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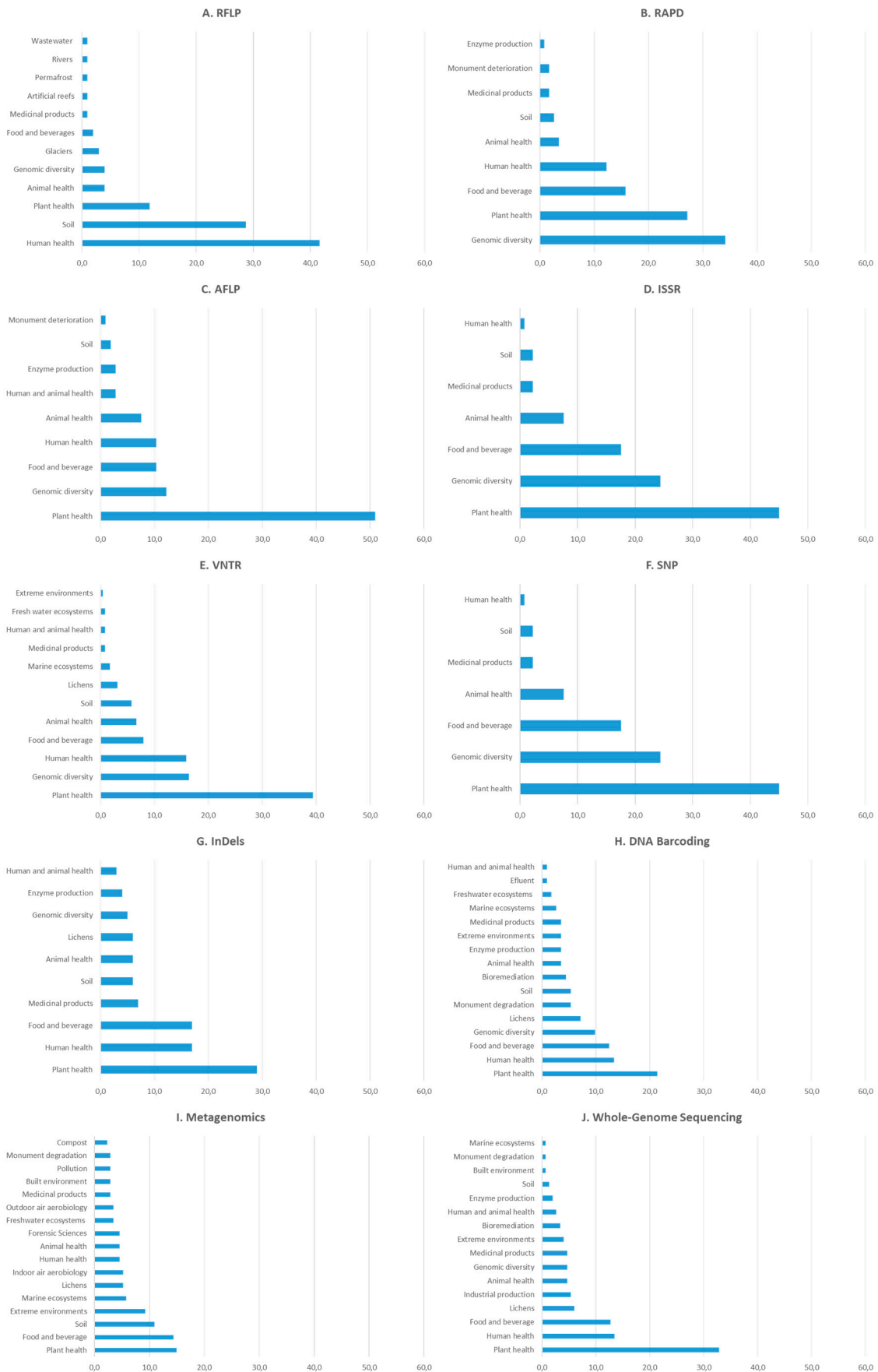
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Supplementary Figure S1. Distribution of the published papers per molecular marker.

Supplementary Table S1. Molecular markers in fungi: an overview of manuscripts published in the last ten years using RFLP and similar techniques (HRM: high resolution melting; PCR-RFLP: PCR restriction fragment length polymorphism; qPCR: quantitative PCR; tHDA-RFLP: thermophilic helicase DNA amplification and restriction fragment length polymorphism; T-RFLP: PCR-terminal restriction fragment length polymorphism; UMPCR-RFLP: Universal MT-RFLP).

Importance	Molecular marker	Fungal identification	Purpose	Reference
Human health	PCR-RFLP	<i>Alternaria chlamydospora</i>	Identification of the etiological agent of malignant otitis externa	[1]
	PCR-RFLP	<i>Aspergillus</i> spp.	Identification of the clinically important <i>Aspergillus</i> species	[2–4]
	PCR-RFLP	<i>Aspergillus flavus</i> <i>Penicillium chrysogenum</i> <i>Candida glabrata</i> species complex	Identification of the etiological agent of non-invasive fungal sinusitis	[5]
	PCR-RFLP	<i>Candida</i> spp.	Identification of the etiological agent of oral thrush in HIV-positive patients	[6]
	PCR-RFLP	<i>Candida</i> spp.	Identification of the etiological agent of candidemia	[7,8]
	PCR-RFLP	<i>Candida</i> spp.	Identification of the etiological agent of cutaneous candidiasis	[8]
	PCR-RFLP	<i>Candida</i> spp.	Identification of the etiological agent of onychomycosis	[9,10]
	PCR-RFLP	<i>Candida</i> spp.	Identification of the etiological agent of vulvovaginal candidiasis	[11]
	PCR-RFLP	<i>Candida</i> spp.	Identification of medically important <i>Candida</i> species	[12]
	PCR-RFLP	<i>Candida</i> spp.	Identification of the etiological agent of neonatal candidemia	[13]
	PCR-RFLP	<i>Candida</i> spp.	Study of the frequency of <i>Candida</i> species in the oral cavity of narcotics and stimulants smokers	[14]
	T-RFLP	<i>Candida albicans</i> <i>Candida dubliniensis</i>	Differentiation between <i>species</i> associated with superficial and systemic infections	[15]
	PCR-RFLP	<i>Candida parapsilosis</i> species complex	Identification and differentiation of the <i>C. parapsilosis</i> complex species	[16]
	PCR-RFLP	<i>Candida</i> spp. <i>Cryptococcus</i> spp. <i>Histoplasma capsulatum</i>	Diagnosis of invasive mycoses	[17]
	PCR-RFLP	<i>Cryptococcus neoformans</i> <i>Cryptococcus gattii</i> species complex	Identification and differentiation of the species included in the same species complex	[18]

