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GENOME SEQUENCING

The Complete Genome Sequence of Chrysopelea ornata, Ornate Flying Snake

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Biodiversity Genomes

Chrysopelea ornata, commonly known as the ornate flying snake, is a beautiful and unique species of snake found in Southeast Asia. This snake is famous for its ability to glide from tree to tree. The snake's body is slender and long, with a characteristic pattern of black and yellow scales that give it a prominent appearance. The significant feature of the ornate flying snake is its ability to glide. This snake launches itself from a high branch and glide up to 100 meters through the air. The snake's gliding ability is due to its unique physical features, including its elongated ribcage and flattened belly. By flattening its body, the snake can create a greater surface area, allowing it to stay aloft for longer periods. The snake also moves its body in an undulating motion, which generates lift and helps it maintain its balance. It is hunted and smuggled. Here we present you the Whole Genome Sequence of Chrysopelea ornata.

Introduction

Chrysopelea ornata, commonly known as the ornate flying snake, is a beautiful and unique species of snake found in Southeast Asia. This snake is famous for its ability to glide from tree to tree. The snake's body is slender and long, with a characteristic pattern of black and yellow scales that give it a prominent appearance. The significant feature of the ornate flying snake is its ability to glide. This snake launches itself from a high branch and glide up to 100 meters through the air. The snake's gliding ability is due to its unique physical features, including its elongated ribcage and flattened belly. By flattening its body, the snake can create a greater surface area, allowing it to stay aloft for longer periods. The snake also moves its body in an undulating motion, which generates lift and helps it maintain its balance. It is hunted and smuggled. Here we present you the Whole Genome Sequence of Chrysopelea ornata.

Methods

The Genetic sample was of a single snake which was road accident killed. DNA extraction was executed using the Qiagen DNAeasy genomic extraction kit using the standard process. A paired-end sequencing library was constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The library was sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format.

The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Cutadapt-version 2 (Martin 2011). Using MaSuRCA (Maryland Super Read Cabog Assembler) (Zimin et al. 2013) assembled the trimmed sequence.

Results and Data Availability

The genome sequence of Chrysopelea ornata is available on NCBI:

Genome: JAHWGE000000000 (https://www.ncbi.nlm.nih.gov/nuccore/JAHWGE000000000)

BioProject: PRJNA742155 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA742155)

BioSample: SAMN19929648 (https://www.ncbi.nlm.nih.gov/biosample/SAMN19929648).

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