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Composition of sex chromosomes of veiled chameleon (*Chamaeleo calyptratus*, Iguania, Squamata) reveals new insights into sex chromosome evolution of iguanian lizards

Tishakova K.[1, 2]*, Prokopov D.[2], Davletshina G.[2, 3], O'Brien P.[4], Ferguson-Smith M.[4], Giovannotti M.[5], Trifonov V.[1, 2]
[1] *Novosibirsk State University, Novosibirsk, Russia*
[2] *Institute of Molecular and Cellular Biology, SB RAS, Novosibirsk, Russia*
[3] *Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*
[4] *Cambridge Resource Centre for Comparative Genomics, Department of Veterinary Medicine, University of Cambridge, Cambridge, UK*
[5] *Dipartimento di Scienze della Vita e dell'Ambiente, Università Politecnica delle Marche, Ancona, Italy*
* *k.tishakova@.g.nsu.ru*

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Motivation and Aim: The genetic sex determination is widespread among vertebrate animals and has evolved multiple times in different clades. It is assumed that some homologous synteny blocks (HSBs) were involved in the formation of sex chromosome more often than others due to their genetic content. Squamate reptiles represent interesting model organisms to study sex chromosome evolution, because they demonstrate a striking diversity of sex determination systems. In the present work, we investigated the chromosome composition of the veiled chameleon (*Chamaeleo calyptratus,* CCA henceforth) to identify sex chromosomes and study their genetic content.

Methods and Algorithms: We obtained flow-sorted DNA-libraries of chromosomes for *C. calyptratus* and sequenced them using Illumina MiSeq platform. The reads were aligned to the genomes of reference species, such as the green anolis, *Anolis carolinensis* (ACA) and the plateau fence lizard, *Sceloporus thristichus* (STR). A pair of sex chromosomes were identified using PCR-assisted mapping with male-specific RAD-seq markers.

Results: We identified CCA5 as a pair of sex chromosomes. NGS data analysis demonstrated homology between CCA5 and ACA5+ACAX. ACA5 is described in the sex chromosome of pygopodid geckos and skinks, whereas ACAX form the sex chromosomes of most Pleurodont iguanas, soft-shelled turtles and some geckos. These HSBs contain at least three genes, PITX2, SOX5 and SOX10, which may be promising candidates for the role of master sex-determination gene.

Conclusion: Thus, the sex chromosomes of *C. calyptratus* contain the homologous synteny blocks, that are involved in the formation of the sex chromosomes of many reptiles.

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