Foreword.

"***Mens sana in corpore sano***" : a healthy mind in a healthy body.

The health of the Rottweiler, worldwide, lies close to our heart and is embedded in the Constitution of the International Federation of Rottweilerfriends (IFR).

It's reference to the health of all breeding dogs, implies that the Federation and its Memberclubs must pay particular attention to genetic disorders.

For the Rottweiler, Hip Dysplasia (HD) and Elbow Dysplasia (ED) were the first disorders that worldwide led to regulations meant to diminish the genetic affection of the breed.

The measures that were taken by breed clubs and/or kennelclubs, mostly by excluding the dogs that are affected by the disease from breeding, have proven to be quite effective, although not enough to completely eliminate the genetic factor and remove it from the genepool Still they have helped to limit the number of affected dogs and to avoid a lot of suffering.

In this brochure you will find a brief review of just a few of the genetic diseases that are said to have entered the Rottweiler's genepool. [1]

The list is not new, nor the particular diseases on it. Even the way of approaching the problem is known for a long time and was amongst others confirmed in the International Breeding Strategies of the FCI that were approved in 2009.

Indeed, not just for the Rottweiler but for many other breeds too, cynology has sounded a loud alarm concerning an ever more reduced genetic diversity among certain canine breeds, causing not only extreme phenotypes ([2]) but also physical and health problems.

This reduced genetic diversity seems to root so deeply in canine breeds, including the Rottweiler, that many highly unwanted genetic traits and/or disorders are said to be present in such an important proportion that if no resolute action follows, they may threaten to result in the extinction of breeds, especially where the genepool of the dogs that are and/or may be used for breeding is (too) limited. We should not take this warning lightly !

Studies on the amount of inbreeding (or linebreeding) and its negative impact exist and are high on the agenda of scientific and cynological meetings.

Ever more breed associations, national and international and including the FCI, are paying attention to the phenomenon.

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[1] For a list of all (696) Mendelian genetic disorders that were identified in canine breeds : cfr. the study published by the university of Sydney : "Online Mendelian Inheritance in Animals" : http://omia.angis.org.au/home

[2] Highly unwanted by the breedstandard but wanted, introduced, consolidated and promoted only by personal preferences.

As all that concerns the health and conformation of the Rottweiler touches the very core and even the reason of existence of the IFR, it is clear that our Federation cannot and may not remain blind to this evolution but must act in a pro-active manner.

For many breeders, show results have replaced other selection criteria and seduce them into breeding only with well-known show-winning dogs in the hope that their characteristics will be inherited by their offspring so these too will be successful. (and bring an increased puppy-sale).

Unfortunately, the pool of these popular breeding dogs (also called popular sires or "Matador dogs") is very small and when all breeders sip from the same well, this results in an ever more limited pool of breeding dogs, and consequently an ever more limited genetic diversity. How many times have we not said or heard that it seems that certain dogs can be found in almost every pedigree and this worldwide.[3] The knowledge of this fact is not new. Now we must also be aware of the consequences.

What can and must be done ? Well, it is clear that the genepool must be enlarged using a broader base. There can be no discussion about this and I hope this brochure will make this clear.

The IFR cannot impose breeding regulations and the present brochure does not intend to do so.

We do want to create awareness of the problem and to invite the IFR-Memberclubs to discuss and consider an active (common) strategy and at least organize educational programs for their affiliated breeders.

Many measures are thinkable, and the most obvious is of course excluding all dogs from breeding that show a genetic disorder or which are identified (DNA-tests) as to be carriers of the defective genes.

Such measure will however not only also exclude dogs that are valuable because of desired or necessary characteristics, but will limit the genepool even more and would result in an even higher concentration and prevalence of other defective genes.

Is it wise then to test, at the same time or successively, all dogs for all known genetic disorders with the intention of excluding all carriers / sufferers from breeding ?

Most probably not as the impact of such a measure on a breed's genetic diversity and thus its health and conformation, would be even disastrous and have the opposite effect of the one that was aimed at.

Certainly, dogs with defective dominant genes must be excluded. These dogs are ill themselves and automatically excluded or at least should be excluded by any responsible

[3] The "matador effect", or the "popular sire effect" has cynology's attention since 1915 already when Mr. Williams Haynes demanded attention for the phenomenon : a particular male is used to inseminate a large number of females and produces an important proportion of the breed's offspring. These dogs do not only transfer the wanted characteristics but they also lead to more homozygotes carrying recessive alleles that cause diseases and unwanted traits (physical + mental).

breeder.

Carriers of pathological recessive genes may however still be used for breeding, provided the partner is free of that recessive gene and the dog carries positive characteristics that are important for the breed.

The situation becomes more complicated in the case of diseases that are transmitted by the combination of several recessive genes (multi genetic).

What is clear, is that the solution lies with the breeder. A first step must be to make the breeder aware of the existence and implications of genetic disorders and of the dangers of too close and too much inbreeding. Education and communication are the key-words.

It is here that we define the task of the IFR and why we think that the need for an active International Federation of Rottweilerclubs has never been more important than at the moment.

In a world in which breeding dogs, semen and pups are daily sold worldwide, this challenge cannot be met on a national level alone but demands international initiatives.

It is no use to create awareness for only a handful of breeders or even for a whole national pool of breeders if the same awareness does not exist worldwide, especially not in the context of an international exchange of breeding dogs and thus of genes.

To the contrary, if we do not succeed to create a worldwide responsible attitude, this may lead to a consolidation or an introduction of national protectionist measures, neither being in the advantage of our beloved breed.

The present brochure is just a first step towards this educational program and is meant as a first stimulant to make all aware of the problem, to make the breeder understand that he has the solution in his own hands, and to motivate all to respect and do all that is feasible to advance the Rottweiler's health.

Further steps to educate breeders and owners, not only to convince them to honestly test their dogs for the presence of defective genes and to publish the results (and this not only when these show a positive result) but especially to handle this knowledge wisely in their breeding policy, must be taken by the respective IFR-Memberclubs.

Wherever possible, the IFR will put its means and structure at disposal for this.

We are aware that this is an ambitious plan but it is one that must succeed, even if not on a short term. Our beloved breed just cannot afford the option that it would not.

On behalf of the Executive Board of the IFR,

Dirk Vandecasteele
President.

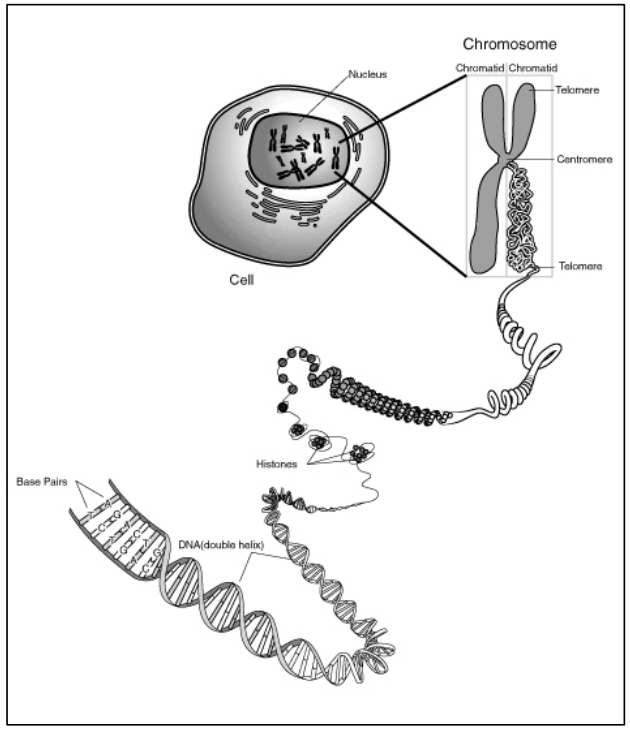
I. AN INTRODUCTION TO BASIC GENETICS.

1. Basic genetics.

The following text about basic genetics[4] certainly does not have the ambition to be complete. That would take a whole book and would even then leave many questions unanswered.

Its only intention is to give a schematic overview of the basic elements of genetics, comprehensible for all but still sufficiently profound to understand how genetics work.

1.1. The cell and its chromosomes.



The body is made of billions of cells which constitute tissues. Several tissues make up organs, such as liver, brain, heart, etc.

Every single cell of the dog contains a nucleus (core) with chromatin that consists of 78 chromosomes[5].

The chromosomes themselves are – simply said – composed of DNA.

Below, we will depict these chromosomes graphically as little staves.[6]

x 39 pair

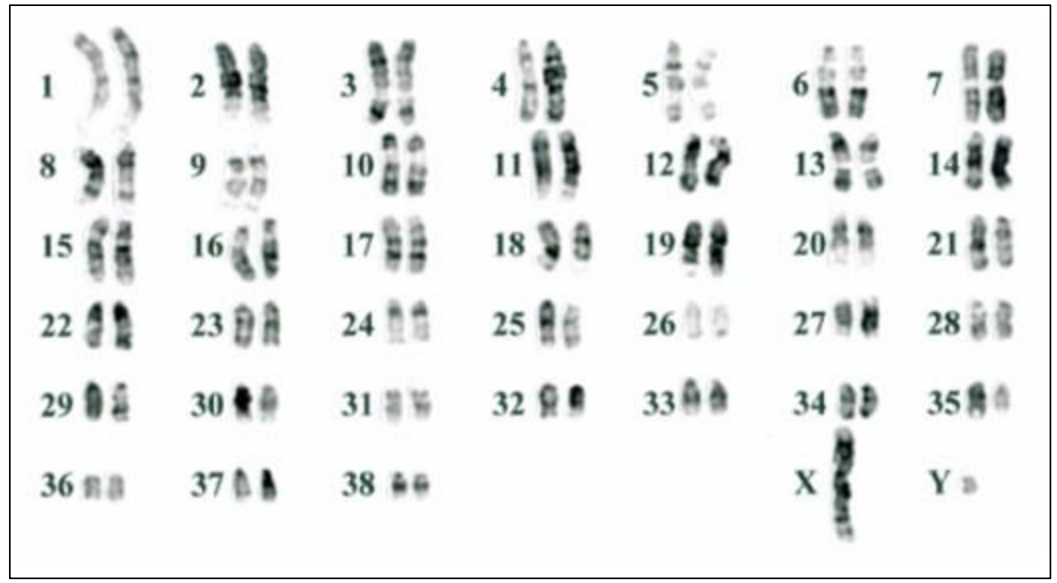
78 chromosomes

[4] The basics of genetics were discovered and published already in 1866 by the Austrian monk Gregor Mendel in his book "*Versuche über Pflanzenhybriden"*. The publication received hardly attention but was "rediscovered" in the beginning of the 20th century and became the basis for modern genetic science. The discovery in 1944 of the components of chromosones (Avery, USA) and in 1956 of the encoding of the hereditary characteristics in the DNA (Deoxyribonucleic acid) by Watson and Crick, were the final breakthrough to modern genetics and its applications.

[5] The human cell contains only 46 chromosomes or 23 pair of chromosomes.

[6] Very often chromosomes are not pictured as a bar but in X-form. This is their temporary shape during mitosis, when they prepare to be devided.

These chromosomes come in pairs, which means that every cell contains 39 pairs of chromosomes.



Each chromosome in a pair is called an autosome (exception : the Y-chromosome or gender-chromosome).[7]

Both autosomes in a pair carry the same (but not necessarily identical) genetic information. For instance : both chromosomes in a pair will carry the genetic information that defines eye color, length of coat, etc … but the content of that information on each chromosome may differ (cfr. infra).

This is the case for 38 of those pairs, only for the 39th pair this is different as one of that pair is the Y-chromosome or the sex-chromosome (all other pairs are XX, this one is XY). It is this Y-chromosome that determines the gender of the pup. Only the male dog carries the XY-pair in its cells and can pass on the Y-chromosome that defines the male gender, the female dog carries only XX-chromosome pairs and can only pass on the X-chromosome.

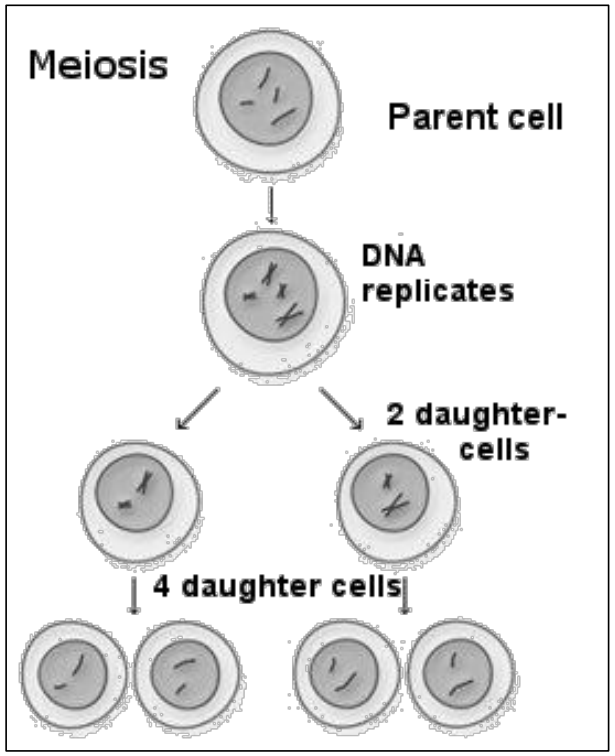
1.2. Sexual reproduction.

Sexual reproduction consists in that the female egg (ovum) and the male sperm cell merge and form a new cell (= zygote). This new cell will then divide itself again and again (through mitosis) and will finally evolve into the body of the pup.

[7] When we say that a gene is autosome recessive or autosome dominant, this means that the gene is located on a X-chromosome and not on the Y-chromosome. Its hereditary nature is therefore not dependant on the gender of the parent-dog.

If the sperm cell and the egg would be normal cells and would each contain 39 pairs of chromosomes, then the new cell (zygote) that is a fusion of both, would not contain 78 chromosomes or 39 pairs, but would contain 156 chromosomes or 78 pairs of chromosomes. This would of course be unthinkable and unwanted.

For that reason, the sexual reproduction is preceded by the "meiosis" (reduction division) that splits a body cell (both of the male and of the female) and at the same time also the chromosomes it contains.



I will not dwell on this complex mechanism but let us summarize it by simply stating that during this (multi-phased) division of the cell, each pair of chromosomes is as it were pulled apart or split into the two separate chromosomes.

This leads to new cells that will each contain half of the normal number of chromosomes, or in other words : after the meiosis we are left with two cells that each contains 39 chromosomes.

We call these new cells "gametes" or germ cells and more commonly the sperm cells of the male animal and the egg cells of the female animal.

The mating of the parent dogs brings the male sperm cell to the female egg cell and allows them to merge.

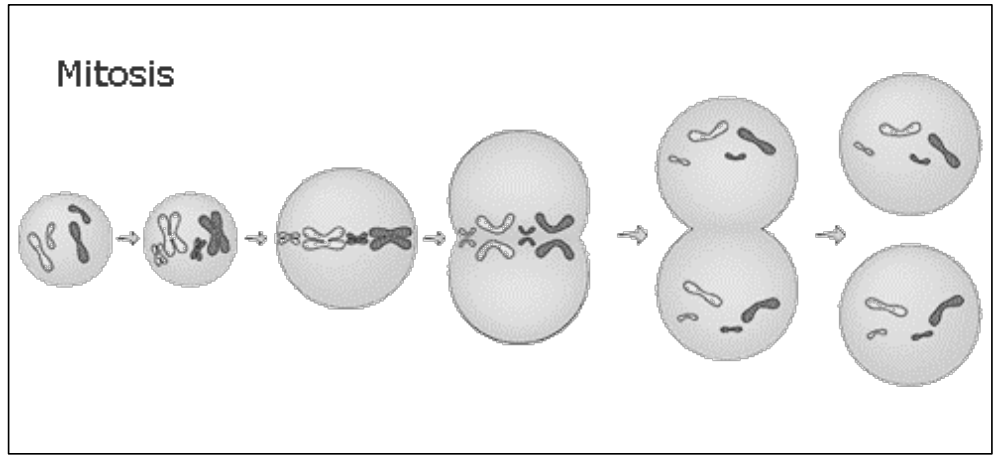
The actual fertilisation consists of the nucleus (core) of the sperm cell entering into the egg cell. Together, they form a new cell (the zygote) that contains all the 39 chromosomes of the sperm cell and all the 39 chromosomes of the egg cell.

In other words, this zygote contains again 78 chromosomes that will form again 39 pairs and it is this new cell that will evolve by mitosis (cell division, this time not splitting the pair of chromosomes but by splitting the chromosomes themselves so the new cell has the same number and identical chromosomes as the mother cell) into the later body of the Rottweiler pup.

