Telomere Estimates by Quantitative PCR in American Kestrels Birds

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Telomeres are highly conserved repeated sequences found at the ends of linear chromosomes. Measuring telomere length has been used to estimate the ages of individuals in several species. The research presented here focuses on developing telomere length estimates in the American Kestrel (*Falco sparverius*), using Quantitative Polymerase Chain Reaction (qPCR). The verification of a primer pair that can amplify a reference gene and serve to normalize the telomere qPCR data is vitally important. The gene for glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was preferably chosen because it occurs in a single copy in most birds. However, the Kestrel genome has not been sequenced making primer design challenging. We used a bioinformatics approach to find regions of the GAPDH gene that are conserved between chicken and several species of raptors. We also checked several published GAPDH primers reported in the literature. Here, we report the sequence and efficiency of qPCR primers that can be used for telomere length studies in the American Kestral.

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