Genetic Diversity Testing for Swedish Vallhunds

Overview

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

Genetic diversity testing of Swedish Vallhunds is now in the final phase with 105 dogs having been tested at the time of the report below. We feel that more than 95% of the existing genetic diversity will be represented in the present database, but we will continue to update the database as new dogs are tested. The goal is to test enough dogs so that no new alleles or DLA haplotypes are recognized, although it is likely that any additional autosomal alleles or DLA haplotypes will be at very low incidence.

Price: $80
Price reduced to $70 when combined with a diagnostic test.

[ORDER TEST KITS]
Allow 5-10 business days for results.

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

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

Internal Relatedness: The IR value is a measure of genetic diversity within an individual that takes into consideration both heterozygosity of alleles at each STR loci and their relative frequency in the population. It is also an estimate of the genetic relatedness of a dog's parents. Unlike standard genetic assessments, IR puts more emphasis on heterozygosity over homozygosity and uncommon over common alleles. IR values are unique to each dog and cannot be compared between dogs. Two dogs may have identical IR values but with very different genetic makeups

I. Introduction

A. Breed history[1-4]

The Swedish Vallhund (herding dog) is an ancient, national dog breed of Sweden. The Vallhund originated in the county of Västergötland and is also known as the *Västgötaspets* or Swedish cow dog. They were originally used to drive and herd cows over 1,000 years ago, although what they looked like at that time is not known. However, large dogs of the same type have been found buried with their masters in Viking-age settlements in Scandinavia, and their skeletons resemble the modern Norwegian Elkhound, another northern Spitz-type breed. The breed was almost extinct by the early 1940s, but a small group of citizens including Bjorn von Rosen and K. G. Zettersten managed to bring national awareness to the breed. The men scoured the country to find the best remaining specimens, including one male (Mopsen) and three females (Vivi, Lessi, and Topsy). Mopsen and Lessi produced a dog, Jerry 265OTT; a breeding of Mopsen and Vivi produced a female, Tessan 3999VV; and a breeding of possibly Topsy with Mopsen produced Borgalls Mopsan 7871VV. These five offspring were purportedly the foundation of the breed's revival.

The Swedish Kennel Club officially recognized the breed as the Swedish Vallhund in 1943. The Swedish standard was revised in 1963, and the breed became known as Västgötaspet after the Swedish province Västgötland where the breed was revived. The Vallhund has gained some popularity since WWII and is now found in over ten countries.

The Swedish Vallhund is an active competitor in dog agility trials, obedience, rally obedience, showmanship, flyball, tracking, hiking, and herding events. Herding instincts and trainability can be measured at noncompetitive herding events and those possessing good herding instincts can be further trained for competitive herding trials.

B. Physical features

The average height of the Swedish Vallhund, measured at the withers, is approximately 33cm (12.9in) for males and 31cm (12.2in) for females. They have short legs and long bodies and varying lengths of tail from none to normal. The coat is short with a harsher topcoat and a softer and denser undercoat. Coat color varies from grey, greyish brown and greyish yellow to reddish brown, with darker hair on the back, neck, and sides of the body. Lighter shades of the same colors occur on the muzzle, throat, chest, belly, buttocks, feet and hocks. Lighter markings on the shoulders can appear as a harness. Some dogs have a narrow white blaze and white markings on fore and hindlegs and chest. White markings are not to exceed 30% of the body.

People not familiar with the Vallhund are usually well aware of its British relative, the Corgi breeds of Wales that have been further popularized by Queen Elizabeth II. Although the two breeds are quite similar in appearance, the Corgi is shorter legged, longer and stockier than the Vallhund. It is believed by some that Welch Corgis were taken to Sweden in the 8th or 9th century during the Viking conquests in Britain. The historian, Clifford Hubbard thought the Swedish Vallhund was the older of the two breeds.

II. Baseline genetic diversity testing and what it tells us about Swedish Vallhund

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

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

Thirty-three STRs and their alleles were studied in over 105 Swedish Vallhunds (Table 1). Allele and allele frequencies were used to determine basic genetic parameters such as the number of alleles found at each STR locus (Na), the number of effective alleles (Ne) per locus (i.e., the number of alleles that contribute most to genetic differences), the observed or actual heterozygosity (Ho) that was found, and the heterozygosity that would be expected (He) if the existing population is in Hardy Weinberg equilibrium (HWE). HWE is achieved when the selection of mates is random within the population being studied. By definition, the population should not be subject to no positive or negative human selection pressure, but this is usually ignored when referring to a breed within a species. The value F is a coefficient of inbreeding derived from the Ho and He values. A value of +1.0 would occur only if every individual were genetically indistinguishable at each of the 33 STR loci, while a value of -1.0 would be seen when all the dogs were completely different at each of the 33 loci.

