



“Dobermann’s Genetic Management”

Dobermann’s Genetic Management

Translated by Gaia Santangelo

PRESENTATION

After having prepared this work in accordance with a decision taken by the **AIAD National Council** on June 2011, I decided to show it to the IDC president, **Mr Hans Wiblishauser** during the **IDC Presidium** meeting held in September 2011 in order to obtain his approval, and I gladly noted the keen interest of the entire Presidium, shown through the advice of carrying it forward on behalf of IDC, for the benefit of the Doberman world population. The following day, the **General Assembly of IDC Members** unanimously ratified the assignment. The time passed since that ratification was needed to re-elaborate the project, find a sponsor who could guarantee its realization and find a group of qualified researchers to accomplish it. The sponsor is the **Istituto Veterinario di Novara (Veterinarian Institute of Novara)**, belonging to the **“Policlinico di Monza Cliniche Private S.p.A.”** group.

I wish to express my gratitude and thank the President of the **Policlinico di Monza Cliniche Private S.p.A.**, **dr. Michelangelo de Salvo** and the vice president, **dr. Massimo de Salvo** from the bottom of my heart for their sensitivity towards dogs and their liberality.

The realization of the project was entrusted to the **Molecular Genetics Veterinary Service of the autonomous University of Barcelona**, directed by **Dr. Armand Sánchez**. Scientific responsible are: **dr. Armand Sánchez**, Service Director of Veterinary Molecular Genetics of the Autonomous University of Barcelona, **dr. Erik Zini** Scientific Director of the Veterinarian Institute of Novara and I.

For my vision, this ambitious project will mark the start of a scientific study that, as far as I know, has never been conducted or concluded and put into practice for any canine breed.

It may be modified, be a continuous work in progress, improved, but, from now on, the success of the project will rely mainly on the enthusiasm and commitment that each and everyone, **Clubs affiliated to IDC, breeders, members and Dobermann fans** will devote to its realization.

Viva il dobermann
Pierluigi Pezzano



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1.0 INTRODUCTION, BACKGROUND, COMMENTS AND PROPOSALS

For decades, the breeding of canine breeds has been conducted:

- without providing, a unique breed standard interpretation and judgment guidelines to breeders and judges both at a national and at an international level;
- without a clear definition of a target, which means without clearly indicating to breeders which dog they had to breed, with which morphological, attitudinal and character characteristics;
- without defining a selection strategy, which is in any case impossible to define without a target;
- without a method: often, all possible strains of blood and all different morphological types are used in a rambling mixture with no discrimination, since the breeder, lacking specific guidelines, is forced to rely on his unique experience, knowledge, intuition or to follow the trend.

The result is a population of purebred dogs, which is little homogeneous as far as the morphological and attitudinal characteristics are concerned and have unpredictable genetic inheritance. In brief, this represents the top risk.

One of the most revealing and common example of a conceptually and practically wrong breeding approach is the spasmodic research of the trendy stud dog.

This involves the same dog being overused for a large number of bitches in the same kennel or in more kennels at the same time.

This practice significantly reduces the number of dogs for reproduction, unbalancing the number of dogs and bitches and thus it reduces the dog’s contribution to the effective size and genetic variability of the population. In this regard, there is a recent FCI directive which refers to the need of limiting the offspring of both bitches and studs . That directive, suitably adapted to our breed’s needs, could be the beginning of a crucial turnaround for the improvement of the breeders’ strategy and therefore of the Doberman.

The principle on which the AIAD breeding Championship has been based since 1980 is that of proclaiming more than one club champion each year and it is designed to draw the attention on studs of different bloodlines to be used in breeding and therefore it is made to give the proper contribution from the dog to the genetic variability and effective population size of Dobermans. The attitudinal test required to aspiring club champions is intended to direct the breeders to use individuals with outstanding skills and natural qualities for reproduction.

It is well known that Dobermans with outstanding natural qualities have and can give an advantage of genetic fitness, even if they present some morphological faults.

The key strength of the European Doberman is that a the majority of breeders understood that there is just one Standard and that it is necessary to raise a unique breed according to the Standard as far as morphology, attitude and character are concerned. The phenomenon of the two “*non breeds*”, bred under the same Standard, one for morphology and the other one for attitude (and none of them take character into account) is widespread throughout Europe in utility and sport dogs. Thankfully, this phenomenon is far from the culture of the great majority of our breeders.

A second important key point is the passion that the Doberman creates in new generations: all those young people who fill our rings guarantee that our breed will have a future which is going to be much brighter than the present.

