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What's in the Gene Pool?

The founding of the breed - the Gene Pool



Let's pretend these 11 dogs are the "founders" of your breed - they are the first dogs entered into the studbook. All subsequent members of the breed are descended from these dogs <u>only</u>. The breed has a <u>closed gene pool</u>.

All of the genetic variability that will <u>ever</u> exist in your new breed is <u>present in these dogs</u>. Mutations probably won't add new, useful genetic variation because most mutations are detrimental. If the mutated gene is dominant and detrimental, it will likely be weeded out very quickly. If the mutation is recessive, it is not expressed unless an animal is homozygous for the allele by inheriting a copy from each of its parents. In the heterozygote condition, a mutated recessive allele can lurk in the genome for generations without ever causing a problem. So, unless additional "founders" are added to the population at a later date, <u>all of the genes you will ever have to work with in your breeding program are present in these dogs</u>.

In each of these dogs there are at least a few (and perhaps many) recessive genes that could cause genetic disorders. But these disorders will only expressed if a dog is homozygous for the disease allele - it must have TWO copies, one from each parent. As long as the disease genes are <u>rare</u> in the population, very few animals will ever display the illness.

Can the gene pool get bigger? (No!)

Okay, starting with your 11 founder dogs, let's let them reproduce. To keep it simple, we will let them produce only identical copies of themselves - clones.

Now we have 27 dogs, all of which are exact copies of one of the founders. What has happened to the size of the gene pool?

Nothing.

You now have more dogs, and you now have more copies of the genes found in the dogs that had more offspring, like that busy gray dog with the red tongue. So, the <u>frequency</u> of particular alleles is different in this population than in the founders, but the <u>number</u> of different alleles in the population is exactly the same. (We're ignoring the possibility of a mutation for now.)

What if the dogs reproduce normally instead of producing clones? In sexual reproduction, each puppy receives one set of genes from each parent. And, each puppy receives a different mix of parental genes, so each one is a bit different. Also, each parent dog has a different number of offspring and might mate multiple times with different dogs. So the frequency of the various alleles in the population could be very different in this new population than in the founders.

But again, even though there are now more dogs in the population, <u>the gene pool does not get bigger</u>.



In fact, it doesn't matter how large this breed gets - it might someday grow to thousands of dogs - but as long as the stud book is closed, **the gene pool will never be larger than it was when the breed is founded.**

Can the gene pool get smaller? (Yes!)



The gene pool of a closed breed can never get bigger. But it can get smaller.

What if dogs with black ears were less fertile, or had higher puppy mortality, or had some other biological problem? The frequency in the population of the genes causing the black ears would be reduced by natural selection - black-eared dogs would contribute fewer copies of their genes to the next generation. Eventually, by genetic drift (chance) or natural selection, the genes in black-eared dogs would become rarer and rarer, and might eventually be eliminated from the population entirely.

What if breeders didn't like black ears, so all the puppies with black ears were spayed or neutered and sent to pet homes? Those alleles will become less frequent in the population, and they might be eliminated completely because of artificial selection courtesy of the breeder.

The gene pool gets smaller when genes are completely eliminated from the population. It is unlikely that a gene will be restored by chance mutation, and the only other way it can be restored is if an animal is introduced into the breeding population that carries that gene and who reproduces successfully.

In purebred dogs, when the stud book is closed, no new alleles can be introduced into the breed. The loss of an allele is permanent and reduces the heterozygosity in the genome for that gene.

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