The most noticeable aspect of allelic diversity in the Vallhund is the comparatively low number of alleles found at each locus. Although each locus can have as few as 7 and as many as 25 alleles, allele numbers per locus in Vallhund vary from as few as three (e.g., AHTk211) and no more than nine (VGL1063). However, unlike other breeds where one or two alleles predominate, Vallhund allele frequencies are more even among the existing alleles. This indicates that selection of sires and dams has tended to use the full-spectrum of available genetic diversity present at the time of registry closure. Although registry closure precludes outside introgressions, the period following closure is usually a time of intensive breed refinement and selection of animals that will produce puppies breeding true to the standards. It appears that the founding population for the Vallhund were quite "refined" and "true breeding" from the onset, as further supported by the breed history.

Table 1. Allele designation and frequency at 33 STR loci for Swedish Vallhund. The allele that occurs at the highest frequency at each locus is highlighted.

[Table 1 Link](#)

B. Standard genetic assessment of heterozygosity at each autosomal STR locus

It is possible to study human-directed selection pressures by doing a standard genetic assessment of allele and allele frequencies at each of the 33 autosomal STR loci and based on 105 dogs. Each locus is made up of two alleles, one inherited from each parent. The most interesting figure for this type of study is the inbreeding coefficient (F). Only 5 of 33 loci have F values >0.100,

which indicates an inordinate degree of inbreeding. Conversely, 5 of 33 loci have F values ≤ -0.100, indicating a deliberate attempt by breeders to find the most unrelated parents. The remaining 23 of 33 loci are reasonably close to 0.00, or in HWE equilibrium. As occurs with a number of breeds, the inbred loci are cancelled out by the outbred loci, giving the illusion that all 33 loci are in HWE when the measurements are taken for the breed as a whole (Table 3).

Table 2. Standard Genetic Assessment for Swedish Vallhund using 33 STR loci (Updated October 10, 2019)

#	Locus	N	Na	Ne	Ho	He	F
1	AHT121	222	6	3.520	0.685	0.716	0.044
2	AHT137	222	6	2.645	0.604	0.622	0.029
3	AHTH130	222	6	1.828	0.495	0.453	-0.094
4	AHTh171-A	222	5	2.024	0.505	0.506	0.003
5	AHTh260	222	4	2.544	0.649	0.607	-0.069
6	AHTk211	222	3	2.443	0.635	0.591	-0.075
7	AHTk253	222	6	4.550	0.779	0.780	0.001
8	C22.279	222	4	1.910	0.441	0.476	0.073
9	FH2001	222	5	2.251	0.554	0.556	0.003
10	FH2054	222	7	2.096	0.572	0.523	-0.094
11	FH2848	222	5	1.950	0.523	0.487	-0.073
12	INRA21	222	4	2.227	0.554	0.551	-0.006
13	INU005	222	3	1.196	0.167	0.164	-0.016
14	INU030	222	4	1.913	0.459	0.477	0.037
15	INU055	222	4	3.509	0.757	0.715	-0.058
16	LEI004	222	5	3.260	0.590	0.693	0.149
17	REN105L03	222	5	3.732	0.788	0.732	-0.077
18	REN162C04	222	5	3.946	0.716	0.747	0.041
19	REN169D01	222	4	2.592	0.572	0.614	0.069
20	REN169O18	222	3	1.716	0.383	0.417	0.082
21	REN247M23	222	2	1.356	0.284	0.263	-0.081
22	REN54P11	222	3	1.284	0.230	0.221	-0.038
23	REN64E19	222	4	2.269	0.572	0.559	-0.023
24	VGL0760	222	8	4.226	0.770	0.763	-0.009
25	VGL0910	222	5	2.839	0.599	0.648	0.075
26	VGL1063	222	9	4.025	0.761	0.752	-0.013
27	VGL1165	222	6	3.507	0.739	0.715	-0.033