	RFLP	Dermatophytes	Detection of source of dermatophytosis	[19]
	PCR-RFLP	Dermatophytes	Study of the molecular variation analysis of species <i>Arthroderma benhamiae</i> associated with dermatophytosis	[20]
	PCR—RFLP	Dermatophytes	Identification of the etiological agent of dermatophytosis	[21–23]
	PCR-RFLP	Dermatophytes	Differentiation between environmental and clinically isolates	[24]
	PCR-RFLP	Dermatophytes	Study of the molecular variation analysis of <i>Fusarium</i> species associated with dermatophytosis	[25]
	RFLP	Dermatophytes	Identification of the etiological agent of dermatophytosis	[26]
	RFLP-PCR	Dermatophytes <i>Candida</i> spp.	Identification of clinical isolates from hair and skin samples	[27]
	PCR-RFLP	Dermatophytes Non-dermatophytes	Confirmatory test for onychomycosis	[28]
	PCR-RFLP	Dermatophytes Non-dermatophytes	Identification and antifungal susceptibility of species associated with onychomycosis	[29]
	RFLP	<i>Enterocytozoon bieneusi</i>	Identification of <i>E. bieneusi</i> isolated from HIV-infected patients	[30]
	PCR-RFLP	<i>Mucorales</i> species	Molecular diagnosis of rhino-orbito-cerebral mucormycosis	[31]
	RFLP	<i>Pneumocystis jirovecii</i>	Identification of the etiological agent of pneumocystis pneumonia in immunocompromised patients	[32]
	PCR-RFLP	<i>Paracoccidioides</i> spp.	Identification of the etiological agent of paracoccidioidomycosis	[33]
	RFLP	<i>Proteus mirabilis</i>	Identification and phyletic evolution analysis of <i>Proteus mirabilis</i> strains	[34]
	tHDA-RFLP	<i>Pythium insidiosum</i>	Discrimination between species associated with pythiosis	[35]
	PCR-RFLP	<i>Scopulariopsis</i>	Identification of genera associated with opportunistic infections	[36]
	UMPCR-RFLP	<i>Talaromyces marneffeii</i>	Identification of the etiological agent of opportunistic infections in immunocompromised patients	[37]
	T-RFLP	<i>Trichophyton</i> spp.	Identification of the etiological agent of onychomycoses	[38]
	RFLP	<i>Trichophyton mentagrophytes</i> species complex	Discrimination between species among the species complex	[39,40]
	PCR-RFLP	<i>Sporothrix schenckii</i> complex species	Identification of the etiological agent of sporotrichosis	[41,42]
	T-RFLP	Dermatophytes	Identification of dermatophytes in veterinary mycology	[43]
	RFLP	Gut microbiome	Intestinal fungal diversity of sub-adult giant panda	[44]

Animal health	PCR-RFLP	<i>Malassezia</i> spp.	Identification of <i>Malassezia</i> species isolated from animals	[45]
	PCR-RFLP	Yeast	Identification of yeast species isolated from bovine intramammary infection	[46]
	PCR-RFLP	<i>Aspergillus</i> spp. <i>Alternaria</i> spp. <i>Penicillium</i> spp.	Identification of fungal contamination of date palm tissue cultures	[47]
Plant health	RFLP	<i>Beauveria</i> spp. <i>Metarhizium</i> spp.	Plant tissue localization of the endophytic pathogenic fungi	[48]
	PCR-RFLP	<i>Colletotrichum gloeosporioides</i> <i>C. truncatum</i>	Discrimination between fungal species associated with anthracnose in papaya and bell pepper	[49]
	PCR-RFLP	<i>Colletotrichum gloeosporioides</i> <i>sensu lato</i>	Discrimination between strains	[50]
	PCR-RFLP	Endophytic fungi	Identification of endophytic fungi of sugarcane	[51,52]
	T-RFLP	Endophytic fungi	Identification of endophytic fungi of <i>Alpinia officinarum</i>	[53]
	PCR-RFLP	<i>Fomes fomentarius</i>	Discrimination of <i>Fomes fomentarius</i> genotypes	[54]
	PCR-RFLP	Fungal pathogens	Identification of fungal pathogens in potato crops	[55]
	T-RFLP	Fungal phyllosphere fungi	Effects of Summer season and long-term drought in the foliar phyllosphere	[56]
	T-RFLP	<i>Fusarium oxysporum</i> f. sp. <i>fragariae</i>	Study of genetic diversity of the etiological agent of Fusarium wilt in strawberries	[57]
	T-RFLP	<i>Puccinia psidii</i>	Study of genetic diversity of the etiological agent of rust in Eucalyptus spp. and other trees	[58]
Food and beverages	PCR- RFLP	Fungal species	Identification of pineapple spoilage fungi	[59]
	T-RFLP	Yeast	Identification of yeast used in wine fermentation in Chinese enology	[60]
Medicinal products	PCR-RFLP	<i>Ophiocordyceps sinensis</i>	Identification of Chinese caterpillar medicinal mushroom from counterfeit species	[61]
	PCR-RFLP	<i>Cercospora beticola</i>	Analysis of fungicide resistance	[62]
Genomic diversity	RFLP	<i>pfl</i> somatic hybrids	Characterization of somatic hybrids from <i>Pleurotus florida</i> and <i>Lentinula edodes</i>	[63]
	PCR-RFLP	<i>Aspergillus flavus</i>	Study of the molecular variation analysis of <i>A. flavus</i> from clinical and environmental isolates	[64]
	PCR-RFLP	<i>Volvariella volvacea</i>	Identification of A mating-type loci in <i>Volvariella volvacea</i>	[65]

	T-RFLP	Mycorrhizal fungi	Effect of different degrees of salinization	[66]
Soil	T-RFLP	Mycorrhizal fungi	Effect of time and plant composition	[67]
	T-RFLP	Mycorrhizal fungi	Effects of plant composition	[68]
	T-RFLP	Mycorrhizal fungi	Effects of maize expressing the <i>Bacillus thuringiensis</i> Cry1Ab endotoxin (Bt maize)	[69]
	T-RFLP	Mycorrhizal fungi	Effects of local environment and geographical distance	[70,71]
	T-RFLP	Mycorrhizal fungi	Effects of fertilization	[72–74]
	T-RFLP	Mycorrhizal fungi	Effects of geographical distance	[75,76]
	T-RFLP	Mycorrhizal fungi	Effect of poly (lactic) acid (PLA)	[77]
	T-RFLP	Mycorrhizal fungi	Effects of root age from <i>Panax ginseng</i>	[78]
	T-RFLP	Mycorrhizal fungi	Effects of plant composition	[79,80]
	T-RFLP	Mycorrhizal fungi	Effects of till	[81]
	T-RFLP	Mycorrhizal fungi	Effects of host during ecosystem development	[82]
	T-RFLP	Mycorrhizal fungi	Effects of time	[83]
	T-RFLP	Mycorrhizal fungi	Effects of transgenic crops	[84]
	T-RFLP	Mycorrhizal fungi	Effects of long-term effects of multiwalled carbon nanotubes and graphene	[85]
	T-RFLP	Mycorrhizal fungi	Effects of plant organ and development of stage winter wheat	[86]
	RFLP	Mycorrhizal fungi	Effects of season	[87]
	RFLP	Mycorrhizal fungi	Effects of tree harvesting	[88]
	RFLP	Mycorrhizal fungi	Effects of the invasive plant <i>Impatiens glandulifera</i>	[89]
	T-RFLP	Mycorrhizal fungi	Effects of biochar	[90,91]
	T-RFLP	Mycorrhizal fungi	Effects of pentachlorophenol	[92]
	T-RFLP	Mycorrhizal fungi	Effects of tea plantation ages	[93]
	T-RFLP	Mycorrhizal fungi	Effects of herbivory and soil water availability	[94]
	T-RFLP	Fungal communities	Study of fungal diversity of marine biofilms on artificial reefs	[95]
Artificial reefs	T-RFLP	Fungal communities	Identification of fungal succession in the forefield of a receding glacier	[96]
Glaciers	T-RFLP	Fungal communities	Identification of fungal isolates from cryoconite holes on glaciers	[97]
	T-RFLP	Fungal communities	Study of fungal responses to reciprocal soil transfer along a temperature and soil moisture	[98]
	T-RFLP	Fungal communities	Study of the diversity and community structure of fungi	[99]