Also in my opinion our weaknesses are:

- a dominant vision focused largely on economic profits, which is understandable for breeders but goes to the detriment of adequate attention to health, morphologic, attitudinal and character controls;



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- the belief many have that the issue of breeding Dobermans can be reduced into a sequence of more or less planned matings of their bitch with one or more dogs. According to this vision, the reproductive cycle would be reduced to only three events: decision to mate, birth of puppies, sale. This hyper-simplified approach is risky. Each individual breeder should instead develop a breeding strategy, consistent with their culture and vision of the breed. Although it would be appropriate for each strategy to conform with some very general prerequisites defined by the breed clubs and by IDC. First of all, the breeder should aim at selecting their brood females. Only through the careful selection of brood females, generation after generation, can the breeder obtain the predictability of breeding results, thus reducing all risks. Breeding brood females without knowing their breeding history makes the results far less predictable, and therefore the selection and improvement work becomes more risky. In any case, however the breeder has begun his journey, the need to proceed towards a strict and careful selection of brood females is unavoidable: the selection of brood females is not an economic matter, it is a structural matter of the breeding strategy. The breeder should select within the normal type and the strain of blood belonging to their own brood females, aiming at first at consolidation with the careful use of linebreeding. Secondly, they should aim at an improvement using improved studs, having their reproductive qualities defined on statistic basis. However, they have to be aware that in any case, the expected value of the mating depends more on the brood female as in the ability of the stud to improve that specific brood female. Experience shows that a given stud produces the best results only with brood females having certain genealogic characteristics and not with every brood female.
- the ZTP test has a useful and effective role only in some countries, namely in those where it is widespread and commonly used. However, ZTP should become common practice in the world of Doberman breeding, although maybe it should be revised from a regulatory point of view in the part regarding the behavior of the Doberman in unfamiliar situations. By this I mean that in order to allow the widest possible diffusion of ZTP among breeders and members of various clubs affiliated to IDC, it is desirable for each country to adopt its Regulations and ask for the training and qualification of a judge-breeder who judges according to the criteria given by Doberman Verein e V. Prior to the Ztp test, each Doberman must take to a blood test to control the DNA. I would like to better clarify my position. As it is known, the Ztp has the function to indicate to the kennel which animals are suitable for reproduction and exclude those which are unsuitable. The Ztp is an easy test to pass for a normal animal and therefore has a selective function and as such it must be made easily accessible, not reserved just to the chosen few. In this sense, either the Ztp test becomes common practice in the Doberman breeding and the majority of dogs to use in breeding take the test or such test might lose its effectiveness and its value. If in a given country, the dogs who pass ZTP every year are only a dozen, their offspring will be the most sought after and this does not improve the breed the least. If the ZTP test is instead made easily accessible and extended to the whole breeding, it resumes its essential function of preliminary verification, which simple and uniform for the breeding. Over the last few years the test has already become partially known in various countries and it became familiar to many, but now it would be necessary to make a significant step forward;
- In some member countries of IDC the research on hip dysplasia and on other hereditary diseases is left to the initiative of breeders. It should rather be checked and validated by breed clubs and performed on protocols approved by IDC, if not already issued by FCI;
- a unique interpretation of the breed standard, including uniform judgment criteria to be submitted to the approval of the IDC Clubs House and circulated and adopted by all member countries of IDC is missing. Judging criteria may be changed periodically through reasoned and documented proposals contained in the Annual Report of the IDC upon discussion and approval by the IDC committee.



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It seems to me that the initiatives suggested to improve some of the problems listed above along with evaluations including a brief explanation of the choices of the judge (at least in the top events), could improve the performance of our breeding and contribute to the spread of a shared Doberman culture. Moreover, some of these initiatives have already been regulated in several countries. The explanation of the given judgment and of the differences between competitors in a given rank, proceeding by elimination from fourth place up to first, adds value to the work of the judge and makes everybody understand, even if not always agree with, the consistency of his vision on the breed. Another fundamental choice that should characterize the strong determination of IDC members in the fight against the common hereditary diseases, could be to make it compulsory for all candidates to the title of National breeding champion, club champion and IDC Sieger, to produce a certification excluding Dilated Cardiomyopathy (DCM), which must be issued by a Veterinary specialized in cardiology and trusted by the club.

1.1 TARGETS, MEASUREMENTS, GENIC CONTROL, ESTIMATION OF HERITABILITY

The adoption of an integrated and shared program for improvement seems to be the only way to follow in the medium term leading to the acquisition of a uniform breeding culture and to the genetic enrichment of our kennels. Not only the breeding improvement has to be taken into consideration, but also and most of all the defense and protection of the health and quality of life of our Dobermans, which means acknowledging the need to prevent and combat prevalent diseases. This is the bet upon which depends the future of the Doberman.

The first step in planning an improvement program consists in:

1. a clear definition of the breeding goals, which often requires a greater commitment than that used in the execution of the final part of the project, the goals do not necessarily have to be static, but are subject to change in time following the acquisition of new knowhow;
2. the identification of the measures and regulations to follow. At this point, the general use of the ZTP test becomes of vital importance;
3. the investigation on the kind of genic control exerted by the genotype of the individual and / or the population;
4. the estimate of the relative influence of inheritance and environment on the character or characters which are being observed.

The first two steps are common to all methods aiming at improving animal production. Once the goals and the rules for detecting the parameters have been defined, the task of the breeder who wants to acquire and transmit the improvements is the application of the following two steps (3 and 4).

