

Resource Summary Report

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National Plant Germplasm System (NPGS)

RRID:SCR_016785

Type: Tool

Proper Citation

National Plant Germplasm System (NPGS) (RRID:SCR_016785)

Resource Information

URL: <https://www.ars-grin.gov/npgs/>

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Description: Cooperative effort by U.S. state and federal government and private organizations to preserve the genetic diversity of plants. The NPGS aids scientists and the need for genetic diversity by acquiring, preserving, evaluating, documenting and distributing crop germplasm. The NPGS is managed by the Agricultural Research Service (ARS), the in-house research agency of the United States Department of Agriculture (USDA). Funding for the NPGS comes primarily through appropriations from the U.S. Congress.

Abbreviations: NPGS

Synonyms: National Plant Germplasm System, NPGS

Resource Type: data or information resource, portal, organization portal

Keywords: preserve, genetic, diversity, plant, germplasm, agriculture

Funding: U.S. Congress

Resource Name: National Plant Germplasm System (NPGS)

Resource ID: SCR_016785

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260812T044322+0000

Ratings and Alerts

No rating or validation information has been found for National Plant Germplasm System (NPGS).

No alerts have been found for National Plant Germplasm System (NPGS).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Walters C, et al. (2026) Assessing the viability of genebanked seeds from rare, wild plants native to the United States using the D.E.A.D. paradigm. Applications in plant sciences, 14(2), e70035.

Sidhu G, et al. (2025) Genetic diversity and population structure analysis in *Asparagus officinalis*. Journal, genetic engineering & biotechnology, 23(2), 100491.

Pelikan A, et al. (2025) Variation for QTL alleles associated with total dissolved solids among crop types in a GWAS of a *Beta vulgaris* diversity panel. The plant genome, 18(1), e70014.

Lee JY, et al. (2025) Allelic Analysis of the Gli-B1 Locus in Hexaploid Wheat Using Reverse-Phase-Ultra-Performance Liquid Chromatography. Molecules (Basel, Switzerland), 30(3).

Strickland LE, et al. (2024) Plant macrofossil data for 48-0 ka in the USGS North American Packrat Midden Database, version 5.0. Scientific data, 11(1), 68.

Jacquet S, et al. (2023) Evaluating the Response of Glycine soja Accessions to Fungal Pathogen *Macrophomina phaseolina* during Seedling Growth. Plants (Basel, Switzerland), 12(22).

Wang H, et al. (2023) Irradiated Pollen-Induced Parthenogenesis for Doubled Haploid Production in Sunflowers (*Helianthus* spp.). Plants (Basel, Switzerland), 12(13).

Li D, et al. (2022) Assessment of Rice Sheath Blight Resistance Including Associations with Plant Architecture, as Revealed by Genome-Wide Association Studies. Rice (New York, N.Y.), 15(1), 31.

Schneider HM, et al. (2021) Multiseriate cortical sclerenchyma enhance root penetration in compacted soils. Proceedings of the National Academy of Sciences of the United States of America, 118(6).

Groszmann M, et al. (2021) A consensus on the Aquaporin Gene Family in the Allotetraploid Plant, *Nicotiana tabacum*. Plant direct, 5(5), e00321.

Che P, et al. (2021) Developing a rapid and highly efficient cowpea regeneration, transformation and genome editing system using embryonic axis explants. *The Plant journal : for cell and molecular biology*, 106(3), 817.

Kumawat G, et al. (2021) A Major and Stable Quantitative Trait Locus qSS2 for Seed Size and Shape Traits in a Soybean RIL Population. *Frontiers in genetics*, 12, 646102.

Cho K, et al. (2021) Proteomic Determination of Low-Molecular-Weight Glutenin Subunit Composition in Aroona Near-Isogenic Lines and Standard Wheat Cultivars. *International journal of molecular sciences*, 22(14).

Jang YR, et al. (2020) Development of an Optimized MALDI-TOF-MS Method for High-Throughput Identification of High-Molecular-Weight Glutenin Subunits in Wheat. *Molecules (Basel, Switzerland)*, 25(18).

He H, et al. (2020) A high maternal genome excess causes severe seed abortion leading to ovary abscission in *Nicotiana* interploidy-interspecific crosses. *Plant direct*, 4(8), e00257.

Z??st T, et al. (2020) Independent evolution of ancestral and novel defenses in a genus of toxic plants (*Erysimum*, Brassicaceae). *eLife*, 9.

Toubiana D, et al. (2020) Correlation-based network analysis combined with machine learning techniques highlight the role of the GABA shunt in *Brachypodium sylvaticum* freezing tolerance. *Scientific reports*, 10(1), 4489.

Yan F, et al. (2019) Loss-of-Function Mutation of Soybean R2R3 MYB Transcription Factor Dilutes Tawny Pubescence Color. *Frontiers in plant science*, 10, 1809.

Do TD, et al. (2019) Identification of new loci for salt tolerance in soybean by high-resolution genome-wide association mapping. *BMC genomics*, 20(1), 318.

Talukder ZI, et al. (2019) Linkage Mapping and Genome-Wide Association Studies of the Rf Gene Cluster in Sunflower (*Helianthus annuus* L.) and Their Distribution in World Sunflower Collections. *Frontiers in genetics*, 10, 216.