

Resource Summary Report

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[poppr](#)

RRID:SCR_023452

Type: Tool

Proper Citation

poppr (RRID:SCR_023452)

Resource Information

URL: <https://grunwaldlab.github.io/poppr/>

Proper Citation: poppr (RRID:SCR_023452)

Description: Software R package for analysis of populations with mixed modes of sexual and clonal reproduction. Used for genetic analysis of populations with mixed reproduction.

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.7717/peerj.281](https://doi.org/10.7717/peerj.281), [DOI:10.3389/fgene.2015.00208](https://doi.org/10.3389/fgene.2015.00208)

Keywords: genetic analysis, mixed reproduction, mixed reproduction populations, mixed modes, sexual and clonal reproduction,

Funding: US Department of Agriculture ;
USDA National Institute of Food and Agriculture ;
USDA ARS Floriculture Nursery Initiative ;
USDA-Forest Service Forest Health Monitoring Program

Availability: Free, Available for download, Freely available

Resource Name: poppr

Resource ID: SCR_023452

Alternate URLs: <https://CRAN.R-project.org/package=poppr>,
<https://github.com/grunwaldlab/poppr/>

License: GPL v3

Record Creation Time: 20230411T050206+0000

Record Last Update: 20260810T040839+0000

Ratings and Alerts

No rating or validation information has been found for poppr.

No alerts have been found for poppr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

Oreiro EG, et al. (2025) DMI fungicide resistance in *Zymoseptoria tritici* is unlinked to geographical origin and genetic background: a case study in Europe. *Pest management science*, 81(2), 1103.

Resjö S, et al. (2025) Late blight field resistance in potatoes carrying *Solanum americanum* resistance genes (*Rpi-amr3* and *Rpi-amr1*). *GM crops & food*, 16(1), 263.

Zhao K, et al. (2025) Inbreeding and Genetic Differentiation Among Geographic Populations of *Lactarius hatsudake* in Southwest China. *Journal of fungi* (Basel, Switzerland), 11(6).

Shaw CL, et al. (2024) A common multi-host parasite shows genetic structuring at the host species and population levels. *Parasitology*, 151(6), 557.

Tan Y, et al. (2023) The impacts of thermal heterogeneity across microhabitats on post-settlement selection of intertidal mussels. *iScience*, 26(12), 108376.

Rogério F, et al. (2023) Population Genomics Provide Insights into the Global Genetic Structure of *Colletotrichum graminicola*, the Causal Agent of Maize Anthracnose. *mBio*, 14(1), e0287822.

Barbosa CFC, et al. (2023) Genome-Wide SNP and Indel Discovery in *Abaca* (*Musa textilis* Née) and among Other *Musa* spp. for *Abaca* Genetic Resources Management. *Current issues in molecular biology*, 45(7), 5776.

Liu X, et al. (2022) Genome, genetic evolution, and environmental adaptation mechanisms of *Schizophyllum commune* in deep subseafloor coal-bearing sediments. *iScience*, 25(6), 104417.

Nowell RW, et al. (2021) Evolutionary dynamics of transposable elements in bdelloid rotifers. *eLife*, 10.

Edwards TP, et al. (2020) Genetic Diversity and Conservation Status of *Helianthus verticillatus*, an Endangered Sunflower of the Southern United States. *Frontiers in genetics*, 11, 410.

Talavera A, et al. (2019) Genome-Wide SNP discovery and genomic characterization in avocado (*Persea americana* Mill.). *Scientific reports*, 9(1), 20137.

Hopley T, et al. (2019) Gene Flow and Genetic Variation Explain Signatures of Selection across a Climate Gradient in Two Riparian Species. *Genes*, 10(8).

Huo GN, et al. (2016) An investigation into the potential effects of intrapopulation structure and other sources of sampling error, on population genetic studies of the transmission of *Schistosoma japonicum* (Trematoda: Digenea). *Parasites & vectors*, 9, 165.

Kikuchi T, et al. (2016) Genome-Wide Analyses of Individual *Strongyloides stercoralis* (Nematoda: Rhabditoidea) Provide Insights into Population Structure and Reproductive Life Cycles. *PLoS neglected tropical diseases*, 10(12), e0005253.