From the following analysis, it will be better understood that the critical issue for an improvement plan related to a specialized breed such as the Doberman, is given by the objective difficulties to match the economic and improvement needs with those related to protection. Moreover, the breeding strategy of the individual will have to find a balance between genetic variation and consanguinity through the knowledge of the genomic structure of the race.

The management of the genetic variability and the genetic improvement of the Doberman is anyway a primary challenge that the Doberman breeding has to handle with courage and determination, considering the new molecular genetics discoveries and the further on going scientific studies identifying the causes and the genomic localization of some hereditary diseases.

The present genetic variability of this breed constitutes a precious heritage that has to be deeply known to be properly handled and that needs to be strongly defended and preserved for the years to come.

The genetic management of the Doberman population needs particular care not only because of its genetic history, which has broadly been discussed, but mainly due to the recent severe birth reduction in Europe, essentially related to the adoption of fake animalistic rules that are creating an irreparable zootechnical damage and a cultural carnage. If we add to this the **selective pressure** endured by the Doberman, which is



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not always rational, focused and careful, the risk of a further reduction of its genetic variability becomes real.

The common thread of the whole project is based on the following beliefs:

- the selective pressure, however great or little, acts on a given population by affecting the gene frequencies;
- *the Dobermann population will be considered stable when it is going to reach an adaptive peak, obtained through selection, which acts on the entire genetic structure.*

The genetic management of a selected and highly specialized breed such as the Doberman, contributes to its genetic improvement and therefore guarantees its future, growth and diffusion. The genetic improvement cannot be separated from a known, experienced and shared simplified scientific approach. The main aim of our job is to provide the breeders with knowledge and a set of useful and easy to use tools in order to obtain a strong support, based on solid scientific basis so that they can direct their selective choices and obtain healthy and strong Dobermans, *normal* in their morphological conformation and excellent in attitude, nature and character.

However, it is important to keep in mind that the control, the preservation and the improvement of genetic variability, which is fundamental goal for the Doberman, includes reasoned selective goals that should somehow limit the increase of consanguinity in Dobermans and mostly the use of a limited number of dogs in the majority of matings. In particular, the restriction of inbreeding, creates quite a few operational and cultural difficulties. For this reason, the role that IDC will play in the study and in the shared and informed circulation of the choices resulting from the conclusions of the study proposed here will be essential.

As to what stated in the introduction, first of all the problem of assessing the level and the effect of consanguinity in the Doberman population will have to be solved by creating a single file for the registration and the processing of the data related to the descendants contained in each pedigree.

Every year, the data of the newborns will have to be entered in the file. At that point, to certainly determine what the risks of increasing the inbreeding level are, it will be necessary not to see these data as an absolute value, but to correlate them to the genetic improvement of the population.

The increase in the level of consanguinity among the individuals belonging to a certain population is an essential effect of the genetic improvement. The breeders know that if only the best subjects are chosen to obtain the following generation, in the latter there will be newborns which are even more related to one another than those of the previous generation.

Therefore, the genetic improvement increases the animal performance and also the consanguinity, but the latter also to some extent reduces the performance.

Thus, the choices are to be made balancing these two effects. It is also to be taken into consideration that the impact of an increase in consanguinity is not linear: the inbreeding depression is reduced when the levels of consanguinity are low, but when they increase, the problem becomes more evident. Consanguinity is not even the only criterion that can be used to control genetic variability in the population and following only this principle may turn out to be insufficient. Consanguinity strikes when two individuals not related to each other are mated but the genetic variability in the population remains unchanged. The control and the management of inbreeding and genetic variability is a highly complex operation which may require some sacrifice also from the point of view of selection.

If it was necessary to reduce inbreeding, it would be necessary to proceed with a reasoned effort both from IDC and national breed clubs, which should supply the technical tools, and the breeders who are to choose every single mating. Only the awareness from all parties and their joint effort will provide maximum results with minimum sacrifice.



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In any case, the use of concrete and properly supported indicators, provides all the clubs of IDC member countries with powerful means that will be used in the future in the selective choices which will turn out to be useful guidelines for breeders and members.

As to the relationship among Clubs and with IDC, the study will constitute a milestone that will help to understand the bonds existing among all the breeders worldwide.

Once the project comes to an end, the various operational aspects herewith underlined, will have be discussed and extensively dealt with in order to be agreed and planned.

At that point, we will be also able to effectively attribute the breed genetic identity of a single animal (*attribution of the racial identity*), starting from any kind of biological sample: hair, saliva, sperm and blood.

At the same time, it will be possible to determine the level of actual reliability of a paternity test.

These two points could be of crucial importance for the official identification of the selected studs or for the registration of an individual to the breed or in case the animal is of a foreign origin.

But above all, we will be able to know exactly the health condition of the breed and to arrange a reasoned plan of breeding and of containment and eradication of the genetically transmissible diseases prevalent in our breed.

