COMPARISON OF CORE PROMOTERS IN FUGU RUBRIPES AND HUMAN

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Different species may have developed specific modes of transcription initiation of their genes. We have considered two relatively distant vertebrate species, *Fugu rubripes* and human, and compared the content of their extended core promoters covering the range of [–70,+60] relative to experimental transcription start sites. Our study included over 18,000 human genes and 5,000 Fugu genes. We utilized TRANSFAC Professional database Ver.7.4 and all its available matrix models related to vertebrates, as well as the associated Match program ver.1.9. Promoter groups with different GC-content were analyzed in order to reduce potential nucleotide bias. We observed striking differences in the core promoter contents of these two species. We enumerated the most significant differences in transcriptional patterns of Fugu and human. We also determined species specific sets of transcriptional patterns that could be linked to transcription initiation, as well as the most frequent and, separately, the most over-represented patterns in various promoter groups. Our study should contribute to better understanding of the transcription initiation mechanisms in these two species, insights into the impact of 450 million years of evolution on transcription initiation, and better annotation of promoter transcriptional regulatory patterns in different species.