# Inbreeding in Dalmatians

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# Inbreeding in Dalmatians

*James E. Seltzer, Ph.D.*

You have postponed the decision for as long as you can. Now you absolutely must make up your mind. Blossom is a terrific bitch. She epitomizes just about everything you have tried to produce during the many years that you labored carefully to select the ideal mates for successive breedings. Finally, your efforts paid off and you were rewarded with a Dal that finished quickly, took Best of Breed in a regional specialty, and, at three years of age has a CD and two legs toward her Open title. Ch Lotus Blossom of Bali Hai CD is going to be bred. But to whom?

**DEFINITIONS**

**Inbreeding** – The mating of relatives, or, more narrowly, the mating together of animals more closely related than the average of the population from which they come.

**Line Breeding** – The mating of later generations back to some ancestor or its descendents. Line breeding implies at least some level of inbreeding.

**Outcrossing** – Breeding from totally unrelated animals within a given breed.

**Cross Breeding** – The mating of two recognized breeds to establish a new variety or to improve an existing one.

**Assortative Mating** – The mating of individuals that are phenotypically similar. Assortative mating means mating like with like.

Not one to make such important decisions impulsively, you have been contemplating this mating for more than a year and have spent a lot of time carefully observing a number of potential sires for Blossom's first litter. Blossom has an outgoing and affectionate temperament; she moves with grace and elegance; she is typey, balanced, sound, and exquisitely marked. These are characteristics that you are intent on preserving into the next and succeeding generations if you have any way of selecting a stud dog that complements Blossom's virtues and manifests the Dal type for which Bali Hai Dalmatians have always been known.

Finally, after months of observing and studying potential mates, their progeny and siblings, and reviewing pedigrees, health and hearing statistics, you managed to narrow the field to only two Dalmatians. You really like both of these and are finding it difficult to choose between them.

The first candidate, Ch Tonkin Bali's Majesty, is a double uncle of Blossom's, line bred on the famous, Ch Frolictree's Majesty, who also appears many times in the pedigree of Blossom and other Bali Hai Dalmatians. Tonky is a best in show and specialty winner and is currently ranked among the top five Dalmatians in the country. You like this dog, and it is apparent that others do also, for Tonky is one of the most frequently used stud dogs in the breed and is vying for the record for the highest number of champion get. Tonky is the favorite among your trusted Dal friends, most of whom cannot understand your indecision.

The other finalist is Ch Taskmaster of Agrimony who is unrelated to Blossom, at least insofar as a search for common ancestors in their 5-generation pedigrees can reveal. Task has been line bred on Ch Dance of Merlin who was the foundation bitch of the Agrimony line. Dance of Merlin was an import and is not believed to be related to Frolictree's Majesty. Nonetheless, Task exhibits many of the characteristics that you have tried to encapsulate in your Bali Hai line. Because of the similarity, you were even asked by a fellow Dal fancier whether Task is a product of your own breeding.

You have spent a lot of time getting to this point in your breeding program, and you do not want to lose what you have already achieved. Perhaps breeding to Tonky is the better choice. On the other hand …

### *Measures of degree of inbreeding*

You realize that breeding to Tonky will mean a continuation of a fairly tight line breeding program. You have been told that close breeding in this manner and over a prolonged period can be risky, but you are uncertain just what this means. Further, you do not know how one can evaluate the risk when choosing a sire for Blossom's litter. In fact, you wish there were a way to quantify the degree of inbreeding for *any* proposed mating. Geneticists have provided just such a tool.

### Wright's Coefficient

Wright's coefficient is the most commonly used measure of the degree of inbreeding. The coefficient, $F_X$, tells us the proportion of genes for which the inbred animal is likely to be homozygous.[2] To be more precise, $F_X$, when calculated for a limited number of generations, tells us the relative level for which the inbred animal is homozygous compared with the average level for the breed as a whole.

