Genetic Diversity Testing for Bernese Mountain Dog

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 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 will be useful to dog breeders who wish to use DNA-based testing to track and increase genetic diversity as a supplement to in-depth pedigrees. DNA based information on genetic heterogeneity and diversity, along with genetic testing results for desired phenotypes and health traits, can aid in informing breeding decisions.
Genetic diversity testing in Bernese Mountain Dog has been established, and almost all existing alleles at the 33 STR loci and 7 DLA class I and II regions have potentially been identified. As of July of 2021, 100 Bernese Mountain Dogs from the USA and Canada were tested to assess genetic diversity in the breed. We will continue to add new alleles and haplotypes if they are found in the breed, and their respective frequencies will be updated if necessary.

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 and 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 Bernese Mountain Dog

A. Breed History [1-4]

Bernese Mountain Dogs are originally called *Berner Sennenhund*, from the German *Senne* ("alpine pasture") and *Hund* (dog); *Berner* (Bernese, in English) refers to the canton of Bern, the geographical area in Switzerland where the breed flourished. The Bernese Mountain Dog is one of the four Sennenhund-type breeds originating from the Swiss Alps. They were originally used as farm dogs by dairy cattlemen and performed a variety of duties such as companionship, guarding property, driving cattle, and pulling milk and cheese carts. By the late 1800's, the number of Bernese Mountain Dogs dwindled and the quality of to the survivors declined. Then in 1907, a

Swiss breed club was formed under the leadership of Dr. Albert Heim (**Figure 1**), thus revitalizing the Bernese Mountain Dog as a farm and companionship dog. The breed was officially established in 1912.

Figure 1. Dr. Albert Heim (far left) with a pair of Bernese Mountain Dogs in the 1920's.

In 1926, Isaac Scheiss, a Kansas farmer, imported the first pair of individuals to the United States. The American Kennel Club (AKC) registered its first Bernese Mountain Dog in 1937 and classifies the breed in its Working Group. The Bernese Mountain Dog Club of America (BMDCA) was founded in 1968. Currently, the breed is ranked 22 of 196 in popularity among the AKC registries.

B. Appearance [1-3]

The Bernese Mountain Dog is a large and sturdy breed. Adult males measure between 25 and 27.5in (64–70cm) at the shoulder and weigh between 80 and 120lb (35–55kg). Females are slightly smaller at 23 to 26in (58–66cm) at the withers, weighing between 75 and 100lb (35–45kg). Dogs appear masculine, while bitches are distinctly feminine. Their coat is thick, moderately long, and can be straight or slightly wavy. Bernese Mountain Dogs have a distinctive tricolored coat pattern characterized by a black ground color, a clear white chest, and rich rust markings above each eye, on the cheeks (reaching to at least the corner of the mouth), on all four legs, under the tail and on each side of the chest. The white chest marking typically forms an inverted cross, also called a "Swiss cross". Symmetry of markings is desired by breed standards. The tip of the tail is white, and white feet are desired, but the color must not extend past the pasterns. Their noses are always black. Any ground color other than black, as well as blue eyes, are disqualifiers. Individuals are slightly longer than they are tall, with a full, powerful, and balanced body. The back is wide, firm, and level from the withers to the croup. The head of a Bernese Mountain Dog is flat on top with a moderate stop, and the ears are medium-sized, triangular, set high, and rounded at the top. The breed's natural gait is a slow trot, but individuals are capable of speed and agility.

C. Temperament [1-3]

The temperament is self-confident, alert, docile, patient and good-natured. Bernese Mountain Dogs should never be sharp, anxious, aggressive or shy. The breed requires regular activity and exercise.

II. Genetic Diversity of Bernese Mountain Dog

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]. Each STR locus is known to contain 7 to 29 different alleles (average of 15.4 alleles/locus) in the canine 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. 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 100 Bernese Mountain Dog individuals are listed in **Table 1**.

Table 1. Alleles and their frequencies for 33 STR markers in Bernese Mountain Dog (n=100). The allele that occurs at the highest frequency at each locus is bolded.

AHT121	**AHT137**	**AHTH130**	**AHTh171-A**	**AHTh260**	**AHTk211**
80 (0.005)	**131 (0.391)**	121 (0.020)	**219 (0.480)**	240 (0.015)	**87 (0.856)**
96 (0.050)	137 (0.297)	**123 (0.520)**	225 (0.163)	244 (0.252)	91 (0.040)
98 (0.545)	141 (0.025)	127 (0.050)	235 (0.356)	246 (0.213)	93 (0.059)
100 (0.094)	147 (0.094)	129 (0.149)		250 (0.069)	97 (0.045)
102 (0.267)	149 (0.158)	139 (0.262)		**252 (0.282)**	
104 (0.010)	153 (0.035)			254 (0.158)	
108 (0.030)				256 (0.010)	
AHTk253	**C22.279**	**FH2001**	**FH2054**	**FH2848**	**INRA21**
286 (0.163)	116 (0.173)	**132 (0.545)**	148 (0.010)	234 (0.325)	**95 (0.757)**
288 (0.436)	118 (0.248)	136 (0.099)	152 (0.144)	238 (0.080)	101 (0.050)
290 (0.144)	**124 (0.579)**	140 (0.109)	**156 (0.584)**	**242 (0.395)**	103 (0.193)
292 (0.257)		144 (0.020)	160 (0.020)	244 (0.200)	
		148 (0.025)	164 (0.114)		
		152 (0.203)	168 (0.129)		
INU005	**INU030**	**INU055**	**LEI004**	**REN105L03**	**REN162C04**
124 (0.040)	**144 (0.505)**	**210 (0.792)**	85 (0.035)	229 (0.140)	202 (0.233)
126 (0.361)	146 (0.079)	212 (0.064)	**95 (0.787)**	**231 (0.295)**	204 (0.158)
128 (0.480)	150 (0.391)	218 (0.144)	107 (0.134)	233 (0.015)	**206 (0.485)**
130 (0.119)	152 (0.025)		109 (0.010)	237 (0.270)	208 (0.124)
			111 (0.035)	241 (0.280)	

REN169D01	REN169O18	REN247M23	REN54P11	REN64E19	VGL0760
202 (0.005)	160 (0.015)	268 (0.040)	**222 (0.599)**	139 (0.010)	13 (0.208)
212 (0.020)	162 (0.396)	**270 (0.733)**	226 (0.054)	**145 (0.713)**	**14 (0.639)**
216 (0.035)	164 (0.054)	272 (0.064)	228 (0.119)	147 (0.089)	19.2 (0.005)
218 (0.125)	166 (0.005)	274 (0.104)	232 (0.040)	153 (0.188)	20.2 (0.030)
220 (0.810)	**168 (0.465)**	276 (0.015)	234 (0.010)		21.2 (0.020)
222 (0.005)	170 (0.064)	278 (0.045)	236 (0.015)		22.2 (0.074)
			238 (0.163)		23.2 (0.010)
					24.2 (0.015)

