ABSTRACTS

ISCFR 2012

July 26-29, Whistler, Canada

7th International Symposium on Canine and Feline Reproduction

In a joint meeting with

EVSSAR 2012

15th Congress of the European Veterinary Society for Small Animal Reproduction

Editors: Gary England, Michelle Kutzler, Pierre Comizzoli, Wojciech Nizanski, Tom Rijsselaere and Patrick Concannon

Reprinted in IVIS with the permission of the ISCFR Organizers
Applying the canine genome to genetic testing of sires, dams & offspring

Hughes, A1; Dibley, M2; Davison, S2; Fretwell, N1,2

1Mars Veterinary, Gaithersburg, MD 20898, USA; 2Waltham Centre for Pet Nutrition, Freeby Lane, Waltham-on-the-Wolds, Leicestershire, LE14 4RT, United Kingdom.

Angela.Hughes@marsveterinary.com

OBJECTIVES AND METHODS: Many pure-breed dog populations have a limited gene pool and as such, are similar to an endangered species where it is critical to consider the entire population, as well as, the individuals involved in any given breeding. In order to make breeding decisions, breeders are incorporating family history, selecting for favorable phenotypes and utilizing limited genetic information including inbreeding coefficients and specific disease or trait DNA tests. Unfortunately, these genetic resources may not provide a complete overview of a dog’s potential genetic contribution to the breed. We investigated using a multiplex set of SNP markers as a means of evaluating chromosomal haplotypes and homozygosity values within the Dandie Dinmont Terrier breed.

Blood, cheek swab, or frozen semen samples were obtained from a majority of the potential breeding Dandie Dinmont Terriers within the US. Their DNA was typed at over 300 different SNP locations across the genome. For each dog, homozygosity was calculated and the haplotypes inferred utilizing the Phase software. Haplotypes for potential mates were compared to evaluate the suitability of each possible cross in terms of predicted homozygosity within offspring and maintaining rarer chromosomal haplotypes in the breed. We have created a “breeding score” that summarizes the potential heterozygosity across the chromosomes in a cross which allows all potential breedings to be ranked by a single, inclusive factor.

RESULTS: Within the Dandie Dinmont Terrier breed, we identified chromosomes with a large degree of heterozygosity and others that have lower diversity which may be related to traits that breeders have “fixed” in the breed (e.g. coat texture and length, chondrodysplasia). Initial feedback from the breeders has been positive producing healthy puppies and a noted improvement in litter size. Longer term studies are underway to monitor health and physical traits in these dogs.

CONCLUSION: While Optimal Selection should not be the only means of determining a desirable breeding, the diversity of the individuals should be included as a factor in order to maintain the genetic health of the entire breed. This genetic tool is now available for commercial use in over 150 breeds.