

AKC Bearded Collie Stud Book & Genetic Diversity Analysis
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Breed Development

A Scottish Bearded Collie has been in existence since the 1500s. However, the modern breeding and recording of Bearded Collie pedigrees only began in the 1940s from a limited number of founders. Figure 1 below shows a pedigree of a Bearded Collie (far left) back to breed founders. Most breeds originate from a limited number of founders (to the right), and through reproduction and purging arrive at a performance and conformational standard. The breed then enters an expansion stage (large population in the middle) and grows the population over time.

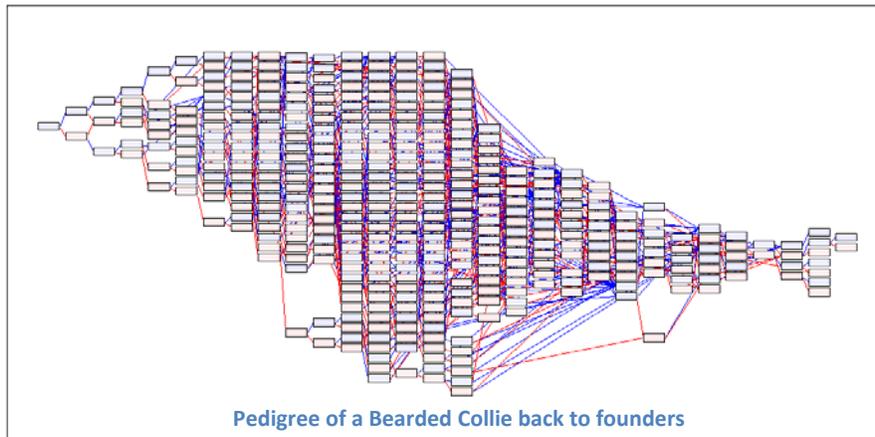


Figure 1

Those dogs who produce desirable offspring for breeding, and whose descendants produce desirable offspring for breeding through generations will increase their influence in the breed. Dogs that do not adhere to or reproduce the standard, or produce inferior or unhealthy offspring are discarded from breeding. Their influence and that of their ancestors will diminish in the gene pool.

Founders

A founder is a dog with unknown ancestry (unknown sire and dam). A genetic analysis of a computerized pedigree database will not distinguish between original founders and those dogs whose pedigree is unknown (even if they came from other registered Bearded Collies). The AKC Bearded Collie stud book database had 22 founders by the 1960s and 24 founders by 1980. All of the original founders are dogs from the UK whose descendants were eventually brought to the US and are therefore included in the AKC stud book.

Founders do not contribute all their genes to the next generation. Offspring only carry half of the genes of a parent, so **it is the number of DIFFERENT breeding offspring that affects the percentage of founder genes which are actually passed on to the population.** Influential Ancestors are dogs who contribute genes to the current population through multiple generations of descendants. They may or may not be founders. Founders may not become influential ancestors if their descendants do not continue to contribute genes to later generations.

Table 1. Influential Ancestors and Founders

INFLUENTIAL BEARDED COLLIE ANCESTORS (FOUNDERS = *)					
Average % of genetic contribution to dogs per decade					
Blue (↑ %); orange (↓ %); yellow (lost influence)					
Dog	1960's	1970's	1980's	1990's	2000's
Bailie of Bothkennar	29.60%	31.70%	32.30%	32.50%	32.60%
Jeannie of Bothkennar	15.50%	12.00%	11.60%	11.40%	11.10%
* Dandy	14.80%	15.80%	16.10%	16.30%	16.30%
Britt of Bothkennar	12.90%	11.70%	11.40%	11.20%	11.20%
Ridgeway Rob	12.70%	17.30%	18.70%	19.60%	19.90%
* Jennifer of Multan	11.90%	7.20%	6.30%	6.00%	5.70%
* Newtown Blackie	8.90%	10.90%	11.90%	12.30%	12.30%
* Mist	7.80%	7.20%	7.20%	7.10%	7.00%
* Jock	6.50%	5.90%	5.70%	5.60%	5.60%
* Mootie	6.50%	5.90%	5.70%	5.60%	5.60%
Brasenose Annabelle	6.20%				
* Brasenose Bonnie	6.20%				
Bess of Bothkennar	4.30%	4.20%	4.50%	4.40%	4.20%
* Dirk	3.90%	3.60%	3.60%	3.50%	3.50%
* Shaggy	3.90%	3.60%	3.60%	3.50%	3.50%
* Lassie	2.80%	4.10%	4.50%	4.60%	4.70%
Bobby of Bothkennar	2.70%	6.90%	7.40%	7.50%	7.70%
* Don	2.10%	2.90%	3.10%	3.10%	3.10%
* Baldi (Worker)	2.10%	2.90%	3.10%	3.10%	3.10%
* Meg (Worker)	2.10%	2.90%	3.10%	3.10%	3.10%
Beasant of Bothkennar		3.50%			
Mister		2.60%	2.90%	3.00%	3.20%

Bailie of Bothkennar (born in the 1940s) is the most influential Bearded Collie in the breed. He contributed on average 29.6% of his genes to all dogs in the 1960s, and his influence has increased to 32.6% of the genes of all Bearded Collies in the 2000s. **One-third of the genes of every Bearded Collie come from Ballie of Bothkennar, even though he does not appear until the 10th generation of most modern dogs.**

Ridgeway Rob contributed 12.7% of his genes to all dogs in the 1960s, and that has increased to 19.9% of the genes to dogs in the 2000s.

