Genetic Diversity Testing for German Shepherd Dogs

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 to determine genetic heterogeneity and diversity across the genome and in the Dog Leukocyte Antigen (DLA) class I and II regions for specified dog populations. This test panel is useful to dog breeders who wish to use DNA-based testing to track and distribute genetic diversity as a supplement to in-depth pedigrees. Information on genetic heterogeneity and diversity, along with DNA testing results for desired phenotypes and health traits, can aid in informing breeding decisions in order to improve the overall genetic health of a breed.

Genetic diversity testing of the German Shepherd Dog is now in the **preliminary results** phase. During this phase, we will continue to test more registered dogs to build the genetic database necessary to provide a more accurate assessment of genetic diversity within the breed. This report is based on 38 registered German Shepherds from the United States (n=26) Canada (n=11) and the Netherlands (n=1). Although results reported herein are preliminary, this cohort of individuals should provide a reasonable picture of genetic diversity in the breed. Allele and DLA haplotype frequencies will be updated as more dogs are tested. It is anticipated that new alleles at the 33 STR loci and additional DLA class I and II haplotypes will be identified in the future, but these will likely be of lower frequency than those detected in this initial population. Please note that some of the diversity metrics reported herein were calculated using 37 out of the 38 individuals.

Results reported as:

Short tandem repeat (STR) loci: A total of 33 STR loci from carefully selected regions of the genome were used to assess genetic heterogeneity and existing genetic diversity within an individual as well as across the breed. The alleles inherited from each parent are displayed graphically to highlight heterozygosity and genetic diversity in individuals as well as breed-wide.

DLA haplotypes: Seven STR loci linked to the DLA class I and II genes were used to identify genetic differences in a region that regulates 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, allergies, and susceptibility to infectious agents.

Internal Relatedness: The IR value is a measure of the genetic relatedness of an individual's parents. The value 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; two individuals from different sources may have identical IR values, but a quite different genetic makeup.

I. Introduction to the German Shepherd

A. Breed History [1-3]

Undoubtedly one of the most popular and recognizable dog breeds in the world, the German Shepherd (*Deutshe Schäferhund*) can be traced back to a dog named Horand von Grafrath, born in 1895 in Frankfurt, Germany (**Figure 1a**). Formerly named Hektor Linksrhein, this male was purchased by Captain Max E. F. von Stephanitz, a German cavalry officer who was largely responsible for the development of the German Shepherd Dog as a breed (**Figure 1b**).

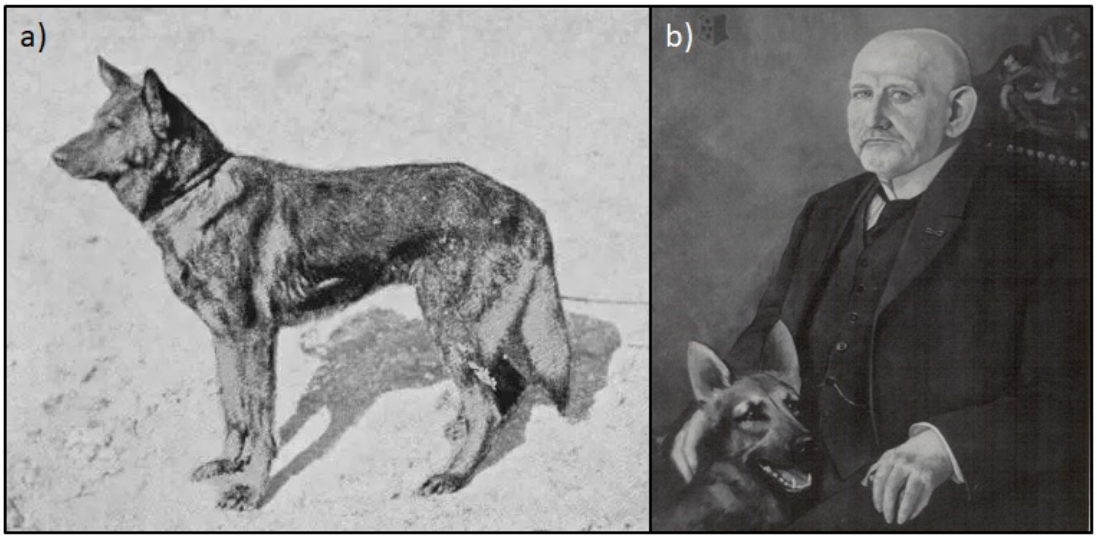


Figure 1. a) Horand von Grafrath (1895-1899), the first registered German Shepherd. **b)** Captain Max von Stephanitz with Horand von Grafrath.

Horand von Grafrath was a grey/yellow sable Thuringian Shepherd (a breed named after a German state), and was purchased by von Stephanitz to serve as a stud in his newly created breeding program. His goal was to develop a breed of working dogs that combined the qualities of Thuringian and Wurtemberg sheepdogs. For that, in 1899 Captain Max von Stephanitz founded and became the first president of the Society for German Shepherd Dogs (*Verein für Deutsche Schäferhunde*). Subsequently, Horand von Grafrath became the first individual registered as a German Shepherd Dog. The main directive of this newly created society was the standardization of the German Shepherd breed, both in terms of work ability and temperament. To von Stephanitz, breeding for beauty was secondary to selecting for the traits he considered essential for a working dog ("utility and intelligence").

In just a couple of decades, the number of individuals grew exponentially worldwide and the German Shepherd became one of the world's most popular breeds, a recognition that still holds to this day. In 1907, Mira von Offingen was the first German Shepherd exhibited in America, more specifically in the states of Pennsylvania and Philadelphia. Just a few years later, in 1913, the German Shepherd Dog Club of America (GSDCA) was founded by Benjamin Throop and Anne Tracy, along with 26 other members. However, in 1917 animosities arising from the USA entering World War I led the American Kennel Club to change the breed's name to Shepherd Dog. At the same time, the German Shepherd Dog Club of America was rebranded as the Shepherd Dog Club

of America. It wasn't until the late 1970's that the breed was registered again as German Shepherd in the United States.

Popularity of the German Shepherd rose rapidly after WWI, driven by famous dogs such as Strongheart (originally named Etzel von Oeringen, 1917-1929) and Rin Tin Tin (1918-1932) (**Figure 2**). Combined, these dogs appeared in over 30 movies and are hugely responsible for increasing the worldwide popularity of German Shepherds as family pets.

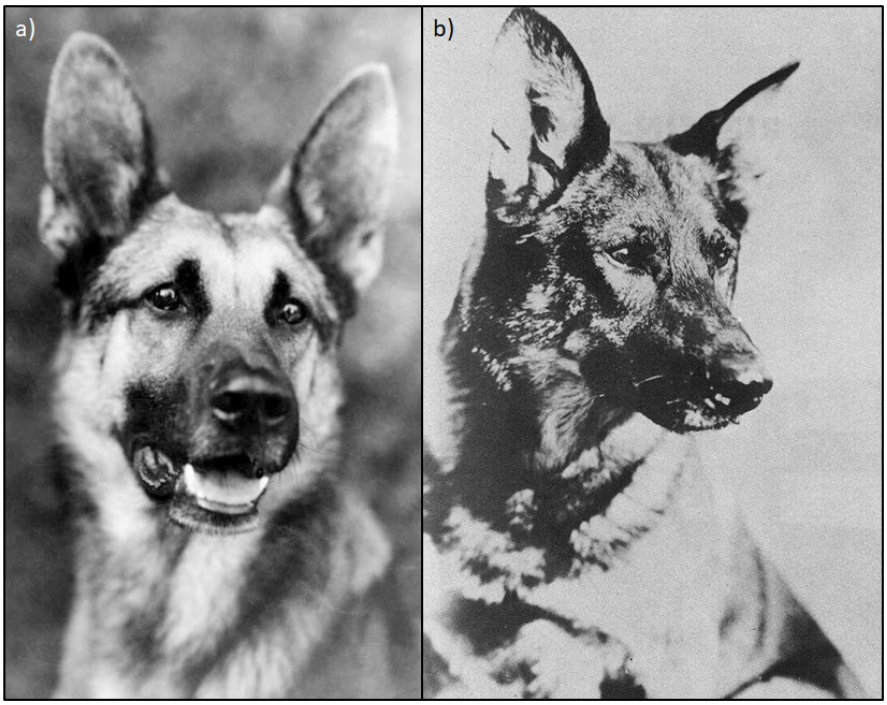


Figure 2. a) Etzel von Oeringen (1917-1929), also known as Strongheart. **b)** Rin Tin Tin (1918-1932). These two male German Shepherds were famous worldwide, appearing in over 30 films.

