

Preserve genetic analysis for the swedish Vallhund

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In the wild it is of great importance that a species has a genetic variation in order for its adaption in its habitat, but it is also important for our pets with a genetic variation for about the same reasons – we can not predict what demands our breeds will stand before in the future and without a variation within the breed we are at worst case risking that a breed is extinct by a new, or a previously unknown disease. That a breed club is up to date with the breeds preserve genetic situation is therefore a way to try to ensure the future.

In the wild it is called a genetic bottleneck when a species due to a sudden change becomes very few, for example in a natural disaster where the vast majority of individuals die. Every dog breed has, evolutionary seen not so long ago, gone through two genetically bottlenecks, when the wolf became dog is one and the second is when the dog became different breeds. In the creation of a breed often very few dogs have been used and these are now the foundation for the entire breed. The genetic variation that was found in the few dogs that initially formed the breed is the maximum ever available. New genetic variation can only be added through mutations, but they are so few that it is of little matter.

Breeding with focus on preserving is different from selective breeding because the preserving breeding is aiming to preserve as much as possible of the diversity, in this report in the shape of genetic variation, that is within the breed. Selective breeding is aiming towards what commonly known as “refining breeding”, that is improving the breed one way or another. Perhaps also aiming towards every individual looking as much alike as possible? Selective breeding and rectifying reduces the genetic variation within the breed.

A preserve genetic analysis purpose is to evaluate a breed's preserve genetic status – to describe how a breed is heading from a preserve genetic perspective. The result is both a follow up on how the work with preserve genetic progresses but can also be used in order to map the faults that exist and to do something about these. Examples of what other breed clubs have done is:

- This month's dog (male) on the website where they are trying to market male dogs that has not yet been used in breeding but are suited for breeding, even if they are not the most successful at dog shows, in contests or whatever seems to be important merits for the breed.
- To clearly inform the breeders about the shortcomings in a breed concerning the genetic preservative perspective and to talk about the importance of “liking differences”.
- To actively contact owners of dogs that are descendants of genetically important dogs in the breed process (and, of course, if there are no reasons against breeding, encourage them to do so).

Method

The method that was used to make this analysis is called pedigree analysis (analysis of pedigrees). This analysis is mainly performed through two different calculating methods, probability calculations and a “gene drop”-simulation. The latter simply means assuming each of the breeds founders (founders is the animals which has founded the population) has two different genetic predisposition in the beginning and then the simulator “drops” these through the pedigree multiple times (I usually use 10 000 times) and the reported value is for example how well represented a single founder is in the population today is an average of the values that has been reported through these simulations. There are two kinds om main types of measurements in a preservative genetics analysis, those who are inbreeding related and those who are directly related to genetic variation.

Data

This analysis is based on data from the database: Worldwide Swedish Vallhund – Västgötaspets Pedrigree Database, by Leonie Darling. However, the analysis is based on the 13 dogs that laid the foundation for the SKK's pedigree - these are thus considered as "founders", that is the start of the pedigree book although some knowledge is available about some of their ancestors.

Inbreeding

The inbreedity is the probability that a genetic predisposition is to combine with the same genetic predisposition (not just a similar genetic predisposition but the same genetic predisposition) in a descendant. Inbreeding in it self is, theoretical, not dangerous but since it consists of the probability of two genetic predisposition to meet themselves it is in practice dangerous since the risk also is larger for deleterious genetic predispositions to meet themselves. Many diseases derives from so called recessive genetic predispositions – those of which two are needed in order to get sick. If the individual only have one it will not get sick and is therefore not a disadvantage in itself. But through inbreeding a sick genetic predisposition may spread very quickly in a population – it is then called an inbreeding depression and it is the inbreeding depression that is the actual problem with inbreeding. Inbreeding depression is the danger with inbreeding.

The inbreeding in swedish vallhund is at an average of 27,02 % which is approximately what one can expect even if its not a very low number. Mating sibling with each other results in an inbreeding of 25 %. It is at approximately the same inbreeding that are found in the Swedish wolf. It is really hard to compare the actual inbreeding between breeds, there fore The Swedish kennel club has chosen for example to have a certain number of generations – to be able to determine which breeds that are “better” and “inferior” in this regard. By only looking at the inbreeding 25 % is a high number. Other breeds that I have investigated accordingly and with accordingly same number of generations has had 10-20 % inbreeding in their extended pedigrees. It is hard to compare The Swedish kennel clubs calculations because they are based on a few generations but in an extended database like this you add more information. In every case I know the inbreeding has gone up when you add more information, because when you add more information it then shows that the individuals in the beginning of the pedigree is related to one another. The inbreed in a closed population is always going to increase, what you can do is keep down the pace inbreeding increases as much as possible. Remember though that the inbreeding itself is not dangerous, it is first when it develops into an inbreeding depression it is so. It is therefore important to keep an eye on the fact that the inbred increase is not unnecessarily high (by never mating animals that are closely related to each other, that is, breeding animals should be less related to each other than cousins) to keep an eye on potentially harmful genetic predisposition and ensure that they do not get spread in the population. If it is possible (as in recessive inherit), it is good to trace where the genetic predisposition comes from and be sure not to mate to inbreed on this on individuals with this genetic predisposition.

The inbreeding, 27%, is calculated on just under 17 generations. Inbred growth over the last two

years is 2%. An inbreeding of two percentage points in two years in an extended family tree is normal. The high level of inbreeding depends more on how the breed is historically managed. The inbred will continue to increase, it is important to keep the inbred increase as low as possible by as far as possible mating individuals who are so far related to each other as possible.

