

Genetic Diversity Testing for Akitas

Overview

The Veterinary Genetics Laboratory (VGL), in collaboration with Dr. Niels C. Pedersen and staff, has developed a panel of short tandem repeat (STR) markers that will determine genetic diversity across the genome and in the Dog Leukocyte Antigen (DLA) class I and II regions. This test panel will be useful to breeders who wish to track and increase genetic diversity of their breed as a long term goal.

Genetic diversity testing of Akita is well established and we feel that almost all of the existing alleles at the 33 STR loci and DLA class I and II regions have been identified. Any new alleles or haplotypes are likely to occur at very low frequency. We will continue to add new alleles and haplotypes when they are found and to adjust frequencies if necessary. We have confirmed that Akita exist as two varieties, Japanese (AKJ) and American (AKA). Blends involving crossing between varieties also have been identified and genetically characterized as intermediate. As of Sept 2018, we have tested 524 dogs from all three of these groups (117 AKA, 341 AKJ and 62 Blends), and the results of our preliminary genetic diversity testing have been updated.

Results reported as:

Short tandem repeat (STR) loci: A total of 33 STR loci from across the genome were used to gauge genetic diversity within an individual and across the breed. The alleles inherited from each parent are displayed graphically to highlight heterozygosity, and [breed-wide allele frequency](#) is provided.

DLA haplotypes: STR loci linked to the DLA class I and II genes were used to identify genetic differences in regions regulating immune responses and self/non-self recognition. Problems with self/non-self recognition, along with non-genetic factors in the environment, are responsible for autoimmune disease.

Internal Relatedness: The IR value is 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 and uncommon alleles over common alleles. 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.

Introduction

The Akita originated from the high regions of Northern Japan (Honshu Island.) Through the last 70 years, they have become separated by breeding, and somewhat by geography, into two breeds or varieties. Both “breeds” originated from the same founder population. During WWII, on the brink of extinction, many Akitas were mixed with other breeds in an effort to save them from government ordered culling in Japan. The American Akita started post war with 166 dogs of all types/colors registered with the Akita Club by 1966. When the stud book was turned over to AKC in 1972, 1,865 Akitas were registered as foundation stock. Akitas continued to be imported and registered with AKC until 1974, at which time the stud book closed to new imports (reopening in 1992). Meanwhile in Japan, after being declared a Japanese Natural Monument in 1931, organized efforts were undertaken, through selective lines, to preserve/restore the Akita to its original breed standard (allowing only three colors of origin). Some of these lines are retained in the American Akita, in the US, Europe and Oceanian countries. Due to American and Japanese Akita breeders pursuing differing standards, the country of origin requested the FCI ([Federation Cynologique Internationale](#)) to split the breed, (effective within FCI June 1999.) In the US and Canada, within AKC ([American Kennel Club](#)) and CKC ([Canadian Kennel Club](#)) the differences are considered two varieties of the same breed. Some favor blending the two types, others vehemently oppose. Some favor the look and personality of one variety over the other, while still others believe that neither is an accurate representation of the original breed.

The genetic information used to formulate the enclosed tables and graphs came from DNA samples of 524 Akita from around the world and include American Akita (AKA) (n=117), Japanese Akita (AKJ) (n=341) and what are known as “blends” (n=62). We believe that the dogs currently tested are reasonable representations of the genetic relationships and diversity that still exist in these varieties, although more AKA need to be tested.

The Canine Genetic Diversity Test and What It Tells Us

A. Population genetics based on 33 STR loci on 25 chromosomes

STR markers are highly polymorphic and have great power to determine genetic differences among individuals and breeds. The routine test panel contains 33 STRs that are recommended for universal parentage determination for domestic dogs by the International Society of Animal Genetics (ISAG) with additional markers developed by the VGL for forensic purposes.

The diversity of alleles at each of the [genomic STR loci](#) and their frequency in the population were used to determine the genetic relatedness and diversity of American Akitas (AKA), Japanese Akitas (AKJ), and Akita blends (AK) from around the world. Allele frequencies differ somewhat between AKA and AKJ and there are some alleles that are specific for AKA or AKJ (Table 1). However, these tend to occur at low frequency and it is possible that they will be found in both breeds if a larger number of AKA or AKJ are tested. Allele frequencies indicate that the Akita blends tested are truly mixtures of AKA and AKJ, but more closely related to AKA than AKJ.

