



CONFERENCE 2010, Edinburgh, Scotland

Dog Genetics and Genomics Workshop

Time: July 29, 2010, 13:30,

Place: Lecture Theatre 4, Edinburgh Conference Centre, Heriot-Watt University

Workshop convenor(s): Alan Wilton, University of New South Wales
Kathryn T. Graves, University of Kentucky

Committee: Barbara Zangerl (seconded onto Committee to assist in absence of contact from other committee members), Cathryn Mellersh, Mathew Binns

Committee Members Present: Alan Wilton, Barbara Zangerl, (Kathryn Graves had clash with Equine Genetics and Thoroughbred Parentage Testing session)

Approximate number of attendees: 100

Length of workshop (hours): 2.5 hours

Will there be another workshop at the next ISAG conference (yes/no)? Yes, there was strong interest in holding a similar session in 2012.

Who will be the convenor(s) of the next workshop?

Alan Wilton, University of New South Wales / Kathryn T. Graves, University of Kentucky

What is the expected number of attendees at the next workshop? 75

What is the expected length of the next workshop (hours)? Two

Report on any business conducted:

The workshop was called to order at 13:30 by Chair Alan Wilton. Seconded Committee member Barbara Zangerl was present, Co-Chair Kathryn Graves had a clash with the Equine Genetics and Thoroughbred Parentage Testing session so could not attend. Committee members Mathew Binns and Cathryn Mellersh were not in attendance at the conference,

The Chair introduced the key speaker, Dr. Elinor Karlsson, who gave a talk entitled "Mapping Complex Traits in Dog Breeds". She gave published and unpublished examples of the use of gene mapping using Genome Wide Association Studies in dogs.

Following questions there were three presentations chosen from the posters. Javier Quilez from Spain spoke on “Homozygosity mapping detects a selective sweep region of 10-Mb in the Boxer genome”. Anne-Sophie Lequarré from Belgium spoke on “LUPA, a European initiative taking advantage of dog genomics to decipher complex human diseases.” and explained the working of the organisation, the projects underway and others for which they are still collecting samples. Next student Assunta Bramante from Italy spoke about “Mc1r, Agouti signaling protein (ASIP) and CBD103 are involved in brindle coat colour of Boxer and Great Dane dogs.”. There was some discussion after this about the cause of brindle being a duplication of CBD103 with one copy containing a 3 bp deletion, $\Delta G23$, as does the black allele.

Nominations were collected for the standing committee before the tea break at 15:00. Nominees were Alan Wilton - Australia (Chair), Barbara Zangerl - USA, Kathryn Graves – USA, Tomas Bergström – Sweden, Kim Summers – UK, Olga Francino Marti – Spain.

The session restarted at 15:30 with about 75 attendees. All nominations were accepted to the standing committee by unanimous vote. The large committee was selected because of the high drop out in participation by committee members in past years.

After the election of committee members the Chair, Alan Wilton from Australia introduced himself and talked on “Not all simply inherited diseases in dogs are easy to find using GWAS.” giving an example of a simply inherited ataxia in Kelpies that has been resistant to discovery. Then PhD student, Louise Downs from UK was introduced to talk about “A 700 Kb region is linked to Progressive Retinal Atrophy in Tibetan Spaniels.” Next Barbara Zangerl from USA talked about “Predicting a 1.5Mb genomic interval for canine lupus erythematosus using GWAS.” There was some discussion after this from Leslie Lyons about whether it was acceptable not to reveal the identification of the disease gene if the study had identified the causative gene. In this case the author did not know the identity of the gene as they had only collaborated on the GWAS analysis.

The final two talks were by Petr Horin, Czech Republic, who spoke on “Genetic diversity of village dogs from North Kenya” and by Päivi Jokinen, Finland, who spoke on “MHC II risk haplotype associated with canine Chronic Superficial Keratitis in German Shepherd dogs.”

The workshop was concluded at 17.00.

Submitted by Alan Wilton, Chair, Dog Genetics and Genomics Workshop Committee

ISAG Dog Genetics and Genomics Workshop Committee for 2012

elected at 2010 workshop

Alan Wilton, Australia (Chair) a.wilton@unsw.edu.au

Barbara Zangerl, USA bzangerl@upenn.vet.edu

Kathryn Graves, USA ktgraves@email.uky.edu

Tomas Bergström, Sweden tomas.bergstrom@hgen.slu.se

Kim Summers, UK kim.summers@roslin.ed.ac.uk

Olga Francino Marti, Spain olga.francino@uab.cat

**Programme for Dog Genetics and Genomics 29th July 2010 -
Lecture Theatre 4, Edinburgh Conference Centre, Heriot-Watt University**

Chair: Alan Wilton, Australia

Time	Abstract No	Speaker and Presentation Title
13:30	W0011	Elinor Karlsson, USA Mapping Complex Traits in Dog Breeds
14:00	P3086	Javier Quilez, Spain Homozygosity mapping detects a selective sweep region of 10-Mb in the Boxer genome
14:20	P5039	Anne-Sophie Lequarré, Belgium LUPA, a European initiative taking advantage of dog genomics to decipher complex human diseases.
14:40	P1004	Assunta Bramante, Italy Mc1r, Agouti signaling protein (ASIP) and CBD103 are involved in brindle coat color of Boxer and Great Dane dogs
15:00		Election of Committee Members
15:05		Break
15:30	P5076	Alan Wilton, Australia Not all simply inherited diseases in dogs are easy to find using GWAS
15:50	P5003	Louise Downs, UK A 700Kb region is linked to Progressive Retinal Atrophy in Tibetan Spaniels
16:10	P5091	Barbara Zangerl, USA Predicting a 1.5Mb genomic interval for canine lupus erythematosus using GWAS
16:30	P3073	Petr Horin, Czech Republic Genetic diversity of village dogs from North Kenya
16:45	P5098	Päivi Jokinen, Finland MHC II risk haplotype associated with canine Chronic Superficial Keratitis in German Shepherd dogs
17:00		Workshop ends