28 VGL1828	222	5	2.340	0.554	0.573	0.032
29 VGL2009	222	5	2.215	0.595	0.548	-0.084
30 VGL2409	222	5	2.769	0.680	0.639	-0.065
31 VGL2918	222	6	1.963	0.464	0.491	0.054
32 VGL3008	222	5	2.826	0.676	0.646	-0.046
33 VGL3235	222	5	1.938	0.455	0.484	0.060

C. Standard genetic assessment of breed-wide heterozygosity

A standard genetic assessment of a breed is usually based on the entire population and values expressed as means (averages) with a standard error (Table 3). The average number of alleles (Na) per locus in this group of 105 dogs was 4.55, but only 2.57 of these alleles (Ne) contributed most to the heterozygosity. These Na and Ne values for Vallhund were among the lowest that have been observed among the various breeds studied to date.

The observed heterozygosity (Ho) across the 33 loci was 0.57, while the expected heterozygosity (He) for a population in Hardy-Weinberg equilibrium was also 0.57. This difference between Ho and He was used to calculate an inbreeding coefficient (F). The mean F value for the 105 dogs was effectively zero, indicating that the distribution of alleles for the population was in HWE. Therefore, the data in Tables 1-3 indicate that Swedish Vallhund lack genetic diversity but that sires and dams are being carefully selected to prevent further inbreeding.

Table 3. Summary of Standard Genetic Assessment for Swedish Vallhund using 33 STR loci. Values are given as mean (average) with standard error (SE). (Updated October 10, 2019)

	N	Na	Ne	Ho	He	F
Mean	222	4.909	2.588	0.570	0.568	-0.006
SE		0.248	0.151	0.026	0.026	0.011

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

We tested 105 Swedish Vallhund from various countries to see how they were related (Fig. 1). PCoA is a graphic portrayal of how closely individual dogs in a defined population are related to each other The graph is a sphere, but for graphic purposes, the geometric planes that most accurately depict relationships in two dimensions are chosen. This is usually coordinates (planes) 1 and 2. As shown in Fig. 1, Swedish Vallhund from several geographically varied countries all belong to a single population.
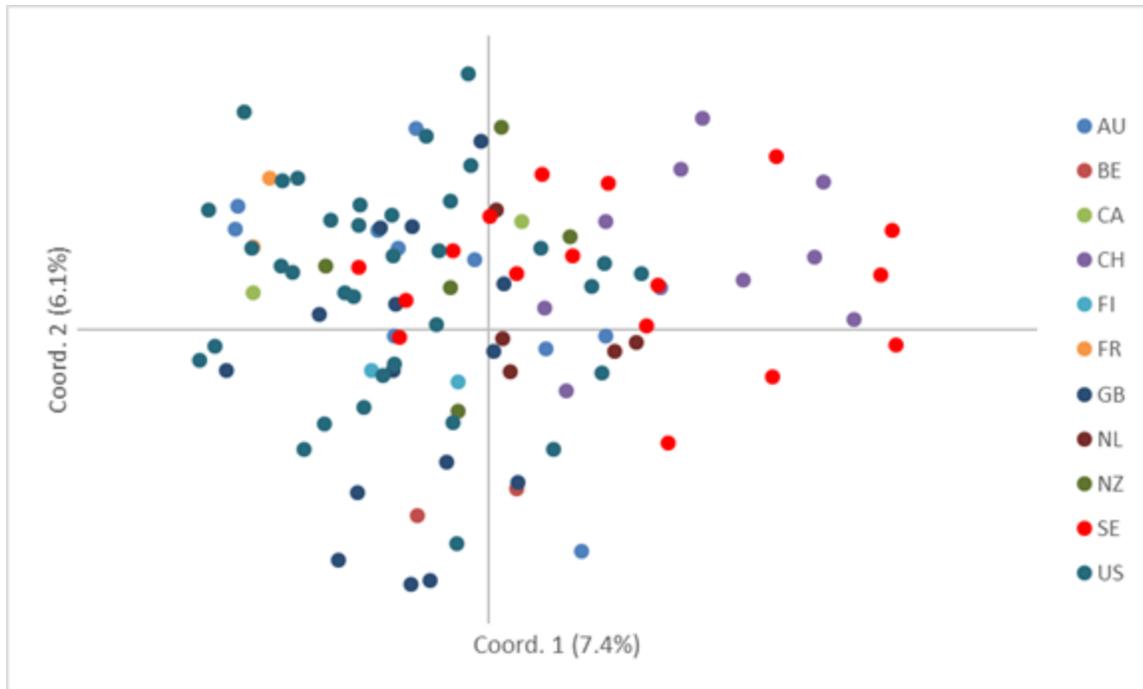
Figure 1. PCoA graph showing the genetic relationship among 105 Swedish Vallhund from various countries of the world.

