

Feb 09, 2023

Version 2

Protocols for the assembly and annotation of snake genomes V.2

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DOI

<https://dx.doi.org/10.17504/protocols.io.5jyl8j6e9g2w/v2>

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GigaScience Press

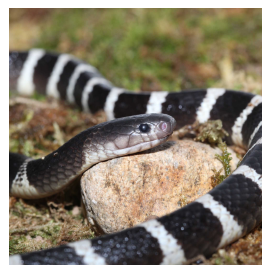
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Collection Citation: Boyang Liu, Liangyu Cui, Zhangwen Deng, Yue Ma, Diancheng Yang, Yanan Gong, Yanchun Xu, Shuhui Yang, Song Huang 2023. Protocols for the assembly and annotation of snake genomes. **protocols.io** <https://dx.doi.org/10.17504/protocols.io.5jyl8j6e9g2w/v2> Version created by **Boyang Liu**

Manuscript citation:

Liu B, Cui L, Deng Z, Ma Y, Yang D, Gong Y, Xu Y, Lan T, Yang S, Huang S, The genome assembly and annotation of the many-banded krait.
GigaByte doi: <https://doi.org/10.20944/preprints202306.0658.v1>

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Protocol status: Working

We use this collection and it's working

Created: February 05, 2023

Last Modified: February 09, 2023

Collection Integer ID: 76433

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

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%.

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Protocol



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DNA extraction protocol for snake genomic sequencing by using AxyPrep™ Multisource Genomic DNA Miniprep Kit

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🔗 The annotation pipeline for the genome of a snake

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