$F_X$ is calculated as the sum of 1/2 raised to the power of (n + n' + 1), where n is the number of generations from the sire back to some ancestor common to both the sire and the dam, n' is the number of generations from the dam back to the same common ancestor, times the factor, $(1 + F_A)$, and the summation is over the separate contributions of each different common ancestor.

$$F_X = \Sigma\,(1/2)^{n+n'+1}\,(1 + F_A) \tag{1}$$

$F_X$ is the coefficient of inbreeding of the animal, x
$F_A$ is the coefficient of inbreeding of the common ancestor, A, when that animal is itself inbred

In many cases, it is easier to first calculate an approximate coefficient[1] as:

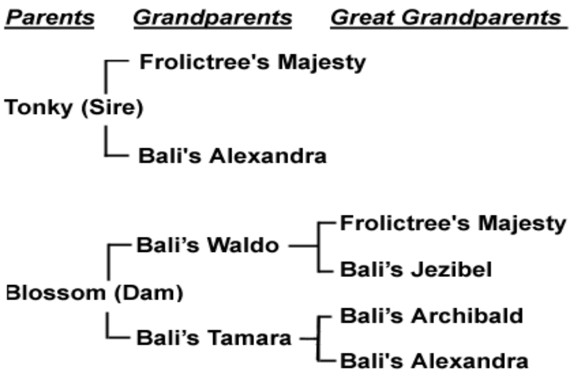
$$F_X = \Sigma\,(1/2)^{n+n'+1} \tag{2}$$

This is a simplified computation, which disregards possible inbreeding of the common ancestors. The coefficient of inbreeding, COI, is a measure of the degree of relationship between the dog's sire and dam. A mating of brother to sister, for example, yields an inbreeding coefficient of 25%, as does a mating of sire to daughter or dam to son.

We should note that the COI will be zero if there are no common ancestors on *both* the sire's and dam's sides of the pedigree. This is true regardless of the number of times that the same ancestor appears in the background of the sire or the dam alone.

Considering only a single term from the series for $F_X$, we can also interpret its value as the probability that at any specified locus on a chromosome, both alleles are identical and were obtained from the same ancestor, A, that is, *identical by descent*. If that ancestor, A, was inbred, then $F_A$ is not zero which implies that the ancestor already had an increased probability of being homozygous at the locus of interest.

Examining the pedigree for a litter resulting from the proposed mating Tonky x Blossom:



We observe that Majesty and Alexandra are both common ancestors. Assuming these ancestors are not inbred, a litter resulting from this mating would be inbred to Majesty at 6.125% and also to Alexandra by 6.125% , and the pups would have a COI of 12.5%. However, Majesty is inbred at 54.5% and Alexandra is inbred at 36.25%. Therefore the total COI for this proposed litter is actually 18.19% which some would consider rather high. Since Task and Blossom share no common ancestors, a litter resulting from that mating would have a COI of 0% despite the fact that Task and Blossom are both inbred.

## Percentage of blood

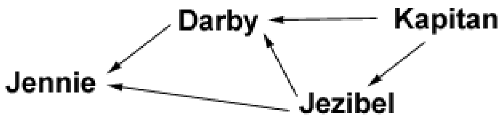
The Percentage of Blood attempts to measure the genetic contribution of a certain ancestor to a selected dog or a proposed litter[2]. It is calculated by summing the contributions for the ancestor each time that ancestor appears in the pedigree, and adjusted by the factor (1/2) raised to the power n, where n is the number of generations back in the pedigree, e.g., for a sire or dam, n = 1 and therefore the Percentage of Blood from either parent is 50%, for a grandsire or grandam, n = 2, giving a Percentage of Blood of 25%, etc. Several popular dog breeding books use Percentage of Blood when discussing inbreeding or line breeding.

If a prominent ancestor appears frequently on one side of a pedigree, say, the sire's side, but does not appear at all on the dam's side, then that ancestor might contribute a relatively high Percentage of Blood. Nonetheless, the inbreeding to this ancestor will be zero. A breeding program that maximizes the Percentage of Blood contribution from an especially desirable ancestor while at the same time minimizes the coefficient of inbreeding might build upon the genetic contribution of the selected ancestor while reducing the risks entailed in inbreeding.

## Relationship Coefficient

Sometimes it is important to know how closely two individuals that share common ancestors are related. Geneticists define the relationship coefficient as the proportion (%) of alleles in two different individuals which are identical by descent[3]. The relationship coefficient between sire or dam and offspring is 50%; between full sibs 50%; between half-sibs 25%. Wright's Coefficient of Inbreeding for offspring produced by mating two individuals is one half the relationship coefficient between the two individuals adjusted for their inbreeding (Van Vleck, p 217).