The first phase of the project is based on three principal lines, which are characterized by a genetic-molecular approach, a genealogical approach, and by a biometric approach, respectively which provide:

1. the definition of the genetic parameters of the population and the analysis of the genetic variability;
2. the assessment of the values of consanguinity and kinship;
3. the assessment of the phenotypic and genetic parameters of the quantitative features selected for the breed and the phenotypic and genetic indexes of the reproducers.

The second phase of the project is characterized by:

- the assessment of the risk factor for both the monofactorial and multifactorial diseases, which are prevalent in the Doberman breed;
- the assessment of the genetic parameters of multifactorial diseases;
- the plan to detect and prevent genetic diseases in the Doberman;
- the detection of recessive diseases carriers through genetic, biochemical and instrumental screenings;
- the indexation of the reproducers and the assessment of the risk factor for the monofactorial and multifactorial diseases;
- the modelling of the control plans and the reduction of the monofactorial and multifactorial diseases;
- the risk assessment of multifactorial diseases for each reproducer;
- the assignment of the individual and racial identity;
- paternity and maternity tests.

The project answers some questions that Doberman breeders, Clubs, owners and fans usually raise. In the discussion of the results, both the data obtained from the registry data and those produced by the analysis of molecular genetics carried out on the genoma of the sampled Dobermans, will be analyzed and discussed with the purpose of advising the breeders in their future choices.



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1.2 GENETIC VARIABILITY

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Genetic variability in a population is important for biodiversity, because without variability it becomes difficult for a population to adapt to environmental changes, which therefore makes a population more prone to extinction. Characterization and evaluation of genetic variability can provide a useful tool for investigating the individualization of suitable strategies in the correct management of the genetic patrimony of canine populations, even if they are characterized by a relatively small *effective population size* (N_e), such as the Doberman’s might be.

In that respect, the tools provided by molecular biology make it possible to deepen our knowledge of the level of variability and of the genetic stratification of our population of Doberman.

This makes it possible to reach high levels of accuracy in the assessment of the principal genetic population parameters that define the fundamental indicators for verification of a correct management of the available resources and enables optimization of the breeding management.

The adoption of optimal strategies of selection that take into account the preservation and improvement of the genes of the canine breed being bred represents, in fact, a fundamental requirement for the recovery, the defence and the valorisation of the canine populations and, with them, of the historical-cultural and ethological values associated with their primary utilisation activity.

Questioning the causes that determine a loss of Genetic Variability is the first step towards responsible management of the future of a breed.

When a breed sets out towards a condition of limited genetic variability, the Club of Breed that manages it has great interest in trying to understand what caused this status quo, but it also must manage conscientiously the breed over which it has responsibility, so as to try to change its course, if the current one is leading the wrong way, and it must find, as soon as possible, suitable remedies, taking advantage of the resources that science provides.

An important aspect in the defence of breeds with a limited effective population size has to do with managing reproduction with a view to maintaining and amplifying genetic variability.

The need to protect genetic variability in canine populations stems from:

- the need to preserve useful allelic forms and to prevent the excessive homozygosis fixation of those allelic variants that bring about genetic diseases.
- the need to preserve a useful variability, in case of possible changes in the selection goals;
- the need to avoid an impoverishment of variability that can cause, furthermore, a reduction in fertility and prolificacy;
- motivations of historical, cultural and ethical order, since genetic variability represents not only a resource to defend and to pass on to those who will have to manage it in the future, but a valuable asset per se.

The general actions to be undertaken within a framework of genetic preservation of the breed include:

1. identification and characterization of the breed, underlining its peculiarity and its potential in terms of contribution to the maintenance of biodiversity and of the relative vocational use;
2. the development of actions that also favour an economic valorisation of the breed, as an effective tool of incentive which is based on the exploitation of those historical-cultural traditions associated with its breeding, and which may give a new impulse to the exploitation and diffusion of the same breed;



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3. the adoption of politics and appropriate normative aiming at involving and finding new synergies among all the interested parties (private citizens, IDC, National clubs and the veterinary and academic world);

In view of the above, it shall appear that monitoring and managing genetic and demographic parameters of a population is of great importance within a framework of genetic preservation.

Generally, nowadays, the term “fatality” can no longer be used, even in connection with a race with a limited effective size or a so-called “relic risk” breed, because molecular genetic studies can indicate the actual genetic variability backup in a population, and because reliable means for managing and enhancing that genetic variability are available with targeted mating plans.

Still generally speaking, in the case of a population faced with a real risk of extinction, an emergency action involves mating as many male breeders as possible - under drastic conditions, in practice using all existing breeders with the obvious exception of those having hereditary taints.

Under these extreme conditions, race selection becomes less important and one is forced to accept as breeders those animals that, under normal conditions, wouldn’t be selected as such.

Fortunately, our Dobermans are not under these conditions yet, and we were able, over the past few years, to maintain a certain level of births, thanks to the fact that in several European Countries it is still possible to cut the tail and to remodel the ears.

Last but not least, this result was achieved by virtue of the strength of mind and the perspicacity of president **Hans Wiblishauser** who has succeeded in upholding the Standard of race of the Doberman. We are grateful to him and to all our German friends and Doberman breeders.