If you want to compare inbreeding rates between races, it needs to be estimated in about as many generations. This is why, for example, The Swedish kennel club chooses to limit the number of generations that are used when you calculate the degree of inbreeding. As I mentioned earlier, inbreedity is a measure of the probability that the same genetic predisposition meets itself and therefore it becomes misleading to limit the number of generations that calculates this probability. However, it can still be interesting to compare the inbreeding rate between races as comparisons. The table below contains the values for inbreeding and the number of generations for Swedish dog breeds that had about the same number of generations in their pedigrees as the Swedish vallhund in 2012 (when I did a study on Swedish breeds, Jansson and Laikre, published in my dissertation).

Breed	Generations	Inbreed
Småland hound	10,1	0,06
Hamilton hound	10,2	0,07
Swedish lapphund	10,4	0,07
Swedish elkhound	11,1	0,08
Drever	11,3	0,07
Swedish vallhund	11,9	0,09

As seen the Swedish vallhunds inbreeding trend follow the trend for swedish breeds, regarding the increase of inbred in the population. My opinion and experience is that swedish breeds generally has quite low increase of inbred.

The swedish mean kinship (MK, which is the mean inbred of the next generation at random mating) is at 25.75 percent. This means that it would be possible to lower the inbred rate by a few percent to the next generation if this was the only factor that had to be taken into account in the breeding work and all individuals were mating everyone. Realistically, the inbreeding increases in a closed population, as said, and it is important to keep the inbreeding as low as possible. In order to drastically affect the inbred positively, you need to find "completely unrelated" individuals - in dog populations, it is often about mixing with another breed, but it is not something usually done until you have real problems with inbred depression.

Effective population size

The effective population size is how big population the population is, purely genetic. It is a way to measure the genetic generation within a breed and indicates to the breeders how important it is to allow as many dogs as possible to breed and how the sex quota is in the breed. One might say that the effective population size is equivalent to how many dogs of those used in breeding that add something to the breed with regard to genetic variation. Remaining individuals can then be considered as copies of already existing genetic material. Unfortunately in dog populations we do not know how many dogs are living or not since this is usually not reported to The Swedish kennel club, but for the population that we imply lives in this analysis, the world's Swedish vallhundpopulation (those born within 12 years of age) applies:

Effective population: 874,76, this I based on 368 males and 539 females. It is in theory pretty easy

to improve the effective population size – to use as much as possible of the variety of the animals who are to be bred the same amount of female individuals as males should be used. In this case we would have wanted 454 + 454 instead of 368 + 539. (I´ve earlier, 2012, counted the effective population only for the Swedish vallhundpopulation living in Sweden – it was only 314 animals.) In summary one could say that since half of the genetically material in an individual comes from its mom and the other half from its dad it is good if the same amount of female individuals as male is used in breeding if you want the largest spread of genetically material as possible.

Gene diversity (GD)

GD is a measurement of the genetically variation that for the swedish vallhund is 74%. Here GD is calculated by giving each founder two allele as "dropped" randomly down through the pedigree. This simulation is done a large number of times and 74% is the mean of what remains (of the original alleles found in founders, the others have disappeared through inbreeding and for purely random reasons). The figure corresponds to approximately 1-MK (mean kinship). If all the random combinations did not effect at all, the diversity would be exactly 1-mk. So when I ran 10,000 simulations for Swedish vallhund, I got that result - which is expected. In order to maintain as much as possible of the diversity of genes, it is important to keep the inbred at as low a level as possible.

Founder genome equivalents (FGE)

The number of FGE is the amount of “fresh” founders that the population corresponds, the number of founders genome that are still in the breed. With other words the amount of unrelated individuals as could number of unrelated individuals who would constitute the same genetic variation as the current population, the number of individuals the unrelated genetic material that remains in the breed would suffice if you put together everything in one and the same dog. For the swedish vallhund it is FGE 1.94, that means that it is hardly equivalent to two genome of the original 13 founders from the founding population. 85 % of the foundation variables have been lost at the present time, most of this variation disappeared when you stopped using descendants after some founders. The situation can somewhat be improved by using lines for underrepresented founders, see next part.

Potentially, it would be possible to get out 3.75 FGE from the population, if it was managed perfectly, as it is the sum of what remains of the founder alleles.

Founder contributions

Founder contribution calculation shows how much of the genes from the breed's different founders that remains in the breed. *It is most important to use descendants after the individuals who are underrepresented.*

Representation: the number och genes in the present population that derived from the actual founder.

Allel-retention: The possibility that a random gene from the founder individual is at all represented in the current population.

Name	Sex	Representation	Allel-retention
Tessy C	Female	0,0001	0,0135
Tessy B	Female	0,003	0,033
Tessy A	Female	0,003	0,0335
Sessan	Female	0,003	0,0445
Jack II	Male	0,003	0,038
Tjappos pappa	Male	0,0119	0,1435
Moppan	Female	0,0267	0,1415
Topsy	Female	0,0407	0,309
Tussi	Female	0,0638	0,36
Lessi	Female	0,176	0,542
Tyra	Female	0,184	0,6475
Tessan	Female	0,2078	0,733
Mopsen	Male	0,2771	0,7155
Sum		1,000	

The value of nurturing the genetical variation

Since the swedish vallhund is affected by numerous problems for which the inheritance is not yet clarified (cushing syndrome, HD etc) it is of great importance to preserve as much genetical variation as possible – genetical variation is the insurance against unseen events for example a genetical disease that spreads fast in the population. If all the individuals is vlosely related many will be carrier of the genetic predisposition The founder alleles that are still existing from the start of the population is therefore important to preserve.