Important to remember is that the new cell (zygote) contains again 38 pairs of chromosomes and that each pair contains one chromosome from the male sperm cell and one chromosome from the female egg cell

This immediately explains why the new cell – and later each cell of the new Rottweiler's

body – contains hereditary information that is half derived from the female animal (mother) and for the other half from the male animal (father).



The important question for the breeder is then of course : which of this information will show up in the body of the pup : will it be the hereditary characteristics of the father or the characteristics of the mother ?

This question brings us to Gregor Mendel's laws but before going into detail on those, first some more information about the chromosome is necessary.

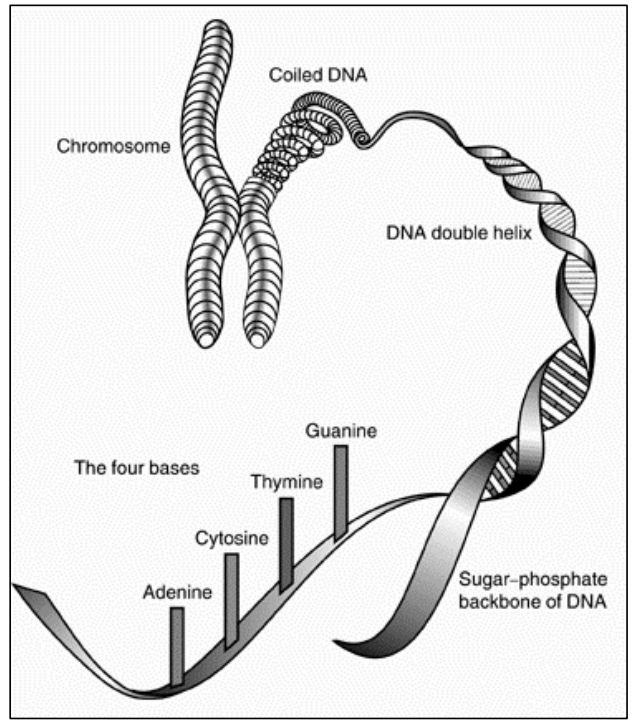
1.3. DNA – genes.

The chromosome consists of a molecule of Deoxyribonucleic acid (DNA) that "twists" around itself like a yarn thread. When we "untwist" it, we see the typical "double propeller structure".

We can imagine the chromosome as a hollow stem that is divided in thousands of segments (loci, cfr. infra) that each houses a gene.

These genes are each responsible for building and defining the characteristics of a specific part of the animal body.

They hold the genetic code for the dog's characteristics and are, simply said, the hereditary



factor that determines how the specific part of the dog's body will develop and will be like. Example : the color of the coat, the color of the eyes, the length of the lower jaw, etc. ... etc. ... etc. ... . [8]

They also define the possible presence of hereditary diseases. [9]

Although there are of course also external influences that determine the development of the body (example : diet, physical exercise, housing, etc. ...), it is the genes that predispose what will be the characteristics of the animal.

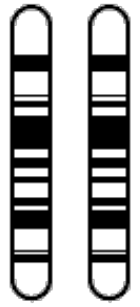
Dogs have approx. 19.000 different genes ! [10]

1.4 Homozygosity - heterozygosity.

Now let us simply imagine a chromosome pair as to be two hollow rods which are each divided into separate boxes (each box is a location or a "locus") in which we find these genes.

On each of the two chromosomes that together form a pair, we find a gene that defines the same characteristic as the corresponding gene on the other chromosome does. For example the length of the coat.

We call those distinct versions of a gene : alleles. They are always located on the same place (locus) on each of both chromosomes of the pair.



Alleles always on the same location : Locus

But while both corresponding genes or alleles define the same characteristic, they do not necessarily carry the same information or in other words they may very well define the same characteristic in a different way !

One of the alleles may for instance be an allele for a dark brown eye, the other allele for a yellow eye.

So remember, all pairs of chromosomes in the zygote (the cell that will develop into the body of the dog), contain a chromosome from the father and one from the mother and while they define the same characteristic (example : the length of the coat) they do not necessarily contain identical information !

The gene on the chromosome from the father may define a short coat while the gene on the chromosome from the mother may carry the information for a long coat.[11]

If both chromosomes carry genes that have identical information for a specific trait, then we speak of homozygosity for that characteristic. If the genes on the other hand carry different information, then we speak of heterozygosity.

Ex.: both chromosomes are carriers of a gene for short coat, then the dog is homozygote for such a coat. If both chromosomes (from the same pair) however carry various information, eg. one gene carries the information for a short coat and the other a long coat, then we say that the dog is heterozygote for this trait.

1.5 Phenotype and genotype.

Now we must introduce two new definitions : phenotype and genotype.

A dog's phenotype is its physical appearance. For example : a dog with a short coat.

The fact that the dog has a short coat, does not necessarily mean that the dog only carries hereditary information that defines such a coat because a dog with a short coat can just as well carry only the gene for a short coat as a gene for a long coat while the latter one

[8] Example : all colors in the canine coat are composed out of only two pigments : eumelanin which is a black pigment and phaeomelanin which is a red pigment, both a form of melanin. White is a lack of pigment. The Rottweiler's colors are black and tan. This particular coloring and its pattern is explained as follows. The B locus in dogs has two possible alleles (although some sources will mention a third allele : the one that defines brindle) : B (which is a dominant gene for black) and b (= a recessive gene for non-black : brown or dark). Dominant black dogs (Kk or KK) are solid eumelanin (they can have white markings but will show no other colors). They cannot show red (tan) in their coat because this black color is dominant and the gene will just not allow any other color to be expressed (the eumelanin can however be modified by other genes to the colors of liver, isabella, blue or even merle). Only dogs who are homozygote "bb" can show other colors in their coat and these dogs will then express whatever genetic information they carry on the A-locus. The Agouti-alleles (the name Agouti is derived from the Agouti = South American rodent with the typical wild markings shown by many mammals) on the A-locus vary between fawn with dark overlay (ay), agouti wolf grey (A+), (the rare) recessive black (As), black and tan (at) and fawn with black mantle (asa). These will (on condition that the B loci hold no dominant B-gene) define which cells will produce black pigment (eumelanin) and which will define the Agouti color. The pattern of the spread of eumelanin, leaving the Agouti spots on the cheeks, muzzle, throat, chest and legs, as well as over both eyes and under the base of the tail, is followed by all genes in the Agouti series.. Conclusion : just like the Dobermann Pinscher, the Rottweiler is a breed that is homozygote "bb" on the K-locus and "atat" on the A-locus.

[9] The dog lover will find many interesting publications, also on the internet, about the canine genome and also about the way growing knowledge of this genome is being used both in veterinarian and human medecines. Cfr. by example : A. R. Boyko, The domestic dog: man's best friend in the genomic era : https://genomebiology.biomedcentral.com/articles/10.1186/gb-2011-12-2-216; M. P. Hoeppner and others, Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts : http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0091172. These articles learn amongst others that the canine genome may even be an ideal model to study disorders that also affect humans through genome wide association. Cfr. the website of the Center for Biotechnology Information, https://www.ncbi.nlm.nih.gov/genome?term=canis%20lupus%20familiaris : "The dog, Canis lupus familiaris, is a useful model organism for medical research due to extensive genetic diversity and morphological variation within the species and to aggressive breeding practices that have resulted in inbred populations of dogs. Many breeds of dog are particularly susceptible to inherited diseases that are also common in humans, such as cancer, heart disease, rheumatoid arthritis, autoimmune disorders, deafness, and heart disease, rheumatoid arthritis, autoimmune disorders, deafness, and blindness."; Elaine A. Ostrander and Robert K. Wayne, The canine genome, http://genome.cshlp.org/content/15/12/1706.full .; Cfr. the website of the University of Sydney, "Online Mendelian Inheritance in Animals" http://omia.angis.org.au/home with mention that of the 969 genetic diseases with Mendelian inheritance that were established in dogs, not less than 400 can be potential models for human diseases.

[10] All the DNA in the chromosomes of one cell is together hardly ± one meter long but even one single DNA-molecule contains enough information to fill an encyclopedia of more than 1000 pages !

[11] I state this here as a simple truth, but it is not and I state it only as an example for easy understanding the basics of how genetics work. In fact, features such as the color and length of the coat are in reality determined by a variety of genetic factors, which is exactly what makes genetics so difficult. For a comprehensive and yet complete discussion on canine coat colours, I refer to Bernard Denis, Judge and Breeder Manual, Coat Colours in Dogs, Diffomédia/Paris.

is not expressed in the dog's appearance.

The genotype is in other words the genetic pattern or information that is carried by the dog's genes, which can not necessarily be seen or understood by just looking at the physical appearance of the dog.

Besides the possibility of an analysis based on a DNA-test, only study and knowledge of the characteristics of the ancestors of the dog, its litter brothers and sisters and their offspring will lead to knowledge on these genetic characteristics.

1.6. Dominant traits – recessive traits.

We have seen that the fusion of the male and female gametes creates a new cell (the zygote) which again contains 78 chromosomes, consisting of 39 pairs.

When the genes on both chromosomes (one chromosome comes from the female egg and the other from the male sperm cell) carry the information for a short coat (homozygous) than this short coat will necessarily occur in the dog's phenotype : the dog's cells simply do not contain any other genetic information that could be expressed.

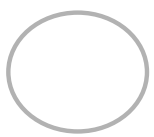
It is different when the genes contain different information (example : the one gene is responsible for a short coat and the other for the long coat) for of course only one of the two characteristics can be expressed. The dog cannot, after all, be long and short coated at the same time.

Nature's solution is that the phenotype reflects only the dominant feature. Even if the dog is a carrier of the recessive feature in its genotype, this will not show in his appearance or phenotype if he carries both the dominant and the recessive gene.

If we accept that the gene for short hair is dominant over the gene for long coat, we say that the short coat is a dominant trait, the long coat a recessive trait.

Study (and experience) learns which traits are dominant or recessive.[12]

All this theory can be explained with a few simple drawings.



cell

Chromosome for a short coat.

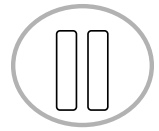
Chromosome for a long coat.

[12] Again, we simplify things by assuming that each characteristic is defined by only one single gene. In reality this is not correct as some traits are defined by multiple genes at the same time, other traits will only appear in case some other genes are absent, or vice versa the presence of some genes will prohibit factors appearing in the phenotype, … In exceptional cases both genes will even be just as dominant as the other one or about just as dominant, … . As I said, genetic science is complex … .

To keep it simple, we picture only one pair of chromosomes but we should not forget that each cell contains 39 pairs.

If a dog is a homozygote for a short or long coat, then both chromosomes in the nucleus carry the same information :

homozygote for short coat

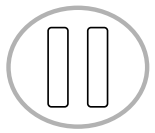


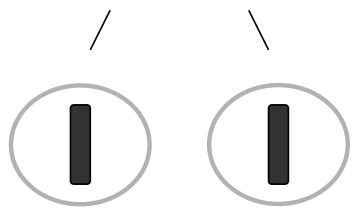
homozygote for long coat.

The one dog will have a short coat, the other one a long coat. This is easy to understand : if the dog is homozygote for a short or a long coat, his cells just do not contain any other information so it is impossible that other information would appear in its phenotype.

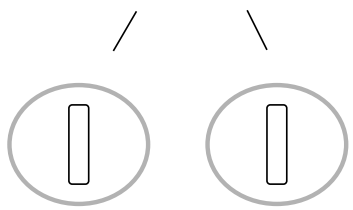
During the meiosis that leads to the creation of the male sperm cell and the female egg cell, the 39 pairs of chromosomes are split and divided over two new cells (gametes) that will each contain 39 chromosomes and no longer 78 chromosomes.

Mother cell



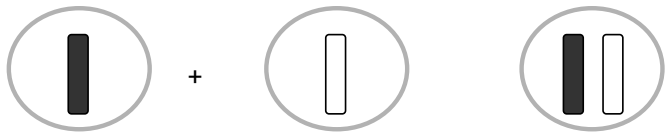


Gametes



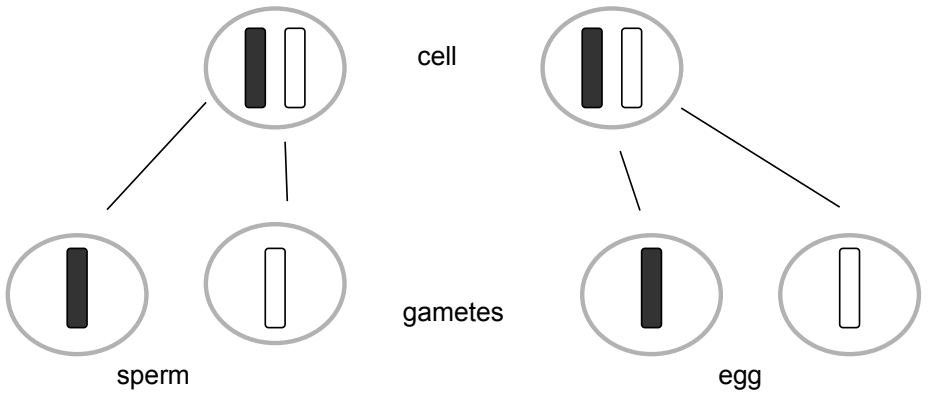
The nucleus of the cell (zygote) that is created because of the fusion of the male sperm cell and the female egg cell, will again contain 78 chromosomes that will form 39 pairs. And as said before, each of those pairs contains a chromosome from the sperm cell and one from the egg cell.

Let us now imagine that the male dog was a homozygote for a short coat and the female dog a homozygote for a long coat. (cfr. drawing). In that case, the zygote cell (and the all the pup's body cells that will develop from that one cell), will contain contradictory information : a chromosome that defines a short coat and a chromosome that defines a long coat.

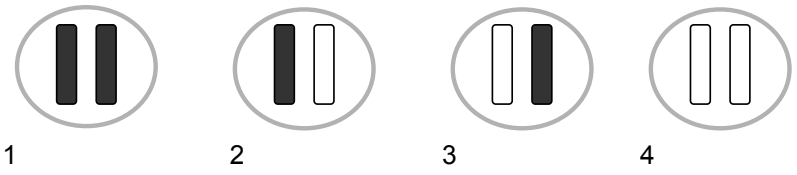


The puppy will in its genotype be a heterozygote for the length of its coat but in his phenotype (outer appearance) he will show a short coat because this is a dominant trait while the gene for the long coat is recessive.

If we now imagine that both parent dogs were heterozygotes for the length of the coat, then we have the following picture :



The fusion of these cells can give us different combinations :



1. homozygote for short coat. The dog will show a short coat. He carries no other information.
2. heterozygote for short and long coat. The dog will show a short coat as this gene is dominant while the gene for a long coat is recessive.
3. heterozygote for short and long coat. The dog will show a short coat as this gene is dominant while the gene for a long coat is recessive.
4. homozygote dog for long coat. The dog will show a long coat as he carries no other information.

A theoretical conclusion that will not be reality in each litter but is a probability that will be proven by statistics over a large number of litters, is that the recessive factor will show in

the phenotype of ¼ of the pups and the dominant factor in ¾ of the pups. [13]

	Short	long
Short	S+S	S+l
long	S+l	l+l

In other words : ¾ will have a short coat, only 1/4 will have a long coat but 2 more will carry the recessive gene for long coat.

Another example would be that one of the parents would be a homozygote for short coat and the other a heterozygote for short and long coat.

The table shows that each pup will have a short coat, even though half of them will be heterozygotes. After all, in this hypothesis each pup will carry the dominant gene for a short coat.

	Short	Short
Short	SS	SS
long	Sl	Sl

It is immediately clear that is much easier to breed for recessive traits than for dominant traits because if a dog shows a recessive trait in his appearance, then it is certain that the dog is a homozygote for that recessive characteristic. Otherwise, he could not show it in his phenotype. Breeding this dog with another dog that shows the expression of the same recessive characteristic in his phenotype will then guarantee that all their offspring will show the same characteristics as neither of the parents carry other genetic information.

By example, the dog with a long coat, which is a recessive factor, can only carry the genetic information for long coat because otherwise this trait could never appear in his phenotype. Breeding two dogs with a long coat (which is of course unthinkable for the Rottweiler as a long coat is an eliminating fault and such a dog cannot be declared breed suitable) can therefore only lead to long coated offspring.