Permafrost	PCR-RFLP	Fungal communities	Influence of water quality on diversity and composition of fungal communities	[100,101]
Rivers	PCR-RFLP	Fungal communities	Identification of fungal isolates from rivers with various contaminations	[102]
Wastewater	ITS-RFLP	Fungal communities	Identification of fungal isolates from textile wastewater	[103]

Supplementary Table S2. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using RAPD and similar techniques.

Importance	Molecular marker	Fungal identification	Purpose	Reference
Human health	RAPD	<i>Candida albicans</i>	Analysis of isolates from clinical sources of hospital in south China	[1]
	RAPD	<i>Aspergillus niger</i> <i>Aspergillus flavus</i>	Molecular characterization of infections in an Iranian educational hospital	[2]
	RAPD	<i>Candida</i> spp. <i>Aspergillus</i> spp.	Survey of opportunistic fungi in the clinical and environmental specimens from Urmia educational hospitals	[3]
	RAPD	<i>Candida albicans</i> <i>Candida glabrata</i>	Molecular epidemiology of strains isolated from intensive care unit	[4]
	RAPD	<i>Scopulariopsis</i> spp. <i>Microascus</i> spp.	Study of the genetic diversity of opportunistic human pathogenic fungi	[5]
	RAPD	<i>Rhizopus microsporus</i>	Identification of the etiological agent of a mucormycosis	[6]
	RAPD	<i>Candida</i> spp.	Study of genetic diversity and relationships among the clinical isolates	[7]
	RAPD-PCR	<i>Candida albicans</i>	Evaluation of genomic polymorphism isolates from patients with vaginitis	[8]
	RAPD-PCR	<i>Aspergillus flavus</i> <i>Aspergillus tamarii</i>	Identification of DNA polymorphisms of isolates from corneal ulcer/keratitis cases	[9]
	RAPD-PCR	<i>Trichophyton rubrum</i>	Genomic polymorphism of <i>T. rubrum</i> isolated from keratinized clinical sources	[10]
Animal health	RAPD	<i>Metarhizium anisopliae</i> var. <i>anisopliae</i>	Study of the genetic diversity among isolates of the entomopathogenic fungus	[11]
	RAPD-PCR	<i>Saprolegnia</i> spp.	Molecular identification of a pathogenic aquatic fungi from rainbow and Caspian trout eggs	[12]
	RAPD	<i>Monacrosporium eudermatum</i>	Study of the genetic diversity of the nematode trapping fungus	[13]
	RAPD	<i>Metarhizium anisopliae</i> <i>Isaria amoenerosea</i>	Study of genetic diversity and pathogenicity of the entomopathogenic fungi	[14]
Plant health	RAPD	<i>Pyrenophora graminea</i>	Study of the molecular phylogeny of the etiological agent of barley leaf stripe	[15]

	RAPD-PCR	<i>Phaeoacremonium parasiticum</i> <i>Phaeacremonium aleophilum</i> <i>Phaeomoniella chlamydospore</i> <i>Fomitiporia mediterranea</i>	Study on genetic diversity of fungi associated with esca disease	[16]
	RAPD	<i>Drechslera teres</i>	Diversity in the Polish isolates from spring barley	[17]
	PCR-RAPD	<i>Fusarium oxysporum</i> f. sp. <i>psidii</i> <i>Fusarium solani</i>	Profiling of etiological agent of guava wilt disease	[18]
	RAPD	<i>Alternaria alternata</i>	Study of the genetic diversity and pathogenicity of the etiological agent of brown spot, leaf spot, and black rot in citrus hybrids trees	[19]
	RAPD	<i>Ustilago maydis</i>	Study of genetic diversity of the etiological agent of smuts in maize	[20]
	RAPD	<i>Sporisorium scitamineum</i>	Study on genetic diversity of the etiological agent of smuts in maizesugarcane	[21]
	RAPD	<i>Lasiodiplodia theobromae</i>	Characterisation of the etiological agent of crown rot disease in banana fruits	[22]
	RAPD	<i>Fusarium oxysporum</i> f. sp. <i>cumini</i>	Study of the genetic variability of the etiological agent of wilt in cumin	[23]
	RAPD	<i>Mycosphaerella pinodes</i> <i>Phoma pinodella</i> <i>Phoma koolunga</i> <i>Ascochyta pisi</i>	Characterization of the etiological agents of ascochyta blight of field pea	[24]
	RAPD	<i>Bipolaris sorokiniana</i>	Study of genetic diversity and phylogeny of the etiological agent of spot blotch disease in wheat	[25]
	RAPD	<i>Myrothecium</i> spp.	Study of genetic diversity of endophytic fungi	[26]
	RAPD	<i>Aspergillus flavus</i>	Characterization of the fungi associated with <i>Vitis vinifera</i> decline	[27]
	RAPD	<i>Phytophthora colocasiae</i>	Study of the genetic diversity of the etiological agent of leaf blight of taro	[28]
	RAPD	<i>Tulasnella</i> spp.	Study of morphological and molecular characterization of fungi isolated from the roots from <i>Epidendrum secundum</i>	[29]
	RAPD	<i>Trichoderma atroviride</i>	Study of genetic variability of strains isolated from a lentil field	[30]
	RAPD	<i>Alternaria lini</i>	Study of genetic diversity of isolates from linseed	[31]

