Why should I be interested in Genetic Diversity for my breed?

Decades and centuries of selective breeding of canines for purebred breeds has resulted in the tightening and restriction of genetics at the breedwide level. This is caused by small groups of founders, popular sires, strict selective pressures and decreased breed numbers due to events like the World Wars. As a result, many breeds now suffer from increasing rates of debilitating complex breed specific diseases. Inbreeding has been proven to affect litter size, and eventually breeds can reach a point when an outcross is necessitated or the breed will become extinct.

Sampling the existing diversity in a breed, and learning how it should be managed, maintained or redistributed, is a vital aspect of being stewards of our breeds. If we maintain a great depth and breadth of diversity, as well as keep inbreeding in litters low, breeds tend to be healthier. We then are happier as breeders, as well as our dogs and our homes! Whether a breed is bottlenecked, depleted of genetics, or has maintained a great amount of diversity, we can help with management.

Nature favors diversity. In nature, species maintain diversity naturally, otherwise they face destruction when confronted with diseases or change in habitat. While purebred dogs are not a species on their own, we restrict their genetic flow as if they were, and therefore must be careful how we manage the breed pools.
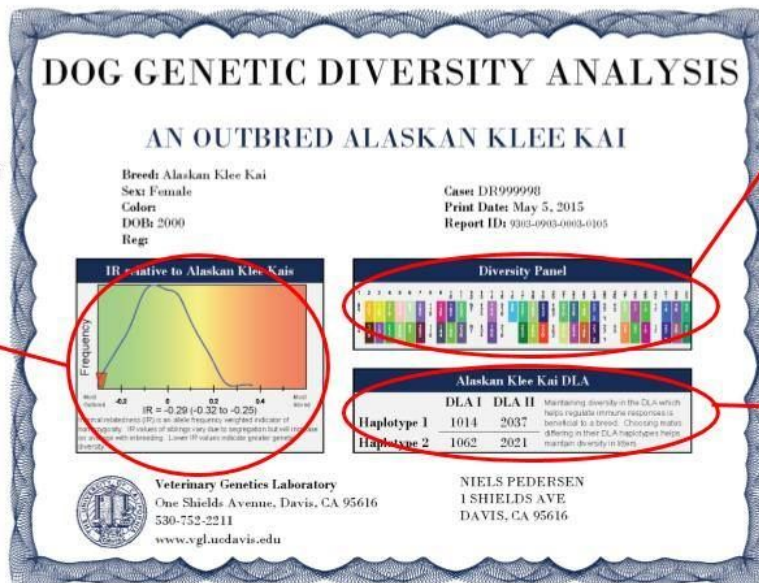
What do you get?

Your Dog's Certificate

Better Bred

This test was developed by world renowned veterinarian researcher, Dr. Niels Pedersen, to equip breeders to maintain their breed's diversity.

This is the inbreeding measurement at UC Davis. The higher the IR, the more inbred. The lower, the more outbred. Breed for litter averages below 0 to produce outbred puppies.

The UC Davis Certificate. What do you get?

DOG GENETIC DIVERSITY ANALYSIS

AN OUTBRED ALASKAN KLEE KAI

Breed: Alaskan Klee Kai
Sex: Female
Color:
DOB: 2000
Reg:

Case: DR999998
Print Date: May 5, 2015
Report ID: 9303-0903-0903-0105

IR relative to Alaskan Klee Kais

Frequency

IR = -0.29 (-0.32 to -0.25)

Diversity Panel

Alaskan Klee Kai DLA

	DLA I	DLA II
Haplotype 1	1014	2037
Haplotype 2	1062	2021

Maintaining diversity in the DLA which helps regulate immune responses is beneficial to a breed. Choosing mates differing in their DLA haplotypes helps maintain diversity in them.

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These are the markers used to map breed-wide diversity. These can be used in breeding programs, like Betterbred, to create breeding tools.

This area names the regions of the DLA, or immune system, of a dog. Numbers in the 1000s are the Class I haplotypes, 2000s the Class II. UC Davis tests the most areas of DLA of any test currently.

Internal Relatedness- is your dog inbred?

UC Davis will release an inbreeding measurement for your individual dog. The higher this number is (more positive) the more inbred your dog. Studies have shown that inbreeding reduces vigor and viability, so is good to reduce in planned litters.

Definition - a measure of genetic diversity within an individual that takes into consideration both heterozygosity of alleles at each STR loci and their relative frequency in the population. Therefore, IR values heterozygosity over

homozygosity. IR values are unique to each dog and cannot be compared between dogs. Two dogs may have identical IR values but with very different genetic makeups. This is an inbreeding measurement. The higher the number, the more inbred (homozygous), the lower the more outbred (heterozygous). This is included on the UC Davis certificate for your individual dog, but does not predict what the dog will produce with another dog.

Dog Leukocyte Antigen - a look at your dog's immune system!

Is your dog's immune system diverse? Does it carry the most common haplotypes for the breed? Are there associated health risks with certain DLA haplotypes?