[\(link to table 1\)](#)

B. Assessment of population genetics using standard measurements

1. Genetic assessment of Akita varieties using genomic STR allele frequencies

The allele frequency data obtained from the 33 STR panel can be used for a standard genetic assessment based on heterozygosity (Table 2). The AKA have an average of 6.64 alleles/loci (Na), while the AKJ had 6.30 alleles/loci. The blends had an average of 5.36 alleles/locus. The higher number of alleles (Na) at each locus for AKA compared to AKJ indicate that contemporary AKA are more genetically diverse.

AKA have an average of 3.03 effective alleles/loci, while the AKJ had only 2.41 and blends 2.67. Effective alleles are the proportion of alleles that contribute the most to heterozygosity. The lower He in AKJ reflects the lower number of alleles at each locus and less genetic diversity, possibly from a smaller number of founders (see DLA haplotypes) in the reconstituted varieties.

The observed heterozygosity (Ho) and expected heterozygosity (He) can be used to calculate a value (F) that is an estimate of the level of inbreeding in a population. An F value of 0 indicates that the population is in Hardy-Weinberg equilibrium (HWE), i.e. mate selection is entirely random. A positive F value means that there is a subpopulation of dogs that are more inbred than the total population, and the higher the value of F, the greater the size of this inbred population. The Ho for the AKA is 0.587 and for the AKJ it is 0.535. The expected heterozygosity if the populations were all in HWE was 0.622 for AKA, 0.543 for AKJ and 0.588 for the blends. Therefore, the index of inbreeding F is highest for AKA (0.056), intermediate for AKJ (0.020), and lowest for blends (0.010). Therefore, although the AKA have more genetic diversity than the AKJ, they also contain a larger proportion of inbred dogs. As would be expected, the blends have the smallest proportion of inbred individuals and the lowest F value.

Table 2. F-Statistics of Akitas using 33 STR loci on 25 chromosomes

		N	Na	Ne	Ho	He	F
American Akita	Mean	129	6.636	3.023	0.584	0.620	0.058
	SE		0.329	0.183	0.026	0.026	0.012
Japanese Akita	Mean	364	6.394	2.396	0.533	0.541	0.019
	SE		0.332	0.129	0.027	0.026	0.009
Blend Akita	Mean	68	5.424	2.680	0.588	0.589	0.003
	SE		0.284	0.148	0.027	0.022	0.024
Unknown Akita	Mean	4	3.545	2.843	0.598	0.598	NaN
	SE		0.177	0.156	0.039	0.030	NaN

C. Differences in population structure as determined by principal coordinate analysis (PCoA)

The data obtained from genomic STRs were used to determine the relatedness of AKA and AKJ to each other based on principal coordinate analysis (PCoA) (Fig. 1). PCoA uses genetic distance based on allele sharing to demonstrate genetic differentiation between individuals in related or unrelated populations. An optimized two dimensional graph portrays the degree of genetic differentiation between individuals and the more distant two points (dogs) are from each other the greater the genetic differences and *vice versa*. This analysis showed that AKA and AKJ were genetically distinct varieties and no registered AKJ segregates with AKAs and no AKA with AKJ. One AKA appears to segregate with AKJ and two AKJ with AKA, which indicates errors in registration or classification rather than interrelatedness. Akitas referred to as "blends" by their owners tend to differentiate more with AKA than AKJ, although some are obviously intermediate between AKA and AKJ, indicating that they are true crosses. Only four Akita blends clearly segregate with AKJ and two dogs of unknown classification (AKU) appear to be blends, although one dog is more closely related to AKJ and another to AKA. The tighter clustering of AKJ than AKA or blends suggests that individual AKJ are more closely related to each other than AKA or blends are related to each other.

