

COMMON AGE-RELATED EXPRESSION CHANGES IN MRNA TRANSCRIPTS IN MOUSE AND HUMAN CNS

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Changes associated with advancing age in mRNA transcript expression levels have been measured in a wide range of animal species, including mice and humans. Identification of homologous transcripts that change to the same degree with age in different organisms may point to common regulatory pathways of aging. We measured age-related changes in mRNA expression levels in 2 month old and 24-month old CB6F1 murine CNS using oligonucleotide microarrays. Using RMA for inter-array normalization and statistical analysis, we compiled a list of over 300 transcript probe sets with a fold-change of greater than 1.3 that significantly changed with age. We compared this list with a published list of human cortical transcript probe sets that also changed with age. 38 common homologous transcripts were found. There was a significant correlation between the mouse and human age-related log₂ fold change of these transcripts ($r = 0.55, p = .0003$). Among the common transcripts identified were GFAP, complement component 4, and deiodinase 2.