ISAG SNP-based Canine Parentage and Identification Panels 2020

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The ISAG workshop for Applied Genetics of Companion Animals was charged with the task to develop standardized single nucleotide polymorphisms (SNP) panels for cats and dogs. These panels are to be used by the ISAG community so data can be shared and be standardized across laboratories, from any country, allowing individual dogs and pedigree registrations to be validated. These standardized panels are then used for in the comparison tests that are conducted by ISAG and its participants. Results from the comparison tests help laboratories to develop their skills and provide quality ratings for the laboratories.

Independently, three groups (Neogen, Orivet, Vetgenomics) had developed panels of SNPs for applications in domestic dog and their breeds. The SNPs and allele frequency information were provided from each group to help develop two (2) panels, a primary and a secondary panel. Panels were primarily selected to be highly informative across many breeds and to include a balanced selection of markers from the three groups. Dr. Oliver Forman from Mars, Inc. provided substantial assistance with the marker selection and data from diverse dog breeds for all the SNP markers. Overall, the following criteria were used to define the dog parentage panels (Excel file – **ISAG Canine SNP Parentage Panels 2020**):

1) Submitted SNPs had allele frequency data from various dog breeds
2) SNPs were ranked as to the allele frequencies to determine informativeness
3) SNPs were selected that performed well with current technologies, including mass spectroscopy, DNA arrays and genotyping by sequencing (GBS).
4) Spacing on chromosomes was considered with attempts to represent each chromosome with more than one marker
5) Markers to assist gender determination were included (*AMEL* and two Y markers).
6) Because of current technology, C/T or A/G SNPs were selected to prevent strand confusion

In addition, the data for the panels in presented in an Excel file with the SNP sequence coordinates defined by the current dog assembly (CanFam 3.1) and all presented in the forward direction of the assembly sequence and the reference alleles defined accordingly. The variants are also provided in the Illumina "Top" strand format, which is to be used for comparison test reporting. The SNPs are identified by their CanFam3.1 chromosome and position. The primary panel has 114 markers and the secondary has 118 markers. Information for *Amelogenin* (*AMEL*) and two Y markers is provided to assist with sex determination.