Known for being loyal, easy to train, and eager to follow instructions, German Shepherds are used in a wide variety of tasks such as pets, police and military work, guard dogs, rescue dogs, explosive and narcotic detection, and guide dogs, among many others. The breed remains hugely popular and numerous, ranking 4 of 200 in the AKC's breed popularity ranking.

B. Appearance [1-3]

The German Shepherd is a large dog breed, with males ranging from 24-26 inches at the withers and weighing between 65 and 90 pounds, and females ranging from a height of 22-24 inches at the withers and a weight of 50-70 pounds. According to the AKC's breed standard, secondary sex characteristics are strongly marked in both sexes. German Shepherds are strong, agile, and well-muscled. They are longer than they are tall, with a desirable proportion of 10 to 8½.

The head is noble and chiseled, the eyes are medium-sized and almond shaped, and the ears are moderately pointed, open toward the front, and carried erect when at attention. The muzzle is long and strong, with a black nose and 42 teeth (20 upper and 22 lower teeth). The neck is strong and

muscular, relatively long, and the withers are higher than and sloping into the back, which is straight. The tail is bushy and hangs in a slight curve when at rest. When the dog is excited or in motion, the curve is accentuated and the tail raised, but it should never be curled forward beyond a vertical line.

The double coat is of medium length; the dense outer coat is composed of straight hairs, is harsh and lies close to the body. The head, legs, and paws are covered with short hair. Most colors are permissible, such as black/tan, black/red, and solid black, for example. Common color schemes include “saddle”, “sable”, and “blanket”. Pale, washed-out colors and blues or livers are serious faults.

Disqualifications include cropped or hanging ears, noses that are not predominantly black, undershot jaws, docked tails, white dogs, and aggression (a dog that attempts to bite the judge).

C. Temperament [1,2]

German Shepherds are known for their motivation to learn and follow commands, traits that make them excellent working dogs. They are eager and alert, and marked by their loyal and protective nature. They are intelligent, obedient, and can be territorial. They are loving family dogs, but can take time to get friendly with outsiders. According to the breed standard as described by the GSDCA, the ideal German Shepherd is a working animal with an incorruptible character, combined with body and gait suitable for the arduous work that constitutes its primary purpose.

D. Health of the German Shepherd [1-4]

1. Lifespan

The breed’s average lifespan is 7 to 12 years of age.

2. Disorders

Common disorders found in German Shepherds, due to their size and genetic background, are elbow (ED) and hip dysplasia (HD). According to the 2021 Orthopedic Foundation for Animals (OFA) statistics, 16.7% of German Shepherds are affected by ED and 17.4% are affected by HD. These are not curable disorders, but can be prevented with a healthy diet, a good exercise program, and most importantly, through informed breeding decisions.

Canine Degenerative Myelopathy (DM) is an inherited neurological disease of autoimmune origin, characterized by a progressive weakness and lack of coordination of the rear limbs that ultimately leads to paralysis, incontinence and muscle atrophy. This disorder is caused by a mutation in the *SOD1* gene, and according to OFA statistics, 14.1% of German Shepherds are affected by this disease. Additionally, 29.4% of individuals are carriers, i.e., even though they are asymptomatic, they can produce affected puppies. Other autoimmune disorders found in German Shepherds include pemphigus foliaceous and systemic lupus erythematosus.

Other inherited disorders found in the breed are Von Willebrand disease (VWD – a blood clotting disorder), progressive retinal atrophy (PRA), pituitary dwarfism, congenital megaesophagus (ME), dilated cardiomyopathy (DCM), and pancreatic acinar atrophy (PAA), among others. German Shepherds can also be affected by bloat – also called gastric dilation and volvulus (GDV), allergies, heart diseases, epilepsy, and hypothyroidism.

The CHIC program is a canine health database sponsored by the AKC Canine Health Foundation and the Orthopedic Foundation for Animals. German Shepherds need to be tested for the following conditions in order to obtain a CHIC certificate:

a) Hip dysplasia through a radiographic OFA evaluation;
b) Elbow dysplasia through a radiographic OFA evaluation;
c) Temperament test – Results of GSDCA temperament test submitted to OFA.

Tests recommended (but not required) by the OFA for German Shepherds include:

a) Cardiac evaluation – Standard congenital cardiac exam with results registered with OFA;
b) Autoimmune thyroiditis through an approved laboratory;
c) ACVO Eye Exam – annually until age 6, and every 2 years thereafter;
d) Degenerative Myelopathy (DM) – DNA tests results from an approved laboratory.

The VGL offers a German Shepherd Dog Health Panel, which offers genetic tests for seven inherited disorders known to occur in the breed. More information can be obtained here: https://vgl.ucdavis.edu/panel/german-shepherd-health-panel.

II. Preliminary Results on Genetic Diversity of 38 German Shepherds

a. Population genetics based on 33 STR loci on 25 canine 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 consisting of those that are recommended for universal parentage determination for domestic dogs by the International Society of Animal Genetics (ISAG) and additional markers developed by the VGL for forensic purposes [5,6]. For each STR locus included in this study, an average of 17 different alleles have been identified across all breeds tested at the VGL so far. Each breed, having evolved from a small number of founders and having been exposed to artificial genetic bottlenecks, will end up with only a portion of the total available diversity (i.e., the total number of alleles). Artificial genetic bottlenecks can include phenomena such as popular sire effects, geographic isolation, catastrophes, outbreaks of disease, and ups and downs in popularity which can lead to increases and decreases in population size. The alleles identified at each of the 33 STR loci and their relative frequencies for the 38 German Shepherds included in this study are listed in **Table 1**.

Table 1. Alleles and their frequencies for 33 STR markers in German Shepherds (n=38). The allele that occurs at the highest frequency at each locus is bolded.

AHT121	AHT137	AHTH130	AHTh171-A	AHTh260	AHTk211
80 (0.03)	131 (0.37)	123 (0.09)	219 (0.11)	**238 (0.38)**	87 (0.24)
88 (0.01)	133 (0.03)	125 (0.01)	**223 (0.43)**	242 (0.22)	89 (0.29)
94 (0.05)	135 (0.01)	127 (0.41)	225 (0.04)	244 (0.03)	91 (0.13)
100 (0.14)	**137 (0.53)**	129 (0.04)	233 (0.42)	246 (0.18)	**95 (0.33)**