We also wanted to see if Vallhund with different coat color formed a single population or varieties within the breed. The 105 Swedish Vallhund clearly belong to a single breed with no clear evidence of genotypic variation related to coat color, such as is seen with Black and Pepper/Salt Giant Schnauzers. Although yellow dogs are found together mainly in one quadrant, the numbers are too small for statistical accuracy and they may have all come from the same kennel and are therefore more closely related.
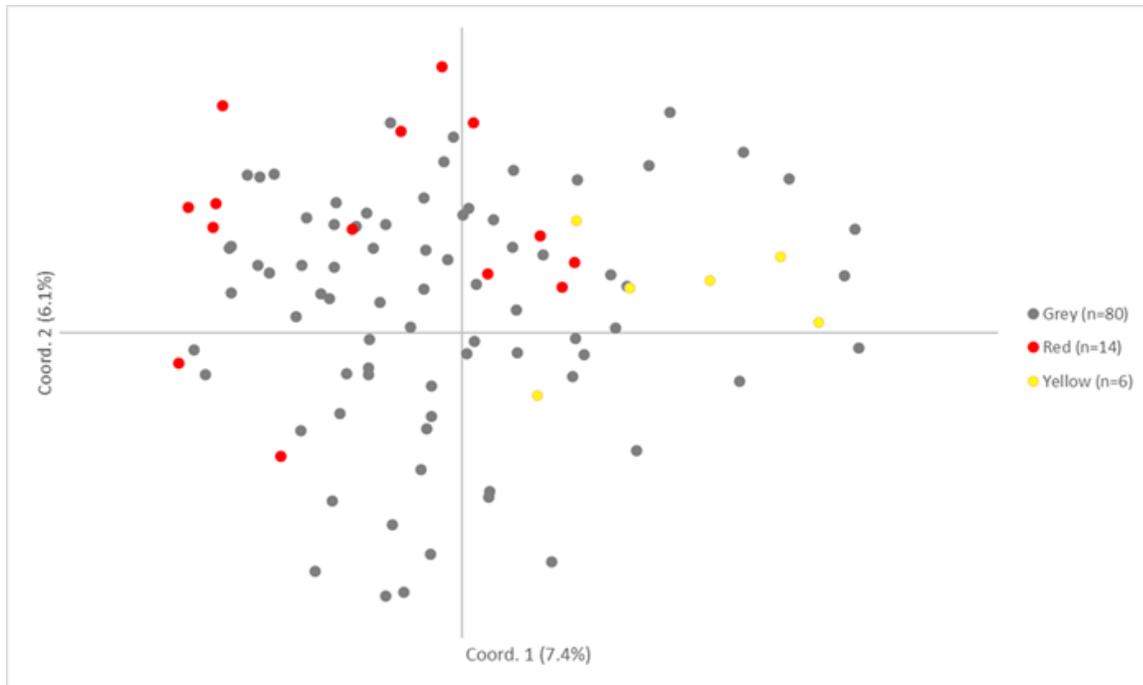
Figure 2. PCoA plot showing the relatedness of individual Swedish Vallhund with coat color being an added variable

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

A. IR values

Genetic assessments such as those presented in Tables 1-3 are indicators of population-wide heterozygosity and do not reflect the genetic diversity of individuals within the population. The genetic diversity of an individual dog is largely determined by the diversity inherited from each of its parents. Internal Relatedness (IR) is a calculation that has been used to determine the degree to which the two parents were related (Table 4). 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 (Fig. 3 -red line). A dog with a value of -1.0 would have parents that were totally unrelated at all 33 STR loci, while a dog with an IR value of +1.0 has parents that were genetically identical at all loci. An IR value of +0.25 is equivalent to offspring of full sibling parents from a random breeding population. IR values >0.25 occur when the parents of the full-siblings were even more related to each other than dogs from a random breeding population.

