	.016	1.994	-.029	1	.506	.009	.0000	-.015
Gc	2	.135	.0032	.127	37.	.019	1.145	-.064	1	.129	.091	.0025	-.050
PGD	2	.297	.0058	.254	37.	.273	1.340	-.170	1	.257	.885	.0033	-.155
PGM	2	.054	.0014	.053	37.	.001	1.055	-.020	1	.054	.001	.0013	-.006
GPI	1	.000	.0000	.000	37.	.000	1.000	.000	0	.000	.000	.0000	.000
Hb	3	.378	.0065	.464	37.	.585	1.867	.185	3	.470	1.415	.0018	.196
PI	7	.541	.0069	.700	37.	1.344	3.313	.228	21	.710	2.100	.0015	.238

MEAN VALUES FOR BIOCHEMICAL LOCI

MEAN	32	.311	.0181	.348	37.	1.485	1.745	.107	16.132	54	.353	16.218	.0021	.119
Abg	3	.467					1.878				.473		.0030	
Cbg	2	.058					1.062				.059		.0014	
Dbg	8	.687					3.192				.696		.0017	
Kbg	2	.134					1.154				.136		.0026	
Pbg	4	.672					3.051				.681		.0003	
Qbg	3	.511					2.044				.518		.0012	
Ubg	2	.183					1.224				.186		.0031	

AVE F .046

AVE F .058

MEAN VALUES FOR BLOOD GROUP LOCI

MEAN	24	.387					2.297				.443		.0021	
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MEAN VALUES FOR ALL LOCI

MEAN	56	.364					1.972				.390		.0021	
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AVE # ALLELES ELEC = 3.200 AVE # ALLELES BG = 3.429 AVE # ALLELES TOTAL = 3.294

GREASEWOOD AREA

LOCUS #	ALS	Ho	VAR	He	N	X	ENA	Fis	X2	df	Heub	X3	VAR	Fisub
Tf	3	.636	.0231	.483	11.	.536	1.935	-.318	1.109	3	.506	.730	.0102	-.258
AlB	2	.273	.0198	.235	11.	.067	1.307	-.161	.284	1	.246	.128	.0108	-.108
ES	1	.000	.0000	.000	11.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
Al	2	.364	.0231	.397	11.	.031	1.658	.084	.078	1	.416	.174	.0071	.126
Gc	2	.091	.0083	.086	11.	.003	1.094	-.057	.036	1	.090	.001	.0062	-.009
PGD	2	.273	.0198	.235	11.	.067	1.307	-.161	.284	1	.246	.128	.0108	-.108
PGM	2	.273	.0198	.235	11.	.067	1.307	-.161	.284	1	.246	.128	.0108	-.108
GPI	1	.000	.0000	.000	11.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
Hb	3	.727	.0198	.490	11.	1.264	1.970	-.484	2.579	3	.513	1.911	.0055	-.417
Pi	5	.818	.0149	.714	11.	.167	3.501	-.146	.234	10	.748	.097	.0013	-.094

MEAN VALUES FOR BIOCHEMICAL LOCI

MEAN	23	.345	.0282	.287	11.	1.285	1.608	-.202	4.887	21	.301	3.296	.0063	-.147
Abg	3	.393					1.648				.412		.0113	
Cbg	1	.000					1.000				.000		.0000	
Dbg	4	.607					2.547				.636		.0054	
Kbg	2	.090					1.098				.094		.0064	
Pbg	4	.546					2.201				.572		.0086	
Qbg	3	.550					2.221				.576		.0064	
Ubg	1	.000					1.000				.000		.0000	

MEAN VALUES FOR BLOOD GROUP LOCI

MEAN	18	.312					1.959				.370		.0056	
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MEAN VALUES FOR ALL LOCI

MEAN	41	.298					1.752				.330		.0060	
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AVE # ALLELES ELBC = 2.300 AVE # ALLELES BG = 2.571 AVE # ALLELES TOTAL = 2.412