VGL0910	VGL1063	VGL1165	VGL1828	VGL2009	VGL2409
12 (0.619)	8 (0.144)	15 (0.040)	14 (0.158)	10 (0.030)	**13 (0.579)**
13 (0.010)	12 (0.168)	16 (0.005)	15 (0.119)	13 (0.074)	17 (0.114)
17.1 (0.005)	13 (0.040)	17 (0.005)	16 (0.203)	14 (0.129)	18 (0.292)
18.1 (0.015)	14 (0.272)	18 (0.149)	17 (0.040)	**15 (0.757)**	19 (0.015)
19.1 (0.040)	15 (0.015)	**21 (0.579)**	19 (0.025)	16 (0.010)	
20.1 (0.010)	16 (0.040)	26 (0.119)	**20 (0.450)**		
21.1 (0.099)	17 (0.005)	28 (0.074)	21 (0.005)		
22.1 (0.188)	18 (0.015)	30 (0.025)			
23.1 (0.015)	**19 (0.277)**	31 (0.005)			
	20 (0.025)				

VGL2918	VGL3008	VGL3235
12 (0.010)	13 (0.015)	13 (0.134)
13 (0.713)	**15 (0.441)**	14 (0.277)
14 (0.218)	16 (0.035)	15 (0.015)
15 (0.010)	17 (0.025)	**16 (0.287)**
16 (0.010)	18 (0.406)	17 (0.178)
17.3 (0.005)	19 (0.050)	18 (0.045)
19.3 (0.035)	20 (0.030)	19 (0.064)

The most noticeable aspect of allelic diversity in the Bernese Mountain Dog is the relatively low number of alleles found at each locus compared to more popular breeds. This number ranged from 3 (e.g., AHTh171-A) to 10 (VGL1063) alleles per locus in the study cohort. Similar to other pure breeds, one allele predominated at each locus, with the remaining alleles reasonably dispersed in frequency. However, a single allele occurred at an especially high frequency in two STR loci (85% at AHTk211 and 81% at REN169D01). This indicates that the genomic regions harboring these loci have been under strong positive selection since the formation of the breed and might be associated with highly valued traits.

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); the observed or actual heterozygosity (**Ho**) that was found; the heterozygosity that would be expected (**He**) if the

existing population was in Hardy-Weinberg equilibrium (i.e., random breeding); and the coefficient of inbreeding (**F**) derived from the Ho and He values.

Table 2. Standard Genetic Assessment of 100 Bernese Mountain Dogs based on 33 autosomal STR loci. SE = standard error.

	Na	Ne	Ho	He	F
Mean	5.61	2.646	0.584	0.578	-0.01
SE	0.32	0.158	0.027	0.024	0.01

The average number of alleles (Na) identified in this breed cohort was low, representing approximately 36% of alleles known to exist at each of these loci in all canids tested at the VGL (5.61 out of 15.4). This number is similar to that of breeds with low genetic diversity such as the American Eskimo Dog (36%) and Flat-Coated Retriever (35%). The observed (actual) heterozygosity of this cohort was 0.584, which was greater than the expected heterozygosity (He) calculated for a population in Hardy-Weinberg equilibrium (HWE). This yielded a coefficient of inbreeding (F) of -0.01, thus indicating that this group of dogs was, on average, 1% more outbred (or heterozygous) than expected for a random mating population. Therefore, it appears that this cohort of Bernese Mountain Dog was carefully selected for maximal unrelatedness. Assuming that this population is representative of the entire breed, breeders have done a good job in maintaining and distributing heterozygosity.

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 similarities in the specific regions of the genome that are associated with each STR marker. Loci with low Ho and He values contribute the least to heterozygosity among individuals, and are most likely associated with traits that define the breed's phenotypic standards. Conversely, loci with high Ho and He values are more genetically variable and can be associated with phenotypic variation among individuals within the breed. Moreover, the F value is a coefficient of inbreeding based on Ho and He; if these two values are equal, F=0 which means that the population is in HWE. The F value will be positive when there is a deficiency of heterozygotes (i.e., fewer heterozygotes than expected), whereas negative F values correspond to an excess of heterozygotes within the population.

The number of alleles (Na) identified in individual STR loci for this cohort ranged from 3 to 10 alleles per locus, while the number of effective alleles (Ne) ranged from 1.35 to 4.89 alleles per locus. Observed heterozygosity (Ho) for an individual STR locus ranged from 0.25 to 0.85, while He ranged from 0.25 to 0.79 (**Table 3**). The relatively high Ho values calculated for most loci in this study cohort indicates that a great deal of genetic diversity is associated with phenotypes that are not critical for the breed standard. This is corroborated by the fact that none of the 33 STR markers showed high inbreeding coefficients (F>0.1), which indicates that this cohort was selected from a relatively more outbred subpopulation.

Table 3. Standard Genetic Assessment of individual STR loci for 100 Bernese Mountain Dogs.

#	Locus	Na	Ne	Ho	He	F
1	**AHT121**	7	2.629	0.604	0.62	0.025
2	**AHT137**	6	3.611	0.743	0.723	-0.027
3	**AHTH130**	5	2.748	0.574	0.636	0.097
4	**AHTh171-A**	3	2.602	0.574	0.616	0.067
5	**AHTh260**	7	4.568	0.792	0.781	-0.014
6	**AHTk211**	4	1.35	0.257	0.259	0.008
7	**AHTk253**	4	3.296	0.644	0.697	0.076
8	**C22.279**	3	2.343	0.594	0.573	-0.036
9	**FH2001**	6	2.775	0.683	0.64	-0.068
10	**FH2054**	6	2.552	0.653	0.608	-0.075
11	**FH2848**	4	3.246	0.72	0.692	-0.041
12	**INRA21**	3	1.63	0.356	0.387	0.078
13	**INU005**	4	2.653	0.663	0.623	-0.065
14	**INU030**	4	2.411	0.624	0.585	-0.066
15	**INU055**	3	1.533	0.347	0.348	0.004
16	**LEI004**	5	1.563	0.347	0.36	0.038
17	**REN105L03**	5	3.874	0.77	0.742	-0.038
18	**REN162C04**	4	3.031	0.614	0.67	0.084
19	**REN169D01**	6	1.485	0.35	0.327	-0.072
20	**REN169O18**	6	2.626	0.634	0.619	-0.023
21	**REN247M23**	6	1.8	0.406	0.444	0.087
22	**REN54P11**	7	2.472	0.554	0.596	0.069
23	**REN64E19**	4	1.813	0.465	0.448	-0.038
24	**VGL0760**	8	2.182	0.614	0.542	-0.133
25	**VGL0910**	9	2.324	0.574	0.57	-0.008
26	**VGL1063**	10	4.898	0.851	0.796	-0.07
27	**VGL1165**	9	2.636	0.624	0.621	-0.005
28	**VGL1828**	7	3.502	0.772	0.714	-0.081
29	**VGL2009**	5	1.676	0.386	0.403	0.042
30	**VGL2409**	4	2.304	0.545	0.566	0.038
31	**VGL2918**	7	1.795	0.426	0.443	0.039
32	**VGL3008**	7	2.745	0.683	0.636	-0.075
33	**VGL3235**	7	4.645	0.832	0.785	-0.06

