AN NGS-BASED APPROACH FOR THE COMPARISON OF LIZARD SPECIES TO DETECT GENOMIC DIVERGENCE AND REARRANGEMENTS

Abstract

Genomic divergence between lizards varies across the timescale of the Cretaceous. The genomic divergence of lizards and the timescale of their divergence can be accurately measured by using NGS-based approaches. The aim of this study is to use NGS-based approaches to compare the genomic divergence of lizards and the timescale of their divergence. The results of this study will provide new insights into the evolutionary history of lizards.

4. GENOMIC CHARACTERISTIC

JELLYFISH

5. Mitochondrial Genome Analysis

6. Genome Assembly & Mapping

7. Genes Under Selection

Future work

The sequencing data obtained were analyzed using 'Jellyfish' and 'mapalign' with the mink genome. The genomic characteristic of the assembled genomic data was compared using the jellyfish genome. The results of the analysis were then compared with the published mitogenome of the mink from the GenBank database. The results of the analysis demonstrated that the mink genome is homologous to the assembled mitogenome of the mink from the GenBank database.

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