Science tells us, however, that a decline in the effective population, i.e. the population that is actually involved in reproduction, has a lethal effect on the survival of any race. Based on this principle we should carefully consider that, since we must intervene as soon as possible to remedy and reduce the prevalence of inherited diseases that plague the Doberman, it will be immediately necessary to gradually or suddenly exclude from breeding any affected individuals. This unavoidable action will naturally lead to a further significant reduction of the effective population.

Under those conditions, an internal change of address as concerns admissibility to shows of Dobermans with docked tail and cropped ears, would be disastrous.

For these reasons, in the name of the Doberman, its history, its reality, its fairness and its future, we hope that the Doberman Verein e.V continue, as they have done so far, to operate with strength and determination to protect the breed.

1.3 GENOMIC MARKERS

The use of genomic markers and sequencers has proved to be an extremely useful tool, in that it has enabled, directly based on molecular information, the assessment of fundamental parameters like the *effective population size* (N_e), the detection of bottlenecks and the determination of the contribution of the founders (founder effect) in the history of the population; the assessment of the level of inbreeding of the individuals, the presence of gene flow and admixture with other breeds, the presence of genetic stratification inside the population and finally the assessment of parameters for the evaluation of intra-race variability, like *gene diversity* and *allelic diversity*

The use of molecular markers can provide an important support for the constitution of a genomic profile that makes it possible to get the maximum accuracy and reliability from pedigree information.

Modern techniques are the best investigation tool for developing suitable strategies in the correct management of the genetic patrimony of canine populations.



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1.4 INBREEDING AND RELATEDNESS

Inbreeding results from the mating of animals that are related. The higher the degree of relation between the two parents, the higher the inbreeding in the children.

Inbreeding is expressed by a coefficient that can assume any value between zero (no consanguinity) and one (maximum theoretically possible consanguinity with auto-reproduction, and therefore the vegetable kingdom).

The coefficient of inbreeding of a subject (Fx), that is equal to the kinship of its parents or to a half of the coefficient of additive relatedness among the two parents, is an indication of the mean percentage of homozygous loci for descent.

In other words, it expresses the mean fraction of the genetic patrimony that an individual receives, identically, both from its father and from its mother, by virtue of the fact that its parents were related.

The calculation of the coefficient of inbreeding of the individuals (Fx) is very useful and it must be carried out and monitored in a breeding, in order to avoid the negative effects that derive from an excessive use of consanguinity.

Inbreeding causes an increase within the population in homozygosis and a reduction in heterozygosis (in the genotype of subjects of consanguineous parents there is a more frequent presence of two identical alleles for a determined gene, which transmitted by the ancestor common to the parents (one through each parent)).

The coefficient of consanguinity increases if mating among relatives is repeated in subsequent generations. By way of example, when mating a male and a female which are born from the same dog yet from different mothers (half-siblings of the father), the coefficient of consanguinity of their puppies will be 0,125.

If this type of mating is repeated, the coefficient of consanguinity will reach the value of 0,219 in the second generation, of 0,305 in the third one, of 0,381 in the fourth generation, of 0,449 in the fifth generation and so on.

A breeder normally tries to avoid mating among first- or second-degree relatives (close relatives), but we must not forget the so-called "back-ground Inbreeding", i.e. the consanguinity that accumulates generation by generation.

It would therefore be necessary to monitor and calculate the coefficient of inbreeding considering the contribution of inbreeding of the common progenitors (*Fa*) in the pedigree for at least seven antecedent generations, with a view to avoiding reaching a critical level of consanguinity.

Consanguinity of a subject does not transfer to its progeny if this is mated to a subject that is not a relative: if two subjects that share kinship yet are not related are mated, the consanguinity in their progeny will be drastically decreased

As concerns what coefficient of consanguinity should be considered dangerous, in other words the value that should not be exceeded, there are conflicting opinions.

In general, we must bear in mind that any coefficient of consanguinity is exempt from the inbreeding depression, and that the negative effects are proportional to such coefficient, and values greater than 0,100 must be kept under close control.

The main objective of this part of the research has been to estimate, for every subject, the values of consanguinity (Fx), the inbreeding coefficient, the kinship coefficient, the medium inbreeding coefficient, the value of its average annual growth, the value of the inbreeding increase per generation in relation with the values of the effective population size (Ne), and therefore to the vitality and genetic variability of the race. For the calculation of a part of these data, use can be made of the database of **WinBreed** that contains over 150,000 pedigrees of Italian and foreign Doberman and which, for almost all the recorded subjects, allows to trace back for fatherly and/or maternal line *over thirty generations*, up to the progenitors of the breed which been born in the last years of the XIX century. To these data, all data from countries members of IDC shall be added, i.e. data relating to Dobermans born in the last ten years and taken directly from the database of different Nations.



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Consequently, these data shall be certified and it will be possible to give breeders a very reliable tool for the definition of programmed mating schemes, aiming at reaching selection targets. Besides, as an application of the study of the values of relatedness, the breeders which have had in the past, and those who currently have, a genetic weight in the Doberman population.

