

DEVELOPMENT OF A RAPID DNA TEST FOR JACK RUSSELL ATAXIA
Progress report
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K. Paige Carmichael, DVM, PhD, DipACVP.
Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens,
GA 30602

Phone: (706) 542-5834
Fax: (706) 542-5828
Email: kpc@vet.uga.edu

Introduction: Jack Russell Ataxia is one of two forms of ataxia identified in the Jack Russell terrier breed. This form of ataxia is characterized by uncoordinated movements, difficulty righting and a broad-based stance that can be recognized in puppies as early as two weeks of age. Most pups show these signs between 4-6 weeks of age and while mentally they are normal, their ability for locomotion becomes progressively worse. We have shown that JRA is an autosomal recessive inherited condition that is passed from clinically normal carrier parents to their offspring.

Objective and Hypothesis: The objective of our research is to develop a rapid DNA test that will enable Jack Russell terrier breeders to identify asymptomatic carriers of the neurodegenerative disease, we call Jack Russell Ataxia (JRA). Such a test would allow breeders to make informed breeding decisions to eliminate the causative mutant gene from their lines. Our hypothesis is that a genetic defect is responsible for JRA in Jack Russells. We also hypothesize that the mutated gene in JRA is not related to the late onset (spino-cerebellar) form of JRA. Our plan is to test this hypothesis by accomplishment of three specific aims. These are:

1. Assembly of DNA samples from an extensive Jack Russell terrier pedigree suitable for analysis.
2. Determination of the canine gene responsible for JRA in Jack Russell terriers.
3. Development of a rapid DNA test to detect the mutation in affected dogs and carriers

PROGRESS TO DATE

Objective 1.

We have examined 77 affected puppies over the course of this study; 3 affected puppies in 1995, 5 in 1996, 11 in 1997, 15 in 1998, and 19 in 1999, 8 in 2000, 8 in 2001 and, 7 in 2002, 5 in 2003 and 1 in 2004. We have collected blood samples and extracted DNA from 743 dogs. Also, using test matings, we were able to show that the late-onset (spinocerebellar) form of ataxia is not related to the early onset form of Jack Russell terrier ataxia.

Objective 2.

We have not determined the gene responsible for this condition in Jack Russell Terriers but have eliminated several candidate genes. We have shifted our focus to also include a more complete screening of the canine genome, 10 Mbp at a time

Objective 3

Our work on the DNA test was hampered somewhat by an incorrectly identified carrier. Once this animal was removed from the study we re-analyzed all of our samples and narrowed the number of possible candidate regions in the canine genome to 12 potential targets. We are currently performing analysis of DNA on these target regions and have managed to eliminate seven of them.

Conclusion.

This study has show slow but steady progress. We have successfully eliminated many candidate genes and are currently investigating others. We are however facing a paucity of blood samples from complete families (carrier parents, and affected and unaffected littermates) on which to run our DNA screening. Donation of blood from complete families like this would be highly appreciated and would allow more rapid progress. We are committed to uncovering the gene responsible for Jack Russell DNA and will continue to work on this project until we develop a test for this disorder.