On the other hand, when we breed two short coated dogs, the possibility exists that the litter will show both short coated and long coated pups. After all, a short coated dog can

[13] These percentages are only statistic probabilities, no certainties to be expected in an individual litter. Cfr. infra.

be a homozygote but can also be a heterozygote or in other words carry both the gene for the long and for the short coat.

Easy ? No, some traits are inherited in an intermediary fashion, meaning not by the simple rule that if one gene is dominant and the other recessive that the dominant gene will then define the phenotype but meaning that the offspring will develop a mixed form of both characteristics (example : half pending ears). Besides this, there is the phenomenon of the so called non-Mendelian inheritance : in case of epistasis and hypostasis, an interaction occurs between dominant genes that are located in different loci. The two dominant genes that both affect the same part or biochemical process in an organism, influence each other and some of the dominant genes cover up other dominant genes. In the case of epistasis, the dominant trait prohibits other dominant genes to be expressed, in the case of hypostasis a dominant gene is supressed by the presence of certain other genes. Cryptomere are dominant genes that remain unexpressed when certain other genes are absent but are expressed when other dominant genes are simultaneously present. Still others traits are the result of “crossing over” which means that during the meiosis, part of a chromosome breaks off and is exchanged with the corresponding part of the other chromosome. This leads to the creation of a “new” chromosome with different characteristics than those of the original chromosome. This “crossing-over” may for example explain a dog having two different eye-colors. The problem is that this “new chromosome” will be inherited by the offspring of the dog, which is unwanted. Still another exception is polygenic inheritance, the phenomenon that a certain characteristic is not defined by one gene but by multiple genes.

To make it even worse, genes can have a complete or incomplete or reduced penetrance.

Penetrance in genetics is the proportion of individuals that carry a particular allele and will actually express that trait in their phenotype.

Some dominant traits will have a penetrance of 100 %, others will have a reduced penetrance. For example, if a gene that is responsible for a particular autosomal dominant disorder has a penetrance of 80 %, then this means that 80 % of the dogs who are carriers of the dominant gene will develop the disease and 20 % will not.

If an allele is highly penetrant, then the trait it produces will almost always be apparent in the offspring that carries the allele. An allele with a low penetrance will only occasionally produce the trait with which it is associated. In cases of low penetrance, which can make it difficult to distinguish environmental from genetic factors.

So again, easy ? No ! Let us therefore safely stick to basics in this brochure.

1.7. G. Mendel’s principles of heredity.

To make the discussion of these rules somewhat easier :

- we call the parent-dogs the P-generation (parentis = parents) and the first generation of descendants the F1 generation, followed by the F2 generation, the F3 generation, etc. …

- we won’t use drawings but letters. For the dominant short coat we will use the capital letter “B” and for the recessive long coat the small symbol “b”. As all chromosomes appear in pairs, we will call the homozygote for the short coat “BB”, the heterozygote will be named “Bb” or “bB” and the homozygote for the long coat will be called “bb”.

In the following calculations, we will assume that we only cross the descendants (= inbreeding, cfr. further in this brochure) because this makes it easier to understand and to define the patterns (in these examples we have knowledge of the ancestors’ genotypes which would not be the case if we bring other dogs into these calculations).

1.7.1. The first rule of Mendel : uniformity.

When we cross two dogs who are homozygote for a specific trait but who differ in that specific characteristic, then all descendants in the F1 generation will have the same appearance (phenotype) for that specific trait.

This shows consistency with the concept of genetic dominance that we saw before.

The pups of the F1 generation will all show the same characteristic of one of the parents : in our example all pups will be short coated and none will be long coated, although all pups also carry the gene for the long coat.

Cfr. the example above of two homozygotes with differing genes for the length of the coat.

BB + bb will in the F1 generation always give the combination Bb

	b	b
B	Bb	Bb
B	Bb	Bb

As the gene for the short coat (B) is dominant over the gene for the long coat (b), the phenotype of the pup will in each combination show the short coat.

For most characteristics, it makes no difference if the dominant gene derives from the male or the female parent. They are called autosomes.

Still, some genetic traits are gender related ! The X-chromosome carries many genes while the Y-chromosome that determines the gender and is only carried and transferred by the male, hardly carries any other genes than the one that defines the gender.

This implies that some characteristics that are found on the X-chromosome and not on the Y-chromosome that is part of the pair, are only transferred by the female with the X-chromosome.

They will appear in the phenotype of the male pup even if the gene is recessive (XY) and are gender-related : the Y-chromosome from the male has no information to counter it.

An example is that both the A and B forms of haemophilia are X-linked recessive traits, which causes males to bleed excessively while females may carry the trait and pass it on but will not develop the disease.

Imagine the female carrier to be XHXh and we breed her to a normal male who is XHY (notice that the Y-chromosome is “empty” or better : does not carry the gene).

The dominant gene is H, the recessive gene is h. The bitch is a carrier, the male carries the dominant H gene on this X-chromosome, none on his Y-chromosome.

The Punnet–square is then as follows :

	XH	Xh
XH	XHXH	XHXh
Y	XHY	XhY

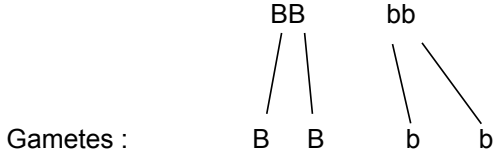
Conclusion : 50 % are male puppies (XY), 50 % are female (XX). The pups (75 %) that carry the dominant gene “H” will not suffer the disease. However, 25 % carries the recessive gene “h” on the X-chromosome and as the Y chromosome does not carry the dominant gene to dominate or neutralise it, the single recessive gene (passed on by the female on the X-chromosome) will make the male pup a “bleeder” … .

1.7.2. The second rule of Mendel : the principle of segregation.

Until now, we only discussed the F1 generation. What happens if we cross the F1 generation with itself ?

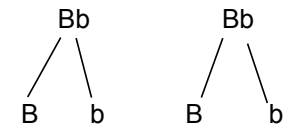
The rule of Mendel can be summarized by stating that inbreeding the F1 generation will lead to a F2 generation of which 75 % will show the characteristic of one of the grandparents and 25 % the characteristic of the other grandparent.

Let’s go back to an example and use the example of the mutated gene that defines (Progressive Retinal Atrophy), being a recessive gene that may lead to blindness (cfr. infra). The healthy gene is dominant B, the mutation is recessive b.



In the F1-generation each pup will carry the genes Bb (cfr. ut supra)

The dogs in this generation will then form the following gametes :



F2 In this generation we will have the following combinations :

	B	b
B	BB	Bb
b	Bb	bb

This means that (statistically) 1 out of 4 descendants (25 %) will be homozygote for the healthy gene, two will be heterozygotes and will be carriers of both the healthy and of the mutated gene and one will be homozygote for the defective gene and will develop the disease.

Because of the dominance of the healthy gene, 3 out of 4 pups (75 %) of the pups will not be sick but 1 out of 4 (25 %) will develop the disease as he will be homozygote for that recessive trait and will not carry the dominant gene for the healthy gene.

Mendel’s rule is therefore correct : in the F2 generation 75 % shows the characteristic of one of the grandparents (healthy dogs) and only 25 % will show the trait of the other grandparent (the one that developed the disease).

Please understand that this is only a very simple example. It would for instance be totally different if we would discuss the inheritance of colors in which multiple other factors, intermediary and even factors of imperfect dominance play a part.[14]

Important to be aware of is that should we have a litter out of two perfectly healthy dogs and experience that one or more pups develop a disease caused by an autosome recessive gene, then this not only proves that both parents are necessarily carriers but also that (according to probability) 50 % of the littermates may be carriers that can pass the mutation on to their progeny … a fact that we may not ignore !

Cfr. infra : the need to test and to publish results. The fact that a dog is healthy, is not a proof that he is not a carrier of a defective gene.

[14] Bernard Denis, oc

1.7.3. The third rule of Mendel : the rule of independent assortment.

Until now, we only discussed parents that differ in only one characteristic but what happens if we cross parents who are homozygotes but differ in two or more characteristics (poly-hybrid crossing).

Take the example of the short coated black dog that is bred to a yellow long coated dog. We will call black and yellow H and h, short and long B and b. Let us assume that both the genes for short and black hair are dominant.

Mendel's third rule is then that genes that are located on different places on the chromosomes, will still be inherited independently of each other or in other words : both characteristics for which the parent dogs differ, will be inherited independently.

The schema is then as follows :

P	BBHH	+	bbhh
Gametes	BH - BH	+	bh bh
F1 - generation		BbHh	

All these pups will be black and short coated. The genotype also carries the gene for yellow and long coat but these are recessive genes and are not expressed.

The F2 generation is born by inbreeding the F1 generation and as we learned, this results in 75% short coats and 25 % long coated pups, also 75% black and 25 % yellow coated.

The formula of Mendel is then :

¾ black x ¾ short = 9/16 black short coated
¾ black x ¼ long = 3/16 black long coated
¼ yellow x ¾ short = 3/16 yellow short coated
¼ yellow x ¼ long = 1/16 yellow long coated

So in the phenotype (just draw the table yourself), we will have 9/16 pups who will carry both dominant traits (and show them), 3/16 + 3/16 will possess both a dominant and a recessive gene of which only the dominant will show in the phenotype and only 1/16 will show both recessive traits and will show them in the phenotype.[15]

[15] There are exceptions to Mendel's rules. For instance, the principle of independent assortment doesn't always apply if the genes are located close together or are linked on a chromosome because in that case the genes are often inherited together ! Also it has been discovered that alleles do not always interact in the same dominant/recessive way and this especially if they are co-dominant of show a different expressivity or penetrance.

	BH	Bh	bH	bh
BH	BB HH	BB Hh	Bb HH	Bb Hh
Bh	BB hH	BB hh	Bb hH	Bb hh
bH	bB HH	bB Hh	bb HH	bb Hh
bh	bB hH	bB hh	bb hH	bb hh

We can apply this formula over and over again, also if we bring in other characteristics like eye color, shape of the ears, etc. ... but of course only if we know which of those characteristics are dominant or recessive … .

We will not go further into the exceptions on these principles as this would lead us far beyond the purpose of this brochure. There are many specialized publications on the subject for those that are interested.

I also want to emphasize that the above mentioned calculations are only theoretical. In reality we will not have 16 pups in a litter and even if we did, the above mentioned ratios would not always be true. Coincidence will always be part of breeding and these ratios are theoretical probabilities. Also, we will of course not always use inbreeding or linebreeding as a breeding policy.

A thorough knowledge of the hereditary characteristics of the parents (and of littermates and ancestors), is an absolute necessity to decrease the factor of chance and to breed with truly smart decisions.

Luckily, and then especially concerning hereditary diseases, science offers a great help because of the development of DNA-tests that allow us to identify the presence of mutated genes that cause diseases.

Knowledge of the dominant or recessive nature of those genes, combined with basic knowledge on how genetics work and how to deal with dominant and recessive genetic characteristics in breeding policies, may and even must help not just to breed the "better dog" but most especially to breed the healthier dog !

II. GENETIC DISEASES

Of course I cannot even attempt to discuss all genetic diseases that have been traced in the Rottweiler's genepool (cfr. the text box). This would by far both exceed my knowledge and the intention of this brochure but it is an option for the IFR Meeting of Breed Wardens and Delegates to ask a scientific report on this and the state of affairs in existing researches. [16]

[16] Genetic diseases that have been established in the Rottweiler's genepool : Aortic Stenosis (Sub-), Cataract, Chronic sesamoiditis, Congenital deafness, Congestive/ dilatative cardiomyopathy, Demodicosis, Dilated cardiomyopathy (DCM),

Moreover, the Rottweiler's genetic affection by certain diseases may even differ from country to country. This will especially be the case for countries or continents that have a closed genepool or had a more or less closed genepool for a long time, by example because of travel distances and/or quarantine rules, as this limited the possibility to exchange breeding dogs and to enlarge the genetic diversity.

This will explain why the prevalence of some genetic affections is more important in some countries than in others and this again why also the public awareness of certain diseases and of the need for testing, may differ.

Still, the following diseases undoubtedly demand attention.

2. Some genetic diseases that have entered the Rottweiler's genepool.

2.1. Hip dysplasia (HD)

I will not venture giving a detailed scientific definition of the disease but refer to the many publications that exist. [17]

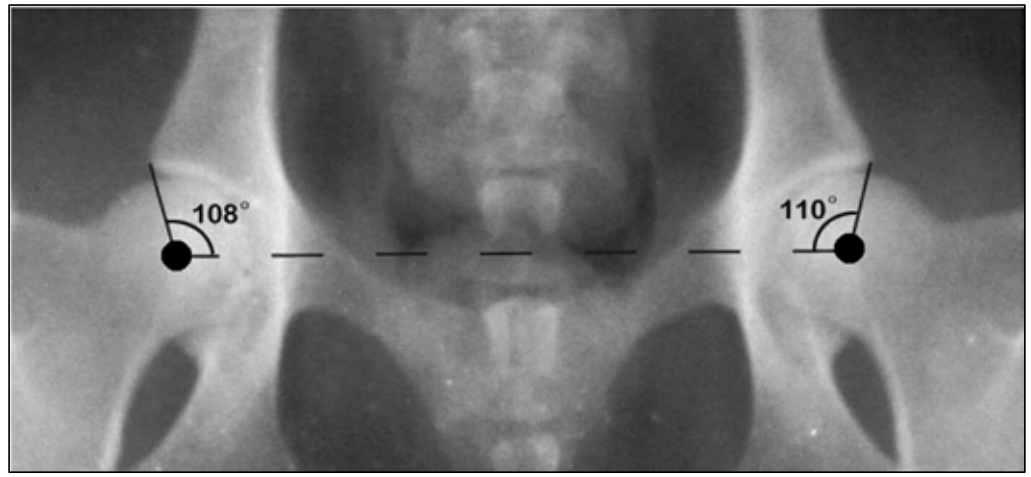
It is a genetic predisposition which increases the probability of the dog developing arthrosis and being disabled. The femoral head does not fit deep enough into the acetabulum (socket) due to laxity of the ligaments and hip capsule, resulting in a joint that does not function smoothly but rubs and wears out.

The symptoms depend on the duration of the disease and the degree of the laxity of the joint and its inflammation. The longer the disease exists, the worse the symptoms become : at an early stage there is a laxity of the joint, at a later stage the joint degenerates and develops osteoarthritis. The dog cannot function fully anymore and suffers severe pain. This leads to a strongly decreased activity, difficulty in moving, hind-limb lameness, …

The diagnose is made by X-Ray photos. The technique used for this is probably standard worldwide : the dog is sedated (or at least should be sedated …) to guarantee relaxation of the muscles. Then the dog is positioned in dorsal recumbence with the hind limbs extended caudally and the femora parallel to the spine, to the table top and to each other. The patellae are centred over the femoral shafts.

Duchenne muscular dystrofy (DMD), Elbow dysplasia, Entropion – Ectropion, Epilepsy, Follicular parakeratosis, Hemofilia B, Hip dysplasia, Histiocytoma (canine cutaneous histiocytoma), Hyperadrenocorticism, Hypertrofic osteodystrofphy, Hypoadrenocorticism, JLPP – Juvenile Laryngeal Paralysis, Leonberger Polyneuropathy, Leukoencephalomyelopathy, Lymphedema, Masticatory myositis, Mitral Valve Insufficiency, Mucopolysaccharidosis, Narcolepsiy, Neuroaxonal dystrophy, Osteochondritiis dissecans (OCD), Osteosarcoma, Patella Luxation, Progressive retina atrofia, Retina Dysplasia, Uveodermatologic syndrome, Vitiligo, Von Willebrands disease, Wobbler syndrome, X-chromosome related muscle dystrophy.,

[17] For a very comprehensible booklet : Frank Comhaire, Understanding canine hip dysplasia, Lambert Academic Publishing,



Here already, the standardization stops as there are several methods to appreciate the photos and to grade the quality of the hip joint (Norberg angle, PennHip, …).[18]

In fact the three most important organisations on the matter use different modes to grade the quality of the hip joint : FCI (Fédération Cynologique Internationale), the OFA (Orthopedic Foundation for Animals), and the BVA/KC (British Veterinary Association/The Kennel Club). [19]

We know that hip dysplasia is a polygenic multifactorial disease, this means that it is caused by a combination of a genetic predisposition (defined by multiple genes) and of external influences such as nutrition, overweight, quality of housing and care, stress, physical strain, environmental conditions, trauma or accidents, … .

Those external factors can more or less easily be managed and by doing this, we can prevent the genetic predisposition to emerge in the phenotype or if it does, to limit its degree and its consequences.