1.5 HERITABILITY OF THE QUANTITATIVE CHARACTERS

When assessing the genetic value of a Doberman, what matters is the information it transfers to its offspring. In order to implement a plan of genetic improvement, it is necessary that those animals be selected which are capable of transmitting to their offspring the group of most favorable alleles. Furthermore, in the gametes, we do not find exactly one of the homologue chromosomes that are present in the parent but, due to a phenomenon called crossing over, a mixture is found of fragments coming from the two original strains. This is the main reason why even two proper brothers may have different reproductive capabilities. One should also consider that the most interesting characters are polygenic, i.e. their capability of expression is the result of the combined effect of several genes, each of which affects the final outcome differently.

Heritability of a character is a precise and well estimable genetic parameter, which can take values from 0 to 1. This coefficient has two major utilizations in genetic improvement: it is used to estimate the additive genetic value of the parent and to predict, based on the improvement strategy chosen, the expected genetic progress in the population, also known as genetic increase. There are, however, several elements which have not been studied in detail:

- 1) the exact number of the genes involved in the manifestation of a single polygenic character is unknown;
- 2) the exact positioning of all these genes within the genome is unknown;
- 3) the exact value of the contribution of each single gene to the ultimate manifestation of the characters has not been determined;
- 4) it is not possible to assess which parental alleles have been transmitted to the son/daughter.

For the time being, therefore, the only alternative is obtaining estimates of genetic indexes starting from the “end”, i.e. from the phenotype data and following a hindsight reasoning.

1.5 ESTIMATION OF GENETIC INDEX

The genetic index is a measure of the true genetic value of an animal of a determined character or, better even, the expected performance of the offspring of an individual. For the estimation of animal reproductive values two information sources are used:

1. the relationship between animals in the population: as it is known, a half of the genes of each parent is transmitted to offspring.
2. phenotypic records, which are measurements of what can be detected, and are the manifestation of the sum of additive genetic effects, non-additive genetic effects and environmental effects, which are specific to each animal.

The measure of a character by itself depends, in fact, on both a genetic component, transmissible to the descent, and on an environmental component, that cannot be transmitted and that can be modified with time.

Among environmental factors for example are the effect of the feeding and the management of the dog that depend only on the ability of the breeder or the owner and not on an intrinsic and transmissible ability of the animal.

Calculation of genetic indexes has the objective to separate the genetic component from the environmental influence, so that a classification of the best animals based on their genetic value is made possible.



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The genetic evaluation can be made only based on characters that have two basic requirements:

- they must be measurable characters. To make a genetic evaluation there must exist phenotypic records that can be both objective and subjective.
- Obviously, the more accurate and objective the records, the more correct the reproductive estimation value;
- they must be heritable characters, i.e. they must be controlled by genes. The higher the heritability of the character, the more accurate the estimation of breeding values.

It is hard to obtain accurate estimations of low heritability characters. The selection goal for us is to obtain an “ideal animal” that has “average” morphologic characters. Each breeder will be able to do different matings in order to obtain in his offspring those biometric data desired. For example, a breeder who has a female low in rear will be able to consult the index of males available for mating in order to select the one that transmits normal height at the withers.

2.0 SAMPLING

Sampling of biological material will involve the collection of peripheral blood, and extraction of Genomic DNA, which are essential material for the Molecular Genetics analyses. Blood has been the preferred matrix, because it is easy to collect and the amount of DNA extracted from this substrate is remarkable, plus it has excellent quality and purity, which are necessary for the storage and the maintenance of the sample.

The Genomic DNA extracted with these methods can be preserved and also used for future objectives of search for years to come.

The logistical organization of the samplings will be planned with the goal of obtaining the greatest number of useful samples for the research in the shortest possible time and, consequently, with the imperative to rationalize the flow of the samples to send to the laboratory while in the meantime rationalizing the collection.

All this will have to respect the necessary timing from the start and the carrying out of the planned research in one year. Considering the above, the subjects used for sampling will be determined on a scientific basis.

2.1 GENOMIC FILE

The samples of DNA, stored and preserved, will form a DNA bank for the creation of a Genomic File of the Doberman breed. The Genomic file not only fixes an image of the currently existing population that is realistic and conservable for the future, but it can also be constantly enriched and widened with the addition of new samples in the years to come.

Thus, we will be able to not only collect the DNA of subjects not related to one another, which will help us monitor the course of genetic variability within the population over the years, but also to collect the DNA of whole families with the purpose of starting the second phase of the project. Thus, through the various generations, it will be possible to monitor the transmission of phenotypic characteristic, of attitude and of the character that the AIAD intends to achieve via the attainment of selection targets. Up to a few years ago it was impossible to investigate the genetic base of attitude and training ability of the individuals. Today, thanks to the information generated from the genetic map of the dog, for the aforesaid characteristics, there are suitable precise chromosomal regions and candidate genes which are realistic subjects of study.

