

Reference datasets for consistency tests of GENAPOPOP 1.0 software: a user-friendly software to analyse genetic diversity and structure in partially clonal and selfed polyploid organisms.

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Datasets companion of the manuscript entitled GENAPOPOP 1.0: a user-friendly software to analyse genetic diversity and structure in partially clonal and selfed polyploid organisms, used to achieve consistency test with Spagedi 1.5 software, and used as reference datasets to demonstrate the new possibilities allowed by GenAPoPop software.

Raw datasets used for testing GenAPoPop 1.0, A user-friendly software for easily compute genetic analyses of autopolyploid populations packaged for Linux, MacOS and Windows; Results obtained from Spagedi 1.5 (Hardy & Vekemans 2001) and GenAPoPop1.0.

Four pseudo-observed genotyping autotetrapolyploid SNP datasets, corresponding respectively to panmictic (A), highly clonal (B), highly selfed (C) and half-clonal-half-selfed (D) reproductive mode scenario. In all these four scenarios, we simulated two populations of 100 individuals each, connected with a migration rate of 0.01 and mutating at a rate of 0.01, genotyped at 10 SNPs. Datasets were recorded 1000 generations after an initial randomly drawing population with equal allele frequencies.

One SNP tetraploid genotyping dataset from two French *Ludwigia grandiflora subsp. hexapetala* populations (aquatic plant from the Angiosperm clade): two populations in which we collected 75 individuals, each genotyped with 36 SNPs using the Hiplex method allowing confident allele dosage (Delord et al. 2018).

One microsatellite tetraploid genotyping dataset on two *Aulactinia stella* populations (sea-anemone from the Cnidaria phylum), sampled on the coast of the arctic ocean. One population of 21 individuals and one population of 15 individuals, both genotyped with 10 microsatellites.