	RAPD	<i>Fusarium solani</i>	Study of genetic diversity and pathogenicity of strains isolated from chickpea	[32]
	RAPD	<i>Fusarium udum</i>	Study of the genetic diversity of the etiological agent of wilt in pigeonpea	[33]
	RAPD	<i>Stemphylium solani</i>	Differentiation among isolates from two varieties of eggplant	[34]
	RAPD	<i>Alternaria</i> spp <i>Cladosporium</i> spp <i>Epicoccum</i> spp <i>Ulocladium</i> spp	Identification of different fungal fruit rot pathogens of date palm	[35]
	RAPD	<i>Diaporthe/Phomopsis</i>	Identification of strains from fruit trees	[36]
	RAPD	<i>Pestalotia</i> sp.	Study of the genetic diversity of isolates of endophytes from different hosts	[37]
	RAPD	<i>Fusarium oxysporum</i> <i>Fusarium solani</i> <i>Fusarium equiseti</i>	Study of the genetic diversity of the etiological agent of root rot in apple	[38]
	RAPD	<i>Fusarium oxysporum</i> <i>Fusarium equiseti</i> <i>Fusarium subglutinans</i> <i>Fusarium proliferatum</i>	Identification and characterization etiological agent of wilt in tomato	[39]
	RAPD	<i>Fusarium moniliforme</i> <i>Fusarium xylarioides</i> <i>Fusarium fusarioides</i>	Study of the genetic diversity and phylogeny of the etiological agent of pokkah boeng disease in sugarcane	[40]
	RAPD	<i>Sclerotium rolfsii</i>	Study of the genetic diversity of the etiological agent of collar rot in chickpea	[41]
	RAPD	<i>Puccinia graminis</i> <i>Puccinia tritici</i> <i>Puccinia striiformis</i>	Molecular characterization of predominant Indian wheat rust pathotypes	[42]
	RAPD	<i>Alternaria alternata</i> <i>Aspergillus neoflavipes</i> <i>Curvularia geniculata</i> <i>Penicillium singorense</i>	Study of phylogeny and genetic diversity of potent endophytic fungi isolated from medicinal plants	[43]
	RAPD	<i>Aureobasidium pullulans</i>	Study of the genetic diversity and population structure in withered grape carposphere	[44]

	RAPD	<i>Sporisorium scitamineum</i>	Genetic characterization of isolates in sugarcane	[45]
Food and beverage	RAPD	<i>Penicillium roqueforti</i>	Molecular and mycotoxigenic identification of fungi in moldy civil cheese	[46]
	RAPD	<i>Aspergillus</i> spp.	Characterization of species associated with commercially stored triphala powder	[47]
	RAPD	<i>Agaricus bisporus</i>	Assisted development of improved strains	[48]
	RAPD	<i>Aspergillus</i> spp. <i>Penicillium</i> spp. <i>Rhizopus</i> spp. <i>Fusarium</i> spp. <i>Alternaria alternata</i> <i>Mucor</i> spp.	Identification of fungi from stored citrus	[49]
	PCR-RAPD	<i>Pleurotus ostreatus</i> <i>Pleurotus sapidus</i>	Differentiation between edible mushrooms	[50,51]
	RAPD	<i>Agaricus bisporus</i> <i>Pleurotus eryngii</i> <i>Lentinus edodes</i> <i>Hypsizygus tessellatus</i> <i>Flammulina velutipes</i> <i>Pleurotus ostreatus</i> <i>Pleurotus djamor</i> <i>Calocybe indica</i> <i>Pleurotus florida</i>	Discrimination between commercial mushrooms	[52]
	RAPD	<i>Aspergillus flavus</i>	Study of the genetic diversity of strains isolates from barley grains	[53]
	RAPD	<i>Aspergillus flavus</i>	Study of the genetic diversity of strains isolates from chilies	[54]
	RAPD	<i>Alternaria solani</i>	Study of the genetic diversity among isolates from potatoes	[55]
	RAPD	<i>Pleurotus pulmonarius</i>	Study of the genetic diversity of edible mushrooms	[56]
	RAPD	<i>Aspergillus flavus</i>	Detection of seedborne <i>Aspergillus flavus</i> from rice cultivars	[57]
	RAPD	Agaricomycetes	Molecular characterization and phylogeny of mushrooms	[58]
	RAPD	<i>Aspergillus</i> spp. <i>Penicillium</i> spp. <i>Saccharomyces cerevisiae</i> <i>Wickerhamomyces anomalus</i>	Identification of contaminative fungi isolated from rye breads	[59]

	RAPD	<i>Monascus</i> spp.	Study of the genetic diversity of strains with culinary and medicinal applications	[60]
	RAPD	<i>Aspergillus niger</i> <i>Aspergillus flavus</i> <i>Aspergillus fumigatus</i> <i>Penicillium citrinum</i> .	Study of the genetic diversity of mycotoxin-producing fungi from contaminated animal feed	[61]
	RAPD	<i>Pleurotus cystidiosus</i> <i>Pleurotus ostreatus</i> <i>Pleurotus flabellatus</i> <i>Pleurotus flabellatus</i> <i>Pleurotus pulmonarius</i> <i>Pleurotus fossulatus</i> <i>Pleurotus eryngii</i> <i>Pleurotus sapidus</i> <i>Pleurotus florida</i>	Study of the genetic diversity of edible mushrooms	[62]
	RAPD	<i>Colletotricum gleosporioides</i>	Study of the prevalence and genetic diversity of mycotoxigenic-producing strains from wheat grains	[63]
	RAPD	Seed-borne pathogenic fungi	Study of genetic diversity of maize seed-borne pathogenic fungi	[64]
Fungal diversity	RAPD	<i>Fusarium verticillioides</i>	Study of the genetic diversity and vegetative compatibility of a major fungal pathogen from cereals in Iran	[65]
	RAPD	<i>Rhizoctonia solani</i>	Study of the genetic diversity in isolates from different agro-ecological zones	[66]
	RAPD	<i>Phytophthora colocasiae</i>	Study of the genetic diversity	[67]
	RAPD	<i>Alternaria alternata</i>	Study of the genetic diversity	[68]
	RAPD	<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	Study of the genetic diversity of populations	[69]
	RAPD	<i>Monilinia fructicola</i>	Study of genetic diversity in strains from the Ebro Valley in Spain	[70]
	RAPD	<i>Fusarium</i> spp.	Study of genetic diversity among 14 different species	[71]
	RAPD	<i>Fusarium semitectum</i>	Study of morphological and genetic diversity of the isolates from cereal grains	[72]
	RAPD	<i>Trichoderma</i> spp.	Molecular characterization of 12 isolates	[73]
	RAPD	<i>Pyricularia</i> spp	Study of the genetic diversity in phytopathogenic	[74]

