

INVESTIGATION OF C. FAMILIARIS FOR DETERMINATION OF GENETIC FACTORS IN LONGEVITY

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Although recent endeavors to discover the mechanisms of the biological aging process have been numerous and successful, there is still much to be learned. Studies of human centenarians have utilized linkage analysis, and many model organisms have also been investigated. From these investigations, it has been noted that genetic factors may play a significant role in aging. Towards the goal of understanding genetic factors contributing to aging and longevity, we are investigating the potential of *Canis familiaris* as a model organism. Limited gene flow, naturally diverse life expectancies, and highly homogeneous populations create an ideal population structure for studying the genetic components of aging in a species with naturally occurring variation in life expectancy (Patronek, et al., 1997). To investigate the canine as a model of human aging, we first gathered height and weight data from 117 American Kennel Club breeds to examine the inverse relationship between lifespan and body size. Regression analysis revealed that smaller breeds generally have longer lives than larger breeds, and this is the first study to analyze data derived from the pet population rather than from dogs referred to specialty practices. Secondly, 54 gene based markers, selected because of their demonstrated contribution to longevity in other organisms or based upon their proximity to the human chromosome 4 marker, D4S1564 (Puca et al., 2001), were added to the canine radiation hybrid map as a basis from which further investigations into aging can be conducted in a gene specific manner. Towards this goal, this group is examining target genes for SNPs to be correlated with extended longevity in those breeds demonstrating exceptional longevity. While the dog is established as a model for study of human hereditary diseases, this effort is the first mechanistically targeted, non-disease specific effort in the dog.