



Differentiated evolutionary relationships among chordates from comparative alignments of multiple sequences of MyoD and MyoG myogenic regulatory factors

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ABSTRACT. MyoD and MyoG are transcription factors that have essential roles in myogenic lineage determination and muscle differentiation. The purpose of this study was to compare multiple amino acid sequences of myogenic regulatory proteins to infer evolutionary relationships among chordates. Protein sequences from *Mus musculus* (P10085 and P12979), human *Homo sapiens* (P15172 and P15173), bovine *Bos taurus* (Q7YS82 and Q7YS81), wild pig *Sus scrofa* (P49811 and P49812), quail *Coturnix coturnix* (P21572 and P34060), chicken *Gallus gallus* (P16075 and P17920), rat *Rattus norvegicus* (Q02346 and P20428), domestic water buffalo *Bubalus bubalis* (D2SP11 and A7L034), and sheep *Ovis aries* (Q90477 and D3YKV7) were searched from a non-redundant protein sequence database UniProtKB/Swiss-Prot, and subsequently analyzed using the Mega6.0 software. MyoD evolutionary analyses revealed the presence of three main clusters with all mammals branched in one cluster,

members of the order Rodentia (mouse and rat) in a second branch linked to the first, and birds of the order Galliformes (chicken and quail) remaining isolated in a third. MyoG evolutionary analyses aligned sequences in two main clusters, all mammalian specimens grouped in different sub-branches, and birds clustered in a second branch. These analyses suggest that the evolution of MyoD and MyoG was driven by different pathways.

Key words: Bioinformatics; Chordates; Evolutionary biology; Myogenic regulatory factors