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

PCoA measures the genetic relatedness of individuals in 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 100 Bernese Mountain Dogs clustered in a way typical of a single population (i.e., a breed) in the PCoA, with individual dogs (represented

by blue dots) reasonably dispersed across all four quadrants (**Figure 2**). Some of the individuals clustered together (red circles) which suggests that they are more closely related to each other than the cohort at large. Conversely, a few dogs appeared as outliers from the main population, seen on the periphery of the PCoA. Overall, this cohort is comprised of individuals as unrelated as possible and is likely to represent the genetic diversity of the breed as a whole.

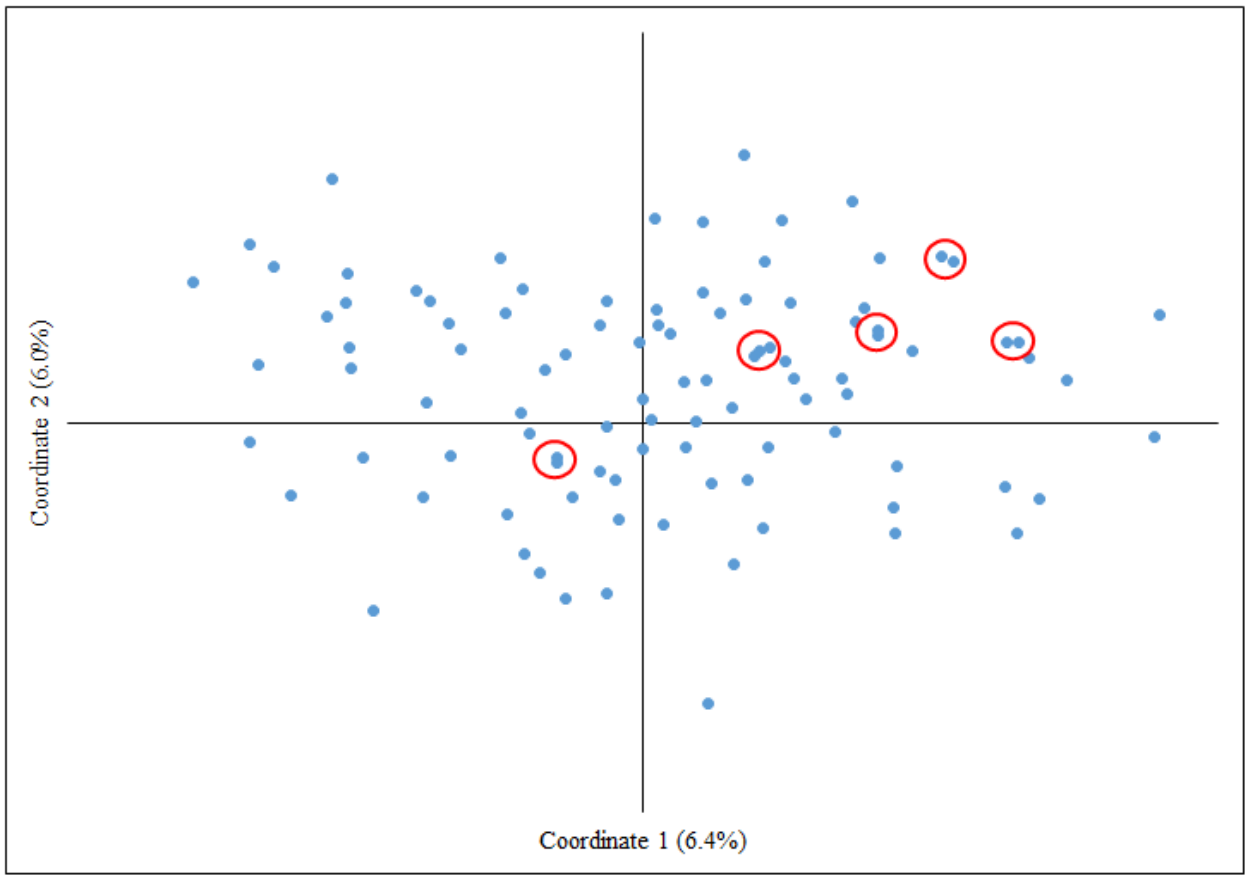


Figure 2. PCoA of Bernese Mountain Dog (n=100) based on alleles and allele frequencies at 33 autosomal STR loci. The closely related individuals are circled in red.

The degree of relatedness of individuals within the breed can be further emphasized by comparing the 100 Bernese Mountain Dogs with a genetically distinct but somewhat closely related breed (the English Mastiff), and a more distantly related breed (Italian Greyhound) (**Figure 3**).
Inter-breed clustering shows separate and well-defined populations, thus indicating that the breeds are genetically distinct as expected. However, this type of comparison accentuates the relatedness of individuals within a breed. The outlier Bernese Mountain Dogs (blue dots) identified in **Figure 2** remain dispersed from the main group of individuals when intra-breed clustering is considered. This pattern corroborates that this cohort of Bernese Mountain Dogs is quite genotypically diverse at the breed level.