Founder dog Dandy contributed 14.8% of his genes to dogs in the 1960s, and that has increased to 16.3% of his genes to dogs in the 2000s. Dandy was the sire of Bailie of Bothkennar.

The above three dogs are the most influential ancestors to today's Bearded Collies. It doesn't matter what type of mating (linebreeding or outbreeding), their significant contribution cannot be altered as they are the basis of the modern breed.

Jeannie of Bothkennar (born December 1943) contributed 15.5% of her genes to dogs in the 1960s, but that has decreased to 11.1% of the genes of dogs in the 2000s.

Founder Jennifer of Multan contributed 11.9% of her genes to dogs in the 1960s, and that has diminished to 5.7% of the genes of dogs in the 2000s.

Founder Brasenose Bonnie and her daughter Brasenose Annabelle were influential in the 1960s, but their influence died out due to their descendants not being propagated.

Beasant of Bothkennar was influential in the 1970s, but his influence died out.

Founder Newtown Blackie's influence has grown from 8.9% in the 1960s to 12.3% in the 2000s due to the proliferation of his descendants.

Mister's influence has slowly grown from 2.6% in the 1970s to 3.2% in the 2000s.

Popular Sires and Influential Ancestors

A popular sire is a dog that is heavily bred upon within a single generation. A popular sire is different from an influential ancestor, because their influence on the breed grows quickly and rapidly without the benefit of observing the effect of their influence and genes on later generations.

Influential ancestors are different than popular sires, because their qualities and influence are constantly evaluated every generation. If they are not producing quality, then their descendants are not bred and their influence diminishes. **The changing influence of ancestors reflects the quality and selection of their descendants for continued breeding.**

Pedigree analysis that shows an increasing influence of a small number of quality ancestors is what is found in all breeds. This is an expected consequence of breed evolution and is not detrimental to the breed.

The AKC Bearded Collie Stud Book Population

The following table summarizes the dogs with listed birthdates in the AKC Bearded Collie Stud Book.

Table 2. Inbreeding Coefficient, Unique Ancestors, % Imports AKC Stud Book

Date of Birth	# of Dogs	Mean 10 Gen IC	Mean All Gen IC	Mean # Unique Ancestors	% Imported Dogs
1960-9	56	14.9%	14.9%	50.9	55.4% (31)
1970-9	1396	19.8%	19.8%	82.1	14.5% (202)
1980-9	1434	23.8%	23.8%	129.0	5.6% (80)
1990-9	1203	25.7%	26.1%	202.8	6.7% (81)
2000-9	723	25.9%	28.1%	293.0	9.0% (65)
2010-on	99	24.2%	29.3%	403.5	15.2% (15)

For dogs in the 2000s pedigrees go back an average of 26.4 generations. Mean number of unique ancestors is the total number of different (unique) dogs present in the pedigree back to founders. This number grows with each generation.

The stud book population expanded and peaked in the 1980s at 1,434 new dogs, then started to decline. The diminished number of breeding dogs found in the stud book dog analysis is mirrored in the declining number of AKC registered litters and pups (Figure 2).