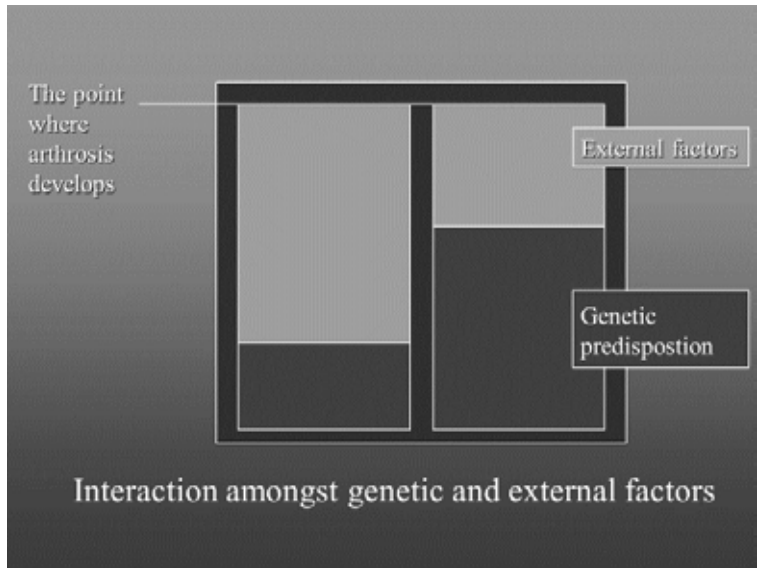
This helps, but does not take away HD as a genetic disease. The known but not yet identified factor is indeed the genetic factor.[20] The hip joint and its function is not defined

[18] Prof. F. Comhaire, Understanding canine hip dysplasia, o.c. The author goes into detail on all different methods and advises the use of the Noberg angle, not using the same uniform values for all breeds but to establish the angle in a representative sample of dogs of the breed and calculate a curve of cumulative frequency distribution so it becomes possible to extrapolate where the angle of an individual dog is situated in relation to that of its breed peers (expressed as a percentile value). This must allow a more relevant and precise percentile ranking of individual dogs. The selection of breeding dogs should take into account the percentile ranking of both parent dogs in order to reduce the prevalence of canine hip dysplasia. Commonly it is accepted that the threshold is a NA of >105°. This might thus be adapted in function of the breed.

[19] Mark Flückiger Prof. Dr.med.vet., Scoring radiographs for canine Hip Dysplasia - The big three organisations in the world, cfr. the website of the committee for dysplasia of Bern and Zurich (Switzerland) for this article that compares the methods that these organizations use : http://www.dysplasie-schweiz.unibe.ch/unibe/portal/fak_vetmedizin/micro_dysplasie/content/e332465/e406506/e406508/Scoring_radiographs.pdf

[20] Cfr. Prof. F. Comhaire, Inbreeding and Hipdysplasia, (http://www.profidog.cz/en/frank-comhaire-pribuzenska-plemenitba-dysplazie-kycelniho-kloubu-dkk/)

by one single gene but by many.



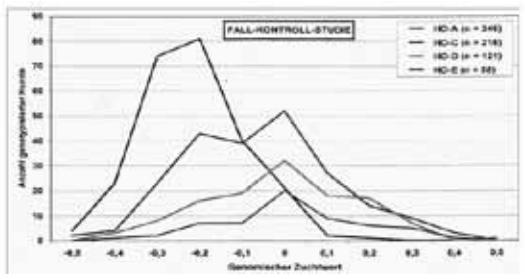
Scientists are doing research for all parts that are directly or indirectly involved in the development of the disease, their (cor)relation with diagnosed HD-affections and for the markers of the genes that are possibly related to those factors and which may allow to identify and locate those genes.

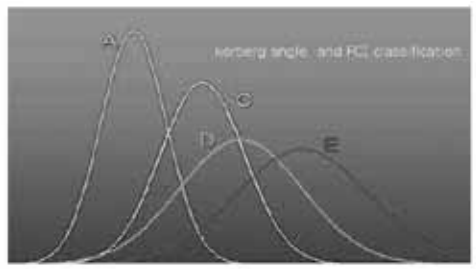
Still, expectations are that it will take many more generations before the prevalence of HD will be sufficiently low to be considered no longer a real threat that is inherent for the breed.

Still, it is not a dream and scientific researches offer hope. In his book "Understanding canine hip dysplasia", Prof. F. Comhaire refers to the work of O. Distl who has identified 17 relevant genetic markers that are involved in the heredity of HD in the German Shepherd and who, based on the relative importance of each of those markers, calculated a genomic breed value. The lower the value, the more it is related to dogs that are free of HD (HD A), the higher the more the dogs are affected with HD (HD C – D). [21]

The Rottweiler should not stay behind in these research programs and we should take

[21] Very interesting is the subsequent study of Prof. Comhaire who, comparing the curves of frequency distribution of the genomic breed value with that of the Norberg angele, both related to the FCI's hip classification, established a striking similarity between both curves. The higher Norberg angles correspond with lower genomic breed values and vice versa. This suggests that the genomic breed value may come to expression in the Norberg angle and inversely, the Norberg angle may possibly be used as an estimate of the genomic breed value. Cfr. Prof. F. Comhaire, Understanding canine hip dysplasia, o.c.





initiatives, especially as we cannot rely on the assumption that studies that concern other breeds will lead to conclusions that will be usable for the Rottweiler too.

Important obstacles for such research programs are indeed all too often an unacceptable lack of information about prevalence and of research materials. A closer cooperation with breed clubs (or the IFR) to make such information available (numerical data, DNA-material of dogs who were diagnosed to be affected or free, data on ancestors, etc. …) might mean a lot for these research programs and for ourselves !

I hear for instance from Prof. Peelman, professor at the veterinary faculty of the university of Gent (Belgium) that he is prepared to discuss such cooperation and he refers to an already successful identification of several causative mutations in other breeds (Malinois and Labrador Retriever) and pending researches about hip- and elbow dysplasia in the Labrador Retriever and Golden Retriever, epilepsy in the Drentse Patrijshond and myokimia/ataxie in the Jack Russell Terrier.

As I said : we cannot stay behind in this … and if we do … we have only ourselves to blame.

Finally, I dare say that the fact that we test our dogs prior to breeding by making an individual diagnosis of the individual dog's affection with HD, is a good thing, even undoubtedly necessary … but only partly efficient. It brings no guarantees, especially if the dog is diagnosed to be HD-free !

As HD is a multifactorial affection, it may very well be that the dog did not develop the disease (or not yet or only in a mild degree) because of the absence of external factors / catalysts but that he is definitely a carrier of all the genetic genes that can cause the disease and can pass those on to his offspring. A "clear" dog is diagnosed to be clear on basis of the photo of his hip joint on the day but it is not diagnosed on his genetic predisposition !

The other way around, the dog that was diagnosed as to be mildly affected, may in theory be so because of external influences (for example an accidental trauma) but may have a genetic predisposition that is less serious than the dog that was diagnosed to be clear.

Such a diagnosis by X-Rays is therefore a great and absolutely necessary help but offers no full guarantee.

For that reason it is necessary, at least opportune, to calculate breed values for HD for each breeding dog, based on the degree of affection of his ancestors, littermates and his (and their) descendants. Such a breed value is then of course to be updated continuously as more information is received and its calculation, management and publication demands continuous human and financial efforts.

Again, this is not new (cfr. the FCI's International Breeding Strategies[22]) but hardly

[22] "Breeding values based on screening results should when possible be computerised to facilitate selection of the breeding stock not only on the phenotypic appearance but also by indicated genotype. **As a general rule the estimated breeding value for a combination should be better than the average for the breed."**

practiced in the canine world (contrary to for instance in breeding programs for horses).[23]

We do see and read an awareness of ever more clubs for EBV as an instrument and it was to be one of the topics (that is : the method to establish and use EBV) of the scientific event of which I sketched the outlines at the Meeting of Delegates in 2015. This issue will now be part of the agenda of the next IFR-Meeting of Breed Wardens.

Another issue is of course the fact that many if not most breeders will not send the X-Ray photos to the assessment committee when the photos are not promising for a good grading. This is short-sighted and on the long term irresponsible : instead of hiding the affection, this information should be made available and so should at the same time a DNA-sample and the dog's pedigree. Only this can lead to successful research and a further decrease of the affection. Again, a reason for education and for creating awareness that the breeder has the future of the Rottweiler in his own hands … . In the Netherlands sending in the photo's for grading is mandatory. An idea that we might all take up with our Kennelclubs and our national orders of veterinarians ?

A questionnaire was recently sent to all IFR-Memberclubs to collect information on the way they and their Kennelclubs deal with HD-affected dogs, how they collect and make information available, if research-programs are going on in their country, if breeding values on HD exist in their country for the Rottweiler, etc. … all this to consider, maybe in cooperation with other breed associations, if an active participation to those programs is feasible.

2.2. Elbow dysplasia (ED):

This is a generic term which covers different problems in the joint, namely OCD of the elbow, a loose fragment or incongruity (= a not correct fit) of the joint. This may occur by itself, but often it involves a combination of different problems. An affected dog will typically limp on its front legs and suffers pain in the elbows. A diagnosis is obtained with the aid of an X-ray.

The disease is multifactorial, which means that there is both a genetic factor as environmental factors (trauma, nutrition, exercise) are involved.

Cfr. ut supra concerning HD.

2.3. Juvenile Laryngeal Paralysis.

The disease is an autosome recessive genetic disease with a progressive nature that affects the nervous system.

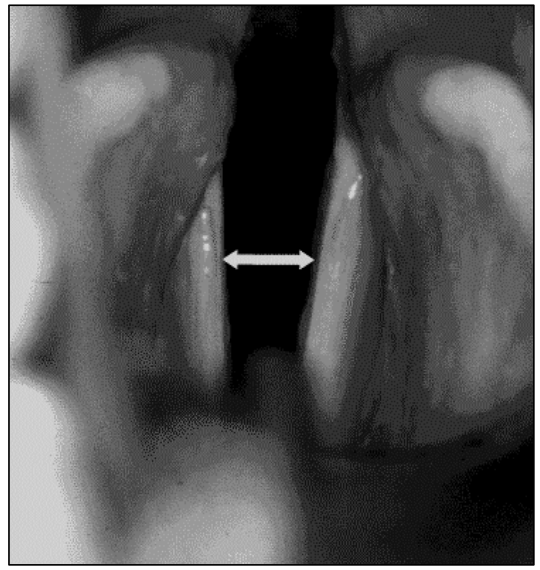
[23] Again in Flanders and based on the obligation for prior testing certain canine breeds (incl. the Rottweiler) on their affection with particular genetic diseases, the government undertook to give financial support to the recognized breeding committees to help them set up a (obligatory) system to calculate breed values. In 2016, a first sum of 30.000 euro was included in the Government's budget and assigned to be used to calculate breed values on hip dysplasia. This will not be sufficient but then again, Rome was not built in one day … .

Our muscles function because of the signals they receive from our brain and that are sent through our nerves.

The larynx also functions because of such signals. When the dog breathes in (expanding the chest), muscles in the larynx contract and pull the vocal cords aside, opening the windpipe and so allowing the air to flow freely into the lungs. The same nerve sends the signals needed to close the larynx again when the dog swallows (so the windpipe is closed and food or saliva cannot enter the lungs and this prevents the dog to choke on it).

However, if a nerve does not function correctly, the muscles do not receive the signals and they become weak or even paralyzed.

The longest nerves usually seem to be the ones that are affected the first and as the nerve that connects the brain with the larynx is one of the longest nerves in the canine body, laryngeal paralysis is often the first symptom of such affection of the nerve system.



The vocal cords are not pulled open when the dog breaths, they vibrate noisily and as they are not fully opened they obstruct the free flow of air into the lungs. As on the other hand they are not fully closed either, the dog may choke on food or water, which can result in pneumonia.

The next longest nerves in the canine body, so besides the one that connects to the larynx, are those that connect the brain with the back legs and these are affected next. The affected dog is struggling getting up and wobbles as he walks. Eventually the front legs will also be affected.

The symptoms do not occur until after weaning age (± 11- 13 weeks), which is why the disease is called juvenile laryngeal paralysis/polyneuropathy or JLPP for short. [24]

We know that JLPP is caused by a recessive gene, which is identified and located.

Its presence or absence can be established by a simple DNA-test which makes JLPP a genetic affection that is "easy" to fight.

Cfr. ut supra where the mechanism was explained of how recessive genes are inherited and under what conditions they can or cannot be expressed in the phenotype (= develop

[24] This explanation of the disease is based on the information found on the website of the University of Missouri-Columbia, College of Veterinary Medicine : http://www.caninegeneticdiseases.net/JLPP

the disease).

Suffering dogs – these dogs carry only the defective gene, otherwise they could not develop the disease - may of course not be bred and they will moreover most probably not reach the age of breed suitability anyway.

The combination of clear dogs (= dogs that are not carriers of the defective gene) offers of course no problem. As these dogs do not carry the defective gene, they cannot pass it on to their offspring and all pups will be clear.

The combination of carriers (heterozygotes) is on the other hand to be very strongly discouraged or even better : this should be forbidden !

The table of Punnet indeed shows that breeding two carriers (Bb) leads to a probability of ending up with 25 % suffering dogs, 50 % carriers who will pass the defective gene on to their offspring and only 25 % clear dogs.

	B	b
B	BB	Bb
b	Bb	bb

Any combination that will knowingly lead to suffering dogs and at the same time to a probability that 50 % of the offspring will again be carriers, must be strongly discouraged and if possible forbidden.[25]

What about the combination of a heterozygote carrier x a homozygote clear dog ?

This combination is to be allowed as it will indeed not lead to suffering dogs but to a probability of 50 % clear dogs and 50 % carriers.[26] Still, we must be aware that 50 % will still be carriers … meaning that this combination should indeed be allowed but used wisely : in case the carrier shows valuable characteristics that are important for the breed.

[25] Again cfr. the FCI International Breeding Strategies : "If close relatives of a dog suffering from an inherited disease or functional disability are used for breeding, they should only be mated to dogs from bloodlines with low or no occurrence of the same disease or disabilities. **If a DNA-test for the disease/functional disability is available, the breeding stock should be tested in order to avoid mating of two carriers**. Mating combinations which from available information increase the risk of serious diseases or functional disabilities or impairment in the progeny, should be avoided."

[26] I underline again that we speak of probabilities and that these percentages may not be understood as numbers that will be expressed in every litter. For example : if the male is a carrier, his gametes or sperm cells each carries only one of the original pair of chromosomes. Some sperm cells (50 %) will carry the chromosome with the healthy gene, the others the chromosome with the defective gene. During the mating, millions of sperm cells "swim" towards the multiple ripened egg cells and it is unsure which sperm cells will reach them and merge with them. The lucky breeder may end up with only clear puppies, the unlucky breeder may end up with only carriers, others with a 'mixed' litter. The same is the case if the father is clear and the mother is a carrier. Her body ripens multiple egg-cells, some with the healthy and others with the defective gene. The lucky breeder's bitch will ripen clear egg cells or will have only the clear ones seminated, the unlucky breeder's bitch will only ripen carrying egg cells or will see only those seminated, … . These percentages are only probabilities, no certainties in an individual litter.

Cfr. also the FCI International Breeding Strategies [27].

Does this mean that it is thus possible to completely remove the recessive gene from the breed ? Probably not. Cfr. the since very long existing care not to breed with long coated dogs and thus the effort to remove the recessive gene for the long-coat, while now and then the trait still occurs, meaning that both parents are carriers.

Still, by crossing only homozygote clear dogs we take away the genetic stamp of the mutation and if (if deemed opportune) heterozygote carriers are crossed with homozygote clear dogs, the prevalence of the defective recessive gene may be halved in every generation !

In our example, we find in the first generation : 2 BB and 2 Bb, thus 50 % free dogs and 50 % carriers. In the second generation, we will have a probability of 6 x BB (clear) and 2 x Bb (carrier). This means a probability of only 2/8 = 25 % heterozygote carriers, 75 % clear dogs and no suffering dogs !

If this is done consistently, the presence of the defective recessive gene may in the long-term lose its threatening nature for the breed.

However, we must even then still warn for the important genetic impact that "matador-dogs" may have if they are a carrier, even if they are only bred to homozygote non carriers.

Cfr. ut supra where we showed that the hidden genetic stamp of a litter out of clear x carrier is just as important as when we cross carrier x carrier : probability demands that 50 % of the progeny will be carriers, only there will now be no suffering dogs.

