Introduction

Certain haematological and serum biochemical phenotypes have been recognised in dogs for many years, but no large scale, systematic studies of the phenotypic diversity of peripheral blood in this species have been undertaken. We aim to carry out a comparative analysis of normal haematological and serum biochemical profiles within a large veterinary database in order to identify possible breed-specific phenotypes.

Materials and methods

Normal haematological profiles were available for 6046 dogs (5447 had machine platelet concentrations within the reference interval); 75 pure breeds plus a mixed breed control group were represented by ≥10 dogs. Normal serum biochemical profiles were available from 3045 dogs (1495 had accompanying normal serum glucose concentrations); 60 pure breeds plus a mixed breed control group were represented by ≥10 individuals. Effects of age, sex and neutering status on haematological and serum biochemical profiles were assessed using linear mixed effects models (LME) while considering breed as a random effect. For those breeds represented by at least 10 dogs, principal component analysis (PCA) was undertaken on all but the mixed breed dogs. For each haematological and serum biochemical parameter the distributions of residuals from LME for all breeds represented by ≥10 dogs were compared with those of the mixed breed dogs by two-sample Kolmogorov-Smirnov (KS) tests.

Results

Haematological profiles

Serum biochemical profiles

Conclusions

This study represents the first large-scale analysis of haematological and serum biochemical phenotypes in the dog and underlines the important potential of this species in the elucidation of genetic determinants of haematological and biochemical traits, triangulating phenotype, breed and genetic predisposition, as well as the urgent need for breed-specific reference intervals.

Reference: Lawrence et al. PLOS ONE 2013; 8(11): e81288