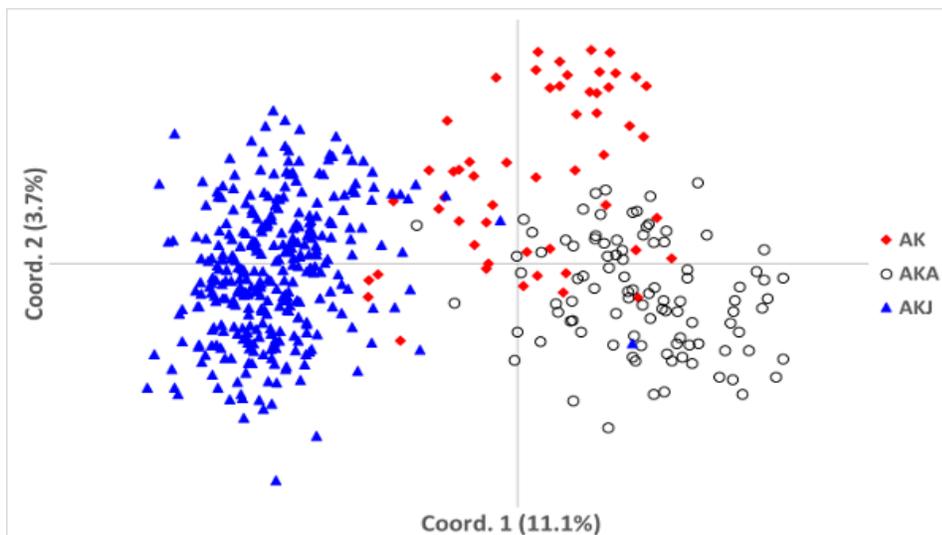


Fig. 1. Top- PCoA of 524 Akitas from three different populations – Akita blend (AK), American Akita (AKA), and Japanese Akita (AKJ)

D. Genetic assessment of individuals within a population using internal relatedness (IR)

The N_a , N_e , H_o , H_e and F values apply mainly to the overall population and not to individual dogs within the population. The genetic diversity of an individual depends not only on the alleles present at each locus, but also on how common or rare each of the two possible alleles is in the population. The commonness or rarity of the two possible alleles at each STR loci can be used to calculate what is called "internal relatedness" or IR. The IR values of a population can then be used to construct a graph with values ranging from -1 to +1. An IR of -1 indicates that the parents of that dog are totally unrelated, while an IR score of +1 indicates that the parents are genetically identical. The average IR scores of puppies born to full-sibling parents from a

random breeding population would be +0.25. The comparison graphs of IR scores for AKA and AKJ provide a great deal of additional information about how individuals in the population are related to their parents.

The median IR value for AKA population is +0.074 (Table 3; Fig. 2), but with individuals scoring as low as -0.270 (most outbred) and as high as +0.383 (most inbred). One half of the population had IR scores of +0.074 to +0.383 and one fourth between +0.159 and +0.383. An IR of +0.25 would be the average score for a litter of puppies born to full siblings from a random breeding population. The fact that the median for the population was near zero (0.074) indicates the average AKA had parents that were as randomly related as possible given the available genetic diversity. However, this is misleading as there are balancing populations of individuals whose parents are either more or less related than the average dog. This more outbred group of dogs is the reason for the left shoulder peak on the IR graph.

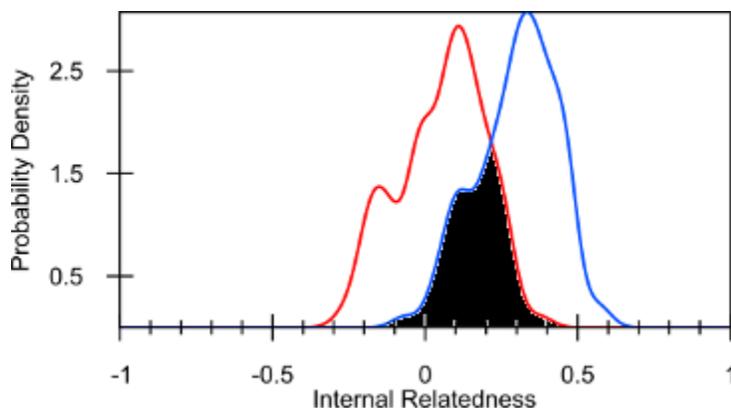


Fig. 2: Distribution of IR estimates in 117 AKA based on intra-breed diversity (Red line), compared with IR adjusted for diversity lost during breed development (Blue line). An estimate of diversity lost because of breed development (area in black) was determined by comparing allele frequencies at the same loci between AKA and randomly breeding village dogs from the Middle East, SE Asia, and the Pacific Islands. The area in black is an estimate of how much available genetic diversity has been retained (41%) or lost (59%) in during the evolution of contemporary AKJ. Retention of 41% village dog diversity is above average for pure breeds.

IR scores for AKJ are given in Fig. 3 and Table 3. The least inbred dog scored -0.394 and the most inbred dog 0.472. One half of the dogs have IR scores from +0.017 to +0.472 and one fourth have scores from +0.100 to +0.472. However, the IR peak is bimodal, suggesting that there two populations make up the curve, one that is more outbred than average and one that is more inbred.