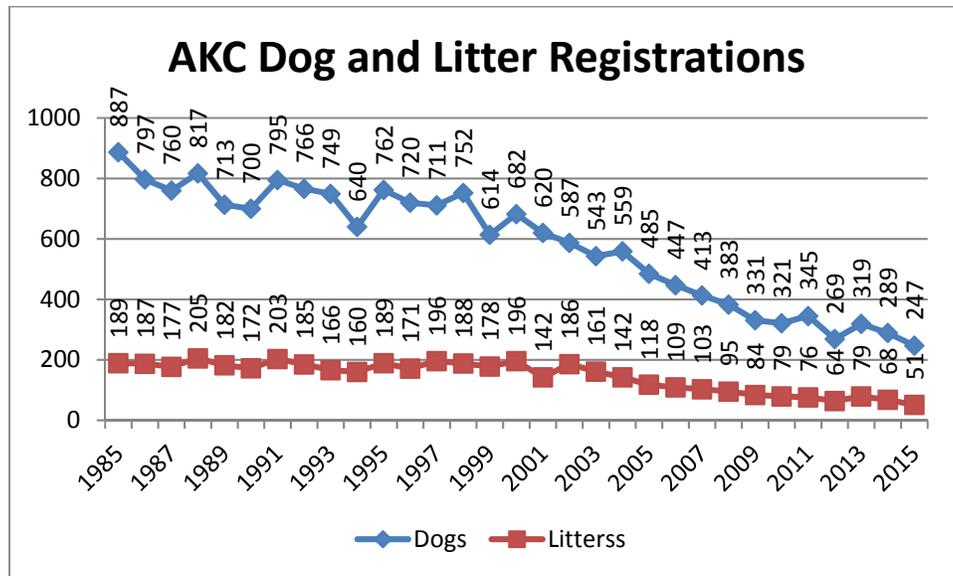


Figure 2.

The diminishing number of breeding dogs and registrations since the 1980s has occurred with most other breeds. With some breeds it was a reflection of the economy in the 1980s and 1990s. For many breeds this trend has reversed and the number of registrations has increased in recent years. However, the Bearded Collie population’s significant decline began around 2001 and has progressed relatively unabated to the present time. The cause of the decline in Bearded Collie breeding cannot be determined by this analysis. However, the decline can have a significant impact on the genetic diversity, health, and vitality of the breed. This aspect is discussed under [Breed Health](#).

Inbreeding Coefficients

The **inbreeding coefficient** is a measurement of the relatedness of the sire and dam of each mating. All genes come in pairs – one from the sire and one from the dam. The inbreeding coefficient represents the percentage of homozygosity of gene pairs due to inheritance from common ancestors. Homozygosity is when the pair contains the same gene (aa or AA) as opposed to heterozygosity which is where there is an unlike pair (Aa). Homozygosity can increase the expression of both positive recessive traits and detrimental recessive disorders.

The **average (mean) all generation inbreeding coefficient** includes all dogs back to founders (see Table 2). This number can only increase over time in a closed population (where no “new” unrelated dogs are being added). It is expected to increase quicker during initial generations as the breed establishes the population and the superiority of influential ancestors. The average inbreeding coefficient based on all generations back to founders in the Bearded Collie for the 2000s is 28.1%, and this is fairly typical for a more recently established, smaller population breed with a pedigree database that goes all the way back to founders.

The average 10 generation inbreeding coefficient of the most recent generations gives an indication whether the breed is utilizing the breadth of its gene pool to select breeding stock, or concentrating on popular sire lines that narrow the breadth of the gene pool. A decreasing 10 generation average inbreeding coefficient shows that the average mates are less related than those of the prior generation and represents an expanding gene pool. The 10 generation mean IC for the Bearded Collie has slowly gone up to 25.9% in the 2000s – indicating a popular sire effect. It went down to 24.2% in the (yet to be completed) 2010s, showing an expanding influence of a broader population background.

The breed-wide average 10 generation inbreeding coefficient for Bearded Collies is a little higher than for most breeds (10 generation inbreeding coefficient closer to 20). However, this average 10 generation inbreeding coefficient is typical for a smaller population, more recently established breed with a similar number of generations from founders as the Bearded Collie. Large, populous breeds once had similar average inbreeding coefficients when their populations were much smaller.

As a tool, the inbreeding coefficient when averaged between matings can give a broad generalization of genetic trends in the breed. The types of matings between individual dogs in a breed (outbreeding versus linebreeding) have no effect on the breed's genetic diversity. Rather, it is the selection of individuals used for breeding. If breeders are utilizing dogs from the breadth of the gene pool, then the genetic diversity of the population is being maintained.

High or low inbreeding coefficients of individual matings should not be a goal in choosing matings: Rather the coefficient should follow the selection goals of concentrating quality and health through the genes of superior ancestors (linebreeding), or bringing in desirable genetic and phenotypic background to compliment or correct the mate (outbreeding).

Breeder diversity in the types of matings and breeding individuals they select is what provides breed-wide genetic diversity. When breeders all run to one area of the gene pool and start doing the same thing (like the popular sire effect) the genetic diversity of the breed declines.

The percentage of imported dogs entered into the AKC studbook has increased each decade from the 1990s on. This did not change the trend of the average 10 generation inbreeding coefficient in the 1990s or 2000s, but this statistic did go down in the 2010s. The question is whether imported dogs have greater quality than existing AKC dogs, are less related (though all go back to the same founder base), and/or have different frequencies of health issues than current AKC dogs. For some of these questions, breeders of imported dogs may not know the answer unless individual health and deep pedigree analyses are evaluated and compared to other dogs. Utilizing a global breed population can help with diversity issues. **Care must be taken that imported dogs do not become popular sires and displace other existing, quality family lines through non-breeding.**

Population genetic benchmark indices were designed for endangered populations of randomly breeding natural species. These indices predict the number of equally contributing founders that would be expected to produce the same genetic diversity as in the population under study. Unequal genetic contributions by founders through linebreeding decrease the founder equivalents and reflects a greater loss of the genetic diversity that was initially present from all of the founders. **All genetic indices are expected to decrease over generations in closed populations.** These indices are useful in captured and endangered species, but in dog breeds they just show the linebreeding and selection that establishes and fixes breed characteristics. Natural species evolve through random breeding and the absence of artificial selection. Dog breeds evolve through planned breeding and directed artificial selection.