102 (0.62)	141 (0.01)	**131 (0.45)**		248 (0.03)	97 (0.01)
104 (0.11)	151 (0.04)			252 (0.16)	
108 (0.01)	155 (0.01)				
112 (0.03)					
AHTk253	**C22.279**	**FH2001**	**FH2054**	**FH2848**	**INRA21**
286 (0.07)	116 (0.41)	132 (0.33)	**152 (0.43)**	232 (0.03)	91 (0.08)
288 (0.74)	118 (0.09)	140 (0.01)	156 (0.03)	236 (0.04)	**95 (0.62)**
290 (0.07)	124 (0.04)	**144 (0.36)**	160 (0.05)	238 (0.04)	97 (0.04)
292 (0.03)	**126 (0.46)**	148 (0.28)	164 (0.14)	**240 (0.43)**	99 (0.18)
294 (0.11)		152 (0.03)	168 (0.32)	242 (0.42)	101 (0.08)
			172 (0.03)	244 (0.04)	
INU005	**INU030**	**INU055**	**LEI004**	**REN105L03**	**REN162C04**
110 (0.18)	146 (0.46)	210 (0.20)	**85 (0.55)**	**227 (0.41)**	200 (0.12)
124 (0.30)	**150 (0.49)**	214 (0.08)	95 (0.39)	231 (0.22)	204 (0.08)
126 (0.50)	152 (0.05)	**218 (0.49)**	103 (0.03)	233 (0.09)	**206 (0.38)**
128 (0.01)		220 (0.24)	107 (0.03)	235 (0.09)	208 (0.05)
				241 (0.18)	212 (0.37)
REN169D01	**REN169O18**	**REN247M23**	**REN54P11**	**REN64E19**	**VGL0760**
212 (0.38)	158 (0.04)	268 (0.13)	226 (0.41)	139 (0.01)	12 (0.13)
216 (0.59)	162 (0.26)	**270 (0.78)**	232 (0.04)	143 (0.04)	**13 (0.37)**
218 (0.01)	164 (0.16)	272 (0.01)	**234 (0.47)**	145 (0.04)	14 (0.01)
220 (0.01)	166 (0.17)	278 (0.08)	236 (0.01)	147 (0.08)	18.2 (0.04)
	168 (0.33)		238 (0.07)	153 (0.18)	19.2 (0.03)
	172 (0.01)			**155 (0.64)**	20 (0.01)
	178 (0.03)				20.2 (0.11)
					21.2 (0.21)
					22.2 (0.08)
					23.2 (0.01)
VGL0910	**VGL1063**	**VGL1165**	**VGL1828**	**VGL2009**	**VGL2409**
16.1 (0.01)	8 (0.01)	14 (0.01)	15 (0.04)	9 (0.03)	**15 (0.33)**
17.1 (0.30)	9 (0.01)	**15 (0.22)**	16 (0.03)	11 (0.26)	16 (0.26)
18.1 (0.04)	10 (0.13)	16 (0.04)	17 (0.04)	13 (0.18)	17 (0.14)
19.1 (0.32)	11 (0.05)	17 (0.22)	**19 (0.87)**	14 (0.22)	18 (0.18)
20.1 (0.13)	**12 (0.36)**	22 (0.07)	20 (0.01)	**15 (0.30)**	19 (0.08)
21.1 (0.14)	13 (0.34)	23 (0.01)	22 (0.01)		
22.1 (0.05)	14 (0.07)	25 (0.03)			
	18 (0.01)	26 (0.22)			
	20 (0.01)	27 (0.09)			
		28 (0.08)			
VGL2918	**VGL3008**	**VGL3235**			
13 (0.13)	10 (0.04)	13 (0.01)			
14 (0.18)	**15 (0.62)**	**14 (0.42)**			

15 (0.18)	16 (0.03)	15 (0.39)
16.3 (0.01)	17 (0.05)	16 (0.14)
18.3 (0.03)	18 (0.18)	17 (0.01)
19.3 (0.08)	19 (0.07)	19 (0.01)
20.3 (0.03)	20 (0.01)	
21.3 (0.26)		
22.3 (0.09)		

The number of alleles found for each STR locus in German Shepherd was relatively low, ranging from 3 (INU030) to 10 (VGL0760, VGL1165). Moreover, a single allele was predominant (found in 50% or more of the cohort) at 10 out of the 33 STR loci (bold in **Table 1**), which indicates that these alleles were present in the foundation stock and were retained in high frequency in the population due to being linked to breed-defining phenotypic traits. This finding is typical of pure dog breeds. It is noteworthy that the percentage of STR loci in which a single allele was identified in a disproportionately high frequency (30%) is relatively low in this breed, so the goal for German Shepherd breeders should be to maintain and keep re-distributing allele frequencies by conserving and breeding rare lines/families. Additional alleles for the 33 STR markers will be identified as more individuals are tested, but likely at low number and frequency.

b. Assessment of population diversity using standard genetic parameters

Alleles for each of the 33 STR loci listed in **Table 1** and their respective frequencies are used to determine basic genetic parameters for the population (**Table 2**). These parameters include the number of alleles found at each locus (**Na**); the number of effective alleles (**Ne**) per locus (i.e., the number of alleles that contribute most to genetic differences/heterozygosity); observed heterozygosity (**Ho**); expected heterozygosity (**He**) if the existing population was in Hardy-Weinberg equilibrium (i.e., random breeding); and the coefficient of inbreeding (**F**) derived from Ho and He values.

Table 2. Genetic Assessment of 38 German Shepherds based on 33 autosomal STR loci. SE = standard error of the mean.

	Na	**Ne**	**Ho**	**He**	**F**
Mean	5.79	3.096	0.623	0.637	0.02
SE	0.31	0.188	0.023	0.022	0.015

The average number of STR alleles identified in this study cohort (Na = 5.8) corresponds to approximately 34% of the average number of alleles identified by the VGL across breeds (see **section IIa**). This means that 66% of the genetic diversity known to exist at these 33 STR loci has been lost in the modern German Shepherd. However, the number of effective alleles (Ne) constitutes a more relevant metric for genetic diversity, since these alleles have the greatest genetic influence on heterozygosity levels. The average number of effective alleles per locus (Ne) was

estimated at 3.1 for German Shepherds; this indicates that most of the heterozygosity was determined by one-half of the alleles segregating in the breed (**Table 2**).

Additionally, results from **Table 2** show that the mean observed (Ho=0.623) and expected heterozygosity (He=0.637) values were similar, thus yielding an inbreeding coefficient (F) of 0.02 for this cohort (**Table 2**). This value suggests that this group of 38 German Shepherds was a product of random breeding (i.e., were close to Hardy-Weinberg equilibrium in which F=0). In other words, sires and dams of the study population were as unrelated as possible. Therefore, even though genetic diversity is relatively low in this breed, these results indicate that breeders appear to be doing a good job of evenly distributing the existing diversity by mating individuals as unrelated as possible based on this preliminary study.

Although these findings provide an estimate of genetic diversity at the breed level, a better picture of heterozygosity at an individual level can be obtained by looking at Internal Relatedness (IR) scores. This diversity metric should be used by breeders to select the most unrelated mates possible in order to continue redistributing the genetic diversity currently existing in German Shepherd (see **section e** below).

c. Standard genetic assessment values for individual STR loci

Allele frequencies can be also used to perform a standard genetic assessment of heterozygosity at each of the 33 autosomal STR loci used in this study (**Table 3**). This provides an estimate of genetic diversity in the specific regions of the genome that harbor each STR marker. Again, it is important to assess the number of effective (Ne) alleles, as these have greater impact on heterozygosity. **Table 3** shows that this metric ranged from 1.3 (VGL1828) to 5.8 alleles (VGL1165 and VGL2918). Based on allele frequencies per locus, observed heterozygosity (Ho) values ranged from 0.26 (VGL1828) to 0.82 (REN169O18, VGL1165, VGL2918); locus-specific expected heterozygosity (He) values were in general similar to their respective Ho values, ranging from 0.24 (VGL1828) to 0.83 (VGL1165 and VGL2918).

Microsatellite loci with the lowest Ho values contribute the least to heterozygosity levels across the breed, because they are most likely linked (i.e., inherited together) with genes associated with genetic traits that are important for the breed's phenotypic standard and thus show less variability. Conversely, a high Ho value means that a locus has greater genetic diversity (variability) across the breed. These loci may be in linkage with genes associated with phenotypic variation among individuals.

Based on Ho and He values estimated for each STR locus, inbreeding coefficients (F) for German Shepherd ranged from -0.12 (AHTH130) to 0.22 (C22.279) (**Table 3**). High inbreeding values (F > 0.1) were estimated for only four of the 33 STR loci (or 12%, bolded on **Table 3**) – fewer than most breeds studied at the VGL so far. High inbreeding levels suggest that these loci have been under strong positive selection since breed development, and thus lack diversity. However, these high levels are balanced by the other loci with F values around or below zero (thus indicating outbreeding), leading to an average inbreeding value of approximately zero estimated for the cohort (see **Table 2**).

Table 3. Standard Genetic Assessment of individual STR loci for 38 German Shepherds. Individual STR loci with high inbreeding coefficients (F>0.1) are bolded.