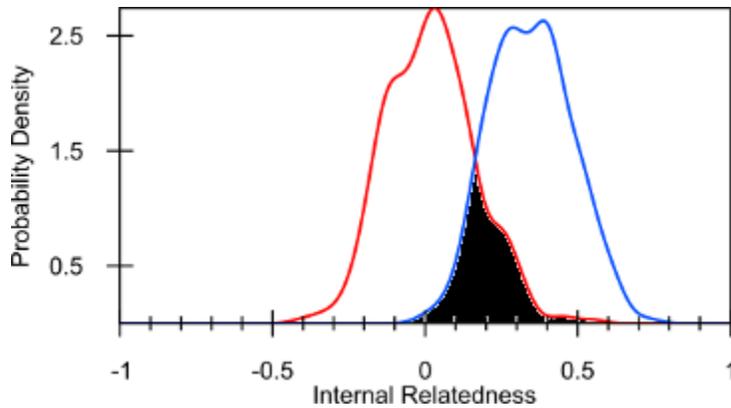


Fig. 3: Distribution of IR estimates in 341 AKJ based on intra-breed diversity (Red line), compared with IR adjusted for diversity lost during breed development (Blue line). Diversity lost because of breed development was determined by comparing allele frequencies at the same loci between AKA and randomly breeding village dogs from the Middle East, SE Asia, and the Pacific Islands. The area in black is an estimate of how much available genetic diversity has been retained (24.4%) or lost (75.6%) during the evolution of contemporary AKJ.

Table 3: Statistical parameters used to interpret IR and IRVD curves for Akita varieties

	IR.AKA	IRVD.AKA	IR.AKJ	IRVD.AKJ	IR.AK	IRVD.AK
Min.	-0.27047	-0.07716	-0.39463	-0.02253	-0.15077	0.1447
1st Qu.	-0.0363	0.19351	-0.1114	0.22496	-0.0364	0.1957
Median	0.07376	0.29458	0.017433	0.30114	0.07023	0.2744
Mean	0.05209	0.28265	0.009961	0.32057	0.06585	0.2915
3rd Qu.	0.1587	0.37968	0.100388	0.40061	0.14864	0.3812
Max.	0.38328	0.56886	0.472032	0.66693	0.2936	0.4602

E. Estimation of genetic diversity lost during breed creation using village dogs as a gold standard

The IR values can also be used to give an approximation of how much genetic diversity has been lost during breed development and subsequent evolution. This is done by comparing the frequency of a given allele in an Akita variety with the frequency of that allele in a population of village dogs from the Middle East, SE Asia, Taiwan and other Pacific island nations such as Brunei and the Philippines. Contemporary village dogs are largely unchanged from the ancestors of almost all modern dog breeds. This adjusted value is known as the IR-Village Dogs or IRVD.

Adjustment of the IR values for diversity lost, using village dogs as the gold standard (blue curve), caused a marked shift of the curve to the right in the AKA (Fig. 2). The median IRVD value was +0.301, with a range of -0.023 to +0.670. This means that the average AKA is about as closely related as offspring of full sibling village dog parents, providing that the parents of the sibling pair were random members of the village dog population. IRVD values progressively greater than +0.25 would mean that the parents of the sibling pair were also increasingly more related than dogs from a large, genetically diverse, random breeding population. The graph of IRVD values for the AKJ shows an even greater shift to the right than for the AKA, with the

median value for the population being 0.301 with individuals ranging from -0.023 to +0.625 (Fig. 3). A crude estimate of the proportion of available canine genetic diversity that still exists in AKA and AKJ can be obtained by comparing the overlapping area (black in Fig. 2 and 3) of the two curves. AKA have retained 41% of the genetic diversity that exists in contemporary village dogs while AKJ have retained 24.4%. This is another indicator besides comparative H_o , N_a and N_e values that present-day AKA are more genetically diverse than AKJ.

F. Population genetics based on STR-associated DLA class I and II haplotypes

In addition to the markers used to estimate relatedness, which reflect genome-wide diversity, a set of STRs associated with specific genes in the DLA region (the canine Major Histocompatibility Complex) was identified and used to measure genetic diversity associated with immune function (see sidebar).

