Evidence for sex-disparity in the development of atrial fibrillation in Irish Wolfhounds
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Dilated cardiomyopathy (DCM) is characterised by cardiac ventricular chamber enlargement and systolic dysfunction which often leads to the development of rhythm disturbances, congestive heart failure and death. The aetiology of DCM is complex in that genetic factors, myocardial ischemia, hypertension, toxins, infections and metabolic defects have been implicated. Irish Wolfhounds are a breed with high incidence of DCM which is often associated with the development of atrial fibrillation. There is a well-established sex-disparity in the incidence of cardiovascular disease in humans, and studies of canine heart disease often have an over-representation of male dogs implying that there may also be a sex bias in the development of canine heart disease.

Data collected over a 30 year period on atrial fibrillation in Irish Wolfhounds has been analysed with respect to the age of onset and the proportion of males and females affected. The data was transformed to normal using a square root transformation. An independent samples t-test was carried out to establish whether there is a mean age difference between the age of onset in male and female dogs and a chi-squared test was performed to establish whether male dogs are more likely to develop atrial fibrillation than females. All statistical analysis was done using the statistical computing software, R Project for Statistical Computing (http://www.r-project.org/).

There was a significant difference (p = 0.0001, 95% CI 6.09 - 18.77) in mean age of onset in males (53 months) compared to females (65 months), however there is a lot of overlap between the sexes with some females developing atrial fibrillation at a young age and some males developing it late on in life. Male dogs were significantly more likely (142/767 18.5%) to develop atrial fibrillation than females (137/999 13.7%, p = 0.006). Few studies have identified single genetic mutations which might be responsible for canine DCM and combining the effects of sex and loci associated with DCM might be more effective in predicting DCM than the impact of a mutation at an individual locus alone.