

Thesis abstract

Patterns of telomere length change with age in aquatic vertebrates and the phylogenetic distribution of the pattern among jawed vertebrates

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In this thesis, I aimed to assess the application of telomeres, the protective caps that the ends of chromosomes, as a novel age determinate for aquatic vertebrates in order to overcome the limitations of the commonly applied increment based ageing methodology. More specifically, I sought to correlate the natural changes in telomere lengths (*TeL*) with chronological ageing in multiple species of teleosts, chondrichthyans, and a species of pinniped.

Species of teleosts and chondrichthyans had significantly different rates of *TeL* change with age and these rates of change were strongly correlated with longevity. *TeL*-at-age relationships were characterised by a large degree of inter-individual variability of *TeL* within all age classes, limiting telomeres to at best assigning broad age classes. Alternatively, telomeres may be better suited as indices of animal condition, by providing a measure of the 'physiological' age of individuals, reflecting the accumulated effects of ageing and stress events throughout life; thus animals with shorter telomeres in spite of their younger chronological age may be biologically old. In total, five of the nine teleosts examined showed significant *TeL*-at-age relations, as did the species of pinniped.

None of the six chondrichthyan species showed this relationship.

Interestingly, these findings highlight that patterns of *TeL* change with age are highly variable within the jawed vertebrates (gnathostomes) – thus, telomere change cannot be characterised by a single pattern for all gnathostomes. In fact, there are three patterns of *TeL* change with age in the gnathostomes:

- (i) declining *TeL*
- (ii) increasing *TeL*; and
- (iii) no significant change in *TeL*.

However, identifying the selective factors responsible for the assignment of and transitions between states of *TeL* change with age are hampered by a lack of the understanding of the overall evolutionary patterns of *TeL* change.

Therefore, I sought to outline the phylogenetic distribution of patterns of *TeL* change with age in the gnathostomes to determine the evolutionary origin(s) of this trait. Two alternative hypotheses for the evolution of *TeL* change were tested by ancestral state reconstruction in a set of 40 gnathostomes. The most likely/parsimonious pattern of *TeL* change in the common

ancestor to all gnathostome lineages was determined, i.e. *Tel* change with age was not present ancestrally and has since evolved independently in divergent gnathostome lineages, with some secondary losses. I was also able to elucidate the evolutionary history of transitions between patterns of *Tel* change within the available gnathostome lineages, with the birds and teleosts displaying the highest rates of evolutionary lability of patterns of *Tel* change with age through repeated transitions/reversions from the ancestral state.

This macro-evolutionary analysis identified relatively rapid evolutionary patterns of *Tel* change with age in two gnathostome clades. However, as highlighted by the high inter-

individual variability of *Tel* within all age classes, furthering an interpretation of the biological and biochemical causes and consequences of variable patterns of *Tel* change will require a focus at the species level and a shift to following individuals through out their lifetime.

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