

IN SILICO ANALYSIS OF THE CONSERVATION OF LEUCISM-RELATED GENES IN VERTEBRATES

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Abstract

Leucism is an anomaly of the pigmentation of the skin of animals and manifests itself as the total or partial loss of the natural color of the species, and can affect parts of or the entire body of an individual. This change is caused by gene mutation, or by changes in expression in the some genes related to melanin synthesis. Related to this anomaly are the genes EDN3, EDNRB, KIT, MITF, PAX3 and SOX10, responsible for the migration and differentiation of melanocytes; this genes are highly conserved and indicate that they have some important function for the survival of organisms. The aim of the present study was to analyze in silico the conservation of Leucism-related genes in vertebrates and to evaluate the phylogenetic relationship of the same. The NCBI database was used to obtain vertebrate mRNA sequences. Then, global and local alignment was performed the significance of the data by E-value. Phylogenetic analysis was based on the construction of a Bayesian inference phylogenetic tree. Among Leucism-related genes, only EDN3 was significantly conserved. Possibly EDN3 is the main candidate gene for the leucism induction. It was found that the phylogeny of mammals selected (after alignments) for tree construction did not allow a well resolved relationship. While for the order Rodentia the relations corroborate with phylogenies already found in the literature. Birds and mammals were grouped into distinct groups.

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