IR scores ranged from a low of -0.260 (parents least related) to a high of 0.435 (parents most related), with a mean (average) value of -0.005 (Table 4). One half of the dogs have IR values between -0.115 and +0.085, which are respectable IR scores. One fourth of the population had IR scores from -0.115 to -0.239, indicating a population that was produced by parents that were as unrelated as possible. However, one fourth of the dogs had IR scores of +0.085 to +0.435. This proportion of dogs are quite inbred and even above the level of offspring of full-sibling village

dog parents. The highly inbred and outbred populations cancel each other out in the breed-wide standard genetic assessment based just on unadjusted allele frequencies.

Table 4. IR vs IRVD comparison for Swedish Vallhund (n=105)

	IR	IRVD
Min	-0.260	0.079
1st Qu	-0.115	0.233
Mean	-0.005	0.323
Median	-0.012	0.306
3rd Qu	0.085	0.404
Max	0.435	0.620

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

The IR values can also be used to give an approximation of how much genetic diversity has been lost during breed development and subsequent evolution. This is done by comparing the frequency of a given allele in Swedish Vallhund with the frequency of the same alleles in a population of village dogs from the Middle East, SE Asia, Taiwan and other Pacific island nations such as Brunei and the Philippines. Contemporary village dogs are largely unchanged from the ancestors of almost all modern dog breeds. The resultant frequencies are then used to calculate the IRVD.

A comparison of IR values (red curve) and IRVD values (blue curve) can be used as a rough estimate of how much of the genetic diversity available in contemporary village dogs has been maintained in modern Swedish Vallhund. A rough estimate based on areas under the curve (black), indicate that Swedish Vallhund have maintained only 7% of the total genetic diversity thought to still exist among all (village) dogs. This is the lowest amount of available genetic diversity found in any of the breeds tested to date.
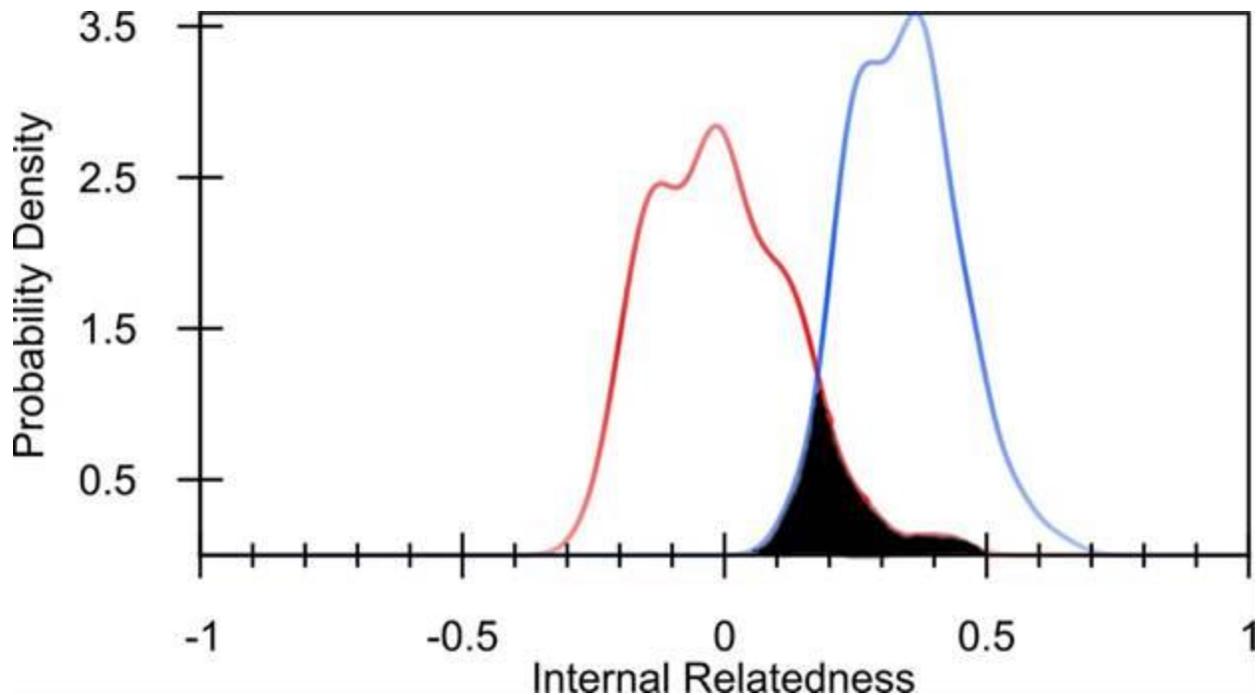
Figure 3. Distribution of IR estimated in Swedish Vallhund (n=105) based on intra-breed diversity (red line). The blue line shows adjusted IR values (IRVD) based on the frequency in village dogs of the same alleles identified in Swedish Vallhund (blue). The black area is an estimate of the amount of genetic diversity still present among dogs that has been retained in Swedish Vallhund, i.e., 7%.