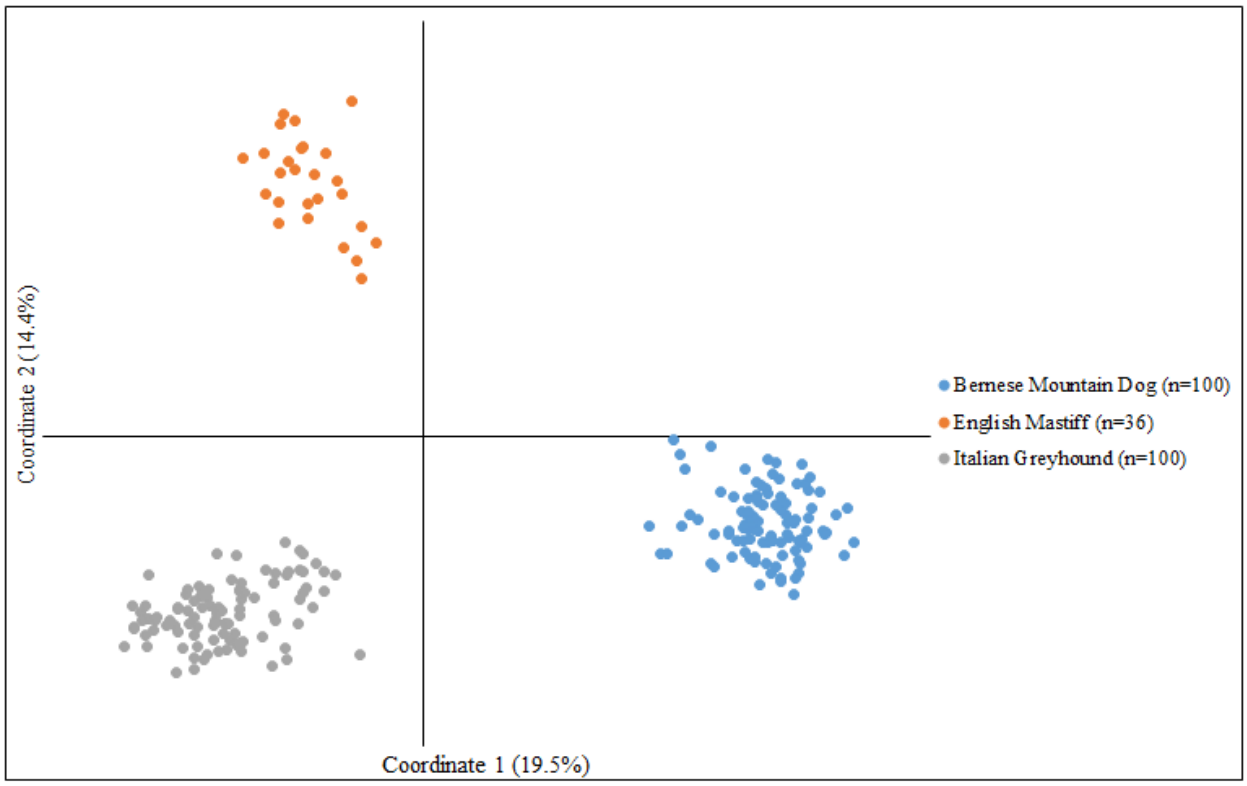


Figure 3. PCoA graph comparing intra- and inter-breed relatedness of Bernese Mountain Dog (n=100) with English Mastiff (n=36) and Italian Greyhound (n=100).

E. Internal relatedness (IR) of individuals and the population as a whole

1. IR testing

Genetic assessments such as those presented in Tables 1-3 are indicators of population-wide (mean heterozygosity), and do not reflect the genetic diversity given to individuals by their parents. Internal Relatedness (IR) is a calculation that has been used to determine the degree to which the two parents of an individual dog are related. The IR calculation takes into consideration homozygosity at each locus and gives more importance to rare and uncommon alleles. Rare and uncommon alleles would presumably be present 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 a 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 above 0.25, the more closely related are the parents and grandparents of the sibling parents.

Table 4 summarizes the IR values for the 100 Bernese Mountain Dogs tested. The most outbred dog in the population had an IR score of -0.24, while the most inbred dog in the group had an IR score of +0.28. This wide range of IR values shows that the degree of parental relatedness varies greatly in this cohort, a typical finding for almost all pure breeds of dogs. One-half of the Bernese Mountain Dogs used in this study had IR scores equal to or greater than -0.0065 and 25% of the dogs had IR scores of 0.073 or greater. This means that this cohort is comprised of a small group of inbred dogs (IR>0.25) which is balanced by an equal sized group of strongly outbred dogs (IR

scores ranging from -0.24 to -0.08). Therefore, IR scores provide a more accurate representation of heterozygosity in individual dogs than the breed-wide averages obtained from the standard genetic assessment.

Table 4. Internal relatedness (IR) values calculated using allele numbers and frequencies in 100 Bernese Mountain Dogs. The IR values can be adjusted to reflect how these same dogs would score if they were to exist in a large population of village dogs (IRVD).

	IR	IRVD
Min	-0.2401	0.0153
1st Quartile	-0.0874	0.2576
Mean	-0.0065	0.3172
Median	-0.0101	0.3136
3rd Quartile	0.0731	0.4071
Max	0.2836	0.5736

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

The IR values obtained from known alleles and their frequencies can be used to approximate the amount of genetic diversity that has been lost as a breed evolves from its oldest common ancestors to the present day. Village dogs that exist throughout the SE Asia, the Middle East and the Pacific Islands are randomly breeding descendants of dogs from which most modern breeds evolved. The known 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). Therefore, the IRVD score approximates how the IR score for a Bernese Mountain Dog would compare to other village dogs if its parents were also village dogs.

Figure 4 shows that the curve representing IRVD scores for the 100 Bernese Mountain Dogs (blue line) is shifted to the right of their actual IR scores (red line). Roughly 75% of this cohort have IRVD values of 0.25 or greater (**Table 4**, **Figure 4**), which means that if they were found among village dogs, they would all be considered offspring of at least full sibling parents. This is a result of the low amount of available village dog genetic diversity that has been retained in Bernese Mountain Dogs.

Moreover, the gray area in **Figure 4** represents the overlap between IR and IRVD curves (16.8%), which is an estimate of the amount of genetic diversity in present-day randomly breeding village dogs that still exists in contemporary Bernese Mountain Dogs. This amount of genetic diversity is slightly over half of the retained genetic diversity (25%) found in all canids tested at the VGL to date (section IIB).

The finding that this cohort of Bernese Mountain Dogs have retained only a small amount of available canid genetic diversity can be explained by different phenomena such as artificial genetic bottlenecks – geographic isolation, natural and man-made catastrophes, breed refinement, popular sire and dam effects, change in interpretation of breed standard, etc. The first loss of diversity probably occurred in the late 1800's, when the number of Bernese Mountain Dogs rapidly declined before Dr. Albert Heim restored the breed. Additionally, founder effects can explain the low retained genetic diversity found in this group of dogs.

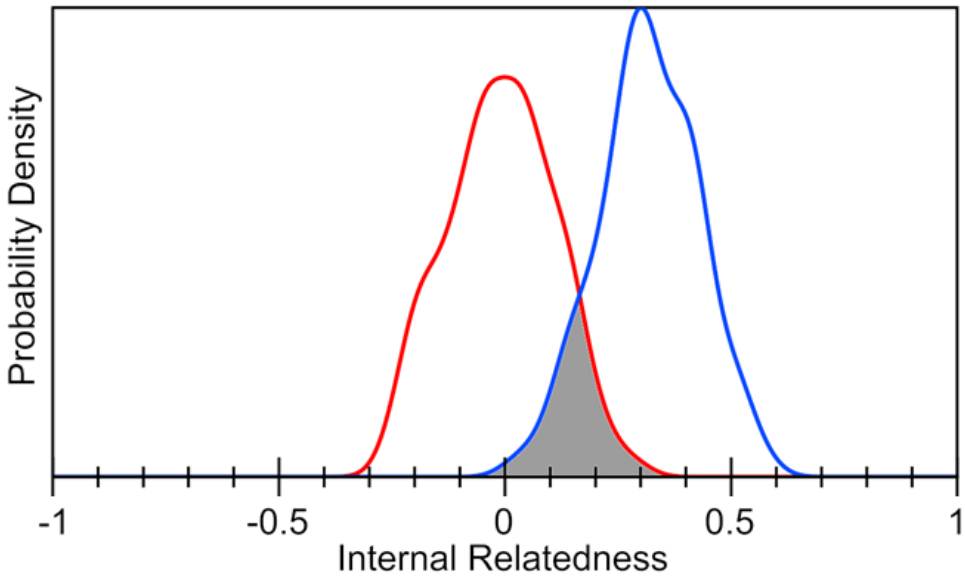


Figure 4. Distribution of IR (red line) and IR-village dog (IRVD) (blue line) values for Bernese Mountain Dog (n=100). The overlap between the curves (gray) represents the degree of allele sharing (16.8%) between this breed and village dogs.