The STR-based haplotype nomenclature used in this breed diversity analysis is based on numerical ranking with the first haplotypes being identified (in Standard Poodles) being named 1001, 1002, ... for DLA class I haplotypes and 2001, 2002, ... for DLA class II haplotypes. It is not unusual for various dog breeds to share common and even rare haplotypes, depending on common ancestry. Haplotypes with lower numbers have been recognized in other breeds, while higher numbers are more apt to be more breed specific. The numerical nomenclature used by VGL for DLA class I and II haplotypes does not correlate with numerical rankings used by others.

Each dog has two DLA class I and two DLA class II haplotypes, one inherited from each parent. There are more than 150 known class I and nearly 100 known class II haplotypes among all dogs, but because of genetic bottlenecks involved in breed development, most breeds will only end up with a small portion of these haplotypes. AKA possess 11 different

Dog DLA and STR haplotype diversity.

The DLA consists of four gene rich regions making up a small part of canine chromosome 12. Two of these regions contain genes that help regulate normal cell- (Class I) and antibody-mediated (Class II) immunity. Polymorphisms in these regions have also been associated with abnormal immune responses responsible for autoimmune diseases. The Class I region contains several genes, but only one, DLA-88, is highly polymorphic (with many allelic forms) and is therefore most important for immune regulation. Specific alleles at the four STR loci associated with the DLA88 are linked together in various combinations, forming specific haplotypes (Table 5). Groups of genes and their alleles that are inherited as a block, rather than singly, are called haplotypes. The class II region also contains several genes, three of which are highly polymorphic, DLA-DRB1, DLA-DQB1 and DLA-DQA1. Specific alleles at STR loci associated with each of the three Class II genes are strongly linked and inherited as a single block or haplotype (Table 6). One haplotype comes from each of the parents. The linkages between alleles within Class I or II regions are very strong; while linkages between regions of the DLA that are more distant from each other, such as Class I and II, are weaker. There are almost two million base pairs separating the class I and II regions, thus allowing for some genetic recombination to occur. This recombination is most apparent between the common DLA class I and II haplotypes, forming unique "extended DLA class I-II haplotypes. Extended class I-II haplotypes are inherited as a single block of genes.

class I and 11 different class II haplotypes, while AKJ have 11 class I and 10 class II haplotypes (Table 3), indicating that both varieties came from a similar number of founders. Six of 11 class I haplotypes in AKA and 5 of 10 class II haplotypes are shared between the two varieties. AKA have 6 unique DLA class I haplotypes and AKJ have five, while AKA have five unique DLA class II haplotypes and AKJ also have five. This suggests that about one-half of founders for AKA and AKJ came from the same lines, while the other half were from different lines.

AKA and AKJ tend to share the same major haplotypes, such as 1029, 1081, 2037 and 2056. However, relative frequencies of these haplotypes vary between AKA and AKJ, with 1029 occurring 18.4% vs 25.7%, 1081 37.9% vs 15.2%, 2037 18.4% vs 25.4%, and 2056 59.2% vs 17.1% in respective varieties (Table 3). Three DLA class I haplotypes in AKA (1029, 1081 and 1082) and four in AKJ (1029, 1061, 1081 and 1092) were found in 77.6% and 88.4% of each respective variety. Two DLA class II haplotypes in AKA (2037, 2056) and four in AKJ (2035, 2037, 2056, and 2057) were found in 77.6% and 89.7% of the respective variety. The major class I and II markers in AKJ were present at similar frequency, while 1081 (40.3%) and 2056 (59.0%) were much higher than other major haplotypes. The haplotype and haplotype frequencies of Akita blends were more closely related to AKA than to AKJ (Table 3).

Table 3: DLA class I and II haplotype and their frequencies in different Akita populations

DLA Class I Haplotype Frequencies (Updated Oct 9, 2019)					
DLA1 #	STR types	American Akita (n=99)	Japanese Akita (n=357)	Blend Akita (n=59)	Unknown Akita (n=4)
1006	387 375 293 180	0.056	--	--	--
1014	375 373 287 178	--	--	--	0.1
1029	380 365 281 182	0.167	0.249	0.161	0.3
1040	380 371 277 186	0.010	--	--	--
1045	376 371 277 186	0.005	--	--	--
1061	380 365 281 183	0.030	0.182	0.068	0.1
1067	376 373 277 178	0.015	0.006	0.017	--
1081	395 379 289 178	0.384	0.148	0.322	0.3
1082	390 373 277 184	0.212	0.017	0.127	0.1
1083	395 375 277 186	0.101	0.084	0.246	0.1

