ISAG Conference 2006, Porto Seguro, Brazil

Dog Genome Mapping Workshop

The workshop was called to order at 1:30 PM by Chair Kathryn Graves. Committee members Matthew Binns and Alan Wilton were in attendance. Cathryn Mellersh was unable to attend. Approximately 30 people were in attendance.

Three short invited presentations were given based on information presented in the poster sessions. Questions were taken after each presentation.

Dr. Hugo Murva Escobar from the Small Animal Clinic, University of Veterinary Medicine, Hanover Germany presented his work on the canine HGMB1:RAGE complex and its apparent importance in cellular functions that may affect various cancers in dogs. Basically preventing HGMB1 from binding to the RAGE receptor may inhibit tumor growth factors and limit invasiveness.

Dr Karina Guziewicz from the University of Pennsylvania presented her work on the bestrophin gene, in which they have identified two mutations, one a missense mutation that creates a premature stop codon and a second that results in an amino acid change. The first mutation is found in Great Pyranees, Mastiffs and Bullmastiffs, the second has been found in the Coton du Tulear. Interestingly both mutations result in similar phenotypes. This work is an example of the phenotypic candidate gene approach, using the human condition (Best Disease) to suggest the bestrophin gene as a candidate. The mutations were not found in 12 other breeds unaffected by multifocal retinopathy.

Dr. Alan Wilton of the University of New South Wales, next gave a presentation on his three areas of interest. His group has identified the causative mutation for neuronal ceroid lipofucsinosis in Australian Border Collies. He estimates that the percentage of carriers in Australia is 3%. The mutation is a C>T transition in the CLN5 gene. He has been able to design an allele-specific assay for this mutation. He next spoke about Trapped Neutrophil Syndrome, also present in Border Collies. The mutation can be traced to an ancestral sire. Use of microsatellites in linkage disequilibrium studies has not been successful in identifying a strong candidate gene but has enabled him to eliminate one or two genes from consideration. The third segment of his talk dealt with his work on the dingo. The dingo is likely related to other wild dogs such as the New Guinea Singing Dog. He emphasized that because dingos are dogs and can crossbreed freely with domestic dogs, pure populations of dingos are becoming endangered.

The final speaker was Dr. Heidi Parker from the National Human Genome Research Institute at NIH. Her presentation was entitled “Population Structure and Complex Traits:Methods for Mapping in the Dog Genome” but she expanded it to give an overview of some of her most recent projects. Her premier study, labeled “Phy-Do” examined the phylogenetic relationships between dog breeds based on haplotype conservation. A minimum of 5 dogs of each of 132 breeds were analyzed with a panel of 96 microsatellite markers. The observed LD between markers indicated different breeds had conserved haplotypes that resulted in the breeds being clustered into groups: The Ancient/Asian, Mastiff, Herding/Sighthound, Modern Hunting and a fifth group containing small terriers. Some breeds fell between groups.

She then gave several examples of specific disorders in breeds and how the breed clusters could be used to identify and confirm candidate genes for these disorders. Collie Eye Anomaly, Addison’s Disease, Malignant Histiocytosis and Transitional Cell Carcinoma are all disorders that have been or are currently being looked at by her group. First the primary affected breed is studied and then other breeds within the same group are looked at to determine the possible range of affected breeds and what genetic or phenotypic differences occur around the locus of interest in related breeds.

There is also a project on morphology and selection concerning breeds in which achondroplasia has been selected for. Plans to use the 26,000 Affymetrix SNP chip are in place, although a 60k SNP chip is on the horizon. Results will be compared across affected breeds.

There were several questions for Dr. Parker. The floor was opened to comments and attendees were encouraged to give summaries of their work.
Alyson Ruhe of the University of California at Davis announced that they had posted a Canine Linkage Map (http://www.vgl.ucdavis.edu/research/canine/projects/linkage_map/data/)

accessible through the Veterinary Genetics Lab website and offered it as a tool to researchers. Gregoire Leroy from France stood and expressed concern about bias in conclusions on breed-specific research because breeds within countries are relatively isolated and there may be important genetic differences between breed populations in different countries. Peter Kesners from Australia mentioned his group's study of the MHC region genes DQA, DQB and DQR and the use of these genes in a family study of genomic matching.

The chair thanked all speakers and participants and reminded everyone that it would be time to elect a new committee at the 2008 conference. The workshop was adjourned at 3:30PM.

Respectfully submitted,

Kathryn T. Graves
Chair
University of Kentucky