F. 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 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, which can cause autoimmune diseases, allergies, and resistance/ susceptibility to infectious diseases.

The Class I region contains several genes, but only one, DLA-88, is highly polymorphic (i.e., 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**). Haplotypes are groups of genes (and consequently their alleles) inherited as a block, rather than individually.

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 STR loci associated with the three class II genes are strongly linked, and often inherited as a single haplotype (**Table 6**). An individual inherits one haplotype from each of the parents. The STR-based haplotype nomenclature used in this breed diversity analysis is based on numerical ranking: class I haplotypes (originally identified in Standard Poodles) are named 1001, 1002, and so on; class II haplotypes are named 2001, 2002, etc. It is common for different dog breeds to share common and even rare haplotypes for these loci, depending on common ancestry.

1. DLA class I and II haplotypes existing in the Bernese Mountain Dog

Ten DLA class I and nine DLA class II haplotypes were identified in this study cohort (**Table 5**). DLA1 haplotype 1160 was the most frequent, being identified in 56% of the dogs tested; the most frequent DLA2 haplotype was 2024 (55% frequency). The remaining DLA1 and DLA2 haplotypes were identified at lower frequencies (<=15%) in the population. DLA 1160 and 2024 are in linkage and inherited as a larger extended haplotype. The predominance of a single 1160/2024 haplotype

in this group of Bernese Mountain Dogs is typical of pure dog breeds and indicates the importance of a single founder or a founder line in the creation of the breed.

Table 5. DLA class I and II haplotypes identified in Bernese Mountain Dog (n=100) with their respective frequencies. The haplotype with the highest frequency for each class is bolded.

DLA1 Haplotype	STR types	Frequency (%)
1006	387 375 293 180	6.5
1016	382 371 277 178	2.5
1030	380 373 293 178	1.5
1068	380 373 287 181	6.5
1094	395 375 277 176	15.0
1121	380 371 277 183	9.0
1160	**386 369 289 176**	**56.5**
1221	380 365 293 180	1.5
1256	386 365 281 180	0.5
1267	386 375 277 176	0.5

DLA2 Haplotype	STR types	Frequency (%)
2001	343 324 284	1.5
2005	339 322 280	15.5
2007	351 327 280	7.5
2012	345 322 280	0.5
2021	339 324 268	2.5
2024	**343 323 280**	**55.5**
2053	343 324 280	6.5
2071	339 322 286	9.0
2118	347 327 280	1.5

DLA haplotype analysis showed extensive DLA I and DLA II haplotype sharing with 46 other dog breeds (**Table 6**). Interestingly, the predominant DLA I haplotype 1160 (56.5%) was also found at a similar frequency in the Borzoi (58.5%), but not in linkage with DLA II haplotype 2024. Only one haplotype was found to be unique to Bernese Mountain Dogs: DLA1 haplotype 1267, with a frequency of 0.5%. Not surprisingly, one DLA I haplotype (1221) was found to be shared exclusively among Bernese Mountain Dog, Saint Bernard and Mastiff (**Table 6**). Similarly, one DLA II haplotype (2118) was found at lower frequencies in Bernese Mountain Dog and Mastiff (1.5% and 5%, respectively), but not in other breeds (**Table 6**). This indicates at least one common and unique ancestor for these two breeds.

Table 6. Sharing of specific DLA class I and II haplotypes between Bernese Mountain Dog (highlighted in blue) and other dog breeds tested at the VGL (n=46).

DLA1 #	STR types	Bernese Mountain Dog (n=100)	American Eskimo, Standard (n=62)	American Eskimo, Miniature (n=38)	American Eskimo, Toy (n=14)	American Akita (n=155)	Japanese Akita (n=507)	Blend Akita (n=59)	Alaskan Klee Kai (n=591)	Barbet (n=68)	Border Collie (n=60)	Berger Picard (n=110)	Black Russian Terrier (n=145)	Biewer (n=121)	Biewer Yorshire Terrier (n=53)	Biewer Terrier (n=186)	Yorkshire Terrier (n=16)
1006	387 375 293 180	0.065	--	--	--	0.081	--	--	--	--	--	--	0.041	--	--	--	--
1016	382 371 277 178	0.025	0.008	0.04	0.11	--	--	--	--	--	--	--	0.01	0.025	0.019	0.013	0.03
1030	380 373 293 178	0.015	0.008	0.03	--	--	--	--	--	0.029	0.008	--	--	0.459	0.349	0.495	0.31
1068	380 373 287 181	0.065	--	--	--	--	--	--	--	--	0.217	--	--	--	0.009	--	--
1094	395 375 277 176	0.15	--	--	--	--	--	--	--	--	--	--	0.014	--	--	--	--
1121	380 371 277 183	0.09	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1160	386 369 289 176	0.565	--	--	--	0.003	--	--	--	--	--	--	0.031	--	--	--	--
1221	380 365 293 180	0.015	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1256	386 365 281 180	0.005	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1267	386 375 277 176	0.005	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

DLA1 # (cont.)	STR types	Bernese Mountain Dog (n=100)	Giant Schnauzer (n=287)	Havanese (n=686)	Italian Greyhound (n=1126)	Irish Setter (n=49)	Irish Red and White Setter (n=71)	Irish Wolfhound (n=56)	Lakeland Terrier (n=119)	Labrador Retriever (n=207)	Llewellin Setter (n=99)	Magyar Agar (n=77)	Polish Lowland Sheepdog (n=30)	Toy Poodle (n=179)	Miniature Poodle (n=330)	Poodle (n=3848)	Rat Terrier (n=39)
1006	387 375 293 180	0.065	0.044	0.0459	--	--	0.07	--	--	0.036	--	--	--	0.003	0.003	0.0482	--
1016	382 371 277 178	0.025	0.045	0.2004	0.0613	--	--	--	0.008	0.01	0.025	--	0.03	0.028	0.027	0.0213	0.05
1030	380 373 293 178	0.015	--	0.0022	0.0298	--	--	--	--	0.051	0.025	--	--	--	--	0.0025	0.03
1068	380 373 287 181	0.065	0.051	0.0146	--	0.01	--	0.08	--	0.041	--	--	--	0.011	0.015	--	--
1094	395 375 277 176	0.15	--	--	--	--	--	0.223	--	--	--	--	--	--	--	--	--
1121	380 371 277 183	0.09	--	0.0051	--	--	--	--	--	--	--	--	--	--	--	--	--
1160	386 369 289 176	0.565	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1221	380 365 293 180	0.015	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1256	386 365 281 180	0.005	--	--	--	--	--	--	--	--	--	--	--	--	--	--	0.01
1267	386 375 277 176	0.005	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