Locus	Na	Ne	Ho	He	F
AHT121	8	2.39	0.58	0.58	0.004
AHT137	7	2.41	0.58	0.58	0.009
AHTH130	5	2.67	0.7	0.63	-0.12
AHTh171-A	4	2.64	0.63	0.62	-0.02
AHTh260	6	3.91	0.71	0.74	0.045
AHTk211	5	3.77	0.71	0.73	0.033
AHTk253	5	1.78	0.42	0.44	0.036
C22.279	**4**	**2.57**	**0.47**	**0.61**	**0.225**
FH2001	5	3.21	0.68	0.69	0.006
FH2054	6	3.19	0.76	0.69	-0.11
FH2848	6	2.69	0.66	0.63	-0.05
INRA21	5	2.32	0.63	0.57	-0.11
INU005	4	2.66	0.61	0.62	0.031
INU030	3	2.21	0.55	0.55	-0.01
INU055	4	2.96	0.63	0.66	0.046
LEI004	4	2.16	0.55	0.54	-0.03
REN105L03	5	3.74	0.68	0.73	0.066
REN162C04	5	3.29	0.74	0.7	-0.06
REN169D01	4	2.01	0.47	0.5	0.059
REN169O18	7	4.27	0.82	0.77	-0.07
REN247M23	4	1.6	0.34	0.37	0.084
REN54P11	5	2.52	0.63	0.6	-0.05
REN64E19	**6**	**2.18**	**0.45**	**0.54**	**0.173**
VGL0760	10	4.6	0.79	0.78	-0.01
VGL0910	**7**	**4.27**	**0.63**	**0.77**	**0.175**
VGL1063	9	3.73	0.74	0.73	-0.01
VGL1165	10	5.82	0.82	0.83	0.015
VGL1828	6	1.32	0.26	0.24	-0.09
VGL2009	**5**	**4.07**	**0.61**	**0.76**	**0.198**
VGL2409	5	4.19	0.76	0.76	0
VGL2918	9	5.86	0.82	0.83	0.016
VGL3008	7	2.35	0.53	0.57	0.083
VGL3235	6	2.82	0.61	0.65	0.062

d. Differences in population structure as determined by Principal Coordinate Analysis (PCoA)

PCoA measures the genetic relatedness of individuals within a population. The data is computed in a spherical form, but often presented in the two dimensions that most closely represent its multi-dimensional form (usually coordinates 1 and 2). The closer individuals cluster together around the

XY axis, the more closely related they are to each other. The 38 German Shepherds used in this study clustered as expected for a pure breed in the PCoA, with dogs reasonably dispersed across all four quadrants (**Figure 3**). A few pairs of genetically similar individuals were observed in this cohort (red circles) based on STR genotypes.

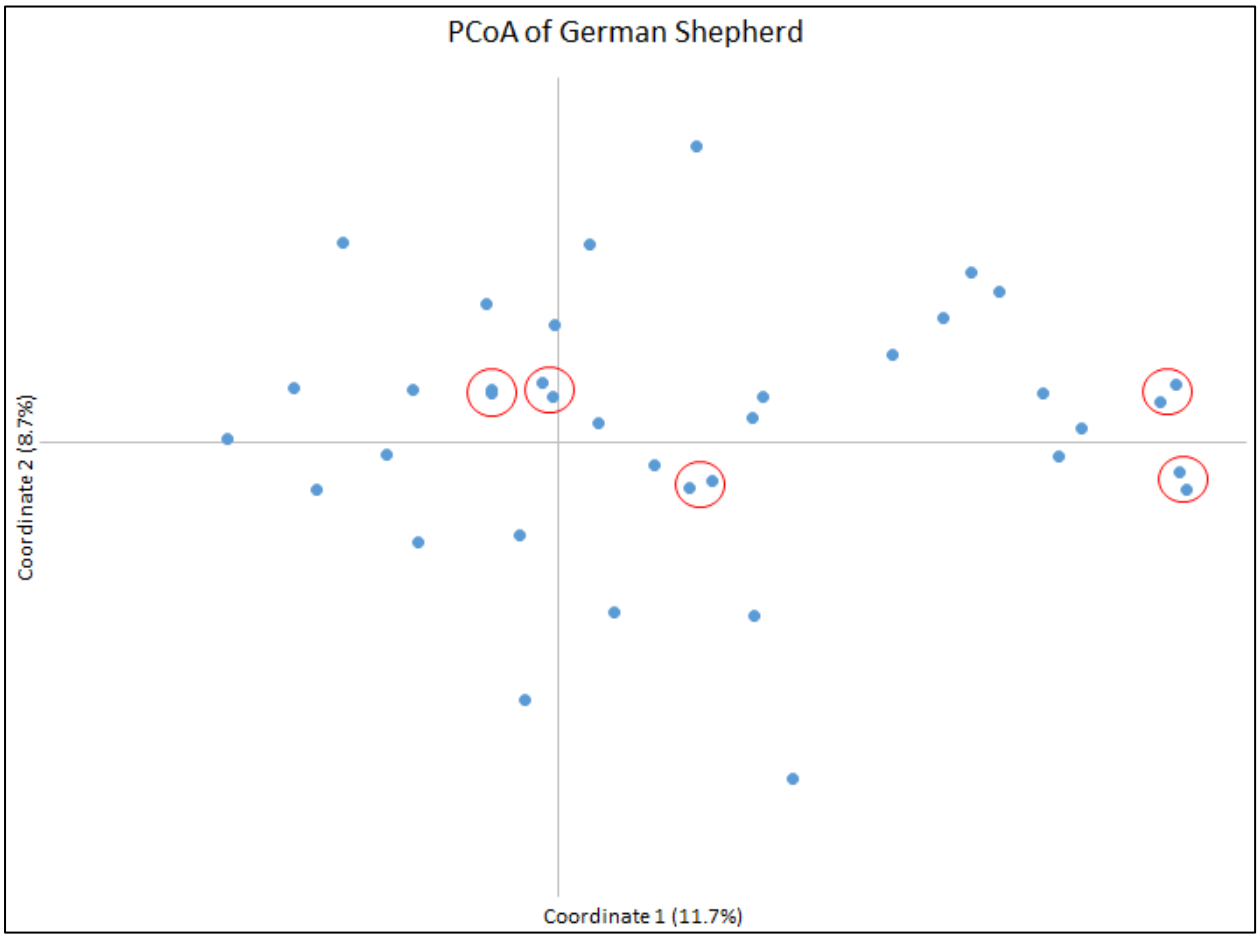


Figure 3. PCoA of German Shepherd (n=38) based on STR alleles and their frequencies at 33 autosomal loci. Red circles indicate pairs of genetically similar individuals.

The degree of intra- and inter-breed relatedness can be further assessed by comparing this cohort of German Shepherds with other breeds, such as the closely related Shiloh Shepherd, and the more distantly related Irish Wolfhound (**Figure 4**). Inter-breed clustering shows separate and well-defined populations, thus indicating that the breeds are genetically distinct as expected. The two Shepherd breeds are clearly related, given their proximity to each other along the X-axis of the PCoA plot, but are genetically distinguishable. However, clustering of each breed in the plot indicates that German Shepherd is more genetically diverse than Shiloh Shepherd and Irish Wolfhound, due to a relatively more "diffuse" scattering of individuals along the Y-axis. This is corroborated by our previous reports (see https://vgl.ucdavis.edu/canine-genetic-diversity/irish-wolfhound and https://vgl.ucdavis.edu/canine-genetic-diversity/shiloh-shepherd). Interestingly, a couple of individuals bridged the two Shepherd populations (red circles), which might indicate either a high degree of German Shepherd introgression into the Shiloh Shepherd individual (grey dot), or a breed misclassification (**Figure 4**).

