

Resource Summary Report

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Japanese Research Center of Genetic Resources NARO Genebank project

RRID:SCR_013259

Type: Tool

Proper Citation

Japanese Research Center of Genetic Resources NARO Genebank project
(RRID:SCR_013259)

Resource Information

URL: http://www.gene.affrc.go.jp/index_en.php

Proper Citation: Japanese Research Center of Genetic Resources NARO Genebank project (RRID:SCR_013259)

Description: Research Center of Genetic Resources is central coordinating institute in Japan for conservation of plants, microorganisms, and animals related to agriculture. NARO Genebank coordinates this activity in collaboration with network of institutes throughout Japan. Conducts exploration, collection, characterization, preservation, and distribution service of microorganism genetic resources, animal genetic resources raised in Japan, and plant genetic resources.

Synonyms: Japanese Research Center of Genetic Resources National Agriculture and Food Research Organization Genebank project, NARO Genebank

Resource Type: biomaterial supply resource, material resource, tissue bank

Keywords: Japan, conservation, plants, microorganisms, animals, agriculture, NARO, genebank

Resource Name: Japanese Research Center of Genetic Resources NARO Genebank project

Resource ID: SCR_013259

Alternate IDs: SCR_013288, nlx_80440, nlx_64563

Record Creation Time: 20220129T080315+0000

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Ratings and Alerts

No rating or validation information has been found for Japanese Research Center of Genetic Resources NARO Genebank project.

No alerts have been found for Japanese Research Center of Genetic Resources NARO Genebank project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 94 mentions in open access literature.

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

Syafaah A, et al. (2026) Involvement of Phytohormone Responses of Rubber Leaves after Pestalotiopsis microspora Infection Revealed with Transcriptome Analysis. The plant pathology journal, 42(2), 191.

Noda Y, et al. (2025) Diurnal Regulation of SOS Pathway and Sodium Excretion Underlying Salinity Tolerance of Vigna marina. Plant, cell & environment, 48(6), 3925.

Ito M, et al. (2024) Single candidate gene for salt tolerance of Vigna nakashimae (Ohwi) Ohwi & Ohashi identified by QTL mapping, whole genome sequencing and triplicated RNA-seq analyses. Breeding science, 74(2), 93.

Han Y, et al. (2024) Characterization and risk assessment of novel SXT/R391 integrative and conjugative elements with multidrug resistance in Proteus mirabilis isolated from China, 2018-2020. Microbiology spectrum, 12(2), e0120923.

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Edet OU, et al. (2024) Genomic analysis of a spontaneous unifoliate mutant reveals gene candidates associated with compound leaf development in Vigna unguiculata [L] Walp. Scientific reports, 14(1), 10654.

Kobayashi A, et al. (2024) How have breeders adapted rice flowering to the growing region? Journal of integrative plant biology, 66(12), 2736.

Toda Y, et al. (2024) Reaction norm for genomic prediction of plant growth: modeling drought stress response in soybean. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(4), 77.

Kalambhe DG, et al. (2024) Trichinella spp. in Slaughtered Pigs of India: From Neglected Disease to an Emerging Food Safety Threat for Public Health. Transboundary and emerging diseases, 2024, 7550006.

Chigira Y, et al. (2023) Mating Types of *Ustilago esculenta* Infecting *Zizania latifolia* Cultivars in Japan Are Biased towards MAT-2 and MAT-3. *Microbes and environments*, 38(3).

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O'Brien A, et al. (2023) Predicting CRISPR-Cas12a guide efficiency for targeting using machine learning. *PloS one*, 18(10), e0292924.

Mansouri S, et al. (2023) Genetic diversity of merozoite surface protein-5 (MSP-5) of *Plasmodium vivax* isolates from Malaria patients in Iran. *BMC infectious diseases*, 23(1), 807.

Wang X, et al. (2022) Characterization of a halotolerant GH2 family ??-galactosidase GalM from *Microvirga* sp. strain MC18. *Protein expression and purification*, 194, 106074.

Li H, et al. (2022) Comparative Transcriptome Analysis Reveals Molecular Insights in Overwintering *Monochamus alternatus* (Coleoptera: Cerambycidae). *Journal of insect science* (Online), 22(3).

Wada KC, et al. (2022) Genetic effects of Red Lettuce Leaf genes on red coloration in leaf lettuce under artificial lighting conditions. *Plant-environment interactions* (Hoboken, N.J.), 3(4), 179.

Tanaka S, et al. (2022) Asymbiotic mass production of the arbuscular mycorrhizal fungus *Rhizophagus clarus*. *Communications biology*, 5(1), 43.

Noda Y, et al. (2022) Diversity of Na⁺ allocation in salt-tolerant species of the genus *Vigna*. *Breeding science*, 72(4), 326.

Shibaya T, et al. (2021) Development of PCR-based DNA marker for detection of white carrot contamination caused by Y2 locus. *Breeding science*, 71(2), 201.