Results of the same search have indicated the existence of a clear inverse correlation between body weight and longevity of the dog, and precise chromosomes were located, defining a series of QTL (*Quantitative Trait Locus*), that are statistically significant, both in the existing inverse correlation between body weight and longevity, and in the ability to influence only longevity or body weight alone.

In the near future, in order to study the Dobermans genetic basis of these same characteristics, it will be fundamental to be able to access all samples collected and stored in the Genomic archive in consequence of the research of the present project.



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This Genomic File has not only the function of historical memory but it also takes on a fundamental value, if it is constantly updated through generations, so that it can be used for obtaining precious genetic information from the DNA of the Dobermans that, in a few years, will have ceased to exist. IDC will thus be able to follow and guide with effective and solid methods the course and the attainment of its own selective objectives of genetic improvement of the breed.

3.0 ALLELIC CONDIVISION AND BIOLOGICAL CONSANGUINITY

From the analysis of the genealogies of the subjects typified with genetic markers, we will proceed to the calculation of the coefficient of kinship for all possible couples using the whole genealogy of the pedigree. The level of biological consanguinity among couples of individuals can also be estimated by the level of sharing of alleles per genetic loci. The investigation of paternity based on the DNA is a typical application of this approach.

In the case of parent-son couples, at least an allele must be shared at every locus; it is possible, however, that both alleles are shared, if by chance the son has received from the other parent the same allele of the first parent.

Thus, the index of allelic sharing, defined as number of shared alleles divided by the total number of typified alleles, cannot be < 0.5 for parent-son couples, and it can considerably be also greater than 0.5 if the genetic variability of the loci in point is low, or if the two parents are related.

The same value of 0.5 is found in couples of proper brothers; in this case, however, it is an attended value, since two brothers can theoretically share zero alleles (with a 25% probability) 1 allele (with a 50% probability) and 2 alleles (with a 25% probability). Furthermore, in the case of brothers, the index of allelic sharing can be greater than 0.5 if the genetic variability of the locus is low, or if the parents are related to one another.

3.1 TYPE AND ATTITUDES VS/ GENOMIC PROFILE

The subjects genetically analyzed, if not in possession of ZTP, will be evaluated by a judge appointed by Dobermann Verein e V. for morphological aspects, vocational traits and the character. For these subjects we will formulate a table that shows the number of alleles shared in their allelic genomic, with the same genomic profile obtained for each dog that belongs to the rest of population that was analyzed by the molecular point of view and the judgment given by the experts of the breed, expressed as a score.

The subjects that will have the bigger number of alleles in common with the rest of the analyzed population will be those genetically more similar to the others, while those with a smaller number of alleles in common with the rest of the population will be more varying for genetic profile in comparison to the others.

For this reason these last subjects could be the most appropriate for the selection oriented to beauty and to sport activities with the dog, because they also associate with a good genetic variability also with good morphological and vocational qualities and good character.

One of the applications connected with the project and already widespread is the biological attribution of fatherhood and motherhood. The added value for the animals coming from that certification is, in all likelihood, greater than the typization cost, which, besides, continues to decrease by virtue of the improved analysis techniques. A solid prospect opened by the present research is therefore the possibility of performing gene typization for every Doberman to be sent on to breeding upon request of breeders or owners.

Another application of gene typization is the assessment of mutual combinability of animals destined for breeding.

4.0 SAMPLING OF ANIMALS FOR MORFOLOGICAL EVALUATION

To underline phenotype variability and sexual dimorphism, we will perform morphological measurements on males and females between seven months and seven years of age in occasion of most important Breed Meeting, and each dog will be photographed with systems that allow to also perform the somatic evaluation through a software.



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On each subject in correct position of *placed* and on plain ground, with the specific technical instrument to measure the height and with the meter, the following biometric measurements will be performed:

- height at rear; measured from the ground at the third back vertebrae
- circumference of the chest (measured caudally at the shoulder blade)
- width of the ilium (measured between the external tips of the ilium)
- width of the ischium (measured between the external tips of the ischium);
- length of the back (measured from the tip of the ilium to the caudal point of the ischium)
- circumference of the insteps;
- circumference of the metacarpus;
- height of the back (distance between the floor and the highest point of the back);
- height of the thorax (measured caudally to the shoulder blade);
- length of the trunk (measured from the scapulo-homeral joint to the ischiatic toberosity);
- length of the ear (if it is complete);
- length of the tail;
- length of the head (measured from the mean point of the occipital crest to the mean point of the antero-superior margin of the nose)
- wide of the head (measured in the zygomatic arch)

5.0 TECNICAL TERM DICTIONARY

ALLELE: in genetics, by allele reference is made to any vital form of DNA codifying for the same gene: in other words, an allele is responsible for the particular way in which a hereditary character controlled by that gene is manifested. By way of example, a gene controlling the “eye color” character may exist in two alleles (i.e. in two alternative forms): the “light-colored eye” and the “dark-colored eye”. It must be specified that by allele reference may furthermore be made to the different polymorphism that a non-codifying locus may have.

