

# POPULATION STRUCTURE, INTERPLOIDY GENE FLOW AND ADAPTATION TO POLYPLOIDY IN AUSTRALIAN BURROWING FROGS *NEOBATRACHUS*

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Polyploidy plays important role in evolution, providing a ‘backup’ genetic material and increasing genetic novelty. However, polyploids have to adapt their cellular machinery to the whole genome duplication (WGD) itself. In the autotetraploids, crossovers may occur randomly between each copy during meiosis, compromising regular chromosomal segregation. Adapted to WGDs autopolyploid plants allow only one crossover per chromosome, which leads to successful meiosis. Although recent WGDs have been described in animals, they occur rarely and usually such animals reproduce asexually. *Amphibia* is the only exception among bisexually reproducing vertebrates with multiple independent occurrences of WGDs, for example, frog genus *Neobatrachus* consists of 6 diploid and 3 tetraploid species. This project aims to provide the first description of meiotic adaptation mechanism to polyploidy in animal kingdom using *Neobatrachus* frogs.

1). Here, based on the exome-capture dataset for 446 loci across 87 *Neobatrachus* individuals covering the entire genus, we describe the population structure, interploidy admixture and decline of suitable ecological niche areas in Australian burrowing frogs *Neobatrachus*.

2). In order to come closer to the understanding of the mechanism of meiotic adaptation to WGD in *Neobatrachus*, we assembled and annotated a genome of the diploid *N. pictus*. Then, we compared genetic variation along the genome for multiple whole-genome Illumina-sequenced 8 diploid (*N. pictus*) and 9 tetraploid (*N. sudellae*) individuals, identifying selected regions and potentially adaptive changes in tetraploids. Preliminary results showed that such regions are enriched for molecular function in microtubule motor activity. This suggests modifications at the homologous pairing process during meiosis.