1087	380 371 277 178	0.015	--	--	--
1092	376 379 277 181	--	0.304	0.008	--
1108	382 371 277 180	--	0.001	--	--
1114	380 373 287 183	--	0.001	--	--
1135	388 385 281 180	--	0.006	0.051	--
1149	395 377 277 186	--	0.001	--	--
1160	386 369 289 176	0.005	--	--	--

DLA Class II Haplotype Frequencies (Updated Oct 9, 2019)

DLA2 #	STR types	American Akita (n=99)	Japanese Akita (n=357)	Blend Akita (n=59)	Unknown Akita (n=4)
2007	351 327 280	0.056	--	--	--
2012	345 322 280	--	0.001	--	--
2017	343 322 280	0.015	0.006	0.017	--
2033	339 323 282	0.015	--	--	--
2035	341 323 280	--	0.304	0.008	--
2036	341 327 276	--	0.003	--	--
2037	341 327 280	0.167	0.246	0.153	0.3
2039	345 327 276	0.101	0.091	0.297	0.1
2056	339 323 286	0.591	0.165	0.449	0.4

2057	341 327 286	0.030	0.179	0.068	0.1
2058	345 323 288	0.010	--	--	--
2060	343 323 284	0.005	--	--	--
2061	341 327 296	--	0.003	--	--
2062	345 327 282	--	--	--	0.1
2063	345 327 286	0.005	--	--	--
2069	349 322 280	--	0.001	--	--
2071	339 322 286	0.005	--	--	--
2103	341 323 286	--	--	0.008	--

DLA haplotypes and haplotype frequencies were unbalanced in both varieties, suggesting either that dogs with certain haplotypes were being positively selected or that these haplotypes were dominant among founders of the breed and have subsequently reverted to a state of random selection. A period of intense positive selection after WWII is a historical fact. Whether this period of positive selection returned to a random state over the last 60 years can be answered by doing a standard type genetic assessment of allele frequencies of the seven STR loci that were associated with the various DLA class I and II haplotypes (Table 4).

AKA have a higher average number of alleles per DLA class I or II STR loci (5.43) than AKJ (5.14). The number of effective alleles was also slightly higher for AKA than AKJ (2.79 vs 2.68). Observed heterozygosity (H_o) was about the same for AKA and AKJ (0.573 vs. 0.577) but expected heterozygosity (H_e) was higher than H_o for AKA than for AKJ (0.621 vs. 0.595). This resulted in an inbreeding index (F) of 0.081 for AKA and 0.027 for AKJ. Therefore, the data indicate that the major DLA region is still under some positive selection, more so for AKA than AKJ. Therefore, individuals with certain haplotypes are still inadvertently being favored to a measurable level over others. These haplotypes are most likely the ones occurring at the highest frequency.

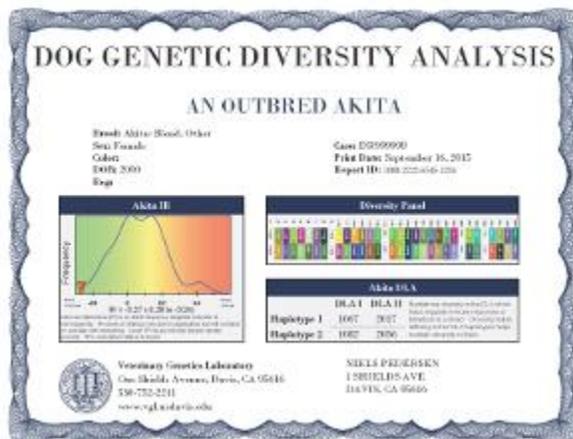
The H_o and H_e values for blends were higher than for AKA or AKJ, reflecting an increase in heterozygosity from outcrossing. The F value (-0.053) was slightly negative indicating that blends were more likely to have parents with different or unusual DLA haplotypes, as also shown in Tables 3, 4.

