

ge·net·ic \jə-ne-tik\ adj

- 1. Biology. pertaining or according to genetics.
- 2. of, pertaining to, or produced by genes; genic.
- 3. of, pertaining to, or influenced by genesis or origins.

di·ver·si·ty \də-vər-sə-tē\ n

- 1. the state or fact of being diverse; difference; unlikeness.
- 2. variety; multiformity.
- 3. a point of different

Definitions from dictionary.com

ge·net·ic di·ver·si·ty

If genetic = origin/genes and diversity = unlike/different, then 'genetic diversity' would be defined as origins unlike/genes different or in proper English: unlike origins or different genes; if one were to delve further into the words diverse/diversity they would find the synonym 'unrelated'.

By Linda Daves Siekert, CVT

chromosome is a visible carrier of genetic information.¹ Each chromosome may contain hundreds to thousands of genes and each gene may have multiple varieties; these variants are called alleles. Every individual inherits one allele from each parent, therefore each individual has a pair of alleles for every gene. If the sire contributes allele A and the dam contributes allele A, the gene pair is homozygous (AA). If the sire contributes allele A and the dam contributes allele B, the gene pair is heterozygous (AB). In truth, there are potentially many different alleles for genes, created through mutations or trading of genetic material during cell division; these allele differences are the basis of genetic diversity.

Examples: The gene for basenji eye color variations may have, but is not limited to, the following alleles which either the sire or the dam can contribute (plus or minus modifiers): dark brown, light brown, dark hazel, light hazel. The gene for tail curl variations may have, but not be limited to, the following alleles (plus or minus modifiers): loose curl, tight curl, semi curl, one curl, double curl, while the gene for red coat variations may have, but not be limited to, the following alleles (plus or minus modifiers): paper bag brown, pale red, light red, medium red, dark chestnut red.

The first successful importation of what became known in the western world as the Basenji occurred in 1936², the first litter born outside of Africa, June 1936³. The first written standard was approved in 1942⁴, six years after the original importers began breeding and selecting for specific traits *they* personally found desirable, though not necessarily commonplace in the source population. Unfortunately, the

original founders sacrificed tremendous amounts of genetic diversity in those first few generations due to their concentration on developing consistency of desired traits through heavy inbreeding.

Using the previously cited examples, let's say the original founders concentrated on dark hazel eyes, tight tail curl and a dark chestnut red coat by breeding phenotype (physical appearance) to phenotype creating a standardized type, i.e. breeding for homozygosity of these three characteristics. By the end of the third generation of breeding, they created their most desired basenji, but at what potential cost?

Let's look. By focusing on breeding phenotype (dark hazel to dark hazel, tight tail curl to tight tail curl, dark chestnut red to dark chestnut red), the following different alleles have potentially been lost: dark brown, light brown, light hazel, large loose curl, small loose curl, one curl, double curl, paper bag brown, pale red, light red, and medium red. No big deal right, since they have created the ideal basenji by culling these (to some) undesirable traits? Two words – genetic linkage. Genetic linkage occurs when certain alleles of different genes, which are physically close to each other, are inherited together.

For the sake of *discussion only*, let's also say the following different genes are linked and are inherited together: the PRA gene is linked to eye color; the HA gene is linked to tail curl and the Fanconi gene is linked to the variations of the red coat color.

To break it down further, we'll also say light brown and dark hazel eye color are linked with the allele PRA carrier, while dark brown and light hazel eye color are linked with

Do we want to preserve genetic diversity, not only for future generations of fanciers, but for the long term viability of our unique breed, or do we just want to breed those picture perfect, cookie cutter show dogs?

the allele PRA clear. Tight curl, semi curl and one tail curl are linked with the allele HA clear; loose curl and double tail curl are linked with allele HA carrier and lastly paper bag brown and medium red are linked with the allele Fanconi clear leaving pale red, light red, and dark chestnut red linked with the allele Fanconi carrier.