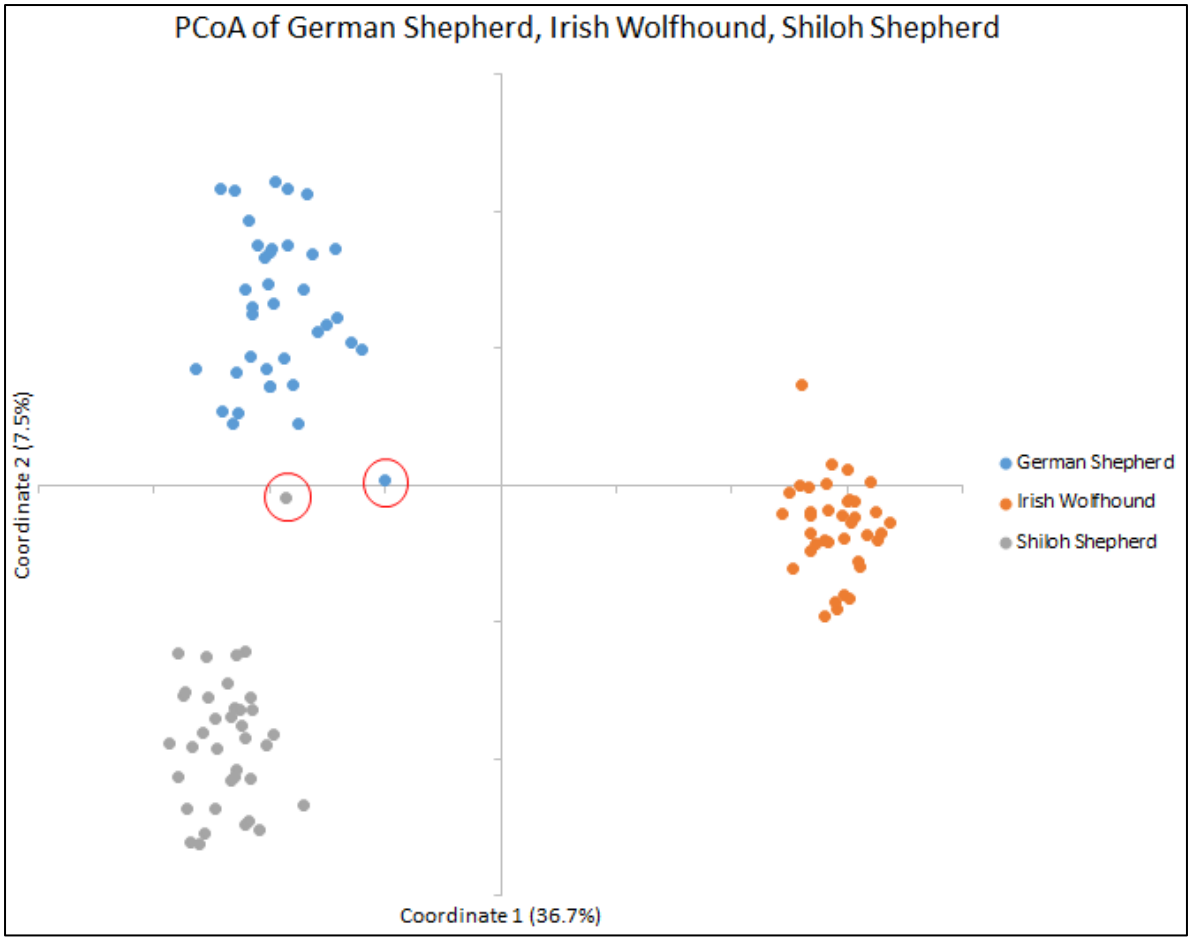


Figure 4. PCoA plot comparing intra- and inter-breed relatedness of German Shepherd (blue dots; n=37) with Irish Wolfhound (orange dots; n=37) and Shiloh Shepherd (grey dots; n=37).

III. Internal relatedness (IR) scores for German Shepherds

a. IR testing and meaning

Genetic assessments such as those presented in Tables 1-3 are indicators of population-wide heterozygosity and do not reflect the genetic diversity inherited by individuals from their parents. Internal Relatedness (IR) is a calculation that has been used to determine the degree of relatedness of parents of an individual dog. The IR calculation takes into consideration homozygosity at each of the 33 STR loci in this study and gives more weight to rare and uncommon alleles, which would presumably be identified in less related individuals. IR scores of all individuals in a population can be graphed to form a curve ranging from -1.0 to +1.0. A dog with an IR value of -1.0 would have parents that are totally unrelated at all 33 STR loci, while a dog with an IR value of +1.0 has parents that are genetically identical at all loci. An IR value of +0.25 would be found among offspring of full sibling parents from a random breeding population. IR values >0.25 occur when the parents of the full sibling parents are themselves highly inbred. *The higher the IR value is above 0.25 for a particular individual, the more closely related are the parents and grandparents of the sibling parents.* **Table 4** summarizes the IR and adjusted village-dog IR (IRVD – see **section e-2**) values for the 38 German Shepherds analyzed in this study.

Table 4. Internal relatedness (IR) and adjusted village-dog IR (IRVD) values calculated using the number of alleles and their respective frequencies for 33 STR loci in 38 German Shepherds.

	IR	IRVD
Minimum	-0.2543	0.0134
1st Quartile	-0.0361	0.1600
Mean	0.0227	0.2424
Median	0.0200	0.2342
3rd Quartile	0.0799	0.3346
Maximum	0.3128	0.4993

The most outbred German Shepherd of the study cohort had an IR score of -0.25, while the most inbred dog had an IR score of 0.31, with a mean IR across the cohort of 0.02. This wide range of IR values is a common finding for pure dog breeds and shows that the wide range of parental relatedness in the study cohort. **Table 4** also indicates that, even though the standard genetic assessments estimated from allele frequencies indicated that the population was randomly breeding (see **Table 2**), IR values suggest that this value can be attributed to more outbred dogs cancelling out more inbred dogs. Close to one-fourth of German Shepherds tested were products of closely related parents (IR values between 0.08 and 0.3), whereas around one-fourth of individuals were outbred (IR values between -0.25 and -0.04).

b. Adjusted IR values (IRVD) as a measure of genetic diversity lost during breed development

Internal relatedness values estimated for German Shepherds can also be represented graphically (**Figure 5**). The IR curve (red line) is trimodal (three peaks): the small peak on the left represents the ~25% most outbred dogs, whereas the small peak on the right represents the ~25% most inbred individuals. Furthermore, the IR values obtained from known STR alleles and their frequencies can be used to approximate the amount of genetic diversity that was lost when a breed was developed from its oldest common ancestors. Village dogs that exist throughout the SE Asia, the Middle East and the Island Pacific region are randomly breeding descendants of dogs from which most modern breeds evolved. The known STR alleles and their frequencies of a given breed can be compared with the same alleles and their frequency in modern village dogs to yield an adjusted IR score (IR-village dog or IRVD) (**Table 4** and **Figure 5**, blue line). In other words, IRVD scores approximate how the IR score for a German Shepherd would compare to other village dogs if its parents were also village dogs.

