

# VCFPOP: performing population genetics analyses for polyploids and anisoploids based on next-generation sequencing variant calling dataset

Kang Huang<sup>1</sup>, Bing Yang<sup>1</sup>, Jincuo Ao<sup>1</sup>, Yuhang Li<sup>1</sup>, Yunxia Cui<sup>1</sup>, Yuchen Kong<sup>1</sup>, Yifan Wu<sup>1</sup>, Derek Dunn<sup>1</sup>, and Baoguo Li<sup>1</sup>

<sup>1</sup>Northwest University

May 9, 2022

## Abstract

Polyploids are cells or organisms with a genome consisting of more than two sets of homologous chromosomes. Polyploid plants have important traits that facilitate speciation and are thus often model systems for evolutionary, molecular ecology and agricultural studies. However, due to their unusual mode of inheritance and double-reduction, diploid models of population genetic analysis cannot properly be applied to polyploids. To overcome this problem, we developed a software package entitled VCFPOP to perform a variety of population genetic analyses for autopolyploids, such as parentage analysis, analysis of molecular variance, principal coordinates analysis, hierarchical clustering analysis and Bayesian clustering. We make this software freely available, downloadable from <http://github.com/huangkang1987/vcfpop>.

## Hosted file

6.pdf available at <https://authorea.com/users/481409/articles/568471-vcfpop-performing-population-genetics-analyses-for-polyploids-and-anisoploids-based-on-next-generation-sequencing-variant-calling-dataset>