The relationship coefficient can be determined by tracing paths using arrow pedigrees. As an example, consider the arrow pedigree below. Jennie's double grandsire is Kapitan and her dam and grandam are Jezibel. Darby was mated to his dam Jezibel to produce Jennie.



To calculate the COI of Jennie we first compute the relationship coefficient between the sire, Darby, and the dam, Jezibel. There are two paths connecting Darby and Jezibel: a direct path from Jezibel to Darby and a collateral path through the common ancestor, Kapitan. The direct path has a single link and the collateral path has two links.

The relationship coefficient is computed as the sum of: .5 (for the link of length one for the path from Jezibel to Darby) plus $(.5)^2$ (for the link of length two for the path from Jezibel back to Kapitan and then to Darby).

$.5 + (.5)^2 = .75$

assuming that Kapitan himself is not inbred. The COI of Jennie is ½ of the relationship coefficient of her sire and dam (.75) which equals 37.5%.

## Major Histocompatibility Complex (MHC)

The coefficients introduced so far are statistical parameters based on the fact that an offspring receives one half of his genes from his sire and the other half from his dam. On average, he receives one quarter of his genes from each of his grandparents. However, he might, in fact, get from 0% to 50% of his genes from any one of his grandparents, and it is this random segregation of the parents genome in the formation of gametes that introduces the element of chance.

With the advent of DNA profiling it has become possible to remove some of the guess-work and actually determine, at least to some degree, the genetic composition of a selected individual. A number of years ago a Dalmatian fancier who was then engaged in the evaluation of tissue rejection in transplants introduced me to his studies in the major histocompatibility complex, MHC, in dogs and other vertebrates[4]. He told me about the existence in dogs of such a complex (DL-A) which is a set of closely linked genes that is best known for its role in the immune system, the production of antibodies, and the rejection of foreign tissue or infectious agents. The basis of immunologic disease is the ability (or inability) to discern self from non-self and to regulate a normal immune response. These genes being tightly linked and lying within a continuous gene region generally segregate as an entity during meiosis, yet as a group they constitute a diverse set of alleles estimated at least 80 million combinations in humans. Higher ordered species have been able to survive ever evolving microbial and carcinogenic insults due, in part, to the diversity of the MHC.

Because a high level of polymorphism (genes occurring in several different forms) at the MHC site is possible, lack of diversity at these loci can be used as an indicator of the inbred status of a population of purebred dogs. Homozygous alleles occurring at the MHC site limit the breadth of response that an individual can mount when challenged immunologically.

# *Consequences of inbreeding*

## General considerations

According to Falconer[5], the most striking consequence of inbreeding is the reduction of the mean breeding value of the individual especially with regard to characteristics related to reproductive capacity or physiological efficiency, the phenomenon known as *inbreeding depression*. Maternal qualities such as litter size and viability are among the most sensitive to inbreeding depression, although other attributes will suffer as well.

Every species and every interbreeding subpopulation within that species carries a number of defective genes that may be lethal or sublethal as homozygotes. The proportion of the population that suffer genetic death (that either die or are incapable of reproducing) because they carry these deleterious genes is called the *load* of the population, and as a result of this *load* the average fitness of the population is reduced. There is little doubt that Dalmatians as well as humans carry a significant genetic *load*, and it is because of this that inbreeding introduces significant risks. Inbreeding increases the probability that these deleterious genes, which are either simple recessives or polygenic, will be paired in the offspring. The more rare the specific gene in the population, the more impact inbreeding will have in bringing it to the fore. As an example: assume a specific defective gene occurs with an average gene frequency of .01 in a breeding population, that is, the gene is found in one out of every one hundred individuals . It will be paired as a homozygote and therefore expressed in a randomly mating population on average only once in ten thousand individuals. However, if the population is inbred with an average COI of 30%, this defect will show up on average in one of every three hundred individuals – a 30-fold increase in the rate of defectives.

Inbreeding with selection can be used in an attempt to eliminate defective genes from the breeding population, and a great deal has been written about such efforts. However, even with very strong selection against the homozygotes, the decrease in the frequency of recessive genes is extremely slow and many generations are required to make even modest gains in eliminating these defects.

At the opposite end of the breeding scenario is the phenomenon that is observed when inbred lines are crossed. The resulting progeny show hybrid vigor or *heterosis*, an increase in those characters that previously suffered a reduction from inbreeding. Generally, the fitness lost in inbreeding tends to be restored on outcrossing. However, a very highly inbred dam because of her own loss of fitness might have difficulty producing a viable litter even when mated to an unrelated dog.