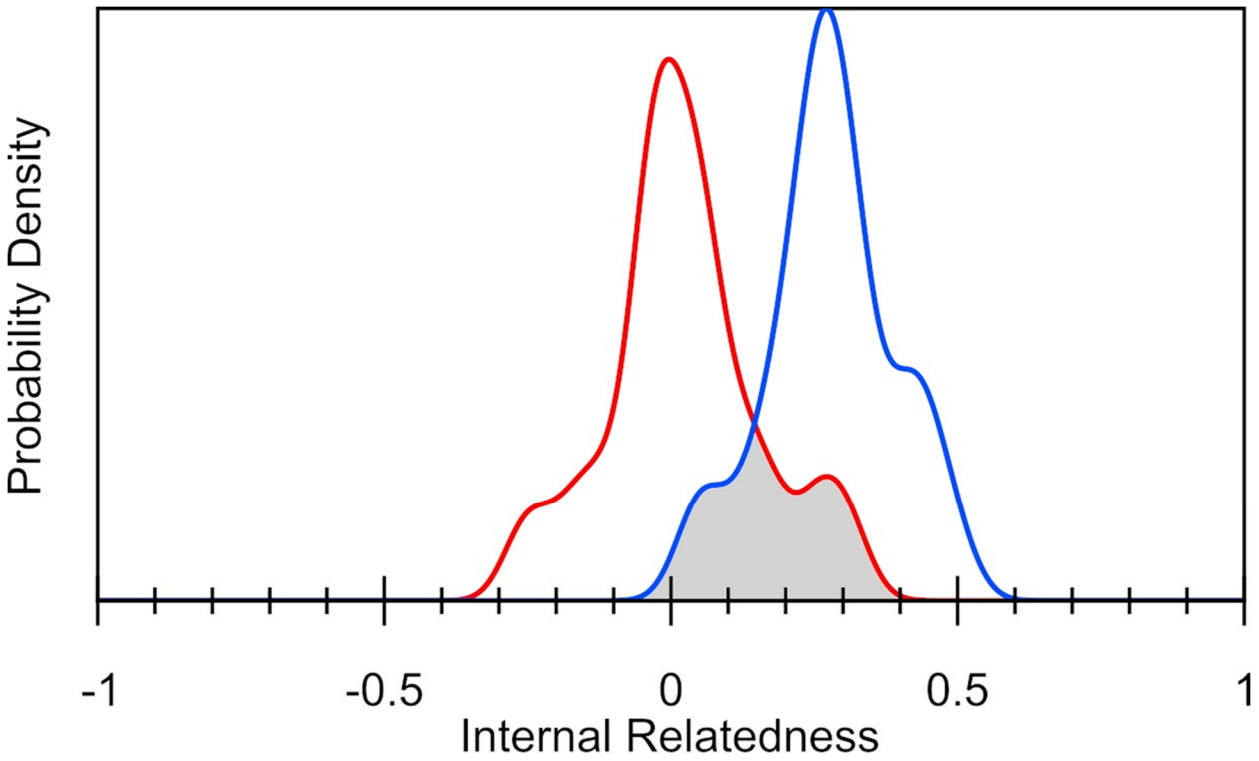


Figure 5. Distribution of IR (red line) and IR-village dog (IRVD) (blue line) values for German Shepherds (n=38). The overlap between the curves (grey area) shows that German Shepherds retain 29.4% of the total genetic diversity existing in randomly breeding village dogs.

The German Shepherd IRVD curve (blue line) is also trimodal but shifted to the right of their actual IR scores (red line) (**Figure 5**). This is because estimated IRVD values ranged from 0.01 to 0.5 (**Table 4**). The IR and IRVD curves overlapped over 29.4% of their areas (shaded in grey). This suggests that German Shepherds have retained around 30% of the total genetic diversity thought to still exist among village dogs from the region considered the ancestral home of most modern breeds. Interestingly, this figure is comparable to the average retained genetic diversity calculated from comparisons with known alleles at the 33 STR loci of all canids tested at VGL, also estimated at 30% (**section IIb**).

c. DLA class I and II haplotype frequencies and genetic diversity

The DLA consists of four gene-rich regions that make up a small portion of 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, which can cause autoimmune diseases, allergies, and resistance/susceptibility to infectious diseases. Breeds that lack genetic diversity in the DLA region are often more prone to autoimmune disorders.

The Class I region contains several genes, but one (*DLA88*) is highly polymorphic (i.e., contains many alleles) and is therefore most important for immune regulation. Specific alleles at the four STR loci associated with *DLA88* are linked in various combinations, forming specific haplotypes

(**Table 5**). Groups of genes (and consequently their alleles) inherited as a block 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 these three loci associated with the three class II genes are strongly linked, and often inherited as a single haplotype (see **Table 6**). An individual inherits one haplotype from each of the parents. It is common for different dog breeds to share common and even rare haplotypes for these loci, depending on breed history and common ancestry.

d. DLA class I and II haplotypes in German Shepherds

Only 8 DLA class I and 9 DLA class II haplotypes were identified in this group of German Shepherds, which is a relatively low number when compared to other breeds tested at the VGL so far (**Table 5**). These numbers are slightly higher than those found in the English Mastiff (6 DLA I and 6 DLA II haplotypes) and the closely related Shiloh Shepherd (7 DLA I and 6 DLA II), and much lower than those of more popular and diverse breeds such as Golden Retrievers (24 and 19, respectively) and Miniature Poodle (33 DLA I and 23 DLA II).

Table 5. DLA I and DLA II haplotypes identified in the German Shepherd study cohort (n=37), as well as their respective frequencies. Haplotypes with the highest frequency are bolded.

DLA1 haplotype	STR types	Frequency (%)
1006	387 375 293 180	7
1045	376 371 277 186	3
1052	**380 372 289 184**	**47**
1054	382 379 277 184	7
1068	380 373 287 181	27
1091	381 371 277 181	1
DLA2 haplotype	**STR types**	**Frequency (%)**
2002	343 327 280	1
2003	343 324 282	1
2007	351 327 280	7
2017	**343 322 280**	**43**
2022	339 327 282	14
2039	345 327 276	3
2053	343 324 280	26

DLA-I haplotypes 1052 (47% frequency) and 1068 (27% frequency) were the most predominant in German Shepherds, being identified in 74% of the study cohort altogether. DLA-II haplotypes followed the same trend, with two predominant haplotypes: 2017 (with a frequency of 43%) and 2053 (26%) (**Table 5**). Since the two DLA-I/DLA-II haplotype combinations (1052/2017 and 1068/2053) were identified in almost identical frequencies, it can be inferred that they are in linkage disequilibrium (i.e., inherited together) as each DLA region is inherited as a block of linked genes from each parent and passed on by descent. Therefore, these DLA-I/DLA-II haplotypes were

present in two closely related founding lines and have been retained in the breed since its development. Although we anticipate that additional DLA-I and DLA-II haplotypes will be identified as more German Shepherds are tested, these will most likely be at lower frequency.

The DLA-I/DLA-II haplotypes identified in German Shepherds are shared with 55 different dog breeds/varieties tested at the VGL (**Table 6**). DLA haplotypes found in a breed can be used to investigate the founder lines and different breeds that were used to create and refine a breed. DLA haplotype sharing is a reflection common distant ancestry. Most of the DLA-I and DLA-II haplotypes found in German Shepherds are extensively shared with a number of other breeds. Not surprisingly, one DLA-I haplotype (1166) was only shared between German Shepherds and Shiloh Shepherds, and found at similar frequencies in both breeds; no DLA haplotypes were exclusively found in German Shepherds (**Table 6**).

Table 6. Sharing of DLA class I and II haplotypes between German Shepherds (highlighted in blue) and other dog breeds/varieties tested at the VGL (n=55).

DLA1 #	STR types	German Shepherd (n=37)	American Eskimo, Standard (n=65)	American Eskimo, Miniature (n=38)	American Eskimo, Toy (n=14)	American Hairless Terrier (n=186)	American Akita (n=160)	Japanese Akita (n=580)	Blend Akita (n=66)	Alaskan Klee Kai (n=652)	Barbet (n=68)	Border Collie (n=64)	Berger Picard (n=146)	Bernese Mountain Dog (n=148)	Black Russian Terrier (n=150)	Biewer (n=136)	Biewer Yorshire Terrier (n=54)	Biewer Terrier (n=218)	Yorkshire Terrier (n=16)	Borzoi (n=149)	Chinook (n=33)	Collie (n=49)	Doberman Pinscher (n=1224)	English Bulldog (n=163)	English Mastiff (n=31)	Mastiff (n=21)	Flat Coated Retriever (n=858)	Great Dane (n=74)	Golden Retriever (n=876)	Giant Schnauzer (n=330)
1006	387 375 293 180	0.07	--	--	--	--	0.084	--	--	--	--	--	--	0.078	0.047	--	--	--	--	0.151	--	--	--	0.003	--	0.02	--	0.014	0.016	0.047
1045	376 371 277 186	0.03	--	--	--	--	0.003	--	--	--	--	0.156	--	--	--	--	--	--	--	--	0.36	0.96	0.0004	--	--	--	--	--	--	--
1052	380 372 289 184	0.47	--	--	--	0.022	--	--	--	--	--	0.016	0.103	--	--	--	--	--	--	--	0.02	--	0.0008	--	0.02	--	--	--	--	--
1054	382 379 277 184	0.07	0.008	0.21	0.32	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	0.0979	--	--	0.003
1068	380 373 287 181	0.27	--	--	--	0.11	--	--	--	--	--	0.211	--	0.064	--	--	0.009	--	--	--	0.06	--	0.0004	--	--	--	0.2721	0.007	0.0462	0.055
1091	381 371 277 181	0.01	--	--	--	--	--	--	--	--	--	--	--	--	0.503	--	--	--	--	--	--	--	0.002	--	--	--	--	0.047	--	0.035
1165	392 369 281 182	0.01	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1166	388 379 277 184	0.07	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

