

Feb 06, 2023

Version 1

Protocols for the genome assembly and annotation of the *Bungarus multicinctus* V.1

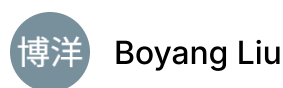
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We use this collection and it's working

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Keywords: Bungarus multicinctus, genome assembly, protocols' collection, genome assembly, continuous genome assembly, genome size, genome, venomous snake, bungarus multicinctus, genomic resource, annotation of the bungarus multicinctus background, molecular mechanisms of toxin production, venomous snake bite, bungarus multicinctus background, toxin production, snake, molecular mechanism, protocols for the genome assembly

Abstract

Background: Snakes are one of the most important wildlife resources and are widely distributed. *Bungarus multicinctus* is a highly venomous snake and is distributed in central and southern China. In recent years, venomous snake bites have gradually increased. Genomic resources are significant for understanding the evolution of a specie and the molecular mechanisms of toxin production.

Find: Here we present a highly- continuous genome assembly of *B. multicinctus*. The genome size of *B. multicinctus* is 1.51Gb. The maximal length of scaffold is 39.68M and the N50 length is 6.55M. The *B. multicinctus* has a GC content of 37.8%.

Files

 SEARCH

Protocol

NAME

DNA extraction protocol for the Bungarus multicinctus by using AxyPrep™ Multisource Genomic DNA Miniprep Kit

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Protocol

NAME

RNA extraction protocol for the Bungarus multicinctus by using TRIZOL reagent (Invitrogen)

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