

EVOLUTION OF PRIMATE GENE EXPRESSION

P. Khaitovich^{1,2}, S. Paabo², M. Somei^{1,2}

¹*Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, 320 Yue Yang Road, Shanghai, 200031, China*, ²*Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig, Germany*

Presenter's Email: khaitovich@eva.mpg.de

Gene expression changes determine species' phenotype in development and are associated with their functional decline in aging. While development is tightly regulated, the transition between development and aging, and regulation of post-developmental changes are not well understood. Here we measured mRNA, microRNA, and protein expression in two brain regions, cortex and cerebellum, of humans, chimpanzees, and rhesus macaques over the species' lifespans. We find that in all species microRNA and gene expression changes taking place during development continue or reverse in aging. The transitions between developmental and aging patterns commonly occur at two distinct time intervals: early childhood and maturity. Surprisingly, many expression changes observed in old age, including the down-regulation of neural genes, initiate in early childhood. Further, we find indications that microRNA and transcription factors regulate both developmental and post-developmental expression changes. Importantly, in cortex, but not in cerebellum, we find significant excess of human-specific gene and miRNA expression changes. Supporting the existing hypothesis, these changes represent a shift in developmental timing in humans, rather than an evolutionary innovation. Genes showing human-specific expression patterns in prefrontal cortex are predominantly involved in calcium signaling, synaptic transmission and long-term potentiation.

Keywords: human, chimpanzee, brain, transcriptome