IV. DLA Class I and II Haplotype frequencies and genetic diversity

The DLA consists of four gene rich regions (classes I-IV) making up a small part of canine chromosome 12. Two of these regions contain genes that help regulate normal cell- (Class I) and antibody-mediated (Class II) immunity. Polymorphisms in these regions have also been associated with abnormal immune responses responsible for autoimmune diseases. The Class I region contains several genes, but only one, DLA-88, is highly polymorphic (with many allelic forms) and is therefore most important for immune regulation. Specific alleles at the four STR loci associated with the DLA88 are linked together in various combinations, forming specific haplotypes (Table 4). Groups of genes and their alleles inherited as a block, rather than singly, are called haplotypes. The class II region also contains several genes, three of which are highly polymorphic, DLA-DRB1, DLA-DQB1 and DLA-DQA1. Specific alleles at STR loci associated with each of the three Class II STR loci are also strongly linked and inherited as a single block or haplotype (Table 5). The STR-based haplotype nomenclature used in this breed diversity analysis is based on numerical ranking with the first haplotypes identified in Standard Poodles being named 1001, 1002, ... for class I haplotypes and 2001, 2002, ... for class II haplotypes. It is common for various dog breeds to share common and even rare haplotypes, depending on common ancestry.

The Swedish Vallhund has the lowest DLA class I and II haplotype diversity of any breed we have studied to date. There are only six DLA class I and four class II haplotypes. However, the haplotype frequency is dispersed over 4/6 class I and 3/4 class II haplotypes. This is different

than many breeds, where a small proportion of haplotypes occur in many dogs. However, this dispersion was predicted based on results from alleles for the 33 autosomal loci. Three DLA class I haplotypes (1177, 1178, and 1179) are unique currently to Vallhund. These unique haplotypes have been inherited by descent from as few as three founders or founder lines, supporting the historical use of one male and three females in revival of the breed. All the class II haplotypes have been found in several other breeds (Table 6), although the 2084 haplotype has only been seen before in a single Biewer terrier (Table 6).

Table 5. DLA class I and II haplotypes found in Swedish Vallhund (n=105) based on four class I STR and three class II STR and their breed-wide incidence.

DLA Class I Haplotype Frequencies (Updated Oct 10, 2019)		
DLA1 #	**STR types**	**Swedish Vallhund (n=221)**
1006	387 375 293 180	0.262
1009	382 377 277 184	0.054
1068	380 373 287 181	0.351
1177	395 373 277 181	0.179
1178	386 365 277 186	0.147
1179	395 375 293 180	0.007

DLA Class II Haplotype Frequencies (Updated Oct 10, 2019)		
DLA2 #	**STR types**	**Swedish Vallhund (n=221)**
2007	351 327 280	0.269
2022	339 327 282	0.054
2053	343 324 280	0.498
2084	339 323 268	0.179

V. Relatedness to other breeds based on DLA class I and II haplotypes

The breed dates to the Viking settlement of England and is thought to have played a part in the development of the modern Welsh Corgi and the Lancashire Heeler (see section VI, B, 3). However, it is uncertain whether the Swedish Vallhund was brought to Wales or the Corgi was taken to Sweden. The DLA class I and II haplotypes are in strong linkage disequilibrium, less subject to recombination, and are inherited as extended haplotypes from each parent. Therefore, they can be useful in looking at how breeds might be related. Table 6 lists several breeds that share DLA class I and II haplotypes with the Swedish Vallhund. The major DLA class I 1068 is present in one-fourth to one-third of Vallhund, Shiloh Shepherd and Flat Coated Retriever. The 2053 DLA class II haplotype is also shared at a comparatively high incidence by these same three breeds, but also occurs in 50% of Vallhund and 61% of Samoyed. There is also minor haplotype sharing among several other breeds (Table 6). Unfortunately, no DLA class I and II haplotype data are available for the Corgi breeds.