Still, a proportional important influence by individual dogs may at the very least slow down the process of reducing the number of carriers, especially in a too closed genepool that has only a limited number of breeding dogs and only a small genetic diversity.

Measures to limit the number of breedings that are allowed per dog may therefore still have to be considered in combination with the aforementioned breed advice.[28]

Cfr. ut supra : " *No dog should have more offspring than equivalent to 5% of the number of puppies registered in the breed population during a five-year period*."

Also, should regulations not aim at a worldwide health instead of the health of only a national population ? May our regulations then allow a carrier to be crossed with a dog that was not tested, by example a foreign bitch whose national regulations do not make prior testing mandatory ? The owner of the carrier may think that this is not his problem … but is this true and correct ? Is the spread and/or consolidation of this lethal mutation

[27] Results from DNA tests for inherited diseases should be used to avoid breeding diseased dogs, not necessarily to eradicate the disease. Dogs shown to be carriers (heterozygote) for a recessive inherited disease should only be bred to a dog that is proven not to carry the allele for the same disease.

[28] We know that in many countries rules exist, some issued by Kennelclubs, others by breed associations and possibly even by legislation, that define a maximum number of mating or litters per dog. Collecting information on such rules and about their wanted / unwanted effects is on the current IFR-Board's agenda. Cfr. the questionnaires that were sent to all Memberclubs.

not all our problem, at least for the dog lover ?

Again, an emphasis on the need for an international approach.

2.4. Subaortic stenosis (SAS):

Subaortic stenosis or SAS is probably the most important cardiac disease for the Rottweiler.

It occurs when the flow of blood from the heart's pumping chamber or left ventricle is restricted. This obstruction is in the area of the heart under the aortic valve.

There are several types of subaortic stenosis but the most common type concerns the subaortic membrane, a shelf-like membrane under the aortic valve. It causes obstruction to the flow of blood from the left ventricle into the aorta. The veterinarian can hear the turbulence that this causes in the blood flow as a heart murmur.

This narrowing can be mild, moderate, or severe. If it is moderate or severe, it can force the heart to work harder and be harmful to the heart's health.

SAS is known to take the lives of seemingly perfectly healthy dogs ! The dog may suddenly faint or drop dead … with no warning and leaving the owner with the question : why ? All too often the owner then refers to a heat stroke or too hard efforts while in reality it was SAS that struck.

The problem is precisely that affected dogs, even severely affected dogs, may not show any signs of disease at all. The owner sees no need for treatment so he does not look for a treatment and especially in case of severe affection this will strongly reduce the life span of the dog.

We know that SAS is a genetic disease. For the Newfoundlander, the disease has been described as being an autosomal dominant trait ! [29] This means that only one of the parents needs to be a carrier to pass it on to his progeny and produce sick dogs (there does seems to be a reduced penetrance).

I find no conclusion that this would be different for the Rottweiler, only that recent studies seem to conclude that it is polygenetic trait.

If the dominant nature of the gene(s) would however be confirmed, this would imply a very concrete danger for our breed and especially in case of further narrowing of its genetic diversity.

Testing is then an absolute necessity ! Indeed, as the affected dog shows no signs of being ill, chances are that if he is not tested, he will be used for breeding, long and possibly even extensively before it suddenly becomes clear that he is affected.

Currently, no DNA-tests are available to detect the gene and a correct diagnosis must be made by echocardiography. Although disputed, a diagnosis by use of stethoscope (auscultation) is said not to be as reliable.

In several countries, many breeders are familiar with the disease and are already now testing their breeding dogs for SAS on a voluntary basis.

The first answers we received on the IFR-questionnaire about SAS learned that an awareness of the disease already exists in many countries and that prior screening is understood as highly advisable but that a structural screening seems to be limited to the UK and especially the USA where for example the breeding regulations of the USRC demand that as of April 2014, all dogs residing in the U.S. and born after April 1, 2012 and used for breeding by USRC members must have an OFA normal cardiac rating prior to breeding.

In Belgium (Flanders) legislation made prior testing on SAS obligatory for some other breeds but, because of its noticeable prevalence (the Rottweiler was / is subject of scientific research) it was recently announced that the Flemish Breeding Commission may suggest that the Rottweiler will complete that list of breeds.

Studies at universities in the United States point at a region on chromosome 21 as the gene's probable location and have established this for both the Rottweiler as for the Golden Retriever. If this is correct, then this may be the case for all affected breeds and would increase the probability that all canine breeds share the same mutation. It might then be easier to develop a DNA-test.

Striking is that in the literature that I find on those researches, there is always mention of the need for more cooperation and support by breeders and breed clubs (amongst others to donate blood- or DNA-samples from dogs that were confirmed to have SAS and/or to be clear).

The same is true for a recent study (2011) at the university in Gent (Belgium) in which the researcher also explicitly deplores the lack of necessary data on the disease's prevalence and the fact that it is difficult to obtain cooperation of breeders, probably because of a fear for their reputation. [30]

Such cooperation – the availability of data and samples - is an absolute necessity for research programs to be relevant and successful. Both healthy dogs and dogs diagnosed with genetic diseases must be known and their pedigrees and DNA-samples should be made available. Only then relevant research is possible.

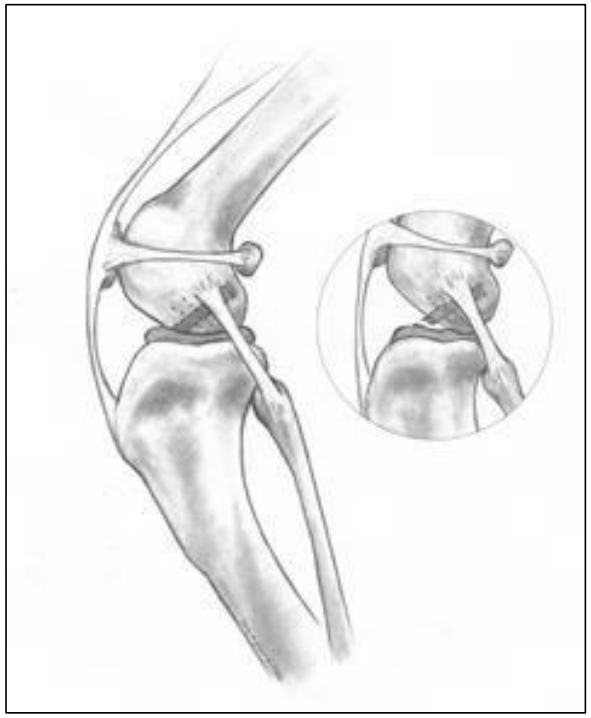
[29] A team of researchers has identified a gene mutation responsible for canine subvalvular aortic stenosis (SAS). The study (University of California) appeared in the September 2014 edition of the journal Human Genetics. The researchers analysed thousands of Newfoundland genes to identify the mutation associated with SAS. The mutation occurs in the phosphatidylinositol-binding clathrin assembly protein (PICALM) gene. Interestingly, according to Dr. Stern, this is the same gene mutation that has been linked to the development of plaque-like lesions in the brains of Alzheimer's sufferers. In addition to the gene analysis, the research team also conducted a pedigree analysis in a family of 45 Newfoundland dogs to look for inheritance patterns of the PICALM gene mutation. They were able to confirm that only one parent needs to carry the mutation to pass it to offspring, and that not all dogs with the mutation develop the disease.
.http://healthypets.mercola.com/sites/healthypets/archive/2015/05/27/subvalvular-aortic-stenosis.aspx

[30] Kevin Caestecker, Subaortastenose Bij De Newfoundland: Klinische Cardiologische Parameters en Genetische Studie, http://lib.ugent.be/fulltxt/RUG01/001/788/889/RUG01-001788889_2012_0001_AC.pdf

This is even more reason, just like for other diseases (cfr. ut supra), for the IFR and its Memberclubs to consider an organized and structured cooperation. A questionnaire to collect information was recently sent to all Memberclubs and the topic will be on the agenda of the next Meeting of Breed Wardens and Delegates.

2.5. Cranial Cruciate Ligament (CrCL). [31]

The cranial cruciate ligament is one of the most important stabilizers of the knee (stifle) joint, the middle joint in the back leg.



Rupture of the ligament causes instability of the joint and is one of the most common orthopaedic causes for hind limb lameness, pain and finally arthritis in the knee.

Diagnosis is made through orthopaedic examination and manipulation of the joint, sometimes completed by radiography, arthroscopy and even CT or MRI scans.

I did not find data on its prevalence but did find a reference to a study in the USA that found that just under 20% of all Rottweilers examined for lameness at university animal hospitals, were diagnosed with CCL rupture (Johnson et al 1994).

It is suggested that Rottweilers are three to seven times more likely to suffer from CCL rupture than the average dog (Whitehair et al 1993, Duval et al 1999) ! [32]

To restore an acceptable function in the knee joint, surgical treatment is usually necessary.

Contrary to humans, canine CrCL is seldom the result of a sudden trauma of a healthy ligament but is usually the result of a slow degeneration (over months or even years) of the ligament.

It is understood as a multifactorial affection, meaning that there is an interaction between

[32] https://www.ufaw.org.uk/dogs/rottweiler-cranial-cruciate-ligament-rupture

a genetic predisposition and external influences (obesity, poor physical condition, skeletal shape and configuration, …)

There seems to be no discussion on the fact that the Rottweiler shows a strong breed related predisposition to the disease. (Morris & Lipowitz 2001, Harasen 2003, Griffon 2010). Cfr. also the high frequency of the disease in both hind legs of the Rottweiler.

I find references to studies showing the inheritance in the Newfoundlander, the Boxer and the Labrador Retriever and even to a study that has found a gene that is likely to be associated with the disease in New Foundlanders but not yet the Rottweiler.

The precise genes that cause the disease seem not to have been identified yet but concrete research is underway (amongst others at the Iowa State University, USA) hoping to develop a genetic test for the condition.

The presence of a significant recessive gene or genes is said to be suspected and dogs with two recessive mutant genes (one from each parent) are at risk of developing the condition but, as penetrance of the gene has been found to be 51%, only about half of these do. The other 49%, with the homozygous recessive genotype (2 recessive genes), do not develop CCL disease. (29) Still, this concerns the New Foundlander and I find no concrete references that specifically concern the Rottweiler.

Such researches and identification of the mutation, would be a great help in remediating the problem. At this moment, there is no DNA-test available to identify carriers or animals that risk developing the condition.

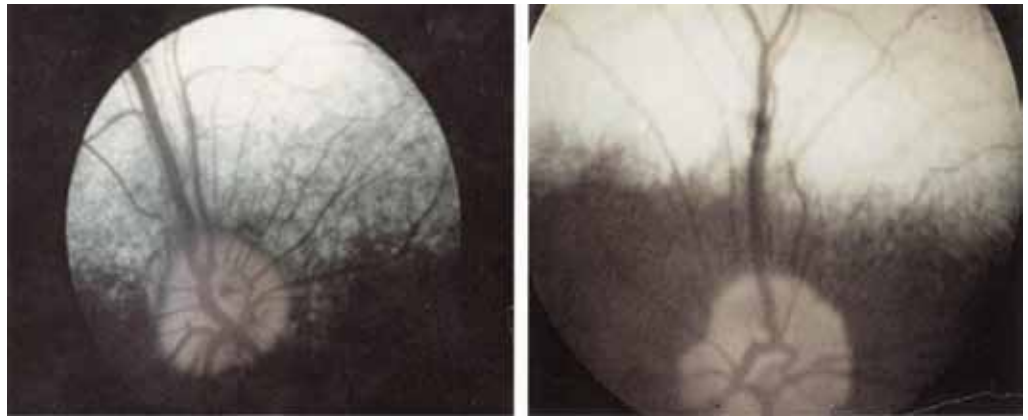
The offspring of one or two parents that have suffered CrCLD will have a high risk of developing the disease, but having parents who did not have CrCLD does not guarantee freedom from the condition. Indeed, the condition usually does not show until after breeding age and after the defective gene(s) are already passed on to the dog's offspring.

Also, as it is a multifactorial condition, it is possible that optimal external factors prevented the condition to develop in the parent dog while the hereditary disposition is nonetheless slumbering in the dog's genetics and waiting to be passed on.

Reality learns that not all breeders are aware of the genetic and thus hereditary nature of CrCLD and do not consider it in their breeding decisions. Again, information and education on the issue is called for.

2.6. **Progressive Retinal Atrophy (PRA):**

Progressive retinal atrophy (PRA) is an eye disease causing the retina to degenerate. The dog will suffer a gradual loss of vision (and often blindness) in both eyes as the retinal cells that sense light (photoreceptor cells) are lost.



Normal retina
|
Affected retina

The most common form of the disease is “generalized progressive retinal atrophy” (GPRA). It comes in two versions, the first one developing already before the age of 6 months and resulting in blindness before the age of 2 years, the other only after the age of ± 3 – 5 years.

In a first stage, GPRA causes a loss of night or dim light vision and later on progresses to an inability to see in bright light and often resulting in blindness.

The diagnosis often comes very late as many dogs compensate for the gradual loss of vision, so owners become only aware of the condition when the disease is already advanced and after the dog has been used for breeding.

This progressive disease is incurable.

General breeding advice is that GPRA sufferers should not be used for breeding but of course, the decision to remove them from the genetic pool can only be taken after they have been diagnosed and chances are real that this is only the case long after the dog has already been used for breeding.

DNA tests are now available but they are breed specific and while I can find them for several other breeds (Schapendoes, Labrador Retriever, Golden Retriever), I have not found one for the Rottweiler.

The disease is said to be an autosome recessive trait but this seems to be breed related as for the Bullmastiff the gene is established to be autosome dominant (!) and for the Samojeed and Siberian Husky to be linked to the X-chromosome.

Should the gene of the Rottweiler also be autosome recessive, then the development of such a test would make it easy to detect the gene and to fight the affection.

I find no concrete data on the prevalence in the Rottweiler but dependent on its importance, an investment in the development of a test that is usable for the Rottweiler might be a good one !

To be followed up upon.

2.7. Osteochondritis Dissecans (OCD)

Osteochondritis dissecans or OCD is a disease of the cartilage. It can affect various joints in a dog’s body.

During the development of the fetus, cartilage is replaced by bone (ossification).

Still, cartilage remains a necessity in every joint. Indeed, in a joint bones meet and there is movement between them. To allow this without harmful friction between the bones, their surface is covered with a layer of cartilage that protects the bone and allows a smooth movement between them.

Osteochondrosis is a pathological condition in which the process of ossification is disturbed, often because of a disruption in the blood supply to the bone. Because of this, the cartilage keeps growing where bone should have been formed. This results in a abnormally thick layer of cartilage, which is far less resistant to mechanical stress than a normal much harder and stronger bone.

In a dog that has developed OCD, the cartilage is damaged or has grown in an abnormal way. Because of this, the cartilage separates itself from the bone or breaks up in small or larger pieces, obstructs the function of the joint and causes an inflammatory condition.

The Rottweiler is one of the large and giant breeds (with the great Dane, Labrador retriever, Newfoundlander, Bernese mountain dog, English setter, ..) that is predisposed to this condition.

Its symptoms that will generally already occur between 4 – 10 months, are :

- lameness (most common symptom and this may be sudden of gradual) of one or more limbs.
- unable to bear the body's weight on a limb with an affected joint
- swollen joints
- experiencing pain in limbs, especially when manipulating the joint
- loss of muscles with chronic lameness

Again I find no concrete data on the proportional prevalence of the disease in the breed but striking is that I found a reference that claimed that already in 1994 it was said that the Rottweiler's predisposition for this condition (in the hock-joint) was hundreds of times greater than in none pure dogs.

I also find it remarkable that (almost) each time I heard about a Rottweiler in my country being diagnosed with OCD, it concerned the elbow or sometimes the shoulder, while most references to a high predisposition in Anglo-Saxon countries concern the hock-joint.

A quick read on the website of Universities Federation for Animal Welfare learns that Rottweilers are genetic predisposed to OCD, and then to hock OCD in particular, but that the causative genes have not been identified yet. [33]

It is said to be likely that multiple genes, as well as environmental influences are important in causing hock OCD in Rottweilers, so again we encounter a multifactorial affection.

Managing the external factors (cfr. ut supra) is then a possibility but does not remove the genetic factor. Determining who the carriers are - those which carry and pass on the gene(s) but do not show the disease themselves - is still not possible yet as we still await the identification of the defective genes and the development of a test to detect them.

Still on this same website, there is the known call to use breeding dogs that have a better breeding value than average for the breed [34].

