

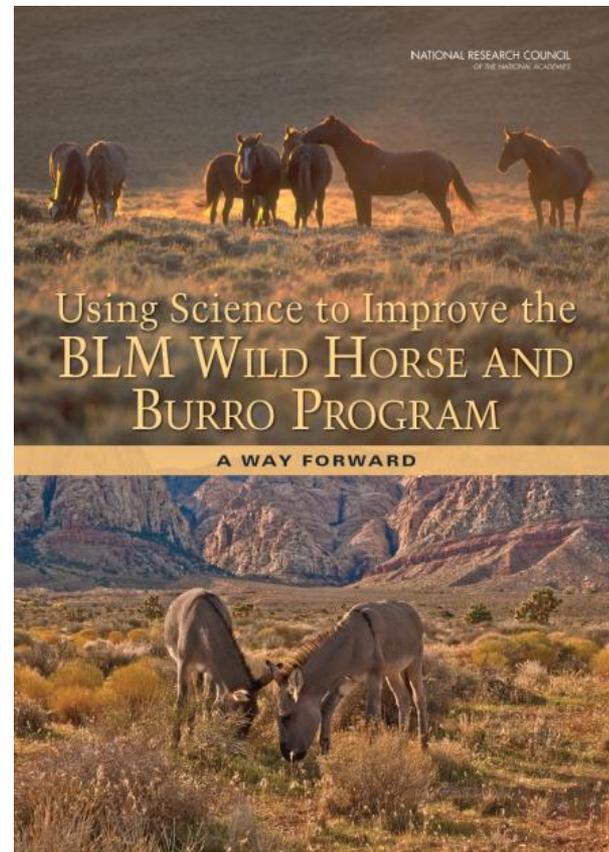
Genetic Diversity in Free-Ranging Horse and Burro Populations

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Statement of task

- What does information available on wild horse and burro herds' genetic diversity indicate about long-term herd health, from a biological and genetic perspective?
- Is there an optimal level of genetic diversity within a herd to manage for?
- What management actions can be undertaken to achieve an optimal level of genetic diversity if it is too low?

Importance of genetic diversity to long-term herd health

- Small herds are likely to suffer from genetic drift, or the loss of rare genetic variants due to chance
- In small herds that are isolated, inbreeding is inevitable
- Fitness costs associated with the loss of genetic diversity due to genetic drift and inbreeding
 - reduced survivorship in disease outbreaks
 - increased incidence of congenital defects
 - reduced ability to respond to and survive changes in the environment

Components of genetic diversity

- Heterozygosity (H_o) – the proportion of individuals in a population that have 2 different variants of a gene
- Allelic diversity (A) – the number of different variants of a gene found in a population
- Coefficient of inbreeding (F_{IS}) – the probability that individuals in a population share alleles that are derived from a common ancestor

Recent genetic studies of WHB

Since 2000, studies have been conducted by E. Gus Cothran at the University of Kentucky and more recently at Texas A&M University

Horses:

- monitor genetic diversity
- assess the similarity of herd lineages to domestic horse lineages
- studies based on 12 highly variable microsatellite loci

Burros:

- monitor genetic diversity
- studies based on 9 microsatellite loci

Is there an optimal level of genetic diversity in a managed herd or population?

Garner et al. (2005) surveyed 108 mammal species including both “healthy” and “demographically challenged”* populations

- Average heterozygosity overall 0.677 ± 0.010
- Average heterozygosity healthy 0.715 ± 0.240
- Average heterozygosity challenged 0.525 ± 0.040

They also demonstrated differences among families within orders of mammals, suggesting that comparisons were most informative when made with closely related species

*experienced population declines, bottlenecks, isolation or reduction in range

Table 5-1 Genetic Diversity Estimates for Free-Ranging and Domestic Horses

Population	Allelic diversity	Observed heterozygosity	F_{is}
Sable Island	5.60 ± 1.35 SD	0.647 ± 0.035 SD	0.070
Sorraia	3.32 ± 0.95 SD	0.450 ± 0.212 SD	-0.061 to 0.018
Domestic breeds from Canada and Spain	5.50 ± 0.42 SE to 8.25 ± 0.57 SE	0.66 ± 0.02 SE to 0.79 ± 0.04 SE	-0.046 to 0.083
South European native horse breeds	5.75 ± 1.54 SD to 8.08 ± 1.93 SD	0.687 ± 0.170 SD to 0.772 ± 0.099 SD	not estimated
Domestic breeds (10 breeds, 191 individuals)	3.6 ± 0.3 SE to 4.5 ± 0.4 SE	0.494 ± 0.057 SE to 0.626 ± 0.058 SE	not estimated
Colonial Spanish horse populations (n=5)	4.00 ± 1.27 SD to 7.73 ± 2.05 SD	0.54 ± 0.18 SD to 0.74 ± 0.10 SD	-0.069 to 0.058
Assateague Island	7.4 ± 1.8 SD	0.794 ± 0.102 SD	not estimated

SD = standard deviation, SE = standard error

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Genetic diversity in horses managed by the BLM