Table 6. A comparison of recognized DLA class I and II haplotypes in several different breeds. There is considerable haplotype sharing between breeds, reflecting the common evolution of modern breeds from indigenous dog populations that were greatly expanded during the Neolithic period.

DLA1 #	STR types	Black Russian Terrier (n=109)	Shiloh Shepherd (n=115)	Labrador Retriever (n=125)	American Akita (n=79)	Golden Retriever (n=690)	Doberman Pinscher (n=420)	Flat Coated Retriever (n=340)	Havanese (n=370)	Samoyed (n=278)	Miniature Poodle (n=242)	Swedish Vallhund (n=105)	Poodle (n=2053)	Giant Schnauzer (n=141)	English Bulldog (n=163)	Biewer (n=94)	Biewer Yorshire Terrier (n=50)
1006	387 375 293 180	0.032	--	0.028	0.044	0.0145	--	--	0.045	0.004	0.002	0.262	0.0482	0.053	0.003	--	--
1009	382 377 277 184	--	--	--	--	--	--	--	--	0.103	0.083	0.052	0.0173	--	--	--	--
1068	380 373 287 181	--	0.248	0.044	--	0.05	--	0.265	0.016	0.029	0.014	0.357	--	0.039	--	--	0.01
1177	395 373 277 181	--	--	--	--	--	--	--	--	--	--	0.171	--	--	--	--	--
1178	386 365 277 186	--	--	--	--	--	--	--	--	--	--	0.148	--	--	--	--	--
1179	395 375 293 180	--	--	--	--	--	--	--	--	--	--	0.01	--	--	--	--	--

DLA Class II Haplotype Frequencies (Updated May 4, 2018)

DLA2 #	STR types	Black Russian Terrier (n=109)	Shiloh Shepherd (n=115)	Labrador Retriever (n=125)	American Akita (n=79)	Golden Retriever (n=690)	Doberman Pinscher (n=420)	Flat Coated Retriever (n=340)	Havanese (n=370)	Samoyed (n=278)	Miniature Poodle (n=242)	Swedish Vallhund (n=105)	Poodle (n=2053)	Giant Schnauzer (n=141)	English Bulldog (n=163)	Biewer (n=94)	Biewer Yorshire Terrier (n=50)
2007	351 327 280	0.032	--	0.032	0.044	0.0145	--	--	0.049	0.004	--	0.271	0.0146	0.053	--	--	--
2022	339 327 282	--	0.057	0.088	--	0.0007	0.002	0.125	0.108	0.092	0.002	0.052	0.0002	0.007	0.015	--	--
2053	343 324 280	--	0.317	0.04	--	0.029	--	0.138	0.039	0.613	0.014	0.505	--	0.043	--	--	0.01
2084	339 323 268	--	--	--	--	--	--	--	--	--	--	0.171	--	--	--	0.005	--

VI. What does this assessment of genetic diversity tell us about contemporary Swedish Vallhund

The DNA results supports the history of the breed having been resurrected from as few as four true-to-type dogs 80 years ago. The breed has the least amount of genetic diversity that we have observed among several diverse breeds that we have studied. The lack of genetic diversity means either that the breed evolved from a few founders or that it is a result of a severe artificial genetic bottleneck. The latter is historically supported by the relatively recent revival of the breed from a reported nucleus of one male and three females. It was purportedly difficult to find remaining dogs with the desired phenotype,[4] so the four individuals may have represented a small and similar phenotypic/genotypic representation of the breed. The breed has only 4/6 major DLA class I haplotypes and 2/4 major class II haplotypes. IR and IRVD values also demonstrate a low level of available genetic diversity. The breed possesses only 7% of the diversity present in village dogs, whereas most larger popular breeds have retained 40% or more. It is said that modern breeds have retained 87% of the diversity that was present at the time their registries were closed. If true for Vallhund, it indicates that genetic diversity was low in the founding population and not subsequently lost.

Although Vallhund lack genetic diversity, this has not necessarily been a problem for the breed. It appears that the founders of the breed were relatively healthy and were spared many of the simple and complex genetic disorders present in pure breeds of dogs. Therefore, they remain comparatively healthy among breeds. In addition to picking founders wisely, either by chance or plan, the breed started off with healthy stock. However, it is also obvious that breeders have done a good job over the decades in maintaining what diversity they had at the beginning by careful selection of the least related sires and dams from among the population at hand.