## Wild populations

There is a revealing picture in an old issue of National Geographic[6]. It depicts a Florida panther seriously afflicted with a skin disease. The caption states: "One of only 30 to 50 of these cats left in the wild, this breeding male…is highly susceptible to the skin fungus, the result of an immune system deficiency probably brought on by inbreeding." As with many other endangered species too numerous to list, these panthers are probably doomed to extinction. As the interbreeding population diminishes, and unrelated mates cannot be found, inbreeding becomes the rule. Genetic diversity is lost, and the group simply succumbs to the mounting burden of its genetic load and an inability to adapt to the demands of a changing environment.

Unless the group is rescued by the infusion of diverse genetic attributes by migrations into the population, *genetic drift* will ultimately lead to the loss of genetic diversity. This loss via genetic drift is especially important in groups with a small *effective population size*, and this number is always smaller than the actual population[7]. As a rule of thumb, an effective population size of about 50 disposes a population to inbreeding depression. However, there is no magic number to determine at which point a species becomes unrecoverable, and there have been some notable successes starting with small populations. For the Mexican wolf, there were three founders captured in the '70s. In 1994, there were 91 living descendants. Though the average inbreeding is over 18% and the Mexican wolf is still endangered, a viable population has been preserved.

## Domestic animals

There has been a great deal of data collected on the effect of inbreeding of domestic and laboratory animals. Willis (p 328) observes that most breeds have evolved following some inbreeding at the start which led to a fairly rapid fixing of the desired breed characteristics when accompanied by culling those that did not measure up. However, excessive inbreeding has been found to be disadvantageous. Notable cases include the Duchess family of Shorthorn cattle which died out after the inbreeding level became excessive and infertility became rife. Inbred guinea pigs show severe declines in the litter size and weaning weight. Inbreeding in pigs has been found to lead to a decline in fertility and the ability to survive. Inbred dairy cows show reduced birth weight, increased early mortality, reduced milk yield and fertility problems. Willis (p 329) cites the effect of inbreeding on a Beagle colony with an increase in neonatal death from about one in 4 for inbreeding below 25% to nearly 3 in 4 when the inbreeding exceeded 67.3%.

An unpublished study has shown an apparent correlation between inbreeding levels and a decline in longevity in Standard Poodles[8]. Falconer (p 248) has cited several inbreeding studies two of which reveal declines in height and IQ scores in humans with increases in inbreeding.

Given the array of problems that can arise from inbreeding, one might ask what barriers nature imposes to minimize inbreeding. There are several mechanisms that are fundamental: the first is an apparent differential fertilization rate that favors gametes which are genetically the most diverse; another is a differential preference by females for mating with males that carry different MHC complexes; and still another is a higher miscarriage rate for fetuses that are homozygous at the MHC site, that is, the father and mother contributed similar MHC genes. Other behavioral barriers include the banishment of male offspring from the group after they reach maturity, and, even in some human cultures, the development of detailed tribal divisions that define which classes may intermarry.

One of the most interesting studies reported on the ability of women to discriminate by scent between individual men according to their respective MHCs, and the observation that women prefer and are more likely to marry men with MHCs that are different than their own[9]. Thereby the parents unknowingly select the proper mate so that their children are more genetically diverse. This same preferential selection of mates to avoid pairing with individuals that are similar at the MHC site has been observed in laboratory mice. Therefore, it seems that given a choice in mate selection, the nose knows. Anecdotal evidence abounds on the refusal of some bitches to mate with the BIS champion that the breeder selects, or if mated, failure to conceive, but nonetheless showing great desire to mate with the mongrel in the neighbor's backyard. Apparently the bitch can smell out the mate that can produce the fitter pups and will, given the opportunity, select him over any others.

Since the MHC genes are the key to immune function, it has been postulated that heterozygosity at the MHC site enhances resistance to a broader variety of diseases than does a homozygous MHC. Failure to respond to the challenges posed by various pathogens: parasites, protozoans, bacteria, viruses and prions can lead to an early death. To properly recognize the variety of possible invaders and to mount the correct immune response, the MHC is endowed with tremendous genetic diversity. If the MHC fails to identify abnormal cells, i.e. infected, foreign or cancerous, they will be allowed to proliferate and cancers or serious infections will result. Conversely, if the MHC sees its own cells as foreign, it will set about to destroying itself with equally disastrous results.