	RAPD	<i>Rhizoctonia</i> spp.	Study of the genetic diversity in phytopathogenic	[75]
	RAPD	<i>Fusarium oxysporum</i> f. sp. <i>raphani</i> ,	Differentiation of isolates of the pathogen among cultivated and wild rocket	[76]
	RAPD	<i>Conidiobolus coronatus</i>	Study of the genetic diversity	[77]
	RAPD	<i>Verticillium chlamydosporium</i>	Genetic characterization of <i>V. chlamydosporium</i> isolated from Pakistan	[78]
	RAPD	<i>Lentinula edodes</i>	Study on the genetic diversity of <i>L. edodes</i> strains	[79]
	RAPD	<i>Fusarium solani</i>	Study of the genetic diversity of the etiological agent of citrus dry root rot	[80]
	RAPD	<i>Aspergillus flavus</i>	Fingerprinting of toxigenic and non-toxigenic strains isolated from different habitats	[81]
	RAPD	<i>Fusarium</i> sp.	Characterization of antibacterial activity	[82]
	RAPD	<i>Botrytis alli</i>	Study of genetic diversity of the agent of onion gray mold	[83]
	RAPD	<i>Aspergillus niger</i>	Comparative sequence analysis of citrate synthase and 18S ribosomal DNA from a wild and mutant strains of <i>A. niger</i> with various fungi	[84]
	RAPD	<i>Trichophyton mentagrophytes</i>	Terbinafine susceptibility and genotypic heterogeneity in clinical isolates	[85]
	RAPD	<i>Aspergillus niger</i>	Study of the genetic diversity among isolates	[86]
	RAPD	<i>Penicillium</i> spp.	Molecular Characterization of Isolates	[87]
	RAPD	<i>Rhizoctonia solani</i>	Study of the genetic variability of isolates of different geographical regions and hosts	[88,89]
	RAPD-PCR	<i>Beauveria bassiana</i>	Study of the genetic diversity	[90,91]
	RAPD	<i>Ganoderma lucidum</i>	Study of genetic diversity	[92]
	RAPD	<i>Fusarium asiaticum</i>	Identification of a novel phenamacril-resistance-related gene	[93]
	RAPD	<i>Sclerotinia sclerotiorum</i>	Study of genetic diversity of strains isolated from eggplant	[94]
	RAPD	<i>Morchella</i> sp.	Study of the genetic diversity	[95]
	RAPD	<i>Aspergillus</i> section Nigri	Study of the genetic diversity of ochratoxin-producing fungi	[96]
	RAPD	<i>Fusarium pallidoroseum</i>	Study of the genetic diversity	[97]
	RAPD	<i>Ganoderma lucidum</i> <i>Leucoagricus</i> spp. <i>Lentinus</i> spp.	Study of genetic diversity among three most frequent species of macrofungi from a tropical forest	[98]
	RAPD	<i>Trichoderma</i> spp.	Study of the genetic diversity	[99]

	RAPD	<i>Colletotrichum falcatum</i>	Study of genetic diversity	[100]
	RAPD	<i>Flammulina velutipes</i>	Study of the genetic diversity	[101]
	RAPD	<i>Bjerkandra adusta</i> <i>Fomes fomentarius</i> <i>Rigidoporus ulmarius</i> <i>Tremetes versicolor</i>	Study of the genetic diversity of macrofungi	[102]
Medicinal products	RAPD	<i>Lentinus edodes</i>	Molecular characterization of shiitake medicinal mushroom strains	[103]
	RAPD-SCAR	<i>Ganoderma lucidum</i> <i>Ganoderma sinense</i> <i>Ganoderma tropicum</i> <i>Ganoderma gibbosum</i>	Differential authentication of the presence of <i>Ganoderma</i> species in medicinal products	[104]
Enzyme production	RAPD	<i>Aspergillus niger</i> <i>Penicillium chrysogenum</i>	Pectinase hyperproduction in fungi Isolates	[105]
Soil	RAPD	<i>Aspergillus</i> spp.	Identification of antibiotic producing fungi from soil	[106]
	RAPD	<i>Glomus</i> spp. <i>Gigaspora</i> spp. <i>Scutellospora</i> spp.	Study of the genetic diversity of arbuscular mycorrhizal fungi	[107]
	RAPD	<i>Trichoderma asperellum</i> <i>Trichoderma longibrachiatum</i> <i>Trichoderma harzianum</i>	Identification of rhizosphere fungi and their antagonistic impact against plant pathogenic fungi	[108]
Monument deterioration	RAPD	<i>Rhizopus</i> spp.	Study of the genetic diversity of fungi associated with the deterioration of historical sandstone monuments	[109]
	RAPD	<i>Aspergillus niger</i> <i>Aspergillus fumigatus</i>	Study of ecologic and genetic diversity of black fungus from associated with the deterioration of stone monuments	[110]

Supplementary Table S3. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using AFLP and similar techniques.

Importance	Fungal identification	Purpose	Reference
Human health	<i>Cladophialophora carrionii</i> <i>Fonsecaea</i> spp.	Study of genetic diversity of the etiological agent of chromoblastomycosis	[1]
	<i>Candida tropicalis</i>	Study of azole resistance genes in the etiological agent of opportunistic infections	[2]
	<i>Apophysomyces variabilis</i>	Determination of environmental sources of the etiological agent of mucormycosis	[3]
	<i>Sporothrix globosa</i>	Study of genetic diversity of the etiological agent of sporotrichosis	[4]
	<i>Hortaea werneckii</i>	Study of genetic diversity of the halotolerant fungus causing tinea nigra	[5]
	<i>Aspergillus fumigatus</i> <i>Penicillium</i> spp. <i>Aspergillus</i> spp. <i>Scedosporium</i> spp. <i>Exophiala dermatitidis</i> <i>Cladosporium</i> spp.	Study of the genetic diversity and prevalence of filamentous fungi in the airways of cystic fibrosis patients	[6]
	<i>Trichophyton schoenleinii</i>	Molecular epidemiology of the etiological agent of <i>tinea capitis favosa</i>	[7]
	<i>Sporothrix</i> spp.	Study of genetic diversity of the etiological agent of sporotrichosis	[8,9]
	<i>Candida auris</i>	Evaluation of <i>C. auris</i> associated with nosocomial infections	[10]
	<i>Paracoccidioides</i> spp.	Study of genetic diversity, population structure, and phylogeography of the etiological agent of paracoccidioidomycosis	[11]
	<i>Coccidioides posadasii</i>	Study of genetic diversity of the etiological agent of coccidioidomycosis	[12]
Human and animal health	<i>Cryptococcus gattii</i>	Study of the origin and genetic diversity of the etiological agent of cryptococcosis	[13]
	<i>Cryptococcus</i> spp.	Study of the environmental distribution	[14]
	Black yeast-like fungi	Identification of fungi associated with lethargic crab disease in the mangrove-land crab	[15]
	Entomopathogenic fungi	Study of genetic diversity of entomopathogenic fungi	[16]
Animal health	<i>Beauveria bassiana</i>	Study of genetic diversity of the arthropod species' parasite	[17]
	<i>Aphanomyces astaci</i>	Transmission from invasive to wild populations of crayfish	[18]
	<i>Metarhizium flavoviride</i>	Study of the genetic diversity of the Hemiptera and Coleoptera species' parasite	[19]
	<i>Acromyrmex echinator</i> <i>Acromyrmex octospinosus</i>	Study of somatic incompatibility and genetic structure of fungal crops in sympatric ants	[20]
	<i>Beauveria bassiana</i>	Study of differential genes expression of the entomopathogenic fungus during infection of lepidopteran larvae	[21]

