



GenAPoPop1.0: Computing population genetic indices and inferring reproductive modes from genotype diversity in polyploid populations.

Solenn Stoeckel, Ekaterina Bocharova, Dominique D. Barloy

► To cite this version:

Solenn Stoeckel, Ekaterina Bocharova, Dominique D. Barloy. GenAPoPop1.0: Computing population genetic indices and inferring reproductive modes from genotype diversity in polyploid populations.. Polyploidy and Biodiversity, Oct 2021, Rennes, France. hal-03810648

HAL Id: hal-03810648

<https://hal.inrae.fr/hal-03810648>

Submitted on 11 Oct 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

GenAPoPop1.0: Computing population genetic indices and inferring reproductive modes from genotype diversity in polyploid populations

Solenn Stoeckel^{*1}, Ekaterina Bocharova^{2,3}, and Dominique Barloy⁴

¹Institut de Génétique, Environnement et Protection des Plantes, UMR1349, INRAE, Agrocampus Ouest, Université de Rennes 1, France.

²Koltzov Institute of Developmental Biology RAS, Moscow – Russia.

³Molecular Genetics Laboratory, Russian Federal Research Institute of Fisheries and Oceanography, Moscow – Russia.

⁴Écologie et santé des écosystèmes – Agrocampus Ouest, INRAE, France.

Abstract

Understanding the ecological and evolutionary impacts of polyploidy, especially on reproductive modes, implies to be able to easily compute population genetic indices and to quantitatively infer the respective rates of clonality, selfing and outcrossing producing current descendants.

We developed a user-friendly software to analyze genotypes of spatio-temporally-sampled individuals, with a special focus on analyzing and interpreting reproductive modes in poly-ploid populations. This software, part of the project ANR Clonix2D, named GenAPoPop (for *Genetic Analyses of Polyploid Populations*), was written using Qt, python and fortran, works on Gnu/Linux, MacOS and Windows, and run locally with no internet connection. It allows computing major population genetic indices for polyploids (F-statistics, linkage disequilibrium, probability of identity, spatial and temporal Fst, genotypic and genetic diversities, etc.) only using a graphical interface and a new method to obtain posterior probabilities of reproductive modes in polyploid populations using temporal genotypings. It aims to ease and broaden the computation of genetic indices in research projects and facilitate polyploid population studies in population genetic courses and student trainings.

We will present the software interface, and provide some results obtained on a tetraploid sea anemone and on a decaploid invasive plant species.

Keywords: population genetics, partial clonality, partial selfing, polyploidy

^{*}Speaker