It has been observed that immune-mediated diseases are occurring with increasing frequency in pure bred dogs. Although the reasons for this are currently not known, several factors are implicated and these include both genetic and environmental influences, including increased use of multivalent vaccines, exposure to toxins and drugs, etc. In addition, the unintentional selection for susceptibility to immune-mediated disease along with desired traits, or a related decrease in the genetic diversity of alleles controlling immune system responses are an important consideration. The creation of a pure breed, by its very nature, is a genetic narrowing of allelic traits. Unfortunately, when selecting for desired characteristics, some degree of diversity is lost throughout the genome, including within the MHC. It is logical to assume that a loss of genetic diversity within the MHC limits both the range of self/non-self recognition and the intensity (too much or too little) of the immune response to stimuli. Indeed, several MHC alleles have been implicated in the pathogenesis of some immune-mediated diseases.[10]

## *Alternative breeding systems*

### Assortative Mating

Dogs can be alike in pedigree, appearance or both. If they are alike in pedigree, they are to some extent inbred. If they are alike phenotypically but unrelated, then geneticists use the term assortative mating if they are bred. It has been observed that matings in human populations tend to be assortative especially for such characteristics as height and IQ scores.

It is obvious that the practioner of assortative mating is attempting to mate best to best according to some commonly agreed upon standard or set of standards, and in order to be successful, one must be able to evaluate potential mating pairs for conformity to this standard. Selection by phenotype is very common in a number of European countries where inbreeding is strongly discouraged. It can also be employed as a mechanism to preserve type among those breeds for which registration is denied if the litter is too highly inbred. According to Willis (p 338), most German breeds are bred with very little inbreeding but much assortative mating and selection. Nonetheless, the result is a very uniform type among the dogs appearing in the show ring.

When assortative mating is applied to broad overall qualities that are generally controlled by large number of gene pairs, there will be some increase in homozygosity, but this will be less than that obtained as a result of deliberate inbreeding. Assortative mating, nonetheless, will increase the resemblance between siblings and between parents and offspring, and for the practiced breeder this is exactly what is desired. Phenotype breeding is still selective breeding, since the breeder is selecting those animals which show the desired traits, while minimizing the probability of doubling up on hidden, undesired ones. Inbreeding, on the other hand, selects for both the phenotypic and genotypic traits, and dramatically increases the probability of producing animals homozygous for defects with the possible concomitant effect of inbreeding depression.

## *Dalmatian population*

### Pedigree database

The author wishes to acknowledge the assistance of Robert VonMayr in providing and allowing the use of the database of Dalmatian pedigrees he has collected and authenticated. This database consists of approximately 20,000 pedigrees with data on sex, date of birth, titles, owner, breeder, and several other items of interest.

### Evaluation of the data

#### *General*

In an effort to assess the average level of inbreeding in Dalmatians this database was used to provide the Dalmatian pedigree information so that the average Wright's Coefficient of Inbreeding (equation 1, above) could be calculated. The computer program used for this purpose was an ad hoc modification of the "Visible COI" program written by the author and available as freeware on the web.[11] Several fundamental authentication procedures were employed in an effort to insure that the pedigree data were valid, and pedigrees that were not complete enough to perform the computations were rejected.

#### ***Number of generations***

Although the computation of the inbreeding coefficient using Wright's formula assumes that the computation can be carried out using an infinite number of generations, as a practical matter it is necessary to fix the number of generations that will be used. Detailed pedigree data is rarely available for any pure breed that allows the computations to be carried back to the origin of the breed, the so-called *foundation event*. Also the computer time required increases exponentially as the generations considered increase. Because of the depth of pedigree information available in the data base and the required computer time for the batch computations, 8-generation pedigrees were used in calculating the plotted Dalmatian COIs and 8-generation pedigrees were also used to calculate the inbreeding of the common ancestors, the $F_A$ factors used in formula 1, above . An 8-generation pedigree includes 510 ancestors – 255 on the sire's and 255 on the dam's sides. If fewer than half of the ancestors were known for either the sire side or the dam side, the data run was rejected.