Plant health	<i>Pseudocercospora griseola</i>	Study of the genetic diversity of the etiological agent of angular bean leaf spot	[22]
	<i>Colletotrichum gloeosporioides</i>	Study of the genetic diversity of the etiological agent of anthracnose	[23]
	<i>Bipolaris sorokiniana</i> (<i>Cochliobolus sativus</i>)	Study of genetic diversity, virulence and population structure of the etiological agent of barley and wheat spot blotch	[24–26]
	<i>Veronaea botryosa</i>	Study of genetic diversity of the etiological agent of asian soybean rust	[27]
	<i>Neotyphodium</i> spp.	Study of the genetic diversity of the endophytic fungi symbiotic with grasses	[28]
	<i>Puccinia striiformis</i>	Study of genetic diversity of the etiological agent of yellow rust	[29]
	<i>Pyrenophora graminea</i>	Study of virulence on barley	[30]
	<i>Fusarium mangiferae</i>	Diagnosis and phylogeny of the etiological agent of mango malformation disease	[31]
	<i>Colletotrichum sublineolum</i>	Study of genetic diversity of the etiological agent of anthracnose in sorghum	[32]
	<i>Mycosphaerella pinodes</i>	Study of genetic diversity of the etiological agent of ascochyta blight on pea	[33]
	<i>Fusarium oxysporum</i> f. sp. <i>acaciae</i>	Study of pathogenicity of fungal species responsible for <i>Acacia koa</i> dieback	[34]
	<i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i>	Study of the genetic diversity of the etiological agent of wilt in tomato	[35]
	<i>Fusarium udum</i>	Study of the genetic variability of the etiological agent of the wilt in pigeon pea	[36]
	<i>Coniophora</i> complex species	Identification of species associated with rotten wood	[37]
	<i>Tilletia foetida</i>	Detection of pathogen on wheat	[38]
	<i>Fusarium solani</i>	Detection of etiological agent of peanut brown root rot	[39]
	<i>Seiridium cardinale</i>	Study of the population structure of the etiological agent of canker in Cupressaceae	[40]
	<i>Hemileia vastatrix</i>	Study of population structure of the etiological agent of coffee leaf rust	[41]
	<i>Diplodia seriata</i>	Discrimination of fungal species associated with grapevine decline	[42]
	<i>Phaeomoniella chlamydospora</i>		
	<i>Phaeoacremonium aleophilum</i>		
	<i>Alternaria alternata</i>	Study of the genetic diversity in toxigenic <i>Alternaria</i> species in wheat	[43]
	<i>Alternaria infectoria</i>		
	<i>Macrophomina phaseolina</i>	Identification of three fruit-rot fungi of banana	[44]
	<i>Fusarium oxysporum</i>		
	<i>Nigrospora oryzae</i>		
	<i>Fusarium oxysporum</i> f. sp. <i>passiflorae</i>	Identification of the etiological agent of fusariosis in passionfruit	[45]
	<i>Venturia inaequalis</i>	Study of genetic diversity of the etiological agent of apple scab within mixed orchards	[46]
	<i>Phaeoacremonium aleophilum</i>	Characterization of the fungi associated with <i>Vitis vinifera</i> decline	[47]

	<i>Phytophthora colocasiae</i>	Study of the genetic diversity of the etiological agent of leaf blight of taro	[48]
	<i>Magnaporthe</i> spp.	Characterization of the fungi associated with rice blast	[49]
	<i>Pyrenophora teres</i> f. <i>teres</i>	Study of virulence factors of the etiological agent of foliar disease net form net blotch	[50]
	<i>Fusarium circinatum</i>	Evidence for a new introduction of the pitch canker fungus	[51]
	<i>Pyrenophora teres</i>	Studies of positional cloning in biparental fungal populations, association mapping of natural fungal populations and population genetics studies	[52]
	<i>Sphaerulina musiva</i>		
	<i>Phakopsora pachyrhizi</i>	Study of genetic diversity of the etiological agent of soybean rust	[53]
	<i>Podosphaera xanthii</i>	Study of genetic diversity and population structure of the etiological agent of powdery mildew in cucurbit	[54]
	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	Study of genetic diversity and virulence factors of the etiological agent of yellow stripe rust on wheat varieties and their mixtures	[55]
	<i>Rhizoctonia solani</i>	Study of differentially expressed genes associated with sclerotial metamorphosis	[56]
	<i>Aspergillus flavus</i>	Characterisation of isolates from peanut fields	[57]
	<i>Fusarium oxysporum</i> f. sp. <i>strigae</i>	AFLP-based marker for diagnosis of the fungi in tropical soils	[58]
	<i>Colletotrichum coccodes</i>	Study of genetic diversity of the etiological agent of anthracnoses and black-dot in crops	[59]
	<i>Sclerotinia sclerotiorum</i>	Study of genetic diversity of the rot producing fungal plant pathogen	[60]
	<i>Fusarium fujikuroi</i> species complex	Distinction of species within the species complex	[61]
	<i>Sporisorium scitamineum</i>	Study of genetic diversity and relationship of the etiological agent of smuts in sugarcane smut	[62]
	<i>Neonectria ditissima</i>	Study of genetic diversity and phylogeny of the etiological agent of fruit tree canker	[63]
	<i>Pyricularia grisea</i>	Study of genetic diversity of the etiological agent of rice blast	[64]
	<i>Fusarium verticillioides</i>	Study of genetic diversity of the etiological agent of rot in maize kernels	[65]
	<i>Blumeria graminis</i> f. sp. <i>hordei</i>	Study of genetic diversity of the etiological agent of barley powdery mildew	[66]
	<i>Fusarium proliferatum</i>	Study of genetic diversity of the fungal pathogen of maize, rice, sugarcane and onion	[67]
	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	Characterization of populations of the etiological agent of yellow stripe rust	[68]
	<i>Alternaria solani</i>	Study of genetic diversity and aggressiveness of the etiological agent of tomato blight	[69]
	<i>Colletotrichum gloeosporioides</i>	Study of the genetic diversity of the etiological agent of anthracnose in water yam (<i>Dioscorea alata</i>)	[70]