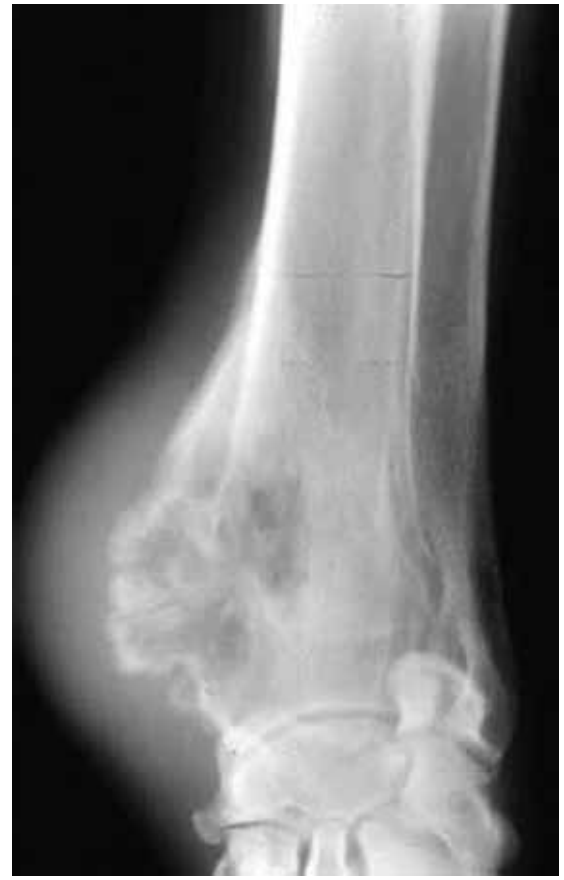
Cfr. ut supra and the FCI's International Breeding Strategies.

Again, a call to establish and use breed values rather than only using individual test scores … and again an issue to be discussed further at the next IFR Meeting of Breed Wardens and Delegates..

[33] http://www.ufaw.org.uk

[34] An Estimated Breeding Value is a tool that helps breeders to make breeding choices that concern inherited diseases (and/or qualities as an EBV can also be made for any trait, so not just for genetic defects but also for highly wanted mental and physical traits). These EBV are not only based on the individual dog's test scores or results but they are based on all known scores and pedigree data from both the individual breeding dog and all its family (ancestors, descendants and also all siblings and again their descendants) to obtain a more effective determination of the genetic traits that the dog may pass to its offspring. An EBV can of course only be calculated for a breed if enough individual dogs have been tested and if their scores are collected and available. Using EBV means that one does not only take the phenotype of the individual animal into account but its more realistic and true (broader) genetic stamp.

2.8. Canine cancers.



lone of us will be unaware that more nd more dogs are said to pass away at young age because of cancer/tumors.

gain worldwide, many scientific esearch programs exist and their ubject and results are published in cientific publications but also, freely vailable, on the internet.

cannot and will not dwell into detail on anine cancers here, especially as the isease comes in many forms.[35]

lot all tumors will have a genetic cause ut still, it is striking that the genetic actor is always part of the suspicion nd thus part of the research.

nly as an example, I refer to canine steosarcoma (OSA), the most ommon primary bone tumor found in ogs that accounts up to 85 % of all alignancies originating in de skeleton.

arger breeds, like the Rottweiler (!), ave a high predisposition for the isease because of their size and weight.

lowever, besides the size and weight-factor, genetic factors have also been established s to induce the development of bone tumors and more precisely, dogs with OSA have een found to have aberrations of the p53 tumor suppressor gene.[36]

For an enumeration and discussion of canine cancers : http://wearethecure.org/learn-more-about-canince-ancer/canine-cancer-library

Mendoza, Konishi T, Dernell WS, Withrow SJ, Miller CW, Status of the p53, Rb and MDM2 genes in canine osteosarcoma, ttps://www.ncbi.nlm.nih.gov/pubmed/9891508 ; Gayathri T Selvarajah, Gene expression profiling of canine osteosarcoma eveals genes associated with short and long survival times, ttps://www.ncbi.nlm.nih.gov/pmc/articles/PMC2746177 ; http://wearethecure.org; ttp://www.caninecancer.com/osteosarcoma; http://www.fitzpatrickreferrals.co.uk/conditions/canine-osteosarcoma ;

Conclusions are therefore that the genetic factor is real and imminent, also for the Rottweiler.

Cfr. the website of the AKC (American Kennelclub) [37] referring to a narrow heritability or in other words to the fact that OSA has indeed genetic causes [38].

The same site explicitly refers to the fact that scientific research established an increased risk of osteosarcoma for the Rottweiler, again because of genetic reasons ! [39]

All these research programs require samples from as many Rottweilers as possible – both from affected dogs and healthy dogs - so genetic influences can be studied. Only this way genes, mutations or abnormalities can be discovered.

Again, a wake-up call for all IFR-Memberclubs and Rottweiler lovers to inquire whether such research programs exist in their country and for a close cooperation. A fine example of such cooperation can be found on the website of the Rottweilerclub of the UK. [40]

Cfr. also the questionnaire that was sent to all IFR-Memberclubs.

[37] http://www.akcchf.org/canine-health/your-dogs-health/bone-cancer-in-dogs.html

[38] Heritability is a statistic used in breeding and genetics works that estimates how much variation in a phenotypic trait in a population is due to genetic variation among individuals in that population. Heritability is estimated by comparing individual phenotypic variation among related individuals in a population.

[39] A major component of this disease in dogs, and possibly in people, appears to be genetic (i.e., heritable). Risk is most accurately defined by body mass, although there is a direct correlation with size as well. In children, osteosarcoma is frequently seen in kindreds with mutations of the retinoblastoma susceptibility gene (RB-1), and this risk is paternally imprinted. In dogs, there are clear breed predispositions. A recent study by Phillips and colleagues published in Genomics (Phillips et al., 2007) showed that the narrow heritability in Scottish Deerhounds was 0.69; in other words, almost 70% of the cause is due to heritable traits. Narrow heritability (h2) is the proportion of the total variability due to genetic factors. It is not surprising heritable factors account for a significant component of risk in Scottish Deerhounds; more than 15% of dogs from this breed die from osteosarcoma. The best-fit model for inheritance of the risk traits in Scottish Deerhounds was a Mendelian major gene with dominant expression. **Furthermore, Comstock and colleagues (Comstock et al., 2006) reported at the 2006 Genes Dogs and Cancer meeting (Chicago, IL) there are 4 regions of the genome that appear to be associated with an increased risk of osteosarcoma in Rottweilers, another breed where risk appears greater than what would be attributable to size alone (incidence estimated at more than 12%).**

[40] For an example of such a cooperation : http://www.therottweilerclub.co.uk/health/bone-cancer-in-rottweilers /

3. Hereditary diseases : Causes and remedies.

3.1. Genetic diversity.

3.1.1. The Rottweiler as a canine breed.

The Rottweiler is a canine breed.

A breed is to be understood as a group of animals that show homogeneity (=the same homogeneous characteristics) in their physical appearance and behaviour (phenotype).

Those particular characteristics distinguish the group from other animals of the same species (in this case the species is "dogs").

Essential in the definition of a breed is that when individual animals are bred together, they pass those characteristics to their offspring. In other words : those characteristics are hereditary.

3.1.2. "In the beginning …"

The "creation" of a breed is established by selective breeding, meaning by selecting and using only individual animals who share the wanted (hereditary) characteristics.

By doing this, the genepool is "closed" so all hereditary influence by animals who do not share those characteristics, is avoided.

Many characteristics are of a recessive nature. To consolidate them in the breed as to be characteristics that are shared and proper to all specimens of the breed and that are guaranteed to be inherited by their offspring, the "art" of creating and maintaining a breed is selecting only those breeding animals that show the most desirable recessive traits (defined in the breed standard) in their appearance and to avoid using animals that show unwanted characteristics ("faults").

Remember : animals that express the wanted characteristics, are homozygote carriers of the desired recessive gene or can be homozygotes or heterozygotes of a desired

dominant gene. Otherwise they could not show those characteristics (cfr. supra) themselves.

Homozygotes for a recessive gene are guaranteed to pass those same characteristics to all their offspring and, if crossed with other homozygotes, will consolidate those traits in the group (breed).

Homozygotes for a dominant gene will do the same while heterozygotes for a dominant gene will pass it on to part of their offspring with a probability of 50 % but again by inbreeding or in other words crossing heterozygote carriers with other heterozygotes or homozygotes, ever more homozygotes will appear who will then be guaranteed to pass the gene to all of their progeny.

3.1.3. Inbreeding, a technique to create or maintain a breed.

Inbreeding means using breeding animals who are very closely related (brother and sister, father and daughter or mother and son, …).

Linebreeding means using related animals but in a less close relation (ex. crossing a female with her great grandfather).

Especially when a breed is being created, the number of dogs that show the desired characteristics in their phenotype and from which breeding animals can be selected, is very limited.

The breeder will therefore very likely select closely related animals for breeding as these will at that time probably be the only ones who share the desired traits and this not by coincidence but because they both possess an identical chromosome that was inherited from a common ancestor.

By inbreeding or linebreeding, chances are that this chromosome will be part of both the sperm cell and egg cell that merge, meaning that the body cells of the pup will carry both identical chromosomes and be homozygote for the genetic information on them.

This is still the same reason why breeders might today chose for inbreeding.[41]

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[41] Imagine wanting to reproduce a dog that has a truly remarkable conformation. When one decides to breed this stud dog to one of his progeny, not less than 75 % of the progeny will be heterozygote carriers of genes that are derived from the stud dog and not less than 25% will be homozygotes or in other words will carry the same chromosomes as the stud dog.

A quick and easy illustration of this. The male carries a pair of chromosomes AB, the bitch CD. This gives the offspring : CA + CB + DA + DB. If we cross the stud with one of his offspring (father AB x daughter CA), this gives us : CA + CB + AA + AB. In other words : all offspring will of course carry genes from the stud dog and in total, 75 % of the genes of the progeny are inherited from the stud dog and 25 % of the offspring will be homozygotic with the stud dog (Coefficient of Inbreeding = 25 %)

Should we cross two littermates, in this example CA x DB, this gives us : CD + DB + AD + AB. Or in other words : now 75 % of the offspring carry genes from the stud dog but in total it gives a slightly better diversity. Now not 75 % of all inherited genes are derived from the stud dog but 50 %. The Coefficient of Inbreeding (COI) is however still 25 %

Also remember: if the dog is a homozygote for a characteristic, he cannot express any other characteristic in his phenotype and cannot pass any other to his own progeny.

Even when in a later stage the number of dogs in the group (the breed to become) increased and more dogs obtained homozygosis for ever more desired traits, this will not immediately have been the case for all traits and/or not for all traits simultaneously. Other dogs will of course have been bred in but to not lose the already obtained homozygosis, probably always as closely related as possible.

This will have been the case over many generations until complete conformation and permanent ([42]) homogeneity of all progeny was obtained or in other words until homozygosis for all or most traits would be obtained.

The same technique, at least of linebreeding, is now used to maintain certain breed specific traits or to emphasize some of them (the latter unfortunately not always within the definition of the breed standard).

3.1.4. Negative effects of inbreeding or linebreeding.

As, by definition, the genepool of a breed is closed and is not affected by external genes, at least not if only purebred dogs are used for breeding, this means that when genetic diseases occur, these are caused by defective genes that already existed and were enclosed in the breed's genepool since its very origins.

The question is : how is it possible that defective genes now suddenly cause so many ill or affected dogs, while those diseases were hardly even known or noticed before ?

Cfr. the disease JLPP of which the Rottweiler lover only very recently became aware and was shocked when learning about its important percentile presence in the genepool. Before, as far as we were even aware of its existence, we were convinced that the affection was proper to the Black Russian Terrier only … . Also, how is it possible that we do not succeed in breeding out some genetic diseases (example HD) although we test our dogs and exclude affected animals from breeding ?

Is this the result of a sudden simultaneous or of a continuously repeated mutation of the genes of a large part of the breed's population ?

Nothing supports this hypothesis and, in fact, we know for certain that such mutations do not happen simultaneously in large proportions of a population.

A gene mutation is a permanent change in the DNA that constitutes the gene. Some mutations will affect only one single DNA string, others will affect a large segment of a chromosome and alter multiple genes.

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[42] Even now, genetic characteristics sometimes appear that prove a common ancestry with other breeds of which dogs must have been used to create the Rottweiler breed. Cfr. the long curly coat and/or white markings that are specific for some other breeds of cattle dogs. Even after so many generations, some recessive genes have survived the degree of homozygotism for the desired Rottweiler coat.

Mutations however start in only one single animal and the dispersion of this mutated / defective gene will then solely depend on its use for breeding and the degree of inbreeding his progeny.

In general terms, we know two sorts of mutations :

- hereditary mutations that already exist since long(er) and that are inherited from a parent.

  These are already existent in the gene that was passed on and will be present in every cell of the dog's body. They are also called "germline" mutations as they were present in the germ cells (cfr. ut supra : the sperm cell of egg cell).

- somatic mutations. These are alterations of the DNA sequence that occur during the dog's lifetime. These changes are usually caused by environmental factors such as radiation (ex. ultraviolet in sunlight) or by an accidental defect while DNA copies itself during mitosis (cell division). [43]

  Such somatic mutations are therefore not inherited from the parents and they will also not necessarily be present in each body cell. Also, they will not be passed on to the progeny of the dog, unless the mutated gene appears in the DNA string in one of the gametes. In the latter case (or if the mutation would happen in the ovum (fertilized egg) at the moment or shortly after the sperm cell and egg cell merge into the zygote, the mutation will after all be present yet in all new body cells that develop by mitosis (cell division starting at the fertilized egg).

  It is thus possible that a dog is a carrier of a mutated gene that was not present in the parent's body and will now pass it on to its own progeny.

  This mutation or defective gene derives from one single animal and its presence in the genepool of a breed will depend on the frequency this animal and its progeny will be used for breeding … and of course on the degree of inbreeding.

Most mutations or defective genes will be recessive. Otherwise, should they be dominant, they would have appeared in a much higher and more expressed manner and much longer ago.[44]

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[43] Mutations that cause diseases are said to be uncommon but are nevertheless existent. Other mutations happen more frequently but have only mild effects, more likely to be "variations" like for instance those that cause perfectly normal differences between individual animals (eye color, bloodtype, etc. ..). Such genetic alterations are called polymorphisms and only very seldom have an impact on health.

[44] My personal opinion is that we should also not underestimate the importance of the change of balance between the wish to maintain and emphasize characteristics of an aesthetic nature and those that concern the dog's utility : beauty versus work. I dare say that for a breed that according to its breedstandard was created for only one reason (to work) and that was put to effective use as a cow driver, it is likely that the breeder gave less importance to aesthetic faults and rather excluded dogs with a lesser or reduced physical or mental functionality and that this natural selection unknowingly but necessarily excluded the carriers (homozygotes for recessive and/or heterozygote or homozygotes for dominant) of the mutated genes that are responsible for disabilities or diseases (example hip dysplasia) . Such natural selection on physical (and mental) functionality may have helped to maintain health and to keep defective genetic homozygosis and thus expressed affections within acceptable

The explanation why these mutations now "suddenly" have an highly enhanced prevalence in many canine breeds and some even have a very noticeable impact on the health of large proportions of a breed is very simple : because of their high (homozygote) presence in the pool of used breeding dogs, which itself can only be explained as a direct (and predictable) result of excessive inbreeding / linebreeding : all breeding to the dog in whom the mutation occurred and/or his/her ascendants and this in a too closed pool of breeding dogs.

By inbreeding or linebreeding, the breeder not only selects breeding animals that show the desired trait in their phenotype (proof that they carry the hereditary information for it) but he deliberately choses closely related dogs that share those characteristics because they inherited the same chromosome from a common ancestor and thus carry the (identical) gene(s) that define(s) the desired traits.

By doing this, he "creates" homozygotes, dogs that can express no other characteristics in their phenotype than those defined by the genes on both identical chromosomes. Their expression is guaranteed as there is no dominant gene that can prevent this.

Unfortunately, those chromosomes carry many more genes than just the one(s) that define(s) the desired characteristics !

They may in fact also contain genes that define highly unwanted characteristics, including genetic diseases and these are of course inherited together with the other genes on the chromosome.[45]

So, by inbreeding to concentrate and emphasize the desired genetic characteristics, one will at the same time just as well concentrate and emphasize the presence of all the defective genes as they are located on the same chromosomes as the desired ones. One comes with the other, the "good" but yes, also the "bad" ones.

We can conclude that inbreeding or using extremely closely related dogs is a breeding technique that is not bad by definition but it should be a well considered breeding decision, not one that is commonly or automatically (on purpose or thoughtless) used by all breeders worldwide, as it has a very noticeable impact on genetic diversity.

