

SCIENCE BYTES: GENETIC LOTTERY or RUSSIAN ROULETTE?

172 Million Chances to get a genetic disorder like Progressive Ataxia.

RETHINKING 5 HETEROZYGOUS CATTLE ALLELES

So you get your genetic test results back and you are happy you have only 5 cattle alleles in your genotype report. But what does this really mean?

The present GeneSeek test looks at 87 alleles at both the paternal and maternal sides. That report would be 5 alleles in 174 or 2.87 %.

2.87 % doesn't seem like much. However, in the bovine genome there are 3 billion base-pairs. So .0287 of 6 billion (maternal and paternal alleles) represents 172,200,000 cattle allele introgressions. That puts your result into the whole genome perspective, not the myopic test sample.

Now one Dc Charolais allele can convert a 1400 pound Charolais-yak hybrid bull into an all white animal.

What potential do the other 172,199,999 cattle alleles have for disruption?

Below is an example of just one disruptive cattle allele:

Progressive Ataxia is an inherited neurodegenerative disease of the Central Nervous System identified in Charolais cattle. It typically appears around 18 months and results in Progressive Ataxia with the end result requiring euthanasia. However, it may take longer to express itself which limits early phenotypic detection.

It is caused by a single base-pair substitution (not unlike the Dc dilution) c.608G>A in exon 5 of K1F1C gene.

It is inherited as an Autosomal recessive as follows:

Alleles: N =Normal, PA = carrier

So:

- N/N Normal not present
- N/PA carrier (not expressed)
- PA/PA expresses Progressive Ataxia (lethal)

Breeding Normal N/N to Normal N/N produces all Normal progeny.

Breeding Normal N/N to Carrier N/PA produces 50% Carrier N/PA and thereby propagates the variant, but produces no affected progeny.

Breeding carrier N/PA to carrier N/PA produces 50% carrier N/PA and 25% PA/PA with Progressive Ataxia plus 25% N/N Normal.

I abstracted this from a UC Davis Veterinary report which claims the incidence within the Charolais breed is as high as 13%. This seems high, because with testing it would be possible to slaughter the carriers and remove them from the gene pool. This becomes a matter of will and integrity.

I write this as within the population of North American yak breeders there have been a small pool of advocates of Charolais-yak hybrids as a short circuit to simulate the Asian white yaks which are ancient hybrids with Indian cattle. There has been some cross breeding with other cattle breeds for meat production and Scottish Highlands, but most notably the Charolais cross has received some measure of popularity.

It is not known at this point how this defect might express itself within these hybrids, but it is likely to manifest in the same lethal manner. Therefore, given the availability of low cost testing, if one is venturing into these white hybrids I would strongly recommend testing these animals for PA alleles before purchasing or breeding them. Due to the lethality of the illness, I would highly recommend slaughtering all PA carriers if revealed.

It goes without saying that most of the other North American cattle breed populations carry some known breed specific genetic defects. These cattle breed associations have identified and developed testing for their breed specific genetic defects. Dr. Cecilia Penedo at UC Davis previously reported that the Imperial black allele as seen in the IYAK and WHYC registered North American yaks is not the black as seen in Black Angus. Dr. Petersen recently confirmed that the North American Imperial yak color is from ancient crossbreeding (prior to -7500 year ago), not more recent hybridization with black cattle breeds.

PURIST NORTH AMERICAN YAK BREEDERS CONTINUE TO OPPOSE INTENTIONAL CATTLE HYBRIDIZATION INTO THE IMPORTED NORTH AMERICSAN YAK GENOME.

172 million is no small number. What other cattle traits lurk below the phenotypic surface?

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