

Horse Coat Color Project

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Scoring Coat Color

- ww because is full color
- gg because does not show signs of silvering
- ee because is not black
- aa because horse is not Ee or EE
- CC because horse is completely pigmented
- dd because no dilution of color
- toto because no large white patches
- oo because no spotting
- Ff or FF because is an ee horse, flaxen points
- pp because no lightening of the hair
- rnrn because there is no roan pattern
- rbrb because no rabicano "coon" markings
- lplp because it is not an appaloosa

Slou
Chestnut colored horse, no black, sorrel mane and tail with white markings.



Mendelian (dominant/recessive):

This genetic interaction means that some alleles of the gene are recessive and some are dominant. To be dominant it must have at least one of the dominant allele and to be recessive it must have 2 of the recessive alleles.

In this horse, we can see that it has black pigment in its hair in certain points, meaning it has at least 1 E allele. If this horse had no black, then it would be an ee horse.



Pleiotropy:

This interaction is where one gene will determine what happens in other

In this picture we see a white foal. This is actually a lethal coat color, where this is the WW allele. If a horse has this it is lethal, it is called Lethal White Foal Syndrome. giving them many neurological defects, hearing defects, and more. This is a pleiotropy.



Incomplete dominance:

This interaction is where one gene does not completely take over another, therefore it allows for both of the genes to come together to make something that is in between the two. In this picture we can see that each of these coat colors genes were incomplete dominance, so they combined to make a roan horse.



Epistasis:

This interaction is when an allele from one phenotype contributes to the effect of the phenotype of another gene, hiding actions of another gene

This picture shows an Appaloosa which has the term epistasis because the gene Lp. This gene is a spotting gene where there is epistasis on all other color alleles.



Qualitative Analysis	
Population size is large X	There are not enough horses for a large population
No migration X	Owners take horses home when not in attendance of the school
No mutations ✓	No Mutations Found
No natural selection ✓	No Natural Selection in captivity on college campus
Random mating X	Selective Breeding
Result: Based on our analysis, we hypothesize that our horse population is not in H-W equilibrium because it failed to meet all five of the required H-W assumptions	

Individual Recessive Allele Frequency and Trends						
	2015 q	2018 q	2019 q	2020 q	Trend	Potential Reason
w	1	1	1	1	No change	Selective Breeding- WW is fatal
g	.85	.97	.89	1	No change	Selective Breeding- on trend to not have greying
e	.67	.63	.65	.89	Unpredictable	migration
a	.75	.41	0	0	Unpredictable	migration
cr	.05	0	0	.32	Unpredictable	migration
d	.91	.95	.96	.97	No change	Selective Breeding
to	1	.93	.94	.97	No change	Selective Breeding
o	1	.98	1	1	No change	Selective breeding-
f	.67	.37	.96	.63	Unpredictable	migration
p	1	.68	.83	.45	Unpredictable	migration
rn	.91	.88	.98	.32	Unpredictable	migration
rb	1	.95	.98	.97	No change	Selective Breeding- Rabicano's are not on trend
lp	1	1	1	.97	No change	Selective Breeding- Appaloosa's are not as desired

Predicted C/Ccr vs Actual C/CCr			
	p^2	2pq	q^2
Predicted	.81	.18	.01
Actual	.9	0	.1

The data collected here we can see our predictions are very close to our actual numbers. We had the majority of dominant C alleles, represents by the p. The Ccr alleles are represented by the q. We had no horses with a combination of the two, unlike we predicted.

The data collected over several years is shown in the table above. The data pertains to the frequency of the recessive allele for each gene (by year) and also determines what kinds of trends are present and why. As you can see, six of the genes are rather unpredictable. Whereas seven of the alleles are fairly consistent. The consistent alleles can be predicted for this sample of horses due to the selective breeding of the horses. Selective breeding follows popular trends in the present culture as far as what is considered desirable, and what is not. As for the six unpredictable alleles, we can attribute their unpredictability to the fact that the horses come from all over, and they all have different owners. Because they come from all over this would be considered migratory behavior and it opens up the door for all kinds of other factors that can play a part in the alleles present.

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Genotype	# of Horses	q[2]	q
ww	20	1	1
gg	20	1	1
ee	16	.8	.894427191
aa	0	0	0
crcr	2	.1	.316227766
dd	19	.95	.9746794345
toto	19	.95	.9746794345
oo	20	1	1
ff	8	.4	.632455532
pp	4	.2	.4472135955
rnrn	20	1	.316227766
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lplp	19	.95	.9746794345

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Phenotype	How many	Genotype	Genotype Frequency from Data
Full Color	18	CC	.9
Diluted to palomino, buckskin, or dark beige with black points	0	CCcr	.0
Diluted to very pale cream color	2	Ccr Ccr	.1

How many C alleles?	How many Ccr alleles?
36	0
$p=.9$	$q=.0$

	p^2	$2pq$	q^2
Predicted	.81	.18	.01
Actual	.9	.0	.1

Anna: I will send you a flowchart with an example on how to do this calculation and if you need more help we can zoom tomorrow or Sunday for 15 min. :-)