



| | | |
|---|---|---|
|  | <p style="text-align: center;"> Institut de Génétique et Développement de Rennes Dr Catherine André et Anaïs Grall Équipe « Génétique du chien » UMR6061, Faculté de médecine 2 avenue du Professeur Léon Bernard 35043 Rennes Cedex Tel : 02 23 23 45 09 Fax : 02 23 23 44 78 http://www-recomgen.univ-rennes1.fr/doggy.html </p> |  |
|---|---|---|

Genetic Research Conducted by the Rennes CNRS

Thanks to the collaboration between the Brittany Spaniels Club and the "Dog Genetics" Team from the Institute of Genetics and Development affiliated with the CNRS in Rennes, France, a project on the genetic causes of the "natural short tail" was undertaken on the 23 different races of the Brittany Spaniel. This work began on the Bourbon Pointer and next expanded to the Brittany Spaniel, the Australian Shepherd, the Pyrenees Shepherd, the Savoie Shepherd, and finally the King Charles Spaniel by the sample selections from the CNRS Antagene Group in Lyon. Furthermore, a partnership with the laboratory of Canine Genetics at the University of Helsinki allowed some Finnish and Nordic dogs to be analyzed as well. The results of these projects were published in English with the October 2008 edition of the scientific journal *Newspaper of Heredity*. Here we present a French summary of this article, including the table of the races studied.

This project helped the Antagene laboratory (www.antagene.com) develop a genetic test, which consisted of an oral swab or a blood test and provided the status of the dog's *T* Gene mutation. Such a screening can help the breeders:

1. Know whether the dog is a "natural short tail" or if the tail was cut;
2. Distinguish if a dog really should be considered an eastern "long tail" or is genetically a "Brachyoure";
3. And better understand the breeding of a "short tail" and a "long tail" that produce statistically 50% short tails and 50% long tails, in comparison to the pairing of two short tails, which still only produces 50% short tails and 25% long tails, with 25% dying *in utero*.

Ancestral T-box mutation is present in many but not all short-tail dog breeds

Marjo K Hytönen^{*1,5}, Anaïs Grall^{*2}, Benoît Hédan², Stéphane Dréano², Samuel J. Seguin², Delphine Delattre³, Anne Thomas³, Francis Galibert², Lars Paulin⁴, Hannes Lohi⁵, Kirsi Sainio¹⁺ and Catherine André²⁺

¹Medical Biochemistry and Developmental Biology, Institute of Biomedicine, Helsinki, Finland.

²Institut de Génétique et Développement, UMR 6061 CNRS, Rennes, France.

³Antagene, Laboratoire de Génétique Animale, Limonest, France.

⁴DNA Sequencing Lab, Institute of Biotechnology, University of Helsinki, Helsinki, Finland.

Article Summary

The dogs present varied morphological characteristics, notably with the lengths of their tails. In many races, certain dogs showed a short tail from birth. The genetic cause of this trait "short tail" had been identified by an English team (Haworth and Al.) in 2001 with the Welsh Pembroke Corgi: it is a matter of encoding the mutation in the *T* Gene, which was already known through the development of the vertebral column in some mice. The observed mutation with the natural "short tail" dogs is a change of a nucleotide (C189G) at the beginning of the gene. In this project, we looked to see if the other races possessed the same mutation of the *T* gene as the standard "short tail." In order to do so, we studied the region of the *T* gene carrying this mutation in 23 other races displaying this phenotype. Altogether we analyzed 360 dogs, 156 of which possessed a natural short tail. The mutation C189G of the *T* gene was rediscovered in the short tail dogs of 17 races (c.f. Picture); for these races, the correlation between the mutation and the phenotype was perfect. For the 6 other races, neither the known mutation nor the coding regions of gene *T* were able to be identified, indicating that for all the races showing this phenotype, the genetic cause is not always equivalent. Thus, for 17 races of the 23 tested, the phenotype "short tail" is principally attributed to the mutation C189G of the *T* gene; on the other hand, for the other six races, a uniform genetic cause still remains to be determined.