Every individual defined as diploid, as the majority of living things, possesses for every character, i.e. for every gene, two alleles, that is two copies; each of the two alleles is present on a same locus (position) on each of the two chromosomes that constitute, in a cell, a couple of homologues.

If on homologue chromosome there is a twin copy of the same allele, the individual is said to be homozygote for that character; if the alleles are different, then he/she is said heterozygote. Every character, within a population, may also be represented by many alleles (although each individual may only carry two).

The set of alleles present in a population is called gene pool. The frequency variability by which alleles appear in the gene pool is a study subject for the portion of genetics called population genetics. Not all alleles result in visible effects in the individual which carries them. If the character they control is manifested, they are called dominant alleles; in the other case, mention is made of recessive genes.

Therefore, an individual may be dominant homozygote, if he/she possesses two dominant alleles; heterozygote, if he/she possesses two different alleles; recessive homozygote, if he/she possesses both recessive alleles.

A dominant allele shall always be expressed, even though the individual is heterozygote. A recessive allele can only be expressed in recessive homozygote individuals. The set of visible characters in an organism is called phenotype, whereas the set of its chromosome complement (comprising therefore both dominant and recessive alleles) is called genotype.

By convention, alleles are indicated by a single letter – a capital letter is used for the dominant allele (e.g. A) and a lower-case letter is used for the recessive allele (e.g. a). Heterozygote (Aa) and homozygote individuals (AA) for a given gene have an A phenotype, because they manifest the effect of the dominant allele, whereas homozygote individuals (aa) manifest the recessive effect and have a phenotype.



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EFFECTIVE POPULATION SIZE (N_e): it defines the number of animals in breeding that could increase the consanguinity if they contributed equally to future generations. The effective Ransom of a population is represented by the relationship among effective number and the real number $N_e = N + \frac{1}{2}$

GENE: it is the hereditary unit of the living organisms. Genes are contained in the genoma of an organism that can be composed of DNA or of RNA and they control the physical and behavioural development of the organism. The majority of genes codify for proteins that are the macromolecules mostly involved in the biochemical and metabolic processes of the cell. Many genes do not codify for proteins, but produce non-codifying RNA, that can play a fundamental role in the biosynthesis of proteins and in gene expression.

GENETIC LOCUS: (or “Locus”, plural “Loci”) in biology and in evolutionistic computation, the term designates the position of a gene or another sequence inside a chromosome.

GENETIC PROGRESS: it is the modifying process of the genetic patrimony with the goal to improve useful characters in a species grown or bred. This process has been often done unconsciously and empirically through the selection of phenotypes that were considered better. Currently, thanks to modern biotechnological techniques, this process is a combination of phenotypic observations, coupled with genotypic knowledge as made available by the study of genomes.

GENERATION INTERVAL (L): it is the time that occurs between the birth of a breeder and that of an individual of the same sex that replaces it.

HEREDITABILITY: index of transmissibility of a quantitative character (h^2), it describes the portion of variability of the character that is due to genetic effects, it is a very important parameter for genetic selection. Characters with high heritability are selectable in an easy way; on the contrary a low heritability indicates that management aspects, rather than genetic ones, determine the observable differences between the animals.

HETEROZYGOSIS: in genetics, heterozygosis is defined as the genetic condition of a cell or an organism constituted by the presence of a couple of different alleles for a gene; the alleles occupy the same loci on the corresponding homologous chromosomes.

HOMOZYGOSIS: in opposition to heterozygosis, it is the genetic condition of a cell or an organism involving the presence of identical alleles for a gene.

INBREEDING COEFFICIENT (consanguinity): it relates to a single individual, and it measures the probability that a subject be homozygote for an identical allele by descent. The coefficient of inbreeding of an individual is equal to the coefficient of kinship of its parents.

KINSHIP: it is the probability that 2 individuals have, in their genetic patrimony, identical copies of the same allele from a common ancestor.

KINSHIP COEFFICIENT: it relates to two different subjects, and it measures the probability that two alleles of the same selected locus at random, one for each of the two subjects, be identical for descent.

POLYMORPHISM: it indicates the existence in a population of more than one allele for a given locus with a frequency greater than 1%

QUANTITATIVE TRAIT LOCI (QTLs) are regions of DNA associated with a particular quantitative character. QTL is strictly associated with a gene that determines the phenotype character in point or participates in its determination.

REAL NUMBERS OF FOUNDER (f_e) AND REAL NUMBER OF ANCESTOR (f_a):

The first one represents the number of founders that have contributed in equal measure and that we expect to always reproduce the same genetic difference.

The second parameter (f_a) is the minimum number of ancestors, not necessarily founders, that explains the complete genetic difference in a population.

This parameter does not completely account for the casual loss of genes from the ancestors in the population of reference, but it completes the information given because it considers the loss of genetic variability produced by an unbalanced use of the breeders and determined by the "bottleneck."

RELATEDNESS COEFFICIENT: it relates to two different individuals, and it measures the probability that they share an identical allele by descent on the one or on the other of the two homologous chromosomes. The coefficient of relatedness is the double of the coefficient of kinship.



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