

Whole genome sequencing of a Japanese endemic pit viper, habu, *Protobothrops flavoviridis* reveals accelerated evolution of venom-related genes enriched in microchromosomal regions.

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Towards the complete characterization of the venomous protein, we conducted the whole genome sequencing of the habu snake, *Protobothrops flavoviridis*. By FACS analysis of peripheral blood cells, we estimated the genome size of habu to be 1.8 Gb. We assembled 98 Gb of whole genome shotgun sequence reads and 26 Gb of Illumina mate-pair reads into the habu genome draft sequence, HabAm1, consisting of 84,502 scaffolds with the total length of 1.4 Gb and the N50 length of 467 kb. We also obtained RNA-seq data in total of 348 Gb from 18 different organs assembled into 367 million non-overlapping transcript sequences. By mapping the transcripts against the draft genome, HabAm1, we extracted exon/intron junction sequences. Using the exon/intron junction information as hints, we identified 25,132 protein-coding genes in total. Through the homology search against the public databases, we identified 20,540 genes with functional annotations. Through the keyword search of venom/toxin related terms against the annotations followed by the manual curations, we identified 284 genes as venom-related genes. Using the synteny with the Japanese striped snake, *Elaphe quadrivirgata*, we anchored 2,639 genes (117.3 Mb in total) onto specific chromosomal regions. We observed a significant enrichment of the venom-related genes onto microchromosomes rather than on macrochromosomes, suggesting the implementation of the genomic architecture in the multiplication and the accelerated evolution in the venom-related genes.

All Welcome

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