Small animal review

There is huge diversity in form, behaviour, disease propensity and longevity in dogs. However, there is little research into variation in life expectancy between breeds.

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McMillan et al (2024) performed a retrospective study using a large UK database to describe variation in longevity estimates based on parentage (purebreed or crossbreed), breed, body size, sex and cephalic index (to characterise the degree of brachycephaly). Phylogenetic clades were examined, and these showed that there was evidence that domestication and artificial selection had an effect on breed lifespan. The authors believe these findings will be of value to owners, breeders and those involved in making decisions regarding breeding to improve canine welfare.

Extending longevity by optimal breeding patterns is clearly desirable, as long as the extra years are of good quality of life. However, it is not always easy to tell the age of a dog or cat in the absence of clear documentation, as recent controversy about the world's oldest dog has shown. My own Jack Russell, who was rescued when she was elderly, seems to have barely aged at all in the last few years, leaving me highly uncertain of her actual age. A study by Pereira et al (2024) might have helped if I had retained any of her teeth from her last dental extractions. Their retrospective study used the dental radiographs of 53 Yorkshire Terriers to evaluate the pulp canal/root ratio, which is thought to be a good indicator of age. Three measurements of the widths of two roots and their pulp cavities were taken at the left and right mandibular molar teeth (309 and 409) and used to calculate the mean pulp canal/root ratio. The pulp canal/root ratio decreased with increasing age, with a moderate negative correlation between age and pulp canal/root ratio noted. The authors suggested this study could contribute to further research into the relationship between pulp canal/root ratio and age in dogs. Further studies into this ratio in different breeds would be useful.

Qi et al (2024) described a completely different method of estimating ageing. This study looked at both wild and domesticated feline species, with a view to optimising management and conservation programmes for wildlife. DNA methylation is a marker of epigenetic ageing which can be used to estimate age from small amounts of biological material. Machine learning was used to build age estimation models from the blood samples of seven Felidae species including domestic cats, Tsushima leopard cats and Panthera species. Mean absolute error of the model was between 1.5 and 2 years for the different species. The models were applicable regardless of the health status of the individuals, which is reflective of the condition of animals in the wild. A common age estimation model for all the different species was not recommended, but one model for the five Pantera spp was considered to be possible. The test was found to be quite inexpensive and since it used low invasiveness of sampling, it was considered to be a practical method of estimating ageing in felines. CA

References

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