

Expanding Friesian breeding

The demand for Friesian horses is higher than ever and the breed is conquering the whole world. That makes it difficult to imagine that there was a time when there were only a handful of true enthusiasts of the breed left. A crusade through Friesland was necessary to collect horses for the studbook and encourage breeders to save the breed from extinction. With that history in mind and given the current popularity of the breed, it seems almost indefensible to start talking about crossing with another breed. Suggesting this causes resistance, which is understandable. Yet there are good reasons for using outcross.

Inbreeding level permanently too high

When the Friesian breed came to the brink of collapse, the population was so small that there was no other option than mating very closely related horses. The total inbreeding over all recorded generations was 4% in 1920 and is now 18%, based on studbook data (a DNA study to confirm this percentage is under way). That is an increase of 14% in ten generations. Over the last two generations, the inbreeding increase has remained well below 1% per generation. Looking back further, the increase per generation was so high that it is actually a miracle that reproduction has been maintained and the breed could grow to its current size. The breed has twice gone through a genetic bottleneck period. This history can be found in books about the Friesian horse, but also in the DNA of every Friesian anywhere in the world. Studbook stallions and stallion mothers from the bottleneck period can be found many times in the pedigree of every contemporary Friesian. At the top is the stallion Danilo 137 with 23% genetic contribution. Because Danilo 137 started his breeding career almost 100 years ago and his genes have been so widely spread in the subsequent ten generations, there is not a single Friesian today that has less than 20% Danilo genes. Almost a quarter of the genes of every Friesian, anywhere in the world, comes from one common ancestor. That is an unprecedentedly narrow basis from which to create a closed breeding population.

The narrow base of breeding animals from which all Friesians today come ensures:

- 1. A lack of genetic variation in our closed population.**

Danilo 137 is at the top, but is certainly not the only stallion with an excessive genetic contribution. The graph in the appendix shows stallions with more than 5% genetic contribution in the current breeding population. The top horses with a contribution >10% are all stallions born between 1900 and 1970. The stallions of that period still largely determine all the genetic properties of today's breeding animals. Of course, selection has taken place over the years and you can therefore assume that the better genes from the better breeding animals of the past have ended up in the Friesians of today. But that is exactly where the problem lies. Selection in a closed population leads to loss of genetic variation within that population. Should the breeding policy change and should we want to select differently, we will find that in our closed population with a very narrow base, there are not enough good genes left to achieve the desired selection result in - for example - the area of health.

2. Mating of relatives becomes inevitable, resulting in inbreeding.

If almost a quarter of the gene package of every Friesian comes from one common ancestor, the contribution to the total inbreeding of that common ancestor is very significant in each and every mating. The attribution to the current total inbreeding for the stallion Danilo 137 is 2.75%. So, of the total average current inbreeding of 18%, 2.75% can be attributed to the contribution of a single founding stallion from the past. For comparison: The final attribution of the later 'preferent' top-stallions Beart 411 and Jasper 366 is 0.19% each. This means that today it takes 15 stallions of the caliber Beart 411 and Jasper 366 (each with large amounts of offspring) to come close to the effect on the total inbreeding of Danilo 137. A stallion like Tsjalle 454 is thought to attribute significantly to the total inbreeding in the population. Yet it takes 25 stallions with Tsjalle's current genetic contribution level to achieve Danilo 137's attribution to inbreeding.

The majority of the Friesian inbreeding problem is inherent to the history of the breed and nothing can be done about that heritage now. New increases in inbreeding can be controlled relatively easy with the current population size and current policy. This does not alter the fact that the vast majority of total inbreeding and the negative effects that are expressed in health problems arise from the genetic bottlenecks in the past. This influence is a given and cannot be eradicated even with the strictest inbreeding policy.

The KFPS advises to avoid close inbreeding in the last five generations when making mating choices. This is good advice, in order to prevent

possible abnormalities in the intended foal. However, this does not prevent inbreeding, the result is only a postponement of inbreeding. Once the common ancestors have moved up to generations above five, breeding animals with a high genetic contribution will eventually contribute to the total inbreeding in today's population. A stallion's ultimate level of contribution to total inbreeding is equal to the square of his genetic contribution divided by two. The advice to avoid close inbreeding in the last five generations has also led to an accelerated shift from genetic differences between animals to genetic variation within individuals. Example: For a mare with a lot of Jochem-blood and no Wessel-blood, a stallion was sought with a lot of Wessel-blood and no Jochem-blood. For a mare with a lot of Wessel-blood and little or no Jochem-blood, a stallion with little or no Wessel-blood was sought. The result is a next generation of breeding animals that show little difference in blood percentage of Jochem and Wessel. This will mean that within a few generations there will no longer be any Jochem-free or Wessel-free breeding animals. So, from that moment on, inbreeding on Jochem and Wessel becomes inevitable.