Reviewed reports from Cothran from 2001-2012
102 HMAs, sample sizes 9-115 (Table 5-2)

	Average	Std dev	Range
Heterozygosity	0.716	0.056	0.497-0.815
Allelic diversity	6.06	1.09	2.58-8.00
Inbreeding coefficient	-0.012	0.071	-0.230-0.133

BLM handbook – critical risk value of heterozygosity is 0.660

- 8 of 102 HMAs below critical risk value

If same standard applied to allelic diversity – critical risk 4.97

- 1 additional HMA below critical risk value

One third (n=34) of HMAs have diversity levels below mean

Genetic diversity in burros

Published Genetic Diversity Estimates for Burros

Population	Allelic diversity	Observed heterozygosity
5 Spanish donkey breeds	8.70 ± 4.40 SD	0.637-0.684
3 Sicilian donkey breeds	6.07 ± 0.72 SD	0.581 ± 0.059 SD

SD = standard deviation

Reviewed reports from Cothran from 2002-2011
12 HMAs, sample sizes 2-49

	Average	Std dev	Range
Burro HMAs			
Heterozygosity	0.408	0.107	0.245-0.551
Allelic diversity	3.333	0.677	1.77-4.11
Inbreeding coefficient	0.093	0.105	-0.084-0.277
Domestic herds (4)			
Heterozygosity	0.450	0.094	
Allelic diversity	4.143	1.386	
Inbreeding coefficient	0.153	0.095	

Management actions to achieve optimal genetic diversity

- Effects of Fertility Control
- Individual Based Genetic Management
- Translocation for Genetic Restoration

Effects of fertility control

The maintenance of genetic diversity depends on the genetic effective size of a herd, which is maximized when

- breeding sex ratios are equal
- family sizes for individuals are equal
- herd sizes do not fluctuate between generations
- Contracepting large numbers of females will reduce both the breeding sex ratio and increase the variance in family sizes and could result in the loss of genetic diversity
- In a harem species such as horses, the number of breeding males is usually less than the number of breeding females
- Reducing the number of males through contraception may allow younger bachelor males to breed, and may not affect the breeding sex ratios or family sizes as strongly
- Prior to implementing these actions, their effects should be tested using a modeling approach

Individual based genetic management

Managing horses as individuals allows for the maximum retention of genetic diversity, but is labor intensive

- monitoring of reproductive success
- recording of pedigree information
- contraception of individuals once their reproductive goal is met

Has been successfully implemented at Assateague Island and Shackleford Banks, but at Assateague it took a long time to reduce herd size and at Shackleford they continue to take off some young horses for adoption

In HMAs where horses can be individually identified, consistently tracked and reliably contracepted, this form of management might be feasible

Translocation for genetic restoration

- The total population of horses on BLM lands is over 30,000 but it is divided into smaller, fragmented units
- If maintenance of genetic variability over the long term is the goal, the effective population size will need to be much higher than even the largest HMA
- Managing some herd populations as a single population would help BLM maintain genetic diversity while also maintaining AMLs
- This will require consistent monitoring of genetic diversity and BLM assisted movements (translocations) of animals between HMAs to augment those with reduced diversity

Translocation for genetic restoration

The report includes some guidance and criteria for translocations including:

- the number of animals to translocate
- the appropriate interval between translocations
- the use of genetic criteria for selecting individuals for translocation
- behavioral and social factors to consider
- implications for translocating horses into herds whose numbers are being controlled by contraception

Other considerations

Aside from concerns about the overall loss of diversity through genetic drift and inbreeding, there are concerns about the expression of genes that cause congenital defects

- The committee recommends that BLM collect data on abnormal phenotypes during all management actions and consult with geneticists and equine veterinarians where phenotypic data suggest genetic disorders

Other considerations

The management of some HMAs is complicated by concerns about associations with Spanish bloodlines or unique morphological traits

- Cerbat Mountain, AZ
- Pryor Mountains, MT
- Sulphur, UT
- Kiger, OR
- The committee recommends that BLM examine in greater depth the genetic constitution of these herds and share the findings with the public
- It is possible that isolation of these herds to maintain genetic purity may lead to the unnecessary loss of genetic diversity

A word about burros

- The total population of burros is only about 5,000 and exists in small, fragmented units
- Genetic studies reveal very low diversity
- Only one of the 12 genetic studies of burro HMAs appears to have been conducted after 2005 - the current status is not known
- Genetic monitoring and translocations to maintain genetic diversity may be more necessary for burros than for horses

Conclusions

The committee recommends that the BLM:

- Continue to monitor genetic diversity as part of routine management of horses and burros
- If genetic diversity is statistically significantly lower in subsequent surveys of an HMA, prioritize HMA for genetic management
- Manage some herd populations as a single population to help maintain genetic diversity
- Collect data on abnormal phenotypes during gathers and consult with geneticists and equine veterinarians where phenotypic data suggest genetic disorders
- Examine the genetic constitution of herds with Spanish bloodlines or unique morphological traits and share the findings with the public so that informed decisions can be made about the sustainability of these herds
- Collect more genetic information on burros