Remember the example above of the stud dog with a truly remarkable conformation : when bred to one of his daughters, not less than 75 % of its progeny will be carriers of genes that are derived from the stud dog and 25 % of the progeny will even be complete homozygotes (= COI of 25 %). Breeding siblings (son and daughter of the stud dog) offers a slightly better diversity (now 50 % will carry genes that are derived from the father) but again 25 % will be homozygotes (COI = 25 %).

Inbreeding is thus a very efficient but also a dangerous instrument, especially if the stud

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proportions, while nowadays breeding policies aim less (or not) at this functionality.

[45] There is a difference between birth defects (congenital defect) and hereditary disorders. The first is the result of a defective development of the foetus and is present at birth. They can be hereditary but not necessarily.

is carrier of a mutation.

Linebreeding seems a healthier but still very effective instrument for the breeder to maintain the dog's conformation and to protect and preserve the traits that he obtained and consolidated in a certain bloodline. It can be used in a kennel for a much longer time than inbreeding and allows to eventually outcross with a dog that has differing ancestors and then ply back to linebreeding and the before already consolidated genes and so end up with the better sum of both.[46]

Still, even then we must be aware that the more the wanted characteristics are consolidated and emphasized, the more the unwanted ones will also be consolidated and emphasized. Worse, the more pronounced the dog will develop the desired traits … the more successful it will be at shows, trials … , the more it will be used for breeding … and the more also the defective gene will put its stamp on the population … (1).

This should not worry us on a limited scale and if the responsible breeder is aware of possible undesired effects and the need for correction when further breeding with this progeny, but when inbreeding or linebreeding becomes an instrument that all breeders use worldwide and especially when they all select the same small number of successful breeding dogs (or their progeny) and so reduce the use of breeding dogs that do not show those traits or not as pronounced (because they differ in their genes), then in the end the diversity of the whole breed may become endangered.[47]

This will more quickly become noticeable in a small or closed genepool, a group of dogs that is isolated from external genetic influence by protectionist regulations, quarantine or for instance when geographic reasons offer an obstacle for easy frequent exchange of breeding dogs.

[46] Outcrossing is breeding two dogs that are the products of line breeding but of two distinctly separate lines. Outbreeding is breeding two dogs who not only are the products of two distinctly separate lines, but are also not the products of line breeding.

[47] Inbreeding leads to a reduced heterozygosis. Literature teaches that it also leads to a reduced general breed quality (lower weight at birth, a deteriorated growth, less vitality, less strength of survival of pups and even an increased number of still-born pups in some breeds, a reduced fertility, a higher increased susceptibility to disease). This is often called an inbreeding depression. Cfr. an article on a study on the topic : N. Pekkala and others, The effect of inbreeding rate on fitness, inbreeding depression and heterosis over a range of inbreeding coefficients, http://onlinelibrary.wiley.com/doi/10.1111/eva.12145/pdf : "Inbreeding (mating between close relatives) increases offspring homozygosity and usually results in reduced fitness. In homozygous genotypes, recessive deleterious alleles are unmasked and benefits of heterozygosity in overdominant loci are lost (Charlesworth and Willis 2009). Genetic drift (random fluctuation in allele frequencies) may also depress fitness by causing deleterious alleles to accumulate and fix in the population (Lande 1994; Lynch et al. 1995a,b). Hybridization among genetically differentiated populations, on the other hand, is known to have the potential to alleviate the effects of inbreeding and drift by increasing heterozygosity in the population (Whitlock et al. 2000). When population size is small, inbreeding and genetic drift both increase because the number of individuals contributing to each generation is limited (Keller and Waller 2002). Consequently, average fitness in a small population is expected to decrease from generation to generation as the level of inbreeding (i.e. homozygosity) increases (Crow and Kimura 1970; Wang et al. 1999; Keller and Waller 2002). Indeed, a positive relationship between population fitness and heterozygosity is often observed in experimental studies and in the wild (see e.g. Keller and Waller 2002; Reed and Frankham 2003; Spielman et al. 2004). As the average homozygosity in a population increases, the difference in homozygosity between offspring of close relatives and offspring from random matings decreases. Therefore, the so-called within-population inbreeding depression (i.e. the reduced fitness of offspring from inbred mating, when compared to offspring from random mating within the same population) is expected to decrease (Wang et al. 1999; Theodorou and Couvet 2006). Low within-population inbreeding depression is commonly observed in populations that have high average level of inbreeding (reviewed in Byers and Waller 1999).

The more closed and limited the number of breeding dogs is, the higher chances become that dogs are mated that both carry the same genetic information. The genetic diversity is low and chances for increased homozygosis (both for wanted and unwanted traits) are high.

When the pool of breeding dogs that are used is large, the genetic diversity of the genepool is larger and the probability that carriers of an identical chromosome or gene are mated is much smaller.

Think of the old folk wisdom that says that the non pure dog is healthier and lives longer. [48]

This corresponds with what is said above : those recessive traits often remain hidden in non pure bred dogs that by definition belong to a more open and diverse genepool while their prevalence is much higher in the pure bred dog for whom chances are also much higher (or deliberately decided upon) to be mated with a partner that carries the same recessive mutation.[49]

Of course we will not always use inbreeding but still, imagine the possible impact of linebreeding or even totally random breeding in a closed genepool with only a limited number of breeding dogs of whom some are carriers of a recessive disorder and worse, imagine if some of those carriers are highly successful showdogs and therefore very popular breeding dogs ![50] If no corrective action is then taken, this would significantly increase the number of homozygotes or in other words the number of dogs that will suffer the disease. [51] We may not let it come to that.

We must be aware of the danger of a too closed genepool and at the very least of the need to make a continuous inventory of genetic diseases and prevalence..

There is no excuse not to. Cfr. also infra about the Coefficient of Inbreeding.

[48] Cfr.A.R. Boyko, oc. : Strong artificial selection has contributed to the diversity of disorders exhibited in dogs. Independent, severe founder effects for each breed cause diseases that are at extremely low prevalence in natural dog populations to, by chance, reach appreciable frequency in one or a few breeds, either from the founder bottleneck itself or through the subsequent propagation of popular sires harboring the variant. In particular, some recessive disorders caused by loss-of-function mutations and some cancers can be rare in humans but common in certain dog breeds (for example, osteosarcoma [52] and amyotropic lateral sclerosis (ALS)-like canine degenerative myelopathy.

[49] There may also be the fact that for none pure dogs, there was more natural selection (less medical attention) which may also have helped to reduce the number of carriers or their chances to breed.

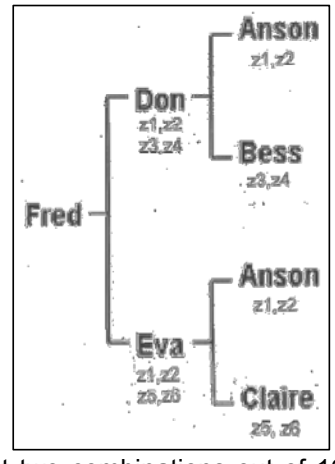
[50] Cfr. FCI-International Breed Strategies : "As a general recommendation **no dog should have more offspring than equivalent to 5% of the number of puppies registered in the breed population during a five-year period.** The size of the breed population should be looked upon not only on national but also on international level, especially in breeds with few individuals."

[51] We are unaware of the precise prevalence of all genetic diseases, not even of the most important or threatening ones. Nor do all kennel clubs calculate or publish the degree of inbreeding of national breed populations. The lack of knowledge of prevalence, is an ever again returning and mentioned obstacle in research programs and can be reproached to a lack of cooperation and communication between researchers, breed clubs and breeders. I look forward to read the answers on the questionnaire that was sent to all IFR-Memberclubs, more precisely to learn about differing experiences or prevalences that concern genetic disorders.

3.1.5. Coefficient of Inbreeding (COI)

As said above, the wish to maintain sufficient genetic diversity, means of course limiting the degree of inbreeding but we may on the other hand not forget the need to maintain or even emphasize breed specific traits, aesthetic or functional and that for this line-breeding or even inbreeding may be called for.[52]

To consider if the balance between these considerations is still sound, we must first be able to quantify them by calculating the "Coefficient of Inbreeding", in short COI.



The COI expresses the probability that the offspring of a certain combination of breeding animals will be homozygotes for a recessive gene.

Computer programs are available to calculate a COI[53].

Still, let's give a simple example by using the following pedigree of the dog called "Fred" and asking ourselves how high chances are for Fred to be a homozygote for the recessive gene "z" of which his grandfather (common for his mother and father) is known to be a carrier.

Drawing the Punnet-table (cfr. ut supra) will teach us that two combinations out of 16 possibilities will be homozygotes, this is a COI of 2/16 = 12.5 %

gametes	z1	z2	z3	z4
z1	z1 – z1	z1 – z2	z1 – z3	z1 – z4
z2	z2 – z1	z2 – z2	z2 – z3	z2 – z4
z5	z5 – z1	z5 – z2	z5 – z3	z5 – z4
z6	z6 – z1	z6 – z2	z6 – z3	z6 – z4

A simple table of the COI obtained by inbreeding :

[52] Cfr. for an interesting article : www.fci.be : Memo on Inbreeding by Prof. B. Denis.
[53] http://www.compuped.com/compuped

Crossing	Coefficient of Inbreeding
Parent x offspring	25 %
Full siblings	25 %
Grandparent x grandchild	12.5 %
Half siblings	12.5 %
Great grandparents / great grandchild	6.25 %
First cousins	6.25 %

The crossing of parent/offspring leads to a COI of 25% - of full siblings to a COI of 25% - of grandparent/grandchild to a COI of 12.5% - of half-siblings to a COI of 12.5% - of great grandparents/great grandchild to a COI of 6.25% - of first cousins to a COI of 6.25%

The question is then of course : which degree of inbreeding is acceptable or still "safe" ? In other words which COI is acceptable without reducing the genetic diversity (which is harmful) ?

The answer is that **the level of genetic diversity must be broad enough to ensure that the inbreeding policies that are being used do not increase the COI from generation to generation.**

The original purpose of the coefficient of inbreeding was to give breeders an instrument to estimate both the benefits and the disadvantages of a certain combination and to decide for an acceptable equilibrium.

The COI still offers this possibility but has also become an instrument to warn for the ever more decreasing genetic diversity in canine breeds.

Most scientific approaches of the problem that I found during my reading tour on the issue, explicitly warn that canine breeds with a too low diversity will necessarily become extinct because of genetic diseases.[54]

This is not just a theory and it is not for nothing that the FCI even prepared an instrument to remediate : a regulation that allows crossing with other breeds if diversity becomes too

[54] An emotional plea : Carol Beuchat, Institute of Canine Biology, Are we watching the extinction of a breed ? "Our dogs are dying of inbreeding. ... None of the things we are doing will cure inbreeding. Scientists can't cure inbreeding. Inbreeding must be cured by breeders." (http://www.instituteofcaninebiology.org/blog/are-we-watching-the-extinction-of-a-breed-or-why-are-we-focused-on-consequence-instead-of-cause)

low to ensure the health and further existence of a breed.[55]

The higher the inbreeding coefficient, the higher the risk of health issues. A low COI will not bring many risks but its effect – seen in the light of the wish to emphasize certain characteristics – will be also low. A high COI may bring the wanted benefits but may also lead to a significant loss of health and vitality.[56]

It is a measurement of risk but doesn't bring any guarantees, also not the guarantee that progeny will yes or no inherit health conditions and it must be clear that knowledge of the COI in a breed cannot replace health tests. Cfr. the fact that such a test can prevent breeding two carriers and thus the probability of 25 % of the pups suffering the disease. This is a direct and certain result that follows only from testing, not from a theoretical consideration.

I will leave further explanation to scientists but it seems **that the COI should not exceed 3.5 %**.

Already as of a COI of 5 %, negative effects become noticeable and as of 10 % there is already a significant loss of vitality and a risk for smaller litters, higher mortality and a significantly increased expression of recessive mutations.[57]

As an example, a recent Belgian study concluded that the Belgian Rottweiler population has a COI between 1.5 – 2.5 % with a still acceptable growth of 0.5 %. It shows only a moderate loss of genetic diversity but even this was deemed serious enough by the researcher to advise calling a halt to an unbalanced use of breeding animals and to lower the standards (breeding regulations) that now reduce or prohibit the use of some animals as breeding dogs. Even introducing strict criteria to reduce the expression of certain affections was said to be discouraged as those might further reduce the diversity of the breed.[58]

The Flemish legislation that followed upon this study, indeed forbids regulations that exclude dogs, even suffering dogs (!), from breeding if they were tested on particular diseases (HD, ED, OCD, DCM) and if the test scores are known. Breeding commissions are recognized and mandated to give breed related advices for the use of the tested dogs.

It will be interesting to learn about the situation in our other IFR-Membercountries and

[55] FCI general and breed-specific guidelines about crosses of breeds and breed varieties – www.fci.be : "*The FCI encourages crosses between breed varieties when it is considered necessary to increase the gene pool with the aim of improving dog health: it is not beneficial for health in dog breeding to have too small populations. "*

[56] A study with standard Poodles showed that dogs with a COI of less than 6.5 %, lived on the average 4 years longer than dogs with a COI of more than 25 %. http://www.dogbreedhealth.com/a-beginners-guide-to-coi

[57] Dr. C. Beuchat, Understanding the Coefficient of Inbreeding (http://www.instituteofcaninebiology.org/blog/coi-faqs-understanding-the-coefficient-of-inbreeding); Cfr. Prof. F. Comhaire, Inbreeding and Hipdysplasia. (pleading for a max COI of 3.25 %) - http://www.profidog.cz/en/frank-comhaire-pribuzenska-plemenitba-dysplazie-kycelniho-kloubu-dkk/

[58] "Inteelt en genetische diversiteit van 23 populaties van honden in Belgie op basis van afstammingsgegevens van de KMSH", 30.06.2012, by lic. Katrien Wijnrocx, dr. Steven Janssens en prof. Nadine Buys Livestock Genetics KU Leuven.
(http://lv.vlaanderen.be/sites/default/files/attachments/RapportInteeltGenetischeDiversiteitHondenBelgie.pdf)

this will of course be discussed at the next Meeting of Breedwardens and Delegates. [59]

3.2. The need to test for genetic diseases.

3.2.1. Is there a need to test ?

Of course there is !

We know that the genetic diversity of the Rottweiler breed, just as of so many breeds, is being reduced because of extensive use of in- or linebreeding to obtain or emphasize certain genetic traits and we know that this means also concentrating the mutated genes that come with it.

It may be true that we have been unaware of this for a very long time and that even today we may still not always know the degrees of inbreeding in all countries (COI) nor the precise prevalence of certain diseases.

Still, we cannot pretend that we are not aware of the existence of those diseases, nor of the fact that many of them were in the past hardly heard about while we now hear more and more about affected and suffering dogs, nor of their severe consequences for the dog, nor of their genetic nature and thus the fact that we have the remedy in our own hands, … .

The library but also the internet are inexhaustible sources of information and the interested dog lover will find countless articles and results of researches, some highly specialized and others more popular-written, but all with the same warning : the genetic diversity of canine breeds is decreasing with as a direct result the increasing prevalence of genetic diseases and on the long term the inevitable extinction of the species.[60]

The Rottweiler is certainly not unspoken off in those studies and conclusions, to the contrary !

Science has not only warned us for the phenomenon but has also told us how to deal with

[59] I cannot but refer to the (almost totally) closed pool of Rottweilers that can be used in Germany as breeding dogs and the alleged establishment that the number of carriers of the JLPP mutation in that pool has grown to a percentage of not less than 21 % of the tested dogs. Given the international nature of nowadays breeding, the spread of the mutation is with no doubt a fact. Recent messages that claim that such prevalence would exist for "all" Rottweilers (worldwide) are not documented nor substantiated by relevant test-programs or results but still, the first (unofficial) results we hear from more or less organized or systematic testing (for instance in the UK, also a territory that has been "closed" for a very long time because of quarantine) warn for an indeed high percentile prevalence and at least a much higher percentage than what we expected from a disease that we even thought to be proper to another breed only. Whatever there is, this must be more than an example but a very loud warning for what may already be or what may become if we do not test all our breeding dogs on their possible affection(s) and/or if we do not lower the risk by opening up the available genepool to breed from. This warning should be even louder and more acute for all other more or less closed genepools, regardless if this is the case by protectionist measures, legal quarantine, geographical isolation,… .