As more generations are included in the calculation, the computed COI will increase. For line bred dogs, most of this increase will likely occur in the most recent few generations, and for the hobby breeder these are the most important. Previous generations can add to the COI but usually more slowly because of the reduced weighting in the formula by one-half for each generation back. Unless there are extensive duplicate appearances of the same ancestor in a pedigree, earlier generations are less important. However, genetic *bottlenecks* can arise because of very extensive use of a very popular sire by the breed fancy, or some catastrophic event can occur, e.g. WWII in Europe, that wipes out much of the breed pool, and such events will be evident as sharp rises in the computed COI. Barring such bottlenecks, the computed COI can be expected to increase only gradually with generations considered until the foundation event when it can be expected to rise sharply. It should be noted that the foundation event can occur over a large number of generations and span a considerable number of years; it can relate either to the breedings that created the breed and fixed many of the breed's essential characteristics or to the importation of a limited number of breeding individuals from the country of origin.

Figure 1 depicts the variation in Wright's COI for a single Dalmatian from the database computed using 4 to 10 generation pedigrees. This individual was the result of a full brother-sister mating, which were themselves inbred. The 10-generation COI of more than 43% is considered very high indeed.

## Classes

Information available from the database allows selection of individuals on the basis of a number of criteria. Most of the Dalmatians in the database are titled, and some have both conformation and obedience titles. It was surmised that evaluating the average COI status of all Dalmatians in the database as well as certain subsets might be revealing.

The data graphed in figure 2 is for all the Dalmatians for which there were sufficient data to perform the computations. The total number of Dalmatians considered was nearly 20 thousand of which 8,450 were usable. Although the average breed COI is only 6.34% and many of the Dalmatians in the database resulted from outcrosses with zero COI, there are nonetheless a considerable number that are more than 15% inbred.

### Champions

Sorting the database to include only those Dalmatians that were conformation titled resulted in a usable subset of 3738 individuals. Figure 3 depicts the distribution of 8-generation computed COIs for this subset. The average COI for champions is 6.01% with a maximum of 42.55%.

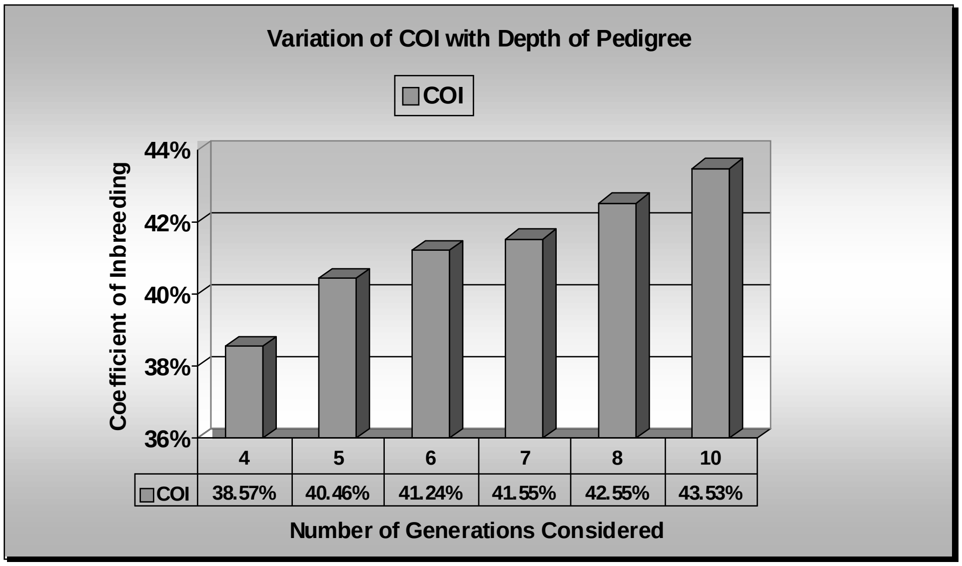


Figure 1 . Example of the variation of the computed COI for a single Dalmatian from the database as the number of generations that are used in the COI calculation is varied from four generations to ten generations.

### Obedience titled

When the database was sorted to include only those Dalmatians that were obedience titled, only 160 usable pedigrees were found. The inbreeding status of this subset reveals an average COI of 4.89% with a maximum COI of 19.16% which is significantly less than the conformation-titled subset.