A lack of genetic diversity does greatly limit a breed's ability to adjust to further artificial genetic bottlenecks, whether they are geographic, catastrophic or genetic disease associated. The breed has suffered at least one new autosomal recessive genetic disorder, a retinopathy. If the frequency of this mutation is high in the breed, it will be difficult to eliminate without losing a portion of linked genetic diversity. If a decision is made to breed for heterozygotes, this further limits the ability to find suitable mates that are both trait free and distantly related. It is also the task of breeders not to succumb to further shortening legs or lengthening the body by introducing the second chondrodystrophy mutation associated with disc disease from a breed like the Corgi.

VI. Health problems of Swedish Vallhund[5-10]

A. Lifespan

The Swedish Vallhund is generally a healthy dog. Its small stature contributes to its longevity, with an average lifespan of 15 years.

B. Health problems of a complex or simple genetic basis

1. Eye problems

Eye disorders include distichiasis, corneal dystrophy, persistent pupillary membranes (PPMs), cataract and retinopathy.[5] Distichiasis is an eyelash that grows from an abnormal spot on the eyelid and causes irritation of the cornea and corneal disease, blepharospasm, and epiphora. The inheritance is unknown.

Corneal Dystrophy is a condition characterized by bilateral, noninflammatory opacity of the cornea and was detected in 0.6% of Canine Eye Registry Foundation (CERF) examinations.[5] It appears as grayish white lines, circles, or clouding of the cornea. Corneal Dystrophy can also have a crystalline appearance.

Persistent Papillary Membranes (PPM) was the most commonly occurring hereditary eye condition in the Vallhund study, occurring in 15% of dogs doing the CERF examination.[5] Persistent pupillary membranes (PPMs) are due to a failure of the uveal tract to regress during embryonic and neonatal life. They usually have no visual consequences. The inheritance is unknown.

About 5% of Swedish Vallhund in one report suffer from cataracts.[5] Cataracts occur in several forms, each of which has slightly different characteristics. Some are primary (not associated with other ocular or systemic disorders) and others are secondary (occur as part of another ocular or systemic disorder). It is difficult to say where cataracts in Vallhund lie in this spectrum, because of the high incidence of other eye disorders including vitreous degeneration, persistent pupillary membrane, corneal dystrophy and retinopathy.[5] Veterinarians commonly classify cataracts based on three criteria, development, cause, and age of onset.

The retinopathy (progressive retinal atrophy-PRA) described in Swedish Vallhund is multi-focal rather than diffuse as in other PRAs, variable in age at onset, progressive over many years and

variable in severity, leading first to night blindness and then to varying degrees of day blindness.[6,7] It was diagnosed in 10% of CERF examinations.[5] Pedigree analysis indicates that the condition is heritable and most compatible with a simple autosomal recessive defect with possible modifying genes. The disorder is not caused by any of the seven known mutations causing progressive retinal atrophy in dogs and diagnosis is by ophthalmoscopic examination by a qualified veterinary specialist.

2. Orthopedic problems

Hip and elbow dysplasia and luxating patella occur at varying incidence in many larger breeds and have become more common is several small breeds as well.[8] The genetics are complex, and the causative mutations may be quite ancient. The Orthopedic Foundation of America evaluated the hip X-rays of over 300 Swedish Vallhund and found 10% to have hip dysplasia, which is. high for a small dog. Elbow dysplasia occurs at about a 3% rate. Luxating patella (loose knee joints) also occurs at a low frequency in the breed.

3. Miscelleneous.

Chronic allergies cause itchy skin and scratching, which can lead to bacterial infections (hot spots).

The Swedish Vallhund has been saved from the serious problem of intravertebral disc disease seen in shorter legged and longer backed breeds such as the Corgi. The Vallhund has the chondrodsysplasia mutation that causes a shortening of the legs and lengthening of the back but lacks the second chondrodystrophy mutation in the same gene (*FGF4*) that further shortens legs, lengthens back, adds stockiness to the frame and leads to abnormal intravertebral disc structure.[9,10] The fact that Corgi have the double *FGF4* mutation, while it apparently does not exist in Vallhund, suggests that the Welsh Corgi's originated from Swedish Vallhund and not the converse.

VII. Information sources

A. Breed history

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