What is the DLA? The DLA is a part of the major histocompatibility complex (MHC) in dogs. DLA plays a critical role in the immune response system and consists of three regions: class I, class II and class III. UC Davis tests the most areas of the DLA of any test out there: a total of 7 regions in both the class I and II. Class II haplotypes are labeled in the 2000s and Class I haplotypes in the 1000s. These values are included on your UC Davis certificate; breeds should attempt to breed for puppies with different haplotypes as well as consider the haplotypes that are not well represented within the breed.

How do your genetics stack up? Common or uncommon?

A dog can be heterozygous (or outbred), and many companies would call this "*high diversity*". This is high diversity WITHIN your dog, meaning that your dog has different genetics received from its sire and dam; *however*, those genetics can still be very common in comparison to the *population* at large. Over time, selecting solely for heterozygosity can lose less common genetics in the population.

A final, but vastly important, aspect of this testing is the analysis of how typical or atypical of genetics a dog may have. As breed pools become restricted, the genetics carried by the majority become more and more common. What does this mean? The breed is bottlenecked, and the diversity that remains becomes less and less common. As this happens, breed specific diseases begin to increase and lifespans decrease. In these breeds, we need ways to redistribute genetics to

improve breed health. BetterBred provides analysis of individuals to aid in redistributing these genes!

Predict your puppies!

Use www.betterbred.com to analyze your results and have accurate predictions for what you will produce in your litters. BetterBred is currently the only online software that predicts what to expect in your litters.
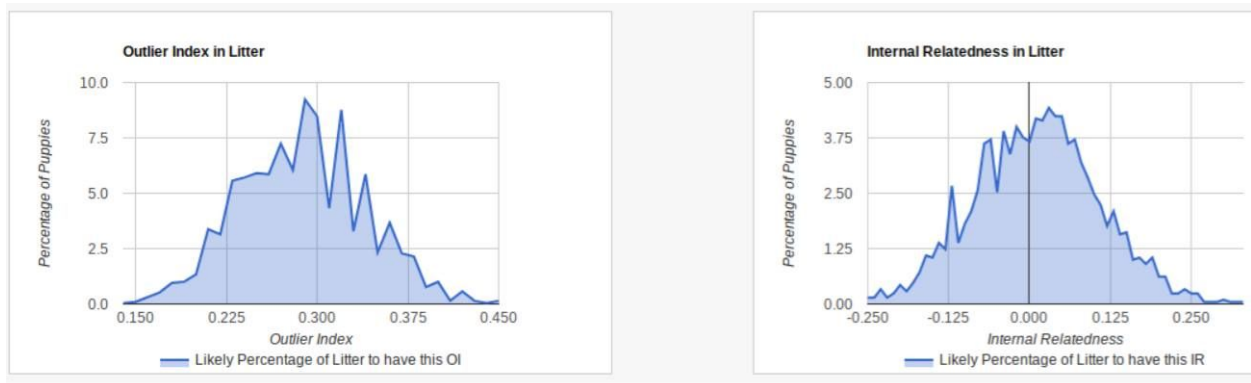
Litter predictions (actual tested litter to follow)

Name	Gender	Outlier Index	Average Genetic Relatedness	Internal Relatedness
Balto	M	0.36	-0.06	-0.02
Yodel	F	0.25	-0.04	0.16
Laika	F	0.20	0.09	-0.25
Happy	F	0.27	-0.03	0.01
Goofy	M	0.30	-0.05	0.02
Kipper	M	0.34	-0.04	-0.03
Hubble	M	0.25	0.01	0.03
Sabi	F	0.31	-0.02	0.00
Pooka	F	0.29	-0.05	0.13
Astro	M	0.29	-0.05	0.16

The following is a discussion of the above litter.

Above is a fully tested litter of standard poodles.

One chart are the actual individual puppies tested at VGL. The other the prediction graphs from their litter simulation (you can see all the pups fall in the ranges predicted).

IR is the inbreeding measurement you will get from UC Davis. The higher the IR, the more inbred the puppy (the more positive the more inbred). This breeding was a relatively close in terms of genetic relatedness breeding I did because of the second consideration: OI

OI stands for outlier index. It tells you how common (or uncommon) a dog is for the population. In bottlenecked breeds (like the standard poodle variety) this tool helps us redistribute our genetics. The higher the OI, the more atypical a dog is for the population (our average at the time was .24, my dam was .21).

Another measure that helps you understand bottleneck influence is AGR, average genetic relatedness. The lower this is, the less related to the dogs in the tested population.

My dam in this case has a lower than breed average OI, meaning she has a lot of bottleneck genetics. She was outbred (a negative IR), meaning not a lot of her genetics are the same from her sire and dam. Because she has so many bottlenecked genes, it's hard to find unrelated dogs (even outliers!).

So my goal in this breeding was to up her OI, or get her next generation further away from our bottleneck. Because the breeding was a closer genetic relatedness, you can see several of my puppies had higher IRs (they are more inbred). I ended up keeping Pooka, Goofy, and Balto intact; all pups with higher than average OI (different genetics for our population). Even with higher inbreeding in some

individuals (my Pooka in particular, who earned a trick dog title at 13 weeks!), it will be easy to reduce that in the next generation because they are less related to more of the population.

This is all really new and complicated, but the big point/takeaway is that littermates can be vastly different from one another! Our selection each generation will impact the future generations of our breeds.