DLA1 # (cont.)	STR types	Bernese Mountain Dog (n=100)	Borzoi (n=136)	Collie (n=49)	Doberman Pinscher (n=858)	English Bulldog (n=163)	English Mastiff (n=26)	Mastiff (n=10)	Flat Coated Retriever (n=690)	Golden Retriever (n=774)	Samoyed (n=191)	Saint Bernard (n=71)	Scottish Collie (n=107)	Shiba Inu (n=127)	Shikoku (n=63)	Shiloh Shepherd, ISSA (n=233)	Swedish Vallhund (n=333)	Whippet (n=77)
1006	387 375 293 180	0.065	0.154	--	--	0.003	--	0.05	--	0.0136	0.005	--	0.037	--	--	--	0.266	--
1016	382 371 277 178	0.025	--	0.04	0.0181	0.095	0.15	0.25	--	0.0019	--	--	0.098	--	--	--	--	0.104
1030	380 373 293 178	0.015	--	--	0.0985	--	0.1	--	--	0.0006	--	--	--	--	--	--	--	--
1068	380 373 287 181	0.065	--	--	--	--	--	--	0.2775	0.051	0.042	0.176	--	--	--	0.264	0.357	--
1094	395 375 277 176	0.15	0.011	--	0.7558	--	--	--	--	--	--	--	0.005	--	--	--	--	--
1121	380 371 277 183	0.09	--	--	--	--	--	--	--	0.0006	--	--	--	--	--	--	--	--
1160	386 369 289 176	0.565	0.585	--	--	--	--	--	--	--	0.016	0.085	0.009	0.012	--	--	--	--
1221	380 365 293 180	0.015	--	--	--	--	--	0.05	--	--	--	0.007	--	--	--	--	--	--
1256	386 365 281 180	0.005	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1267	386 375 277 176	0.005	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

DLA2 #	STR types	Bernese Mountain Dog (n=100)	American Eskimo, Standard (n=62)	American Eskimo, Miniature (n=38)	American Eskimo, Toy (n=14)	American Akita (n=155)	Japanese Akita (n=507)	Blend Akita (n=59)	Alaskan Klee Kai (n=591)	Barbet (n=68)	Border Collie (n=60)	Berger Picard (n=110)	Black Russian Terrier (n=145)	Biewer (n=121)	Biewer Yorshire Terrier (n=53)	Biewer Terrier (n=186)	Yorkshire Terrier (n=16)
2001	343 324 284	0.015	0.661	0.14	0.11	--	--	--	--	0.199	0.142	--	--	--	--	--	--
2005	339 322 280	0.155	--	--	--	--	--	--	--	--	0.008	--	0.014	0.045	0.009	0.027	--
2007	351 327 280	0.075	--	--	--	0.081	--	--	0.0127	--	--	--	0.041	--	--	--	--
2012	345 322 280	0.005	--	--	--	--	0.001	--	0.0618	--	--	--	--	--	--	--	--
2021	339 324 268	0.025	--	--	--	--	--	--	0.2166	--	--	--	--	0.004	--	--	--
2024	343 323 280	0.555	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
2053	343 324 280	0.065	0.226	0.12	0.04	--	--	--	--	--	0.075	--	--	--	0.009	--	--
2071	339 322 286	0.09	--	--	--	0.003	--	--	--	--	--	--	--	--	--	--	--
2118	347 327 280	0.015	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

DLA2 # (cont.)	STR types	Bernese Mountain Dog (n=100)	Giant Schnauzer (n=287)	Havanese (n=686)	Italian Greyhound (n=1126)	Irish Setter (n=49)	Irish Red and White Setter (n=71)	Irish Wolfhound (n=56)	Lakeland Terrier (n=119)	Labrador Retriever (n=207)	Llewellin Setter (n=99)	Magyar Agar (n=77)	Polish Lowland Sheepdog (n=30)	Toy Poodle (n=179)	Miniature Poodle (n=330)	Poodle (n=3848)	Rat Terrier (n=39)
2001	343 324 284	0.015	0.007	0.0539	--	--	--	--	--	0.002	--	0.071	--	0.006	0.012	0.605	0.01
2005	339 322 280	0.155	0.009	0.0022	--	0.04	0.099	0.232	0.004	0.051	0.798	--	--	0.003	--	0.0178	0.08
2007	351 327 280	0.075	0.044	0.0481	--	--	0.155	--	--	0.041	--	--	--	0.003	0.002	0.0161	--
2012	345 322 280	0.005	0.01	0.0044	--	0.06	0.197	--	--	--	0.035	0.078	--	0.047	0.071	0.0057	0.01
2021	339 324 268	0.025	--	0.0036	--	--	--	0.277	--	0.017	--	--	--	0.07	0.055	0.0031	0.03
2024	343 323 280	0.555	--	0.0036	--	--	--	--	--	0.046	--	--	--	0.075	0.011	0.0003	--
2053	343 324 280	0.065	0.059	0.0335	--	0.01	--	0.08	--	0.039	--	--	--	0.014	0.015	--	--
2071	339 322 286	0.09	--	0.0051	--	--	--	--	--	--	--	--	--	--	--	--	--
2118	347 327 280	0.015	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

DLA2 # (cont.)	STR types	Bernese Mountain Dog (n=100)	Borzoi (n=136)	Collie (n=49)	Doberman Pinscher (n=858)	English Bulldog (n=163)	English Mastiff (n=26)	Mastiff (n=10)	Flat Coated Retriever (n=690)	Golden Retriever (n=774)	Samoyed (n=191)	Saint Bernard (n=71)	Scottish Collie (n=107)	Shiba Inu (n=127)	Shikoku (n=63)	Shiloh Shepherd, ISSA (n=233)	Swedish Vallhund (n=333)	Whippet (n=77)
2001	343 324 284	0.015	--	--	--	--	--	--	--	0.1408	--	0.014	--	0.016	--	0.004	--	0.065
2005	339 322 280	0.155	--	--	--	0.015	--	--	0.4181	0.0149	--	0.077	--	--	--	--	--	--
2007	351 327 280	0.075	0.158	--	--	--	--	--	--	0.0136	0.005	0.007	0.005	--	--	--	0.27	--
2012	345 322 280	0.005	--	--	--	--	--	--	--	0.0006	--	--	--	--	0.016	--	--	--
2021	339 324 268	0.025	--	--	--	--	--	--	--	0.0872	--	0.056	--	--	--	--	--	--
2024	343 323 280	0.555	0.011	--	0.0006	0.006	--	--	--	--	0.016	--	--	--	--	--	--	--
2053	343 324 280	0.065	--	--	0.0006	--	--	--	0.1428	0.0304	0.56	0.162	--	--	--	0.328	0.508	--
2071	339 322 286	0.09	--	--	--	--	--	--	--	--	--	--	--	--	0.024	--	--	--
2118	347 327 280	0.015	--	--	--	--	--	0.05	--	--	--	--	--	--	--	--	--	--