HAMMOND AREA

LOCUS #	ALS	HO	VAR	He	N	X	ENA	Fis	X2	df	Heub	X3	VAR	Fisub
TF	4	.667	.0278	.698	9.	.013	3.309	.045	.018	6	.739	.086	.0009	.098
AlB	1	.000	.0000	.000	9.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
ES	2	.111	.0123	.106	9.	.002	1.118	-.048	.021	1	.112	.001	.0087	.010
Al	2	.667	.0278	.494	9.	.543	1.975	-.350	1.100	1	.523	.678	.0007	-.275
Gc	2	.556	.0309	.475	9.	.123	1.906	-.170	.259	1	.503	.098	.0025	-.105
PGD	1	.000	.0000	.000	9.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
PGM	1	.000	.0000	.000	9.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
GPI	1	.000	.0000	.000	9.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
Hb	2	.444	.0309	.444	9.	.000	1.799	-.001	.000	1	.470	.027	.0052	.055
Pl	3	.778	.0216	.641	9.	.263	2.799	-.213	.410	3	.679	.192	.0016	-.146

MEAN VALUES FOR BIOCHEMICAL LOCI

MEAN	19	.322	.0547	.286	9.	.418	1.691	-.127	1.807	13	.303	1.083	.0020	-.065
AVE F														

AVE F -.074

AVE F -.036

Abg	3	.304		1.436		.322		.0161						
Cbg	2	.380		1.613		.402		.0096						
Dbg	5	.745		3.929		.789		.0022						
Kbg	1	.000		1.000		.000		.0000						
Pbg	3	.535		2.152		.566		.0084						
Qbg	4	.647		2.846		.685		.0065						
Ubg	1	.000		1.000		.000		.0000						

MEAN VALUES FOR BLOOD GROUP LOCI

MEAN	19	.373		1.997		.438		.0063						
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MEAN VALUES FOR ALL LOCI

MEAN	38	.322		1.817		.358		.0038						
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AVE # ALLELES ELEC = 1.900 AVE # ALLELES BG = 2.714 AVE # ALLELES TOTAL = 2.235

LITTLE DUCK CREEK

LOCUS #	ALS	Ho	VAR	He	N	X	ENA	Fis	X2	df	Heub	X3	VAR	Fisub
Tf	5	.533	.0178	.630	15.	.222	2.714	.153	.353	10	.652	.495	.0043	.182
AlB	2	.133	.0083	.320	15.	1.633	1.471	.583	5.104*	1	.331	5.350*	.0074	.597
Es	2	.067	.0044	.064	15.	.002	1.068	-.042	.026	1	.066	.001	.0036	-.007
Al	2	.533	.0178	.444	15.	.270	1.799	-.201	.607	1	.459	.390	.0032	-.161
Gc	2	.400	.0171	.320	15.	.300	1.471	-.250	.938	1	.331	.651	.0074	-.208
PGD	2	.333	.0159	.278	15.	.165	1.385	-.199	.594	1	.288	.380	.0080	-.159
PGM	2	.133	.0083	.125	15.	.008	1.143	-.067	.067	1	.129	.015	.0060	-.031
GPI	1	.000	.0000	.000	15.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
Hb	3	.333	.0159	.485	15.	.711	1.951	.313	1.467	3	.502	1.690	.0036	.336
Pl	6	.400	.0171	.602	15.	1.017	2.514	.336	1.689	15	.623	1.919	.0080	.358

MEAN VALUES FOR BIOCHEMICAL LOCI

MEAN	27	.287	.0389	.327	15.	.739	1.652	.123	10.845	34	.338	10.889	.0052	.152
Abg	3	.524					2.102				.542		.0013	
Cbg	1	.000					1.000				.000		.0000	
Dbg	5	.609					2.555				.630		.0056	
Kbg	2	.066					1.070				.068		.0037	
Pbg	4	.709					3.440				.733		.0016	
Qbg	3	.467					1.877				.483		.0065	
Ubg	2	.247					1.327				.256		.0081	

