

The *IGH* E μ 3' Enhancer of the Channel Catfish: Can We Extrapolate Knowledge of Structure/Function Relationships to Other Teleost Species?

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The core region of the E μ 3' transcriptional enhancer that drives the expression of the teleost *IGH* locus has been characterized functionally in two species, the catfish (*Ictalurus punctatus*) and the zebrafish (*Danio rerio*). These studies have suggested important differences: whereas the catfish enhancer acts through an E-box and two octamer motifs, the zebrafish enhancer exerts its major effects through two E-box motifs alone. In this study, the function of the catfish enhancer was re-examined in a broader comparative context within the teleosts. Electrophoretic mobility shift assays of motifs from catfish, zebrafish and *Fugu* were conducted to determine their ability to bind catfish E-protein and Oct transcription factors. Transient expression assays were conducted using a region of the catfish core enhancer that includes a newly-described hybrid octamer/E-box motif. Alignments of sequences (phylogenetic footprinting) homologous to the E μ 3' enhancer region from six teleosts were conducted to determine conserved regions. These studies allowed the following conclusions to be drawn: 1) the important 3'E-box motif described in the zebrafish corresponds, in the homologous region of the catfish enhancer, to an Oct motif with a newly-described negative regulatory function; 2) comparison of the E μ 3' enhancer sequences of six teleosts indicates that while a variety of octamer and E-box motifs are found in this region, strict evolutionary conservation of the important functional elements of the teleost E μ 3' enhancer has not occurred.

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