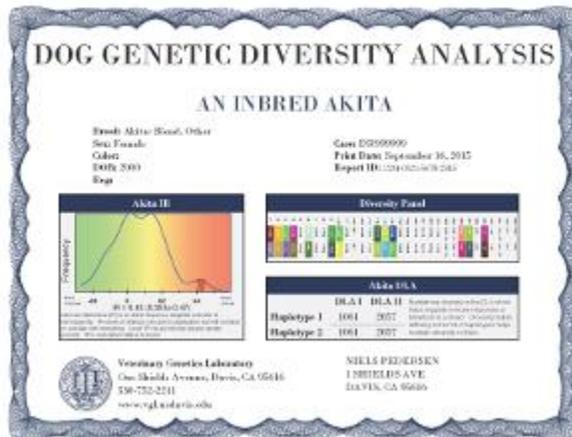
Table 4: Genetic assessment of Akita using the 7 STRs in the DLA region

		N	Na	Ne	Ho	He	F
American Akita	Mean	129	5.429	2.785	0.593	0.620	0.046
	SE		0.445	0.245	0.038	0.034	0.012
Japanese Akita	Mean	364	5.143	2.673	0.575	0.594	0.029
	SE		0.551	0.325	0.036	0.040	0.006
Blend Akita	Mean	68	4.429	3.016	0.657	0.649	-0.015
	SE		0.489	0.281	0.032	0.031	0.031
Unknown Akita	Mean	4	3.714	3.145	0.893	0.665	-0.356
	SE		0.333	0.238	0.047	0.033	0.070

Certificates Providing Genetic Information on Individual Dogs

After a sample is submitted for genetic testing, the identity of the dog and owner will be replaced by a laboratory barcode identifier. This identifier will be used for all subsequent activities. After testing, each owner will be provided with a certificate that reports the internal relatedness, genomic STR genotypes and DLA class I and II haplotypes for the dog(s) tested. The internal relatedness value for the dog being tested is related to the total population.





Genetic Goals for Breeders

The goal for Akita breeders should be to produce a greater and greater proportion of puppies with IR scores less than 0, and with time even lower scores. This can be achieved by selecting parents that are as different as possible in their genomic STR alleles and allele frequencies. It is also important to rebalance diversity within the DLA region. Maintaining existing diversity will require using different combinations of breeding stock, including even those from inbred lines with high IR values. IR values, because they reflect the unique genetics of each individual, cannot be used as the criteria for selecting ideal mates. A breeding pair with identical IR values can have genetically distinct parents and produce puppies significantly more or less diverse than their parents. Conversely, a mating between dogs with high IR values, providing they are genetically different, may produce puppies having much lower IR scores than either parent. A mating between a dog with a high IR value and a low IR value, providing the latter is much different in genomic allele and allele frequencies and DLA haplotypes, will produce puppies much more diverse than the highly inbred parent. Breeders should also realize that a litter of puppies may have a wide range of IR values, depending on the comparative contributions of each of the parents because of genetic recombination. The more genetically diverse and different the parents, the greater the range of IR values in their offspring.

Akita, regardless of variety, have managed to retain a significant amount of genetic diversity compared to some other breeds. However, this diversity is spread across two varieties that have seen very little if any outcrossing for decades. There is also evidence that certain founders have had a disproportionate genetic influence on each of the varieties and that this imbalance is being maintained to some degree by artificial positive selection. The positive news is that Akita breeders have a great deal of diversity to work with, making it possible to rebalance diversity in such a way as to improve health. For instance, previous studies indicate that dogs with the common DLA class I haplotypes, especially in a homozygous state, are at greater risk for autoimmune disorders. Autoimmune diseases are a great problem in the breed. Breeding away from homozygosity in the DLA region, especially involving common haplotypes, is both desirable and easily done using DNA testing.

In brief, potential sires and dams should be first screened for genetic differences in the genome and in the DLA regions by first comparing allele differences at each STR locus, and then at the DLA class I and II haplotypes. Some thought should be given to rare vs common alleles. This information is included on all certificates and on the website. This preliminary comparison will identify promising pairings and if desired, genetic information on the potential sires and dams can then be used to calculate actual IR expectations for their puppies. Puppies, once born, should be tested for their actual IR values, which will reflect the actual genetic impact of each parent on internal diversity. Considerations of mate choices for genetic diversity should be balanced with other breeding goals but improving genetic diversity in puppies should be paramount.

An additional goal of this study is to contribute this genetic information to a web repository, hopefully under the control of the registry. This information could be incorporated into a mate selection service that will allow a breeder to identify, among all the dogs tested, potential mates that would be most ideal for increasing genetic diversity in their litters.