DLA1 # (cont'd)	STR types (cont'd)	German Shepherd (n=37)	Havana Silk (n=44)	Havanese (n=973)	Italian Greyhound (n=1364)	Irish Setter (n=59)	Irish Red and White Setter (n=105)	Irish Wolfhound (n=78)	Lakeland Terrier (n=136)	Labrador Retriever (n=292)	Llewellin Setter (n=152)	Magyar Agar (n=78)	Newfoundland (n=137)	Polish Lowland Sheepdog (n=81)	Toy Poodle (n=232)	Miniature Poodle (n=413)	Poodle (n=5148)	Rat Terrier (n=44)	Samoyed (n=192)	Saint Bernard (n=90)	Scottish Collie (n=119)	Shiba Inu (n=160)	Shikoku (n=84)	Greater Swiss Mountain Dog (n=59)	Shiloh Shepherd (n=60)	Shiloh Shepherd, ISSA (n=270)	Swedish Vallhund (n=510)	Cardigan Welsh Corgi (n=43)	Whippet (n=110)
1006	387 375 293 180	0.07	0.02	0.0504	--	--	0.09	--	--	0.026	--	--	--	--	0.002	0.002	0.04769	--	0.005	--	0.034	--	--	--	--	--	0.2373	--	--
1045	376 371 277 186	0.03	--	--	--	--	--	--	--	0.005	0.003	--	--	--	0.019	0.005	0.00068	--	--	--	0.723	--	--	--	--	0.002	--	0.33	0.005
1052	380 372 289 184	0.47	--	0.0108	0.1859	--	--	0.333	0.011	--	--	0.051	--	--	--	--	0.00029	--	--	--	--	--	--	--	0.317	0.385	--	--	--
1054	382 379 277 184	0.07	0.07	0.1202	0.0143	0.153	--	--	--	0.058	0.092	0.141	--	--	0.002	0.001	0.00019	0.01	--	--	--	0.35	0.006	--	--	--	--	--	0.005
1068	380 373 287 181	0.27	0.24	0.0128	--	0.008	--	0.128	--	0.033	--	--	0.106	0.006	0.009	0.012	--	--	0.042	0.167	--	--	--	--	0.5	0.263	0.3618	--	--
1091	381 371 277 181	0.01	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	0.234	0.012	--	--	--	--	--	--
1165	392 369 281 182	0.01	--	--	--	--	--	--	--	0.164	--	--	--	--	--	--	--	--	--	0.067	--	--	--	--	0.108	0.217	--	--	--
1166	388 379 277 184	0.07	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	0.05	0.043	--	--	--

DLA2 #	STR types	German Shepherd (n=37)	American Eskimo, Standard (n=65)	American Eskimo, Miniature (n=38)	American Eskimo, Toy (n=14)	American Hairless Terrier (n=186)	American Akita (n=160)	Japanese Akita (n=580)	Blend Akita (n=66)	Alaskan Klee Kai (n=652)	Barbet (n=68)	Border Collie (n=64)	Berger Picard (n=146)	Bernese Mountain Dog (n=148)	Black Russian Terrier (n=150)	Biewer (n=136)	Biewer Yorshire Terrier (n=54)	Biewer Terrier (n=218)	Yorkshire Terrier (n=16)	Borzoi (n=149)	Chinook (n=33)	Collie (n=49)	Doberman Pinscher (n=1224)	English Bulldog (n=163)	English Mastiff (n=31)	Mastiff (n=21)	Flat Coated Retriever (n=858)	Great Dane (n=74)	Golden Retriever (n=876)	Giant Schnauzer (n=330)
2002	343 327 280	0.01	--	--	--	--	--	--	--	--	--	0.125	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
2003	343 324 282	0.01	0.023	0.04	--	0.263	--	--	--	--	0.132	0.055	--	--	--	0.265	0.213	0.25	0.38	--	--	0.14	--	0.0004	0.598	--	--	0.1457	0.007	0.0194	0.03
2007	351 327 280	0.07	--	--	--	--	0.084	--	--	0.0115	--	--	--	0.084	0.047	--	--	--	--	0.154	--	--	--	--	--	--	--	--	0.014	0.016	0.047
2017	343 322 280	0.43	--	--	--	0.005	0.009	0.0034	0.015	--	0.029	0.172	0.103	--	--	--	--	--	--	0.007	0.02	--	--	0.215	0.21	0.29	0.0006	--	0.0388	0.002
2022	339 327 282	0.14	0.023	0.21	0.32	0.032	--	--	--	--	--	0.008	--	--	--	--	--	--	--	0.587	--	--	0.0008	0.015	--	--	0.1148	0.101	0.0006	0.003
2039	345 327 276	0.03	--	--	--	--	0.091	0.1026	0.273	--	--	0.148	--	--	--	--	--	--	--	--	--	0.95	0.0086	--	--	--	--	--	--	--	--
2053	343 324 280	0.26	0.223	0.12	0.04	0.005	--	--	--	--	--	0.07	--	0.064	--	--	0.009	--	--	--	0.06	--	0.0012	--	--	--	0.1469	0.007	0.028	0.064
2067	343 322 284	0.04	--	--	--	0.022	--	--	--	--	--	0.07	0.897	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
2080	339 325 276	0.01	--	0.08	0.04	--	--	--	--	--	--	--	--	--	--	0.004	0.009	--	0.03	--	--	--	--	--	--	--	--	--	--	--

DLA2 # (cont'd)	STR types (cont'd)	German Shepherd (n=37)	Havana Silk (n=44)	Havanese (n=973)	Italian Greyhound (n=1364)	Irish Setter (n=59)	Irish Red and White Setter (n=105)	Irish Wolfhound (n=78)	Lakeland Terrier (n=136)	Labrador Retriever (n=292)	Llewellin Setter (n=152)	Magyar Agar (n=78)	Newfoundland (n=137)	Polish Lowland Sheepdog (n=81)	Toy Poodle (n=232)	Miniature Poodle (n=413)	Poodle (n=5148)	Rat Terrier (n=44)	Samoyed (n=192)	Saint Bernard (n=90)	Scottish Collie (n=119)	Shiba Inu (n=160)	Shikoku (n=84)	Greater Swiss Mountain Dog (n=59)	Shiloh Shepherd (n=60)	Shiloh Shepherd, ISSA (n=270)	Swedish Vallhund (n=510)	Cardigan Welsh Corgi (n=43)	Whippet (n=110)
2002	343 327 280	0.01	--	--	--	--	--	--	--	--	0.03	--	--	--	--	0.005	0.08547	0.01	0.003	--	0.004	--	--	--	--	--	--	--	--	--
2003	343 324 282	0.01	0.24	0.2138	0.007	--	--	--	0.761	0.022	--	--	0.004	--	0.422	0.511	0.10334	0.13	0.013	--	0.017	--	--	0.924	--	0.009	--	0.23	0.086	
2007	351 327 280	0.07	0.02	0.0519	--	--	0.195	--	--	0.029	--	--	0.15	--	0.002	0.001	0.01671	--	0.005	0.006	0.004	--	--	--	--	--	--	0.2402	0.12	--	
2017	343 322 280	0.43	--	0.0113	0.2115	--	--	--	0.029	--	--	0.449	--	0.278	0.002	0.001	0.00204	0.02	--	--	--	--	--	--	0.317	0.385	--	0.19	0.241	
2022	339 327 282	0.14	0.07	0.1146	--	0.153	--	0.353	0.176	0.058	0.092	--	--	--	0.006	0.002	0.00049	0.14	0.107	--	--	--	--	--	0.05	0.043	0.0578	--	--	
2039	345 327 276	0.03	--	--	0.0806	--	--	--	--	0.005	--	--	0.288	--	--	--	0.00058	--	--	--	0.71	--	--	--	--	0.002	--	0.31	--	
2053	343 324 280	0.26	0.25	0.0283	--	0.008	--	0.128	--	0.031	--	--	0.106	0.006	0.011	0.012	--	--	0.56	0.144	--	--	--	--	0.525	0.337	0.5324	--	--	
2067	343 322 284	0.04	--	--	0.0004	--	--	--	0.011	--	--	--	--	0.006	--	0.006	--	--	--	--	--	0.225	0.012	--	--	--	--	--	--	
2080	339 325 276	0.01	--	--	--	--	--	--	--	0.168	--	--	--	--	--	--	--	--	--	0.072	0.017	--	--	--	0.108	0.217	--	--	--	

e. Heterozygosity in the DLA region

Due to their physical proximity in canine chromosome 12, the seven loci that define the DLA class I and II haplotypes are in stronger linkage disequilibrium (i.e., have a higher probability of being inherited together) when compared to other parts of the genome. However, the expectation is that, in modern dog breeds, these loci have achieved an equilibrium with other loci across the genome over time due to theoretical random breeding. This assumption can be tested through a standard genetic assessment of each DLA locus (**Table 7**), as well as through an estimate averaged across all loci (**Table 8**).