This disparity between the inbreeding of conformation titled versus obedience titled dogs was not unexpected. Similar results have been observed in other breeds.[12]

## Summary of data

It was an unexpected and pleasant surprise to find that the average inbreeding status of the Dalmatian as measured by Wright's Coefficient of Inbreeding is a relatively low value of 6.34%, at least for this database and using 8-generation pedigrees. Unexpected, because other pure breeds have been found to have significantly higher average COIs; standard poodles, for example have an average 10-generation COI of nearly 19%. Whether this relatively low average COI for Dalmatians is an underestimation because of the limited size of or some unexplained bias inherent in the data set or whether Dalmatian breeders do, in fact, generally opt for outcrosses when selecting breeding pairs cannot be ascertained, yet one hopes it is the latter. In that eventuality, the average genetic health of the breed, relative to other pure breeds, is good, at least with regard to those characters most likely to suffer from inbreeding depression.

Yet within this database it is manifestly clear that some breed lines are highly inbred with inbreeding coefficients of nearly 43% – by any standard, these are highly inbred dogs. The available data does not allow the evaluation of general viability qualities or the correlation of these quali-

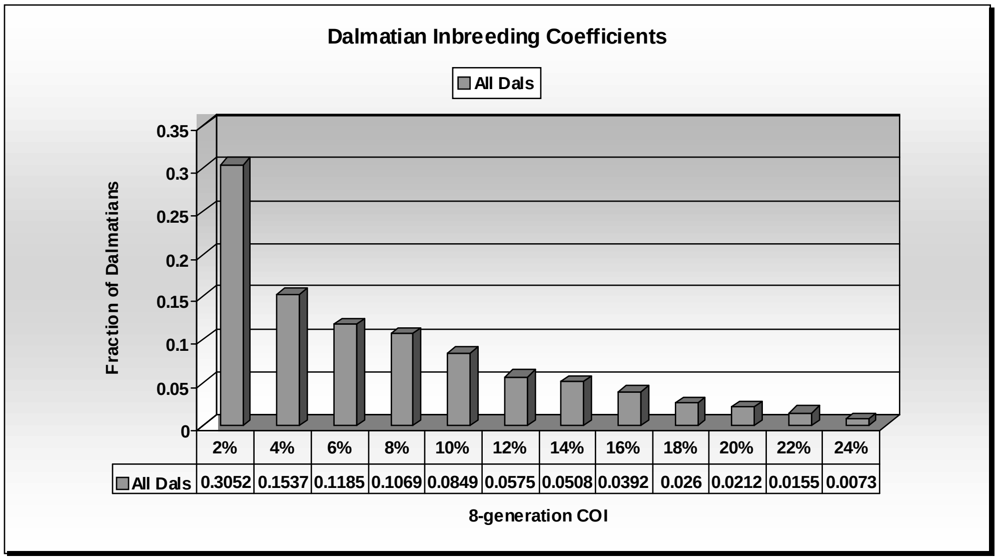


Figure 2. Distribution of 8-generation COIs for all Dalmatians in the database for which there is sufficiently complete pedigree information. [Average COI = 6.34% Standard Deviation = 6.06% Maximum COI = 42.55%]

ties with the level of inbreeding. In general, one expects some degree of inbreeding depression to become apparent even at levels significantly below this number.

It has sometimes been asserted that performance characteristics are most often expressed to a higher degree in outbred dogs. Thus one would expect selection for obedience, field or road work to favor outcrossing. These data actually do reveal a significant difference between the inbreeding status of champions, average COI of 6.01%, and obedience titled Dalmatians, average COI of 4.90%. Selection of breeding mates for obedience very likely is based on demonstrated performance skills and therefore tends to follow assortative rules. Conformation breeders are frequently more closely tied to pedigree analysis and, in attempting to line breed to top show winners, produce litters that are more highly inbred.