Founder Equivalent (Fe) is a measurement of the equivalent total number of equally contributing founders present in the population. For each decade, this has remained fairly steady in the Bearded Collie with 11.11 in the 1960s to 10.89 in the 2000s.

Founder genome equivalents (Fg) is the MINIMUM number of equally contributing founders that can account for the diversity of the population if no genes were lost due to genetic drift; the loss of genes over time just moving from one generation to another. The Fg in the 1960s was 4.63, and is 3.89 in the 2000s.

Effective ancestors (Fa) is the MINIMUM number of ancestors explaining the complete genetic diversity of a population. The Fa in the 1960s was 6.03, and in the 2000s was 5.45.

These numbers show relatively stable indices in the breed and are typical for purebred dog breeds. They would be too low in natural species. In natural species with the absence of selection, there has to be a large buffering population that has as much chance of losing deleterious genes through genetic drift as there is for deleterious genes to increase in the population. These indices are studied to determine if attempts should be made to equalize founder contributions of endangered species, or if new captured animals should be added to the population.

As undesirable phenotypes are selected against in dog breeds, they do not have to depend on random segregation and genetic drift (which happens in nature) to keep deleterious genes in check. As we know that founders in dog breeds do not contribute equally, these indices show that the genes of superior ancestors are being concentrated. **Benchmark population indices that are appropriate for natural and endangered species are not predictive of the genetic health or viability of purebred populations. The genetic health of breeds is not a direct function of homozygosity, genetic diversity, or population size; but of the accumulation and propagation of specific disease liability genes. This can only be determined through genetic screening and valid breed health surveys.** The most important aspect of breed propagation is selection of breeding stock based on health, performance and conformational standards.

Breed Health

As stated above, breed health cannot be predicted based on population indices or measurements of homozygosity; it must be evaluated directly. Some dog populations have a very limited found base, but excellent health. Other breeds with large, diverse gene pools have high frequencies of deleterious genes. The type of mating (linebreeding or outbreeding) will not alter the frequency of dogs affected with breed-related genetic disease, as the causative genes are dispersed in the population. The frequency of affected dogs can only be altered by selection against carriers of deleterious genes. Selection can be based on direct genetic testing, or (if deleterious genes have not been identified) through selection for phenotypically healthy parents from family lines with pedigree depth and litter breadth of normalcy.

The use of genetic tests that differentiate carriers from normal or affected genotypes are beneficial tools, because they allow members of a population to continue to reproduce regardless of their carrier status (when bred to normal dogs) or the carrier risk of their family line. Without a genetic test, dogs with close relatives that are carrier or affected with a genetic disorder would be considered higher risk and selected against. Valid genetic tests increase choices for breeding and decrease the genetic loss in the gene pool from otherwise desirable family lines.

An expanding or large stable population is important so that breeders have increased choices for selection. If a population is contracting, there is a greater chance to lose superior potential breeding dogs,

and diminish the selective advantage for healthy, quality dogs. Smaller generations of Bearded Collies leave less genetic combinations and less prospective mates to choose from. This diminishes the ability to improve the breed. Based on the above indices, it does not appear that the contraction of the Bearded Collie gene pool to date has resulted in a significant narrowing of the breadth of the gene pool. While registration numbers are down, it appears that families have been retained. **However, it is very important that breeders increase their matings and that new breeders are recruited to halt the genetic drain on the gene pool.**

Sometimes breeders are reluctant to breed because they are afraid of producing dogs affected with hereditary disorders. If you don't breed, you are harming your breed through population contraction. Breeders need to do their best to select for health and quality and then see what they produce.

Summary

- As with most breeds, the Bearded Collie population in the US is based on a small number of founders that contribute a large amount of the genes to the current population.
- Average inbreeding coefficients for Bearded Collies are slightly higher than average, but approximately the same as found for other more recently established, smaller population purebred dog breeds.
- Genetic indices show that **while registration and stud book numbers have declined, large portions of the breed gene pool have not been abandoned.**
- Breeders must breed and recruit new breeders to stop the detrimental contraction and genetic loss from the Bearded Collie gene pool.
- Continued selection for health and quality while utilizing the breadth of the breed gene pool and expanding the population should ensure a positive future for the breed.