MEAN VALUES FOR BLOOD GROUP LOCI

MEAN	20	.375					2.190				.436		.0050	
AVE F														

MEAN VALUES FOR ALL LOCI

MEAN	47	.346					1.873				.378		.0051	
AVE F														

AVE # ALLELES ELEC = 2.700 AVE # ALLELES BG = 2.857 AVE # ALLELES TOTAL = 2.765

84-MESA

LOCUS #	ALS	HO	VAR	He	N	X	ENA	Fis	X2	df	Heub	X3	VAR	Fisub				
Tf	6	.889	.0058	.756	18.	.420	4.101	-.176	.556	15	.778	.369	.0012	-.143				
AlB	3	.111	.0058	.202	18.	.736	1.253	.450	3.644	3	.208	3.896	.0072	.465				
ES	5	.706	.0130	.725	17.	.009	3.634	.026	.012	10	.747	.051	.0012	.055				
Al	2	.500	.0147	.486	18.	.007	1.946	-.029	.015	1	.500	.000	.0007	.000				
Gc	2	.118	.0065	.408	17.	3.513	1.690	.712	8.610*	1	.420	8.816*	.0043	.720				
PGD	2	.056	.0031	.054	18.	.001	1.058	-.029	.015	1	.056	.000	.0026	.000				
PGM	2	.333	.0131	.401	18.	.206	1.671	.169	.513	1	.412	.662	.0043	.192				
GPI	1	.000	.0000	.000	18.	.000	1.000	.000	.000	0	.000	.000	.0000	.000				
Hb	2	.167	.0082	.152	18.	.025	1.180	-.096	.168	1	.156	.078	.0057	-.066				
Pi	7	.529	.0156	.650	17.	.380	2.875	.186	.585	21	.670	.746	.0065	.209				
MEAN VALUES FOR BIOCHEMICAL LOCI														AVE F	.121	AVE F		.143
MEAN	32	.335	.0256	.383	17.	.777	2.041	.125	14.117	54	.395	14.619	.0034	.150				
MEAN VALUES FOR BLOOD GROUP LOCI																		
MEAN	22		.300				2.055				.365		.0054					
MEAN VALUES FOR ALL LOCI																		
MEAN	54		.349				2.046				.382		.0042					
AVE # ALLELES ELEC = 3.200														AVE # ALLELES BG = 3.143	AVE # ALLELES TOTAL = 3.176			

SPRING CREEK

LOCUS #	Als	Ho	VAR	He	N	X	ENA	Fis	X2	df	Heub	X3	VAR	Fisub
TF	3	.800	.0400	.660	5.	.148	2.941	-.212	.225	3	.733	.041	.0009	-.091
AlB	2	.200	.0400	.180	5.	.011	1.220	-.111	.062	1	.200	.000	.0207	.000
ES	2	.400	.0600	.480	5.	.067	1.923	.167	.139	1	.533	.312	.0035	.250
Al	2	.800	.0400	.480	5.	1.067	1.923	-.667	2.222	1	.533	1.250	.0035	-.500
GC	1	.000	.0000	.000	5.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
PGD	2	.200	.0400	.180	5.	.011	1.220	-.111	.062	1	.200	.000	.0207	.000
PGM	1	.000	.0000	.000	5.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
GPI	1	.000	.0000	.000	5.	.000	1.000	.000	.000	0	.000	.000	.0000	.000
Hb	2	.200	.0400	.180	5.	.011	1.220	-.111	.062	1	.200	.000	.0207	.000
Pl	2	.400	.0600	.320	5.	.100	1.471	-.250	.313	1	.356	.078	.0208	-.125

MEAN VALUES FOR BIOCHEMICAL LOCI

AVE F - .130

AVE F - .047

MEAN	18	.300	.0316	.248	5.	.545	1.492	-.210	3.084	9	.276	1.682	.0091	-.089
Abg	2	.495					1.979				.550		.0010	
Cbg	1	.000					1.000				.000		.0000	
Dbg	2	.480					1.923				.533		.0035	
Kbg	1	.000					1.000				.000		.0000	
Pbg	2	.465					1.870				.517		.0059	
Qbg	3	.584					2.403				.649		.0054	
Ubg	1	.000					1.000				.000		.0000	

MEAN VALUES FOR BLOOD GROUP LOCI

MEAN	12	.289					1.909				.361		.0052	
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MEAN VALUES FOR ALL LOCI

MEAN	30	.265					1.664				.311		.0075	
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AVE # ALLELES ELEC = 1.800 AVE # ALLELES BG = 1.714 AVE # ALLELES TOTAL = 1.765

