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Aspen's Horse Genes

Allele Description:
ww- fully pigmented, no lethal white
G: G?- born dark, grey out with age. Could be GG or Gg
E: E?- have black skin, but appear a different color. Black pigment on legs
A: A?- black hair is in point on rear and legs. Could be AA or Aa
C: CC- there is no dilution in color because they grey out
D: dd- no dilution of pigment. Born solid color then grey with age
TO: toto- not a paint
O: oo- non-overo horse. No paint coloring, one color
F: ?- not relevant because no red coloring
P: pp- there was no lightening of pigment under her belly. All one color
Rn: rnrn- no roan pattern
Rb: rbrb- no rabicano traits
Lp: lplp- not an appaloosa - the horse still has the alleles, just not the version that would make it an appaloosa

Table 2

Population size is large	Not met-population is less than 30
No Migration	Not Met- Horses are brought in and out of boarding facility
No Mutations	Met- No mutations found
No Natural Selection	Met- No Natural selection in boarding/breeding facility
Random Mating	Not Met- Planned Breeding with stallions

Table 3

	p^2	2pq	q^2
Predicted	81	.18	.01
Actual	.8	.2	0

This example of the population is close to being at equilibrium, but not all of the assumptions are met. So the H-W assumption is not met.

Hypothesis: Does not meet H-W Assumptions

The population size was not met because there are less than 30 horses to breed. There are only three stallions for the broodmares to pick from. Migration was not met because horses are not able to come and go as they please; they are houses in stalls and dry lots. Mutations do not show up because there is no inbreeding occuring in the breeding facility. Since the horses are housed in a facility, there is no way for predators and diseases to interrupt life. There is no random mating that occurs in this facility because humans are deciding what stallion will be bred to the mares. This way of life is not considered to meet the requirements for the H-W Equilibrium.

Mendelian

The 'O' gene is considered Mendelian. Horses will have a white pattern with some black coloring as shown above. The white acts as the dominant color. 'OO' is lethal white, 'Oo" is patterned white, and 'oo' has no white

Incomplete Dominance

Incomplete dominance is the blending of traits. The 'CC^cr' trait shows the red pigment diluted to yellow and the black pigment is not affected. The 'C^crC^cr' trait shows both pigments are diluted to cream. Skin and eye color are also diluted.

Pleiotropy

The 'W' gene is considered a pleiotropy inheritance. It can control other phenotypes that occur under 'WW'. If a horse is 'WW' it can only live a few days because it creates problems with the digestive system.

Epistasis

The 'A' gene is considered Epistasis because the 'A' gene is changed by the presence of 'E'. This means the 'A' will be suppressed and the horse will be black. 'A' has no effect on 'ee'.

Table 1

Genotypes	2015	2018	2019	2020	Trend?	Potential Reason?
w	1	1	1	1	No change	Fatal if not ww
g	.85	.97	.89	.92	Consistent	Most horses grey with age
e	.67	.63	.65	.72	increase	Horses not from FRC
a	.75	.41	0	.32	Decreases and then increases	Horses are not from FRC
cr	.05	0	0	.87	Increases dramatically	Horses are not from FRC
d	.91	.95	.96	.87	Consistent	FRC broodmares are commonly dark bays or sorrels
to	1	.93	.94	.97	Consistent	Low population of Tobianas at facility
o	1	.98	1	1	Consistent	overo pattern not common
f	.67	.37	.96	.32	Decreases	Large sorrel population at the facility
p	1	.68	.83	.74	Increase	Horses not from FRC
rn	.91	.88	.98	.97	Consistent	Low population of roans
rb	1	.95	.98	1	Consistent	low population of appaloosa
lp	1	1	1	1	Consistent	Common gene

This table shows that these 2020 alleles are not within the H-W equilibrium. These certain genes and alleles within our boarding facility fluctuate depending on if they are bred though FRC, whether or not the owner chose them for a certain color, and who's coming in and out of the boarding facility. The data within some common genes such as ww is the same within every equine, however with genes such as aa,ee,cr, they are constantly fluctuating due to the many different reasons as explained above. One example of a gene that changes is the decrease in the "ff" alleles.