In German Shepherds, it case be assumed that the DLA region has indeed reached an equilibrium with other loci regions of the genome. As shown in **Table 7**, the highest number of alleles (Na) identified for a DLA locus was 7 (DLA I-3CCA) and the lowest was 4 (5ACA, 5ACT, and 5BCA). However, similarly to the metrics identified for the genome-at-large, the number of effective alleles (Ne) per DLA locus was roughly half of the total alleles segregating, ranging from 1.61 (5BCA) to 3.12 (DLA I-4ACA). Also similarly to the genome-at-large, coefficients of inbreeding (F) estimated for individual DLA loci ranged from high (F=0.22 for 5BCA) to low (F=-0.18, DLA1131) (**Table 7**). It is likely that additional alleles will be found in the DLA region as more animals are tested.

Table 7. Standard genetic assessment for German Shepherds (n=38) using each of the 7 STRs in the DLA class I and II regions.

Locus	Na	Ne	Ho	He	F
DLA I-3CCA	7	1.789	0.447	0.441	-0.01
DLA I-4ACA	6	3.119	0.737	0.679	-0.09
DLA I-4BCT	5	3.011	0.737	0.668	-0.1
DLA1131	5	2.155	0.632	0.536	-0.18
5ACA	4	1.666	0.378	0.4	0.054
5ACT	4	2.807	0.737	0.644	-0.15
5BCA	4	1.616	0.297	0.381	0.22

When averaged across all DLA loci, the inbreeding coefficient estimated for German Shepherds (F=-0.04, **Table 8**) is lower than that estimated across the genome (F=0.02, **Table 2**). This suggests that the disproportionately high incidence of two DLA class I and II haplotype combinations (**Table 5**) is a result of a single founder line being more extensively used during the foundation of the breed, and not of a more recent artificial genetic bottleneck.

Table 8. Summary of standard genetic assessment for German Shepherds (n=38) using 7 STRs in the DLA class I and II regions. SE = standard error of the mean.

	Na	Ne	Ho	He	F
Mean	5	2.309	0.566	0.536	-0.04
SE	0.404	0.23	0.066	0.045	0.048

f. What does this assessment of genetic diversity tell us about the German Shepherd Dog

The preliminary results reported herein suggest that German Shepherds have limited genetic diversity. This is evidenced by the relatively low number of alleles found to be segregating both in the autosomal STR loci and in the DLA regions. Close to 75% of the study cohort possessed the 1052/2017 and 1068/2053 DLA class I/II linked haplotypes. This indicates that two founders, or closely related founder lines, have contributed disproportionately to the development of the breed. However, the fact that these haplotypes are in equilibrium with the genome-at-large indicates that this disproportionate influence occurred when the breed was founded and has become equilibrated over time.

Certain DLA class I and II haplotypes have been associated with specific autoimmune diseases in certain dog breeds; unfortunately, German Shepherds are often listed as one of the breeds most commonly affected by autoimmune disorders. These include pemphigus foliaceous, systemic lupus erythematosis, and most importantly, degenerative myelopathy (DM). Perhaps the predominance of the aforementioned DLA haplotypes can be associated with the high prevalence of autoimmune diseases most commonly found in this breed. It is important that breeders maintain as much diversity and heterozygosity in the DLA region as possible. Therefore, the best way to reduce the incidence of autoimmune disease is to rebalance both genomic and DLA diversity by outcrossing the dominant and less diverse bloodlines with less common and more genetically diverse lines and not to concentrate on specific genomic STR alleles or DLA class I and II haplotypes.

Breeds that lack genetic diversity, such as the German Shepherd, must be managed much more diligently to avoid further loss of genetic diversity. In this case, breeders have less leeway in dealing with simple recessive or complex polygenic disorders found in the breed, due to the low number of alleles segregating in the population. It is important to note that additional alleles will most likely be identified in the breed as more individuals are tested.

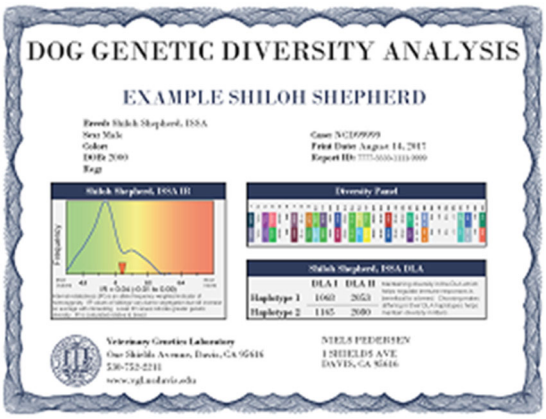
Even though genetic diversity was found to be relatively low in the German Shepherd, the good news is that breeders have been doing a good job of distributing the standing variation via mate selection. This can be corroborated by the inbreeding coefficients estimated for the 33 STR loci across the genome (F=0.02, **Table 2**) and for the DLA region (F=-0.04, **Table 8**). An inbreeding coefficient of zero is attributed to a random breeding population, and the F values calculated for this cohort of German Shepherds approximate this value.

The goal for breeders is to maintain existing genetic diversity by breeding the least related parents possible. Breeders should be aware of this when selecting mates for their breeding programs, in order to redistribute the diversity that currently exists in the breed. The goal is to produce dogs with IR scores lower than zero.

IV. Results of VGL Canine Diversity Testing

a. How will you be given the results of DNA-based genetic diversity testing on your dog?

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 and 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 reported in relation to others in the population. The alleles at each of the 33 STR loci are presented as numbers that correspond to those found in Table 1. Each locus will have two alleles, which can be different (heterozygous) or the same (homozygous). Each allele is inherited from one of the parents. Dogs from closely related parents will be homozygous for more alleles at each locus, or in regions of the genome that are under strong positive selection for phenotypic trait or traits mostly favored in the breed. Dogs with a predominance of rare (i.e., low frequency) alleles will be more distantly related to the bulk of the population than dogs that have a predominance of common (i.e., high frequency) alleles. A sample genetic diversity report is shown below.


DOG GENETIC DIVERSITY ANALYSIS

EXAMPLE SHILOH SHEPHERD

Shiloh Shepherd, ISSA DLA

	DLA I	DLA II
Haplotype 1	1060	2053
Haplotype 2	1165	2080

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b. What should you do with this information?

The goal for breeders should be to continue to produce puppies with IR scores close to zero, and as informed breeding decisions are made, even lower scores. Mates should be preferably selected to avoid homozygosity at any genomic loci or DLA class I and II haplotype; moreover, mating of dogs with less frequent genomic alleles or DLA haplotypes is encouraged. Maintaining existing genomic diversity will require using IR values of potential mates based on the 33 STR loci to assure puppies of equal or greater overall diversity. However, because IR values reflect the unique genetics of individuals, they cannot be used as the primary criterion for selecting ideal mates. Mates with identical IR values may produce puppies significantly more or less diverse than their parents. Conversely, breeding dogs with high IR values (providing they are genetically different) may produce puppies with much lower IR scores than either parent. A mating between a dog with a high IR value and one with low IR value, providing the latter has few alleles and DLA haplotypes in common, will produce puppies much more diverse than the highly inbred parent. Breeders should also realize that a litter of puppies could have a wide range of IR values, depending on the

comparative contributions of each of the parents. The more genetically diverse and different the parents, the greater the range of IR values in their offspring.

The next step is to compare the DLA class I and II haplotypes of the mates. You want to avoid breeding dogs that will produce puppies homozygous for the same haplotypes; once again, less common haplotypes may increase breed diversity in relation to common ones.

Breeders who would like to predict the genetic outcome of puppies of certain sires and dams should screen them for genetic differences in alleles and allele frequencies for the 33 genomic STR loci. Rare alleles should be favored over common ones. This information is included on all certificates and on the breed-wide data found on the VGL website.

V. References

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