The number of DLA class I and II haplotypes (9 and 10, respectively) found in Bernese Mountain Dogs was relatively low and comparable to other breeds with limited genetic diversity such as the Flat Coated Retriever (11 and 10, respectively). It is lower than Giant Schnauzer (14 and 15), Samoyed (13 and 12) and Shiba Inu (16 and 15), and when compared to the diversity in DLA haplotypes of more genetically diverse breeds such as the Golden Retriever (26 and 23) and Miniature Poodle (33 and 23), this discrepancy becomes more evident. This finding suggests that, even though the Bernese Mountain Dog can be considered a genetically diverse breed, a founder effect (or closely related individuals/lines) played a significant role in breed creation.

2. 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 measured by the 33 autosomal STR markers. However, the expectation is that these loci have achieved an equilibrium with other loci in the genome over time, and thus will also be inherited randomly. This assumption can be tested through a standard genetic assessment of each locus (**Table 7**) and averaged across all loci (**Table 8**).

Analysis of individual DLA STR loci shows that observed heterozygosity (Ho) values were higher than or similar to expected heterozygosity (He) values for each locus, indicating a higher than expected degree of heterozygosity in the DLA region compared to other parts of the genome. This is also corroborated by the negative F values found for 6 of the 7 DLA STRs (**Table 7**). A similar conclusion can be reached when considering mean values for observed *vs.* expected heterozygosity and inbreeding coefficient (F) across the region (**Table 8)**. These findings suggest that this cohort was deficient in dogs with the predominant DLA1 1160 haplotype.

Table 7. Standard genetic assessment for Bernese Mountain Dog using each of the 7 STRs in the DLA class I and II regions (n=100).

#	Locus	Na	Ne	Ho	He	F
1	**DLA I-3CCA**	5	2.55	0.62	0.61	-0.02
2	**DLA I-4ACA**	5	2.58	0.63	0.61	-0.03
3	**DLA I-4BCT**	5	2.48	0.62	0.6	-0.05
4	**DLA1131**	5	1.86	0.49	0.46	-0.05
5	**5ACA**	5	2.09	0.54	0.52	-0.03
6	**5ACT**	4	2.57	0.63	0.61	-0.03
7	**5BCA**	4	1.3	0.23	0.23	0.019

Table 8. Summary of standard genetic assessment for Bernese Mountain Dog using 7 STRs in the DLA class I and II regions (n=100).

	Na	Ne	Ho	He	F
Mean	4.71	2.2	0.54	0.52	-0.03
SE	0.17	0.17	0.05	0.05	0.008

III. What does this assessment of genetic diversity tell us about contemporary Bernese Mountain Dog

This study confirmed that this cohort constituted a single breed based on alleles and their frequencies for the 33 autosomal STR loci, as well as intra- and inter-breed genetic clustering based on PCoA. The estimated amount of retained genetic diversity for Bernese Mountain Dog based on a comparison to indigenous dogs was 16.8%, or slightly over half of the average retained diversity of all breeds tested by the VGL (25%). Although this retained diversity is low compared to a number of other breeds, genetic diversity parameters investigated herein show that breeders have maintained a high level of heterozygosity within the breed cohort analyzed through mating practices. Standard genetic assessment for heterozygosity values and PCoA graphing indicate that the average dog in the population is a product of parents that are as unrelated as possible. Finally, comparatively low Internal Relatedness (IR) scores also corroborate these findings at the individual level.

IV. Health of the Bernese Mountain Dog

A. Lifespan

The Bernese Mountain Dog is considered a short-lived breed, with a lifespan of 7 to 8 years [2, 7, 9]. Most other breeds of similar size have median longevities of 10–11 years [8].

B. Diseases

1. Cancer

A comprehensive health survey conducted by the BMDCA in 2005 showed that 67% of Bernese Mountain Dog deaths occur due to some form of cancer [9]. In other breeds this rate is, on average, 27% [2]. At least two forms of cancer are reportedly inherited in Bernese Mountain Dogs: mast cell cancer and histiocytic sarcoma (formerly known as malignant histiocytosis [9]. The BMDCA include the Histiocytic Sarcoma Risk Test submitted to Antagene as an optional test for breeding dogs per its guidelines [10].

2. Degenerative Myelopathy (DM)

Individuals affected by this disease usually present clinical signs in adulthood, which include gradual muscle wasting and loss of coordination typically beginning in the hind limbs. Disease progression continues until the dog is unable to walk. In late stages of the disease, dogs may become incontinent and the forelimbs may be affected. Affected dogs may fully lose the ability to walk 6 months to 2 years after the onset of signs. The BMDCA Board of Directors recommend genetic testing for the genetic mutations that cause DM in breeding Bernese Mountain Dogs (*SOD1A* and *SOD1B*) [10]. A dog that has 2 copies of the *SOD1A* mutation is clear by exclusion for *SOD1B*, and vice versa. A dog that carries one *SOD1A* mutation and one *SOD1B* mutation is considered 'At Risk'. The VGL currently offers a test for the *SOD1A* mutation (https://vgl.ucdavis.edu/test/degenerative-myelopathy).

3. Progressive Retinal Atrophy (PRA)

Progressive retinal atrophy (PRA) is a medical classification that represents several inherited forms of retinal degeneration that are caused by mutations in different genes. One of these disease forms that affects Bernese Mountain Dogs is called Progressive rod-cone degeneration (PRCD). The age of onset and rate of progression vary among breeds, but retinal changes can be identified by screening performed by a veterinary ophthalmologist from adolescence to early adulthood. Most PRCD-affected dogs have noticeable visual impairment by 4 years of age, typically progressing to complete blindness. This disease is extremely rare in Bernese Mountain Dogs; however, the BMDCA Board of Directors recommends an eye examination by a boarded ACVO

Ophthalmologist in breeding dogs to prevent the mating of PRA-affected individuals [10]. The VGL offers genetic testing for the mutation that causes PRCD in several dog breeds (https://vgl.ucdavis.edu/test/pra-prcd).