Breeding animals with high contribution levels will ultimately contribute to a loss of diversity and an increase in total inbreeding in the population. The breed has survived two bottleneck periods, but has not emerged completely without residual symptoms. Every horse veterinarian in the Netherlands can list conditions that are more common in Friesians than in other breeds. The veterinarians at Wolvega Veterinary Clinic came up with the following list:

Conditions and problems that are more common in the Friesian breed:

1. Esophageal dilation (megaesophagus)
2. Aortic rupture
3. Degeneration of the ball-bearing apparatus (intermediate tendon)
4. Dwarfism
5. Hydrocephalus
6. Gastric overloading and gastric rupture
7. Chronic progressive lymphedema
8. Dystocia
9. Coxofemoral abnormalities such as hip dysplasia
10. Bilateral corneal dystrophy
11. Loose Processus extensorius
12. Tail and mane eczema
13. Ossification of hoof cartilage
14. Dystichiasis

15. Susceptibility to leg scab and rasp
16. Retained placenta
17. Reduced defense against parasitic worms
18. Increased risk of complications during recovery from surgery

Dwarfism, hydrocephalus and dystichiasis can be traced back to three known gene defects that have spread throughout the population and are expressed through inbreeding on a common carrier.

In the case of esophageal dilation, it is suspected that it is also a gene defect, which, under the influence of environmental factors (or perhaps other genes), is only expressed in some of the homozygous recessives. In this way, carriers and unrecognized sufferers can pass on their defective genes to their offspring. There are indications that this happened on a large scale. If this suspicion is confirmed, it will be very difficult to responsibly reduce the frequency of the defect in the population through selection.

With all the other conditions and problems on the list, we are still in the dark as to where exactly the higher sensitivity of Friesians comes from.

Reasons could be that:

1. More gene defects are found that have arisen somewhere in the population and are expressed through inbreeding.
2. The genetic component of sensitivity was already present in the narrow genetic base of the breed and has become a breed characteristic.
3. 'Weaker genes' linked to other characteristics have been fixed in the population.
4. Inbreeding and the associated decrease in heterozygosity lead to items from the list occurring more frequently.

Genome selection

If you choose to address the hereditary basis of health problems within the closed population, success depends on locating the less favorable genes in the population. This can be done in the - currently common - manner of combining a lot of phenotype information from individuals and their relatives into an estimate of the genetic predisposition per animal. It is also possible using genome selection. The technical possibilities exist to determine genome information of many individuals. Linking data from those individuals to phenotype information about which condition was expressed and under what circumstances means you are able to identify 'risk genes'. The possibilities are

there, but at the moment the recording of individual health information (clinical observations) is inadequate. When health problems are the result of inbreeding depression/lack of heterozygosity, selection will not lead to the desired result.

Suppose that it will be possible to identify animals with 'risk genes' in the near future. Due to the breed's bottleneck history, there is a good chance that exclusion of animals with these 'risk genes' will lead to a further narrowing of the genetic basis. Result: A new genetic bottleneck and a handbrake on genetic progress towards breeding goals.

The moral of this story is that we have to accept the current health status of the Friesian breed for the time being and settle for very little genetic progress towards the breeding goal if we continue to breed within a closed population. That is certainly no reason to abandon closed population breeding. Genome selection offers opportunities that must be seized. But we must take into account the real chance that Marije Steensma's PhD research, currently carried out for the KFPS studbook, will conclude that there is too little genetic variation left and that the selection space is running out.

Shortage of selection space

The driving force for every breeder is improvement. To search for a stallion that excels in characteristics A and B for your mare that excels in characteristics C and D and then cross your fingers and hope for a foal that excels in A, B, C and D. Statistically it should be possible to approve a few stallions every year where that goal has been more than successfully achieved: stallions for which everyone agrees that they have added value in terms of bloodline and selection characteristics. In practice this is not the case. Many selection characteristics are involved in the process of becoming a breeding stallion. Veterinary findings, semen and X-ray examinations and foundation problems result in a first major selection. The stallions that remain, can never excel at everything. There are characteristics in every new studbook stallion that are just barely acceptable. The higher you go up the breeding pyramid, the more difficult it becomes to find a stallion that matches in terms of bloodline and rises above the level of your mare in genetic potential. Then the idea may arise that 'more of the same' breeding is the highest result that's achievable. This always comes with the risk of setbacks and, on balance, means you're 'breeding backwards'. Taking all this background into consideration, it is understandable that a number of top breeders feel the need to look outside the closed population of the Friesian breed.

Added value of expanding Friesian breeding

The Friesian horse has a strong position in the spectrum of equestrian uses and that strong position has been acquired despite the bottlenecks in its history and despite inbreeding. The strength of the Friesian horse and its distinction from other breeds lies in its character, stature and breed typicality (color and abundant mane, tail and socks). The average Friesian is a great utility horse for recreation and sports. Compared to open sport-oriented breeding of, for example, the KWPN, there is on average an understandable lag in genetic progress in movement characteristics. A target group is now emerging of users who would rather choose a horse that is somewhere between the average sport-bred warmblood horse and the Friesian. There lies a challenge for breeders who want to combine the best of both worlds in one (hybrid) offspring. In terms of longevity, vitality and health, expanded breeding has, due to the strong inbreeding in the closed / pure population, significant added value compared to just continuing to breed purely.