	<i>Petriella setifera</i>	Study of genetic diversity	[71]
	<i>Fusarium oxysporum</i> f. sp. <i>elaeidis</i>	Study of genetic diversity of the etiological agent of fusarium wilt disease of oil palm (<i>Elaeis guineensis</i>)	[72]
	<i>Magnaporthe oryzae</i>	Study of differentially expressed genes associated with appressorium formation in the rice blast fungus	[73]
	<i>Fusarium tricinctum</i>	Study of genetic diversity of the etiological agent of root rots of alfalfa	[74]
	<i>Quambalaria pitereka</i>	Study of genetic diversity of the fungal pathogens of <i>Corymbia</i>	[75]
Food and beverage	<i>Fusarium verticillioides</i>	Study of genetic diversity, fumonisin production and pathogenicity in isolates from maize	[76]
	<i>Aspergillus flavus</i>	Study of genetic diversity of aflatoxin producing fungi in maize	[77]
	<i>Pleurotus spp.</i>	Study of genetic diversity of edible mushrooms	[78]
	<i>Fusarium verticillioides</i>	Identification of the fungus on finger millet in Uganda	[79]
	<i>Agaricus bisporus</i> var. <i>burnettii</i>	Study of the ability of to produce mushrooms at high temperature	[80]
	<i>Aspergillus spp.</i>	Study of genetic diversity of aflatoxin producing fungi in marketed spices	[81]
	<i>Aspergillus flavus</i>	Study of genetic diversity of aflatoxin producing fungi in food and feed samples	[82]
	<i>Coprinus comatus</i>	Study of genetic diversity	[83]
	<i>Aspergillus pseudonominus</i>	Study of genetic diversity of aflatoxin producing fungi in nuts	[84]
	<i>Aspergillus flavus</i>	Study of genetic diversity of aflatoxin producing fungi in the cattle feed	[85]
	<i>Aspergillus parasiticus</i>		
	<i>Aspergillus novoparasiticus</i>		
	<i>Aspergillus arachidicola</i>		
	<i>Aspergillus pseudocaelatus</i>	Identification of food contaminants in corn kernels	[86]
Genomic diversity	<i>Cochliobolus miyabeanus</i>	Study of population structure, gene flow and recombination of on cultivated wildrice	[87]
	<i>Cryptococcus spp.</i>	Environmental isolation and characterization of fungal species from living trees	[88]
	<i>Aspergillus flavus</i>	Study of biogeography and phylogeny among isolates	[89]
	<i>Candida glabrata</i>	Differential expression of aldo-keto-reductase in azole-resistant clinical isolates	[90]
	<i>Lentinula ssp.</i>	Study of genetic relationships among shiitake mushrooms.	[91]
	<i>Phoma macrostoma</i>	Biological and genetic characterization of isolates with bioherbicidal activity	[92]
	<i>Fusarium spp.</i>	Study of genetic diversity among isolates	[93]
	<i>Botrytis cinerea</i>	Isolation of genes related to abscisic acid production	[94]
	<i>Leptosphaeria spp.</i>	Study of the genetic diversity and occurrence of on <i>Brassica oleracea</i> and <i>B. napus</i>	[95]
	<i>Dichomitus squaleus</i>	Study of genetic diversity of the etiological agent of white rot	[96]

	<i>Ganoderma lucidum</i>	Study of genetic and metabolic diversity	[97]
	Arbuscular mycorrhizal fungi	Study of genetic diversity	[98]
	Root-endophytic fungi	Study of community structure and dynamics of plant-associated fungi	[99]
Enzyme production	<i>Myceliophthora</i> spp.	Study of the genetic diversity and phylogeny of thermostable enzymes producing fungi	[100]
	<i>Corynascus</i> spp.		
	<i>Tricoderma reesei</i>	Study of the genetic diversity of cellulolytic enzyme producing fungi	[101]
	<i>Aspergillus</i> spp.	Study of the genetic diversity of the glucose dehydrogenase producing fungi	[102]
Soil	<i>Rhizopogon roseolus</i>	Study of genetic diversity of the an ectomycorrhizal fungus	[103]
	Arbuscular mycorrhizal fungi	Distinction between root system and rhizosphere soil arbuscular mycorrhizal fungi of <i>Prunus mume</i>	[104]
Monument deterioration	<i>Sarcinomyces</i> spp.	Identification of the fungi contributing to the blackened areas on outdoor marble statues	[105]
	<i>Phaeococcomyces</i> spp.		
	<i>Sporobolomyces yunnanensis</i>		

Supplementary Table S4. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using ISSR and similar techniques.

Importance	Fungal identification	Purpose	Reference
Human health	Dermatophytes <i>Candida</i> spp.	Study of genetic relationships and isozyme profile from strains from Egypt and Libya	[1]
Animal health	<i>Beauveria</i> spp. <i>Metarhizium</i> spp.	Diversity of indigenous fungus from a commercial banana field and their virulence toward <i>Cosmopolites sordidus</i>	[2]
	<i>Metarhizium</i> spp.	Study of genetic diversity of the fungal pathogen, causing epizootics in burrower bugs	[3]
	<i>Isaria</i> spp.	Species clarification of <i>Isaria</i> isolates used as biocontrol agents against <i>Diaphorina citri</i> (Hemiptera: Liviidae)	[4]
	<i>F. incarnatum-equiseti</i> <i>F. fujikuroi</i>	Study of genetic diversity of entomopathogenic fungus	[5]
	<i>Metarhizium rileyi</i>	Study of genetic diversity and population structure of the etiological agent of green muscardine in silkworm	[6]
	<i>Lecanicillium</i>	Identification of entomopathogenic fungi	[7]
	<i>Beauveria bassiana</i>	Study of genetic diversity of isolates	[8]
	<i>Helicoverpa gelatopoeon</i> <i>Diabrotica speciosa</i> <i>Beauveria bassiana</i> <i>Purpureocillium lilacinum</i>	Study of genetic diversity of entomopathogenic fungi and its implications for biological control of tobacco pests	[9]
	<i>Beauveria bassiana</i>	Study of acaricidal and pathogenic effects of the entomopathogenic fungus on engorged females of the fowl tick (<i>Argas persicus</i> , Argasidae)	[10]
Plant health	<i>Pseudocercospora griseola</i>	Study of genetic diversity of isolates of the fungal bean pathogen	[11]
	<i>Pyrenophora graminea</i>	Study of the molecular phylogeny of the etiological agent of barley leaf stripe	[12]
	<i>Macrophomina phaseolina</i>	Study of genetic diversity of isolates from sesame	[13]
	<i>Ustilago stamina</i>	Study of genetic diversity of the etiological agent of smuts	[14]
	<i>Inonotus obliquus</i>	Study of genetic diversity among 21 strains of plant parasites	[15]
	<i>Colletotrichum</i> spp.	Study of genetic diversity of the etiological agent of bitter rot in apple	[16]
	<i>Bremia lactucae</i>	Genetic diversity in lettuce plantations	[17]
	<i>Colletotrichum gloeosporioides</i> sl	Genetic structure of isolates from the etiological agent of anthracnose in papaya	[18]
	<i>Colletotrichum sublineolum</i>	Study of genetic diversity of the etiological agent of sorghum anthracnose	[19,20]