Now let's go back and look at those 'perfect' basenjis our founders created in the first few generations of inbreeding: dark hazel eyes (PRA carrier), tight tail curl (HA clear) and a dark chestnut coat (Fanconi carrier). Another way of looking at it would be – by breeding away from a light hazel eye or paper bag brown coat color, we could inadvertently breed towards PRA or Fanconi or any number of maladies not yet known to the breed. The tradeoff? Perfect, cookie cutter, to the standard, homozygous basenjis!?

Angela Hughes, DVM, Ph.D, Veterinary Geneticist reports, "Studies demonstrate that decreased genetic diversity in a canine population negatively impacts litter size, puppy viability, nurturing, libido, skeletal uniformity and health." ⁵

In order to create a line of dogs that consistently produce a standardized type, breeders have selected for homozygosity through



heavy in or line breeding which focuses on perpetuating a few desired ancestral genes. Lines are preserved by continually breeding closely related dogs, some of whom have inbreeding coefficient's greater than 50%, while occasionally dipping into other lines with similarly high inbreeding coefficient's, in the belief this occasional "outcross" is what creates and maintains genetic diversity. However, any ensuing offspring could have similarly high inbreeding coefficients based on the same genes on both sides doubling up.

The Inbreeding Coefficient (IC) determines (as a percentage) the probability of two identical alleles being passed down from an individual's ancestors. The higher the IC, the greater the chance of identical alleles (homozygosity), the lower the IC, the greater the chance of different alleles (heterozygosity). Example: Breeding a Dalmatian to a Pointer, two breeds who have very similar structural phenotype, would have a very low IC (~0%) due to their not having any common ancestors from which to inherit the same allele. This is why the Dalmatian Backcross project worked.6 If genetic diversity is dependent on unrelated alleles, then low IC's, which encourage gene differences, would seem quite necessary for a breed's long term viability; wildlife conservationists, who deal with very limited captive gene pools, select breeding pairs in such a way as to produce low IC's whenever possible.7

The answer to genetic diversity with a small gene pool like the basenji is not the perpetuation of individual lines with high IC's, while occasionally dipping into another line, because we are dipping into the same ancestral gene pool each time. Closely related parents will only increase the IC of their offspring, not decrease it to a more desirable genetically diverse IC of less than 10%. If wild-life conservationist's goals are to maintain genetic diversity by creating offspring with low ICs, shouldn't we do the same, especially since our breed has the ability to do so?

Basenji breeders currently have the unique opportunity to go to the source pop-

ulation and bring back potential founders. Jo Thompson, Ph.D wrote about the importance native stock has in maintaining genetic diversity for the 2008 BCOA Native Stock Studbook Petition used to encourage the AKC to again open the AKC Studbook to imported stock;

"Sound population genetics suggests that an effective population size could require as many as 300 *unrelated* individuals in order to have a population large enough to maintain normal amounts of *additive genes to retain 95 percent heterozygosity* for 100 years. [emphasis added]"

This is still a relevant passage, and will be until such time as the breed fancy is able to procure a significant number of unrelated individuals from Africa, access to the source population is no longer obtainable, or the AKC closes the Studbook once and for all.

Do we want to preserve genetic diversity, not only for future generations of fanciers, but also for the long term viability of our unique breed, or do we just want to breed those picture perfect, cookie cutter show dogs? A tough question but one that need not be either/or in my opinion; breeders can still breed for desirable and homozygous physical traits via two minimally related phenotypical dogs with low IC's (10% or less) thereby maintaining important genetic diversity while creating standardized type.

The most important lessons I learned when I first began to consider breeding were a) do no harm and b) leave the breed better than I found it; producing closely related, uber-type basenjis at the cost of diminishing genetic diversity fulfills neither lesson.

¹www.medterms.com

²ASP basenji.org timeline

³www.pedigrees.zandebasenjis.com/

⁴www.zandebasenjis.com/brit42.htm

⁵AKC GAZETTE, May 2011

⁶users.nbn.net/jseltzer/dal_poin.html

⁷bowlingsite.mcf.com/genetics/inbreeding.html

⁸www.basenji.org/NativeStock/
Application/BasenjiStudbookPetition.pdf