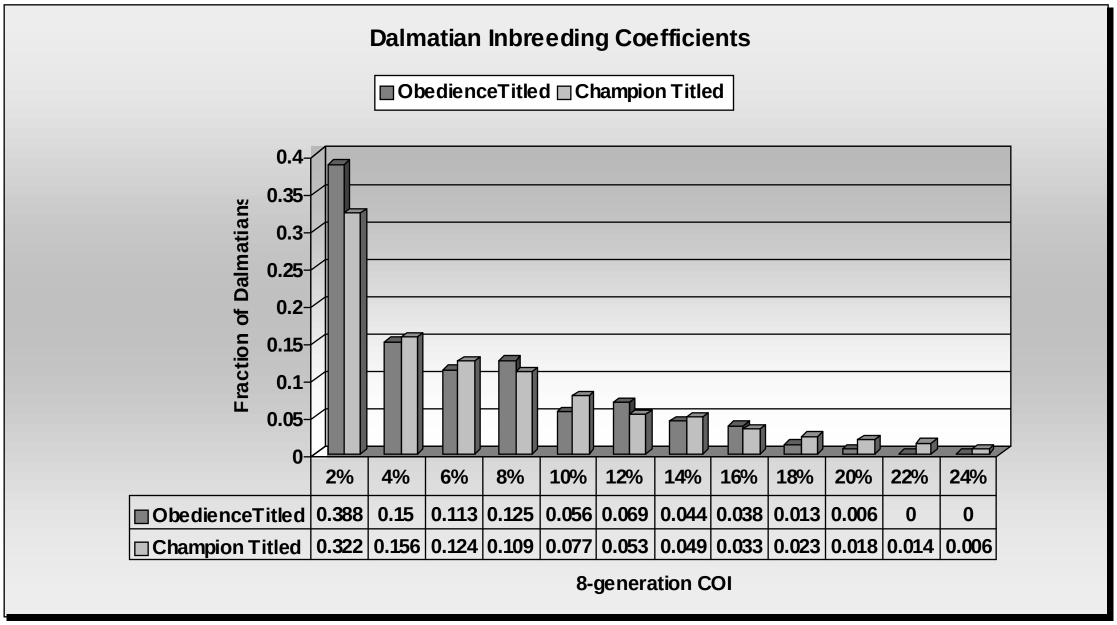


Figure 3. Distribution of 8-generation COIs for all Champion and Obedience titled Dalmatians in the database for which there is sufficiently complete pedigree information. [Champions: Average COI = 6.01% Standard Deviation = 5.96% Maximum COI = 42.55%; Obedience Titled: Average COI = 4.89% Standard Deviation = 4.55% Maximum COI = 19.16%]

## *Moving Forward*

In this article, we have provided an overview of a few of the issues from population genetics that are relevant to breeders of purebred dogs. Of necessity the discussions have been brief, and the interested reader is encouraged to spend a number of quiet hours in a local college library pursuing further research in this important and dynamic field. There is also a wealth of material available on the Web, and those with Internet access would be well advised to visit Dr. John Armstrong's canine diversity web pages (ref. 8, below).

The decision on the best choice of a mate for your bitch, Blossom, remains. Should Blossom be mated to Tonky and continue tight line breeding, or is the better choice a mating to Task which is an assortative mating? The determination of breeding policies within any breed line involves a complex of issues and is based on both short term and long term goals. Yet in this simple, hypothetical example the choice seems clear: preservation of type is possible by the assortative mating, and the risks inherent in inbreeding are avoided. Except for an almost irresistible drive to join the rest of the crowd and breed to the current top stud dog, nothing is to be lost and much to be gained by following the lonelier path of using another dog of lesser fame but comparable quality.

Issues deriving from studies of population genetics that face a breed club are much broader in scope than those confronting individual breeders, for it is a primary mission of such clubs to promote the health and welfare of the breed, and genetic health is an essential ingredient in this effort. While individual breeders will have their own immediate objectives, breed clubs must look into the more distant future and pursue policies that secure a healthy future for the dog breed well into the next millennium. Policies that promote genetic diversity, preserve non-deleterious but rare alleles, and inhibit the almost inevitable increase in average breed homozygosity with the passage of time should be seriously considered. Genetic bottlenecks that derive from the rush of breeders to use the current top winning stud dog should be discouraged – especially since this type of popular sire clustering can have a more global impact in these days of rapid shipments of chilled and frozen semen. Plaudits for dogs that are top producers of champions would be more meritorious if based on "batting averages", numbers of champions produced per puppy sired, rather than raw numbers of champions sired, the latter statistic simply promoting more numerous breedings to the same dog.

This quick look at the inbred status of Dalmatians provides encouragement. An 8-generation view of the database does not reveal extensive inbreeding except in a few breed lines. With further effort, it should be possible to augment the database with health and life span data to allow for more detailed studies. Such studies should attempt to correlate general health and longevity with the level of inbreeding thereby providing data for Dalmatian breeders to make reasonable risk assessments when contemplating matings that involve significant levels of inbreeding.

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