4. Von Willebrand disease (vWD)

Von Willebrand disease (vWD) is an inherited bleeding disorder resulting from a lack or reduced level of a normal blood clotting protein called von Willebrand factor (vWF). Disease presentation varies from asymptomatic to spontaneous hemorrhaging and prolonged bleeding after injury, surgery, or giving birth. Age of onset varies with some dogs only becoming obvious "bleeders" later in life. Without medical intervention, uncontrolled bleeding can result in death. This disease is rare in Bernese Mountain Dogs; genetic testing for vWD is considered optional by the BMDCA [10], and the VGL offers this test (https://vgl.ucdavis.edu/test/vwd-type-1).

5. Elbow Dysplasia (ED)

This potentially crippling condition affects the elbow joint. Elbow dysplasia can result in lameness and affect puppies as young as 5 months. The only way to confirm and evaluate ED is by x-ray. The BMDCA recommends an OFA or OVC evaluation for ED in breeding dogs [10]. This condition is believed to be inherited, since ED is less likely to be present in puppies born to parents that do not possess the condition. Further studies are needed to evaluate this hypothesis [9].

6. Entropion and Ectropion

These conditions affect the eyelids, resulting in damage to the dog's eye. Entropion is a condition in which the eyelid rolls inward, causing irritation to the surface of the eye. Ectropion is the reverse, in which the eyelid rolls out serving as a "catcher's mitt" for tiny bits of debris that can irritate pink tissues on the inside of the eyelid [9]. Eye examinations by a boarded ACVO Ophthalmologist are recommended for breeding dogs to prevent the use of individuals with such ocular disorders in breeding programs [10]. Entropion and ectropion are believed to be inherited, but further studies are needed to evaluate this hypothesis.

7. Sub-aortic Stenosis (SAS)

This heart condition is characterized by a fibrous band below the aortic valve that causes a partial obstruction to the blood flow of blood leaving the left ventricle. This condition may cause sudden death, as many dogs do not show previous clinical symptoms [9]. Since SAS is known to be inherited in some dog breeds, it is hypothesized that this is the case in Bernese Mountain Dogs. However, studies are needed to test this hypothesis. The BMDCA recommends a cardiac evaluation by a boarded ACVIM cardiologist in all breeding dogs [10].

8. Osteochondritis Dissecans (OCD)

This disorder can lead to crippling arthritis when to a lack of blood supply to the bone underneath the cartilage of a joint leads to its death. Like some dysplasias, there are genetic components to this disease, although there are no scientific studies in Bernese Mountain Dogs to help determine the heritability of OCD [9].

9. Hip Dysplasia (HD)

As is the case of most medium and large sized dog breeds, Bernese Mountain Dogs can also suffer from hip dysplasia. HD results from an unstable hip socket and subsequent degenerative arthritic changes that result from this instability. HD can affect young puppies, but more frequently leads to a degenerative, sometimes crippling, arthritis in mature dogs [9]. Clinical manifestations vary greatly; some dogs do not show clear symptoms, whereas for others the disease is completely debilitating. Hip dysplasia examinations are recommended for breeding dogs (OFA, PennHIP) [10].

10. Hypothyroidism

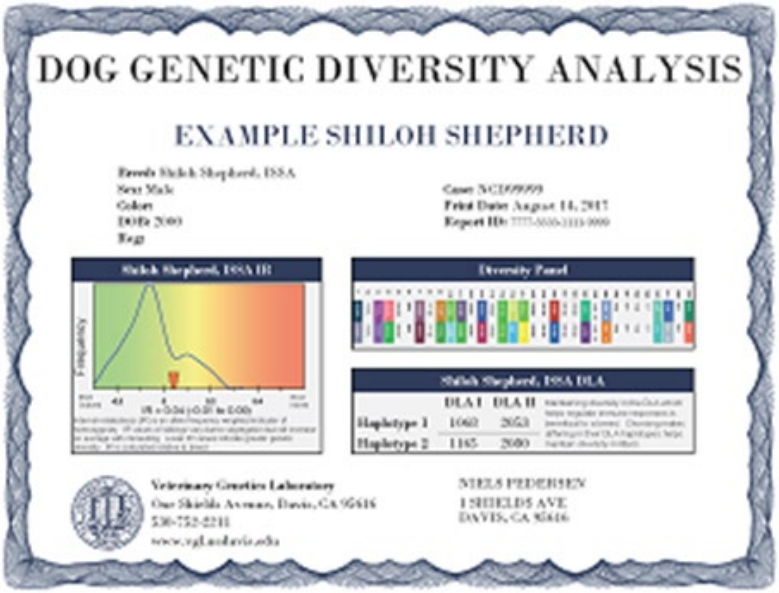
This disorder is rather frequently identified in Bernese Mountain Dogs. Disease presentation can include coat changes (dryness, brittleness, brown pigmentation, and sparseness), changes in temperament (tiredness and lack of motivation), subfertility or infertility, and weight gain [9]. When diagnosed properly, this condition is easily treated with good results. A thyroid profile per OFA is optional per BMDCA guidelines [10].

Due to these common medical issues, the BMDCA suggests that owners and breeders of Bernese Mountain Dogs should do phenotype and/or genotype screening for the aforementioned issues, and submit the results to Berner-Garde (the online health and pedigree database that is available free of charge).

V. 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.



B. What should you do with this information?

DNA testing for genetic diversity in the Bernese Mountain Dog shows a low, but acceptable, level of genome-wide genetic diversity and a relative lack of inbreeding in the study cohort. The number of DLA1 and DLA2 haplotypes identified in this cohort is on the low side compared to other dog

breeds, but like other purebreds, one specific extended haplotype (1160/2024) was found in approximately half of the dogs tested. This is an indication that a single founder or closely related founder lineage has played an outsized role in the desired breed standard. Therefore, the breed needs to be more carefully managed than breeds with larger amounts of genetic diversity, such as the Golden Retriever or the Standard Poodle, for example. Therefore, it is important to closely monitor existing diversity into the future both across the genome and in the DLA region. We believe that this can be most accurately done with DNA testing and the use of interrelatedness scores and DLA1/2 haplotypes to better balance and maintain genetic diversity and as a supplement to in-depth pedigrees.

If the breed were to consider increasing genetic diversity by further genetic introgressions, DNA testing of dogs intended for such introgressions would also be essential to preclude deleterious mutations and to ensure that the added DNA is properly incorporated into the existing population.

The goal for breeders should be to continue to produce puppies with IR scores lower than zero, and with time, 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 common 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. Given the genetic diversity observed in the DLA region in Bernese Mountain Dogs, this approach can be successful if properly implemented.

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.

Finally, results from this study can also contribute the genetic information from Bernese Mountain Dogs to a web repository. This information could be incorporated into a mate selection online service that will allow a breeder to identify, among all the dogs tested, potential mates that would be most suitable to increase genetic diversity in their litters.

VI. References

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