Resource Summary Report

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UNITE

RRID:SCR_006518
Type: Tool

Proper Citation

UNITE (RRID:SCR_006518)

Resource Information

URL: http://unite.ut.ee/index.php

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Description: A fungal rDNA internal transcribed spacer (ITS) sequence database (although additional genes and genetic markers are also welcome) to facilitate identification of environmental samples of fungal DNA. Additional important features include user annotation of INSD sequences to add metadata on, e.g., locality, habitat, soil, climate, and interacting taxa. The user can furthermore annotate INSD sequences with additional species identifications that will appear in the results of any analyses done. UNITE focuses on high-quality ITS sequences generated from fruiting bodies collected and identified by experts and deposited in public herbaria. In addition, it also holds all fungal ITS sequences in the International Nucleotide Sequence Databases (INSD: NCBI, EMBL, DDBJ). Both sets of sequences may be used in any analyses carried out. UNITE is accompanied by a project management system called PlutoF, where users can store field data, document the sequencing lab procedures, manage sequences, and make analyses. PlutoF intends to make it possible for taxonomists, ecologists, and biogeographers to use a common platform for data storage, handling, and analyses, with the intent of facilitating an integration of these disciplines. A user can have an unlimited number of projects but still make analyses across any project data available to him.

Abbreviations: UNITE

Synonyms: unite: A molecular database for the identification of fungi

Resource Type: service resource, storage service resource, data analysis service, data or information resource, data repository, database, production service resource, analysis service resource

Defining Citation: PMID:20409185, PMID:15869663

Keywords: sequence, barcoding sequence, internal transcribed spacer sequence, rdna, gene, genetic marker, internal transcribed spacer, dna, FASEB list

Funding:

Availability: Creative Commons Attribution-ShareAlike License, v3 Unported, The community can contribute to this resource

Resource Name: UNITE

Resource ID: SCR_006518

Alternate IDs: nlx_61947

Old URLs: http://unite.zbi.ee

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250426T055857+0000

Ratings and Alerts

No rating or validation information has been found for UNITE.

No alerts have been found for UNITE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1664 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Liu S, et al. (2025) Genetic modification of the shikimate pathway to reduce lignin content in switchgrass (Panicum virgatum L.) significantly impacts plant microbiomes. Microbiology spectrum, 13(1), e0154624.

Jara-Servin A, et al. (2025) Microbial Communities in Agave Fermentations Vary by Local Biogeographic Regions. Environmental microbiology reports, 17(1), e70057.

Contreras-Negrete G, et al. (2025) Agricultural Practices and Environmental Factors Drive

Microbial Communities in the Mezcal-Producing Agave angustifolia Haw. Microbial ecology, 87(1), 181.

Rasuk MC, et al. (2025) Insights into the lemon (Citrus limon) epiphytic microbiome: impact of the biocontrol yeast Clavispora lusitaniae 146. BMC research notes, 18(1), 11.

Tu X, et al. (2025) Responses of fungal communities at different soil depths to grazing intensity in a desert steppe. PeerJ, 13, e18791.

Lucia Z, et al. (2025) More Than Meets the Eye: Unraveling the Interactions Between Skin Microbiota and Habitat in an Opportunistic Amphibian. Microbial ecology, 87(1), 176.

Li D, et al. (2025) Seed microbiomes promote Astragalus mongholicus seed germination through pathogen suppression and cellulose degradation. Microbiome, 13(1), 23.

Tan JJM, et al. (2025) Efficient Degradation of Industrial Biowaste via In-Vessel Composting-Technical and Microbial Assessments. Bioengineering (Basel, Switzerland), 12(1).

Liu J, et al. (2025) Fertilization Induced Soil Microbial Shifts Show Minor Effects on Sapindus mukorossi Yield. Microorganisms, 13(1).

Martins V, et al. (2025) Subregional pedoclimatic conditions with contrasted UV-radiation shape host-microbiome and metabolome phenotypes in the grape berry. Food chemistry: X, 25, 102139.

Martin I, et al. (2025) The fungal microbiota modulate neonatal oxygen-induced lung injury. Microbiome, 13(1), 24.

Sun S, et al. (2025) Effects of Enterococcus faecalis Supplementation on Growth Performance, Hepatic Lipid Metabolism, and mRNA Expression of Lipid Metabolism Genes and Intestinal Flora in Geese. Animals : an open access journal from MDPI, 15(2).

Chao H, et al. (2025) Litter quality modulates changes in bacterial and fungal communities during the gut transit of earthworm species of different ecological groups. ISME communications, 5(1), ycae171.

Zhou Y, et al. (2025) Deciphering the Distinct Associations of Rhizospheric and Endospheric Microbiomes with Capsicum Plant Pathological Status. Microbial ecology, 88(1), 1.

Kyle KE, et al. (2025) Untrimmed ITS2 metabarcode sequences cause artificially reduced abundances of specific fungal taxa. Applied and environmental microbiology, 91(1), e0153724.

Liu-Xu L, et al. (2025) Isolation and characterization of a new Leptobacillium species promoting tomato plant growth. Scientific reports, 15(1), 930.

Bak GR, et al. (2025) Changes in the potato rhizosphere microbiota richness and diversity occur in a growth stage-dependent manner. Scientific reports, 15(1), 2284.

Diakaki M, et al. (2025) Spinach seed microbiome characteristics linked to suppressiveness against Globisporangium ultimum damping-off. FEMS microbiology ecology, 101(2).

Drahun I, et al. (2025) Characterisation of the bacteriomes harboured by major wireworm pest species in the Canadian Prairies. Insect molecular biology, 34(1), 203.

Hou Q, et al. (2025) Active restoration efforts drive community succession and assembly in a desert during the past 53?years. Ecological applications : a publication of the Ecological Society of America, 35(1), e3068.