The method of transmission can be described as having a "lethal" dominance. In other words, a single of the two transferred alleles suffices to constitute a "short tail," while the embryos with the two transferred alleles die in utero. Furthermore, in our study, no living dog has displayed the mutation during the homozygote state, which confirms the lethal quality of this mutation in the homozygote state.

In order to study the consequences of the *T* gene mutation for the size of the carriers, we compared the number of puppies bred from two short-tail parents to the number of puppies from two long-tail parents. For the race of the Swedish Vallhund, our Finnish colleagues observed a decrease of 29% of the size of the carriers if the two parents are "short tail." According to data from breeders, for the Brittany Spaniels and the Bourbonnais, we did not observe a significant difference between the carriers when two short-tails or two long-hairs were mated. In this article, we have proved that the mutation C189G of the *T* gene was responsible for the phenotype short tail in 17 races of the 23 studied. The dogs showing the mutation can be either Anoures or Brachyours. The genetic or non-genetic causes of these two forms are still fundamentally unknown: it is either a question of another mutation in the same gene, a gene affecting the number of vertebrae, the dose of the products of the *T* gene, or some environmental factors disrupting the important stages of development. Again, nothing has been documented on this subject. For the 6 short tail dogs which do not display this mutation, other genetic factors that determine the Anoure and/or Brachyours remain to be discovered.

We would like to thank all of the breeders, owners, and veterinarians for sending samples and everyone from the Brittany Spaniel Club, particularly Rock Willems, Christian Dagorne, and Anka Obrist.

Table

Results of the sequence mutation of the T gene for the 23 races displaying the phenotype short tail at birth.

- 1 : Total Number of Dogs
- 2 : Number of Long-tail Dogs
- 3 : Genotype at the C189 position of the T gene
- 4 : Number of Short-tail Dogs
- 5: Genotype at the C189 position of the T gene

| | Long Tail | | Short Tail | | |
|---|-----------|----|------------|----|-----|
| | 1 | 2 | 3 | 4 | 5 |
| 17 races for which the short-tail dogs displayed the C189G mutataion of the T gene | | | | | |
| Australian Shepherd | 70 | 42 | C/C | 28 | C/G |
| Austrian Pinscher | 2 | 1 | C/C | 1 | C/G |
| Australian Bouvier | 2 | 0 | | 2 | C/G |
| Braque du Bourbonnais | 25 | 16 | C/C | 9 | C/G |
| Brazilian Terrier | 17 | 7 | C/C | 10 | C/G |
| Brittany Spaniel | 18 | 4 | C/C | 14 | C/G |
| Croatian Shepherd | 3 | 1 | C/C | 2 | C/G |
| Swedish/Danish Farm Dog | 2 | 1 | C/C | 1 | C/G |
| Jack Russel Terrier | 10 | 7 | C/C | 3 | C/G |
| Carélie Bear Dog | 6 | 3 | C/C | 3 | C/G |
| Mudi | 10 | 5 | C/C | 5 | C/G |
| Polish Shepherd | 28 | 10 | C/C | 18 | C/G |
| Pyreneese Shepherd | 64 | 57 | C/C | 7 | C/G |
| Savoie Shepherd | 17 | 15 | C/C | 2 | C/G |
| Schipperke | 12 | 4 | C/C | 8 | C/G |
| Spanish Water Dog | 7 | 3 | C/C | 4 | C/G |
| Swedish Vallhund | 22 | 6 | C/C | 16 | C/G |
| 6 races for which the short tail dogs did not display the C189G mutation of the T gene | | | | | |
| Boston Terrier | 4 | 0 | C/C | 4 | C/C |
| English Bulldog | 5 | 0 | C/C | 5 | C/C |
| King Charles Spaniel | 22 | 13 | C/C | 9 | C/C |
| Miniature Schnauzer | 6 | 4 | C/C | 2 | C/C |
| Parson Russel Terrier | 3 | 2 | C/C | 1 | C/C |
| Rottweiler | 5 | 3 | C/C | 2 | C/C |