The technical breeding laws at a glance:

1. Known and unknown gene defects that only occur in one of the two parent breeds will not be expressed in the first generation of outcross horses (F1).
2. Health problems that occur more often in pure Friesians due to a lack of heterozygosity will never occur more often in the F1 than the average of the incidence levels of the two parent breeds.
3. In open populations, breeding animals can be found that have a significant advantage over the pure Friesians in terms of universal breeding goal characteristics (such as the quality of the basic gaits and sporting aptitude among the top warmblood studbook registered stud stallions). That advantage largely ends up in F1.

The potential genetic progress in F1 compared to the original Friesian is therefore great in the areas of health, longevity, functional build, quality of the basic gaits and sports aptitude. The trade-off is a loss of typical Friesian characteristics, which are often homozygously anchored in the pure breed. In practice, it appears that a growing group is willing to accept that change for the benefits of the hybrid.

Pitfalls of hybrid breeding

- An owner of a Friesian mare who has had several disappointing breedings will inquire with the owner of a very attractive F1 stallion whether he is available for stud service. Perhaps some foreign blood can make a positive contribution. There is a good chance that this will end up a disappointment. It is comparable to a breeder who wants to breed a palomino and looks for the most beautiful palomino stallion to breed with. Characteristics that are positively expressed

through heterozygosity are by definition not stable when breeding. F1 is full of genetic variation, but the question is what part of this diversity will end up in the next generation.

- Blood is thicker than water. The top breeder, who has found a very beautiful horse outside of the pure Friesian population and saw her expanded Friesian breeding crowned with a dream F1, feels the urge to breed with it sooner or later. She has enjoyed a wonderful sporting career and she thinks it is time for a foal. What she misses most about her F1 mare is the forelock and the socks. The most logical choice is a Friesian studbook stallion that is known as the sire with the most hair. It does not matter which studbook stallion she ultimately chooses. In all cases, approximately 60% of the stallion's gene package will come from ancestors that can also be found in the pedigree of her F1 mare. In the F1 mare, 30% of the genes come from the same common ancestors. While the F1 was still free of inbreeding, one backcrossing immediately produces an offspring with 9% inbreeding ($2 \times (1/2 \times 0.6) \times (1/2 \times 0.3)$). Another backcrossing results in 13% inbreeding, with the associated risk of inbreeding problems.

The continued F1 pairing

As previously stated, F1 is full of genetic variation. As long as that variation in an individual from two unrelated parents has been combined, that variation does not present itself available for selection. If you mate F1's with each other, this results in a shift from genetic variation within individuals to variation between individuals. From that moment on, genetic variation is expressed in the form of phenotypic differences between animals and selection opportunities arise. This also makes it useful to test those differences against the Friesian breed standard and the Friesian breeding goal. A lot of phenotypic variation, especially in terms of breed-typical characteristics, will ensure that in the first generations a significant proportion will score inadequately on Friesian type, but will score well above average on functional build, legs and gaits. The alleles responsible for the Friesian-typical characteristics have not disappeared, but are less expressed due to heterozygosity. Selection response will be large and in the long term a 'synthetic' or 'expanded' new breed population will be created that will increasingly resemble the original pure Friesians. It is not the case that, with the transition to a synthetic new breed, all Friesian gene defects will be a thing of the past. From 100% to 50% Friesian blood will cause a decrease in allele frequency, but it remains important to continue to localize the risk genes and select accordingly.

No foreign blood in the KFPS main book

The biggest concern for anyone who cares about the Friesian breed is the risk that foreign blood will cause the breed, as we know it, to be lost. If there is already a beginning of willingness to do something with foreign blood, this leads to the tendency to leave the door open just slightly for breeding animals with a little foreign blood. These must be animals that meet the Friesian breed standard as much as possible on all fronts. As indicated earlier, this method will not solve the inbreeding problem. The amount of foreign blood required to demonstrably improve vitality and longevity in the entire population is so great that the loss of the breed as we know it today is inevitable. If current research shows that the genetic variation within the pure population is not sufficient to continue breeding responsibly within the closed population, that scenario is appropriate. Even after the current genetic research project has been completed, it is unlikely that an unambiguous assessment will be made as to whether the genetic variation is sufficient. An answer to that question is always subject to considerations. How much decrease in average lifespan do we still consider acceptable? How much loss around birth or during the rearing phase is considered still acceptable? How much genetic gain in hind leg strength do you want to sacrifice to make the breed healthier? Etc.... etc.....

These are all questions for which not every breeder will come to the same decision. We must give each other that space. You do not have to be against breeding in a closed population to be in favor of expanded Friesian breeding and you do not have to be against expanded Friesian breeding if you yourself strive for genetic progress in the closed Friesian population.

Both movements can reinforce each other. In addition, there is no legitimate reason to open the KFPS main book for foreign blood now or in the future. The best way to expand towards a new synthetic Friesian breed is to use the same breeding goal as the KFPS is currently using, but a separate breeding program and registration.

The Friesian breed benefits from stubborn breeders who look for suitable breeding animals outside the closed population. The Friesian breed also benefits from stubborn breeders who remain loyal to the pure Friesian. The Friesian horse benefits most from agreement that both choices are defensible.

Genetische Contributie van Stempelhengsten