Heritable diseases/problems of the Akita

Akita suffer from a long list of disease conditions, most of which are heritable either as complex (polygenic) or Mendelian (usually simple recessive) traits. A list of diseases identified in Akita can be found at: <http://akitarescue.rescuegroups.org/info/file?file=s197m7036.pdf> and at https://en.wikipedia.org/wiki/Akita_%28dog%29#Health. The largest number of heritable diseases on this list involves the immune system, either in the form of autoimmune disease or allergies. Autoimmune disorders include several skin disorders (sebaceous adenitis, pemphigus foliaceus, pemphigus vulgaris, uveodermatitis syndrome or VKH), autoimmune thrombocytopenia, autoimmune hemolytic anemia, Addison's disease, thyroiditis/hypothyroidism, immune mediated polyarthritis and SLE or SLE-like syndromes, myasthenia gravis, and renal amyloidosis. Allergic conditions include atopic dermatitis. Simple Mendelian diseases include VonWillebrand's disease, microphthalmia, glaucoma, progressive retinal atrophy, degenerative myelopathy, oligodontia and enamel hypoplasia. Complex genetic traits involving the skeleton include hip and elbow dysplasia, chondrodysplasia, osteochondritis dissecans, spondylosis, patellar luxation and dwarfism. Like many larger breeds of dogs, Akita suffer a high incidence of specific cancers, usually tumors of connective tissue (sarcomas) such as hemangiosarcoma, undifferentiated sarcomas, malignant melanoma, osteosarcoma, or of the lymphoid system (lymphoma/lymphosarcoma). Cryptorchidism and umbilical hernias are commonly seen in puppies of breeds that are more highly inbred. Epilepsy is another complex genetic condition that appears to increase in frequency as a breed suffers more inbreeding. Bloat is a problem seen in many larger deep chested breeds.

A number of these health problems can prove rapidly fatal, but many are either tolerable or manageable with treatment. Therefore, the reported lifespan is 10-12 years. Although many of the health conditions of the breed are manageable, the cost of veterinary care and difficulties coping with managing treatment has led to many Akita being euthanized or abandoned to shelters, where breed specific rescue groups may find them and try to place them in new homes. The fact that Akita are long-lived leads some to conclude that the breed is genetically sound, when in fact it suffers more from heritable disorders than almost any other breed.

Except for a small number of unique genetic conditions, usually of a simple recessive nature, most of the heritable disorders of Akita are ancestral in origin, i.e., the genetic risk factors have been in domestic dogs for a long time and many precede the Victorian era when pure breeding became a norm. The more inbred a breed becomes; the more simple and complex risk factors are concentrated, and the more heritable disease problems occur. Pure breeding involves closing registries to new genetic diversity and inbreeding to fix certain phenotypic traits. Because of closed registries, pure breeds are susceptible to many different types of artificial genetic bottlenecks, including small founder populations, geographic isolation, catastrophes such as famines and war, popular sire and bloodline effects, changes in popularity and population size, etc. There is no doubt that both AKA and AKJ are quite inbred, although the conditions behind this inbreeding are somewhat different. AKJ most likely suffer from a small founder population, while AKA started with a larger genetic base. However, the AKA has suffered more from inadvertent or deliberate non-random mating with dogs having 1081 and 2056 class I/II haplotypes. This is most likely a result of a popular sire effect, but further research is required to make this determination. Additional research is also needed to see if there is an association between specific DLA haplotypes and autoimmune disease.

There is some wisdom in outcrossing between the two varieties, as each contains some unique DLA class I and II haplotypes and there are some differences in allele frequencies at the genomic level. Attempts should also be made to identify additional diversity by testing DNA from dogs across a wider geographic area as well as in long isolated pockets from the home or other countries. Additional genetic diversity may also be present in related breeds.

Conclusion

American and Japanese Akita are closely related but genetically distinguishable varieties of a single breed. Founding dogs were selected independently from among remnant bloodlines that survived WWII and bred without subsequent introgression in Japan and America. Although some original dogs may still exist in their home region, most of the genetic diversity that remains for the breed is likely retained across and within contemporary American and/or Japanese varieties. DNA testing could prove beneficial in identifying remnants of genetic diversity and re-balancing existing diversity. Outcrossing between varieties is at an early stage and could prove important for improving breed health.

Other Information

[A CONVERSATION ABOUT SA IN JAPANESE AKITA INU WITH DR. NIELS PEDERSEN](#)
[By Peter van der Lugt](#)