[60] For an article on the correlation between a decreased genetic diversity and the prevalence of HD : Prof. F.Comhaire, The Relation between Canine Hip Dysplasia, Genetic Diversity and Inbreeding by Breed. (http://file.scirp.org/pdf/OJVM_2014051310255066.pdf)

it.

On the long term, only broadening the pool of breeding dogs and consciously striving for genetic diversity will offer the solution, or in other words : using breeding dogs that do not share the same inherited genetic information. [61]

Talk to any veterinarian or scientist and most, if not all, will say that life, thus health, must have total priority over the wish to maintain breed characteristics as those are mainly of an aesthetic nature.

Cynology on the other hand, will take the debate to a more complex level, in fact the need to balance on the one side the need for healthy dogs and for which a wide genetic diversity is needed, on the other side the wish to preserve and emphasize the breed's characteristics while this is in a considerable extent only feasible by selecting breeding dogs that share inherited chromosomes and because of this show a reduced genetic diversity.[62]

Stepping away from this breeding policy would reduce homozygosity and be harmful for cynological conformation … a further unbalanced inbreeding will concentrate defective genes and may on a long term threaten the existence of the breed … where is the balance ? What is the solution ?

Testing our dogs prior to breeding, may not be the final answer but it is at least part of the solution and one that is feasible on a short term.

We cannot depend on natural selection anymore and may not wait until nature lets the disorder emerge and the progeny suffer.

Many mutations are recessive (for example JLPP) and we know that if both parents are carriers (heterozygote carriers, not homozygote sufferers), that they will not develop the disease themselves. They will not show any symptoms of the disease and there will be no visible warning of the slumbering presence of the mutation. They will be considered to be perfectly healthy and will be used for breeding … .

They will then both transfer the defective gene to their common offspring and those again to their offspring … until a pup develops the disease and suddenly proves that both its parents are carriers and so were their ancestors.

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[61] With the words or Mrs. C. Beuchat in her article : Are we watching the extinction of a breed : "What's the problem here? Breeders are looking to science for solutions to health problems, and the scientists study genetics and disease. But the dogs are dying of inbreeding, and that is the problem we need to fix. We are focused on consequence when the solution lies in the cause. We are continuing to enjoy our cigarettes while we toss money at lung cancer research and assume that with hope, prayer, and patience things will get better. We are learning a lot about the problems that are caused by inbreeding, but we are not solving the problem.
(http://www.instituteofcaninebiology.org/blog/are-we-watching-the-extinction-of-a-breed-or-why-are-we-focused-on-consequence-instead-of-cause)

[62] Cfr. http://www.thekennelclub.org.uk/health/for-breeders/inbreeding debating this balance.

Unfortunately, by then the harm is already done : the pup is conceived, born and will die a horrible death and a significant part of the progeny will be affected.

This, while a simple prior DNA-test and basic knowledge about how to deal with its result, could have prevented so much harm.[63]

So yes, testing is a must !

Other genes are not recessive but are dominant. This means that even the heterozygote carrier will develop the disease.

If such a disease becomes visible at a young age, then chances are that the dog will not live to a breeding age and/or that as a sick dog he will not be used for breeding.

Unfortunately, some of these diseases only emerge at a later age and because of this, only after the carrier (= carrier of both a healthy and a mutated gene) has already been used for breeding and has passed the mutation to his offspring ! Cfr. ut supra : Subaortic Stenosis (SAS).

Also, even though for example SAS is a dominant trait and the carrier will always develop the disease, this can happen with a variable expression : some develop the disease in a mild or moderate manner that will not always be noticed or recognized as such, others will develop the disease in a severe manner but even then the affection remains hidden until a sudden manifestation at only a later age : the dog fainting, dropping dead … .

Again, before this occurrence, the dog may very well already have been used extensively for breeding and have passed the gene to a large number of pups who will all develop the (life threatening) disease.

Again, prior testing the dog on its possible genetic affection might have prevented much harm.

I repeat the question and its answer : is testing necessary ? Of course it is !

Preventing the dispersion of defective or mutated genes and breeding them out again, is only possible by breeding with unaffected dogs, which means :

- with dogs that are not carriers of a dominant gene
- in the case of recessive genes, only with combinations in which at least one of the partners is not a carrier [64]. (and of course not a sufferer).

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[63] Cfr. FCI International Breeding Strategy : "Results from DNA tests for inherited diseases should be used to avoid breeding diseased dogs, not necessarily to eradicate the disease. **Dogs shown to be carriers (heterozygote) for a recessive inherited disease should only be bred to a dog that is proven not to carry the allele for the same disease."**

[64] Cfr. the FCI International Breeding Strategy : "Dogs shown to be carriers (heterozygote) for a recessive inherited disease should only be bred to a dog that is proven not to carry the allele for the same disease".

Given nowadays possibilities, it must be clear to all dog lovers that breeding without prior knowledge of a possible affection with a gene that may cause a lethal disease, is just not acceptable.

The health of the dog must have priority over the wish to possess the highest tin cup or the wish for economic gain.

It is the responsibility of national kennelclubs and Rottweilerclubs to express their concern in their breeding regulations, not in the least by recommending or even imposing some particular tests prior to breeding.

I remember warning at the Meeting of Delegates of the IFR in 2013 that if cynology sits still, legislators may step in ! Well, not long afterwards, this became the case in Flanders (region of Belgium) where current legislation makes it obligatory to test all Rottweilers prior to breeding on Hip- and Elbowdysplasia, Dilated cardiomyopathy (DCM) and Osteochondritis Dissecans (OCD) and an obligatory test on SAS will probably shortly follow.

Let it be a lesson for us all : we must act in a proactive, not a defensive way.

We must act now but without forgetting what is necessary on the long term.

3.2.2. Must we test for all diseases ?

Some will now react shocked but the correct answer is probably : no, we must not test on all genetic diseases and we must not try to remove all defective genes from the genepool.

We know that all dogs carry defective genes and that “totally clear” dogs do not exist.

Nobody knows how many defective genes exist in a breed’s genepool. Some sources say that each individual dog carries at least 3 to 5 mutated genes.

The higher the coefficient of inbreeding (COI), the more effect of such genetic disorders (for example HD and cataract) was established in canine breeds (Labrador, German Shepherd, Cocker Spaniel) that were subject of researches.[65]

Several DNA-tests to detect the presence of a mutation are available. Some of them are “cocktails” and can be used to identify multiple mutations by doing one single test.

Many of those tests are however breed-related and not yet developed for the Rottweiler. Why not ? Possibly because of a lower prevalence and so a lack of need for those tests or, maybe, because the Rottweiler lover just was not interested enough yet and research was not yet initiated or supported ?

[65] I hear that in Belgium, 80 % of Golden Retrievers originate from only 2 popular sires. This is an extreme example whereby the Coefficient of Inbreeding is relatively low, but the genetic diversity is strongly reduced, resulting in increasing prevalence of epilepsia, hip dysplasia and cancer(s).

Doing all known tests on all breeding dogs and trying to find even more tests to identify also all other recessive genetic defects in an attempt to breed only with totally “clear” dogs towards a perfectly clear breed pool, is not realistic and would probably even have an extremely harmful impact on the genetic diversity of the breed.

No dogs are totally clear of mutated genes. They can be declared “clear” for the genes that they were tested for but they will then still carry (many) other mutations and pass those on to their offspring.

Should we decide to exclude all known carriers of all known defective genes and then test the remaining dogs on even more mutations to exclude again all carriers, we would only decrease genetic diversity and would concentrate other recessive mutations that are now not yet expressed but would now too become so concentrated that they would become homozygote in the genotype and emerge in the phenotype.

This would in other words lead to an ever smaller pool of breeding dogs, while at the same time the carefully bred and valuable breed specific characteristics of all excluded dogs would go lost.

Closing the genepool even more, is certainly not an answer.[66]

We must respect nature. It may sound hard but genetic defects exist and will always exist. They should be fought where necessary and realistic but we must make balanced decisions, indeed with particular attention for the health of the dog but also with respect for breed specific characteristics, including a correct temperament, a correct conformation, a correct and breed specific functionality, …

There may be no discussion on the fact that breeding combinations that will or will probably produce sick (= affected) offspring, must be avoided or forbidden. We should therefore not breed with sick dogs as they are homozygotes for the recessive mutation or homozygotes or heterozygotes for a dominant defective gene and will certainly pass the gene to their offspring.

There may also be no discussion on the necessity to test for genes that are responsible for life-threatening or life-shortening diseases (for example Juvenile Laryngeal Paralysis, Subaortic Stenosis) nor about the necessity to test for genes (if DNA tests are not existent : for symptoms of those disorders) that cause serious pain or that reduce the essential functionality and quality of life (hip dysplasia, elbow dysplasia, OCD, …).[67]

We must indeed test our dogs on those affections and deal wisely with the results, but even then not necessarily by resolute excluding all affected dogs or carriers from

[66] Cfr. the FCI International Breeding Strategies : As a general rule, a breeding programme should never exclude more than 50% of the breed; the breeding stock should be selected from the best half of the breed population.

[67] Cfr. the FCI International Breeding Strategies : “Screening should only be recommended for diseases and breeds where the disease has major impact on the dogs’ functional health”.

breeding.[68]

To the contrary, all conclusions learn that the genepool must be as broad as possible, even if this means using dogs that are mildly affected or are heterozygote carriers of a recessive mutation.[69]

Not wanting to re-invent the wheel, I refer to the text that was published by the FCI on International Breeding Strategies.

Concerning the necessity to limit inbreeding :

- To preserve, or preferably extend, the genetic diversity of the breed, matador breeding and heavy inbreeding should be avoided.
- Mating between siblings, mother to son or father to daughter should never be performed.
- As a general recommendation no dog should have more offspring than equivalent to 5% of the number of puppies registered in the breed population during a five-year period. The size of the breed population should be looked upon not only on national but also on international level, especially in breeds with few individuals.
- As a general rule, a breeding programme should not exclude more than 50% of the breed; the breeding stock should be selected from the best half of the breed population.

The same text guides concerning the selection criteria :

- Only functionally and clinically healthy dogs, with breed typical conformation, should be used for breeding; i.e. to only use dogs that do not suffer from any serious disease or functional disabilities.
- If close relatives of a dog suffering from an inherited disease or functional disability are used for breeding, they should only be mated to dogs from bloodlines with low or no occurrence of the same disease or disabilities. If a DNA-test for the disease/functional disability is available, the breeding stock should be tested in order to avoid mating of two carriers.
- Mating combinations which from available information increase the risk of serious diseases or functional disabilities or impairment in the progeny, should be avoided.

[68] Example, the legislation in Flanders that imposes obligatory testing of the Rottweiler prior to breeding, explicitly forbids all regulation that limits the use of a dog for breeding if it was tested on the concerned genetic disorders. Part of the legislation is that the results of those tests must be collected and made available by a recognized breeding committee for all who is interested. It is left to the wisdom and appreciation of the breeder to use that knowledge when deciding to use the dog or not.

[69] Instead of resolutely excluding dogs (which may in some cases be necessary of course), regulations might also choose to give breeding advice on the combinations that are allowed, encouraged or discouraged. Of course for this, scientific guidance is called for.

- Screening results (positive or negative) for phenotypic appearance of polygenetic diseases should be available in open registries. The results should be used to aid the selection and combination of breeding dogs.
- Breeding values based on screening results should when possible be computerised to facilitate selection of the breeding stock not only on the phenotypic appearance but also by indicated genotype. As a general rule the estimated breeding value for a combination should be better than the average for the breed.
- Screening should only be recommended for diseases and breeds where the disease has major impact on the dogs' functional health.[70]
- Results from DNA tests for inherited diseases should be used to avoid breeding diseased dogs, not necessarily to eradicate the disease. Dogs shown to be carriers (heterozygote) for a recessive inherited disease should only be bred to a dog that is proven not to carry the allele for the same disease.
- Health issues that cannot be diagnosed by DNA-tests or screening programmes should have equal impact in the breed specific breeding programmes.

I cannot add to this, only the firm intention of the IFR-Board to discuss this in the context of the IFR and to create actual awareness, not just talking about it on social media but demanding for concrete action and this, if feasible, coordinated on an international level and with scientific guidance.

[70] It is clear that the FCI expresses the concern that testing on all known genetic diseases would lead to excluding too many dogs from breeding and would limit the genepool even more. Therefore, there should be no obligatory testing on disorders that are not life-threatening or life-shortening but that are for example only of an aesthetic nature or that have only mild effects on the dog's health, functionality and life-quality.

An example of such a genetic disease that is not life-threatening is "Vitiligo", a skin disease that manifests through skin depigmentation. The condition is believed to be genetic and may be immune mediated. The condition is not life threatening, but more of an aesthetic nature. The extent to which the condition affects the dog is variable, some will experience full depigmentation while others will only have a depigmented nose. Its prevalence is unknown to me and I have only heard about the disease occurring in some Scandinavian lines.

Final plea

As said before, this brochure is only meant to discuss basic genetics and to create awareness of the problem of too close inbreeding or linebreeding and its correlation with the prevalence of genetic diseases.

The need to make the Rottweiler lover aware of this threat cannot be ignored and covers the need for scientific education on basic genetics, on genetic diseases and their correlation with line- and inbreeding and for guidance on the instruments that are available to fight the problem : amongst others the establishment and use of EBV and of COI, the need for more homogeneity in diagnostic and grading methods, the need for testing and for the publication of testing results and of course the need to cooperate with existing research programs.

I sincerely hope that the International Federation of Rottweilerfriends will actively support the idea of an international cooperation on the issue and ultimately of a common breeding strategy that transcends the individual litter but concerns the Rottweiler as a breed and then as a breed with a clear definition as a working breed, with characteristics understood on the basis of utility and health.

Sitting still is not an option, at least not if we hold the health and future of the breed close at heart.

Facta, non verba. The eyes of the Rottweilerworld are on us and rightfully so.

Dirk Vandecasteele
President of the IFR-Board.

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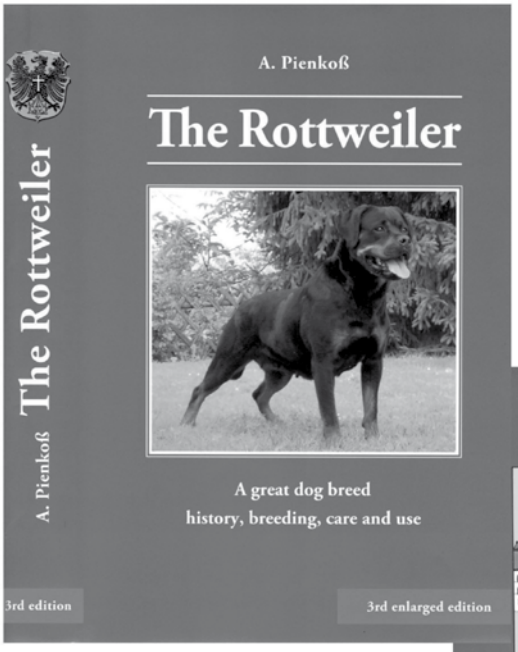
The Rottweiler

By A. Pienkoss



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This book is far more than just a description of a breed. Here, the reader learns about the historical development of dog breeding – a subject not everyone is familiar with – and about cynology in Germany.
The work is enhanced by numerous scientific articles written by renowned cynologists and behaviourists. The author appreciates the use of illustrations and uses plenty of them to help explain the text. Tips on how to keep and train dogs complete the book. Pienkoss' was a dog lover and the experience he gathered over a period of many years is evident here. This book is a gift – by writing it, the author has rendered a valuable service to us all.

Herbert Stemann in
„Deutscher Hundesport" 3/1984

Here was someone, who wrote down everything he knew about Rottweilers and his experience with them and made a book of it. It was not just anyone, it was Adolf Pienkoss. Perhaps that is why the book is a little like him: comprehensive, multi-faceted and not easy to digest in one sitting. One must take one's time. Some sections are fascinating and the reader is eager to read on; others are read more critically or only with great difficulty and some will be deferred until later, when problems arise and expert advice is needed. It is not a book for beginners; it is a reference book which has become indispensable to everyone devoted to the Rottweiler.

Fr. Schwandt in
„Rottweiler-Nachrichten" 3/1983

This new edition of Adolf Pienkoss' book guarantees that future generations will also be able to share his wealth of knowledge and experience with Rottweilers. This book is an essential reference work for all real Rottweiler lovers and breed fans. At the same time, this new enlarged edition shows how in today's ever faster changing society and the consequences thereof – positive or negative – greater demands are made of us and of our Rottweilers.

Henrik Bagdasarian
Public Relations ADRK e.V.
7/2008

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