

## **Genetic studies of Chiari-like Malformation with Syringomyelia (CM/SM) in the Cavalier King Charles Spaniels (CKCS)**

A recent grant from the American Kennel Club Health Foundation (#954) with matching funds provided by ACKCSC and Cavalier Club USA has allowed our genetic studies to continue. The team brings together a range of expertise:

### **Human Geneticists**

Dr Guy Rouleau Director of CHU Sainte Justine Research Centre in Montreal (formally at McGill University)

Dr Zoha Kibar CHU Sainte Justine Research Centre) lead investigator of Grant #954 and is doing the fine-mapping

### **Veterinary Neurologist**

Dr Clare Rusbridge responsible for phenotypic information, ensuring it is consistent.

### **DNA Collection and Database**

Penny Knowler collates this information, including the pedigrees.

### **Statistical analysis.**

Dr Marie-Pierre Dube (University of Montreal)

A new whole genome scan using the innovative canine SNP (single nucleotide polymorphisms) genotyping technology is planned in the near future. When the geneticists look for genes they compare dogs that have the condition with those that don't i.e. 'normal dogs'. It is the latter that we are specifically looking for the next stage. Since Syringomyelia can develop, sometimes slowly, over a period of years. For this reason we are looking for dogs that have been MRI'd

### **Over 5, but preferably over, 7 years of age and do not have SM**

**plus any close relatives that may have been MRI'd - siblings, half siblings and offspring. These dogs can be any age.**

**Blood** in EDTA (pink or purple topped tubes to prevent clotting) is the best source of DNA. See 'Instructions for sending blood to Montreal Lab' and send **with sample submission form**

**Buccal swabs** An alternative source is which are sent directly to the lab in Montreal, **with a sample submission form**

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**Please send a copy of the sample submission form, the MRI report and pedigree to Clare Rusbridge. This is to ensure the details are logged and to limit the possibility of samples being lost. The information is also valuable for our collaborator Dr Sarah Blott for her Optimisation Breeding Programme.**

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