	<i>Verticillium dahliae</i>	Characterization of the etiological agent of wilt from different geographic origins	[21]
	<i>Rhizoctonia solani</i> AG 2-2 IIIB	Genetic structure of a population isolated from <i>Agrostis stolonifera</i>	[22]
	<i>Bipolaris oryzae</i>	Study of genetic diversity and population structure of brown spot fungus isolates	[23]
	<i>Knoxdaviesia proteae</i>	Study of genetic characterization of the ophiostomatoid fungi from South Africa	[24]
	<i>Cadophora luteo-olivacea</i>	Identification of the genetic groups of grapevine fungal pathogens	[25]
	<i>Myrothecium</i> spp.	Study of genetic diversity of endophytic fungi	[26]
	<i>Colletotrichum</i> spp.	Study of genetic diversity and differentiation of isolates associated with Leguminosae	[27]
	<i>Ganoderma</i> spp.	Genotyping	[28]
	<i>Fusarium solani</i>	Study of genetic diversity of etiological agent of yellowing disease from black pepper	[29]
	<i>Cytospora chrysosperma</i>	Study of genetic diversity of the etiological agent of cytodpora canker from walnut trees	[30]
	<i>Alternaria alternata</i>	Study of genetic diversity of the etiological agent of potato brown leaf spot	[31]
	<i>Neofabraea</i> spp.	Identification and characterization of the etiological agent of bull's eye rot on apple	[32,33]
	<i>Botryosphaeria</i> species-complex	Molecular identification of the etiological agent of cankers and drying of buds in <i>Eucalyptus</i> sp.	[34]
	<i>Rhizoctonia solani</i> (AG 1-IA)	Study of pathogenic and genetic variation among the isolates of the etiological agent of rice sheath blight	[35]
	<i>Bipolaris sorghicola</i>	Study of genetic diversity of the fungal pathogen infecting sorghum, India	[36]
	<i>Myrothecium roridum</i>	Genetic relationships of isolates from water hyacinth in Thailand	[37]
	<i>Monilinia polystroma</i>	Study of genetic diversity and pathogenicity of a pathogen from cherries	[38]
	<i>Fusarium</i> spp	Study of genetic diversity of the etiological agent of sugarcane wilt	[39]
	<i>Pestalotiopsis longiseta</i>	Study of population genetic structure of the etiological agent of tea gray blight	[40]
	<i>Fusarium oxysporum</i> f. sp. <i>ciceris</i>	Study of genetic diversity and population structure of Iranian isolates of the etiological agent of chickpea wilt	[41,42]
	<i>Ustilago esculenta</i>	Identification and genetic diversity of isolates	[43]
	<i>Calonectria pseudonaviculata</i>	Study of genetic diversity of the etiological agent of boxwood blight	[44,45]
	<i>Diaporthe vaccinii</i>	Identification and characterization of the etiological agent of upright dieback and viscid rot of cranberry	[46]

<i>Fusarium oxysporum</i> f. sp. <i>cumini</i>	Study of genetic diversity among isolates	[47]
<i>Erysiphe pisi</i>	Study of natural incidence and genetic variability of the etiological agent of powdery mildew on peas	[48]
<i>Monascus</i> spp.	Comparative analysis of genetic polymorphisms among <i>Monascus</i> strains	[49]
<i>Alternaria carthami</i>	Study of population structure and virulence analysis of isolates	[50]
<i>Zymoseptoria tritici</i>	Study of genetic diversity of the etiological agent of <i>Septoria tritici</i> blotch	[51]
<i>Fusarium solani</i> f. sp. <i>cucurbitae</i>	Genetic diversity of the etiological agent of crown and root rot of watermelon	[52]
<i>FUSarium proliferatum</i>	Study of genetic diversity of endophytic fungi strains isolated from <i>Belamcanda chinensis</i>	[53]
<i>Macrophomina phaseolina</i>	Study of genetic diversity among isolates of sesame, Iran	[54]
<i>Fusarium</i> spp.	Study of genetic diversity and phylogenetic profiling of the etiological agent of storage rot of ginger (<i>Zingiber officinale</i>)	[55]
<i>Alternaria solani</i>	Study of genetic diversity of the etiological agent of early tomato blight	[56]
<i>Neopestalotiosis</i> sp	Study of genetic diversity of the etiological agent canker disease from guava (<i>Psidium guajava</i> L.)	[57]
<i>Lasiodiplodia theobromae</i>	Study of genetic diversity of the etiological agent of mulberry root rot	[58,59]
<i>Tilletia laevis</i>	Detection of teliospores from closely related species implicated in wheat diseases	[60]
<i>C. gloeosporioides</i> (<i>Fusarium fujikuroi</i> <i>Phaeosphaeria nodorum</i> <i>Botryosphaeria dothidea</i> <i>Pseudofusicoccum ardesiacum</i>	Identification of six fungal pathogens from the different varieties of the mango (<i>Mangifera indica</i> L.)	[61]
<i>Tulasnella</i> spp.	Identification of fungal populations associated to the Australian evergreen terrestrial orchid <i>Cryptostylis ovata</i>	[62]
<i>Colletotrichum</i> spp.	Study of genetic diversity of the etiological agent of anthracnose in fruit crops	[63]
<i>Sarocladium oryzae</i>	Study of genetic diversity of the etiological agent of rice sheath rot disease	[64]
<i>F. oxysporum</i> f. sp. <i>cubense</i>	Study of genetic variation of the etiological agent of <i>Fusarium</i> wilt in banana	[65]
<i>Colletotrichum truncatum</i>	Study of pathological, biochemical and genetic diversity of the etiological agent of anthracnose in chilli (<i>Capsicum annuum</i> L.)	[66]
<i>Magnaporthe oryzae</i>	Study of pathogenicity of rice blast fungus	[67]
<i>Diaporthe</i> sp	Study of genetic diversity of indigenous and exotic species associated with various crops	[68]

	<i>Colletotrichum</i> spp.	Study of genetic diversity of the etiological agent of anthracnose from Mango cv. Nam Dork Mai See Tong	[69]
Genomic diversity	<i>Armillaria gallica</i>	Study of genetic diversity	[70]
	<i>A. alternata</i>	Study of genetic diversity	[71]
	<i>F. oxysporum</i>	Study of genetic diversity	[72]
	<i>Monilinia fructicola</i>	Study of genetic diversity	[73]
	<i>Sclerotium rolfsii</i> <i>Sclerotium delphinii</i>	Study of genetic diversity	[74]
	<i>Mycosphaerella fijiensis</i>	Study of mating-type alleles and M13 PCR markers in the etiological agent of black leaf spot of bananas	[75]
	<i>Hypsizygus marmoreus</i>	Evaluation of growth characteristics and genetic diversity of commercial and stored lines	[76]
	<i>Pleurotus eryngii</i> var. <i>tuoliensis</i>	Study of genetic diversity	[77]
	<i>A. flavus</i>	Study of genetic diversity	[78]
	<i>F. oxysporum</i>	Study of pathogenicity and genetic diversity of isolates from corms of <i>Crocus sativus</i>	[79]
	<i>Tricholoma lobayense</i>	Study of genetic diversity	[80]
	<i>Sporisorium scitamineum</i>	Study of biogeographical variation and population structure of isolates	[81]
	<i>Thricoderma</i> spp.	Study of genetic diversity and biocontrol potential of rhizospheric microbes isolated from tomato and maize	[82]
	<i>Verticillium dahliae</i>	Study of genetic diversity, virulence, and vegetative compatibility in isolates from cotton	[83]
	<i>Blumeria graminis</i> f. sp. <i>tritici</i>	Study of genetic diversity and virulence structure	[84]
	<i>Shiraia bambusicola</i>	Study of genetic diversity	[85]
	<i>A. fumigatus</i>	Molecular Identification	[86]
	<i>Ganoderma lucidum</i>	Study of genetic diversity	[87]
	<i>Magnaporthe oryzae</i>	Characterisation of isolates from rice in peninsular Malaysia	[88]
	<i>Fusarium graminearum</i> <i>F. culmorum</i>	Study of genetic diversity among isolates	[89]
	<i>Stenocarpella maydis</i>	Study of genetic variability of stalk and ear rot disease in corn plants	[90]
	<i>A. flavus</i>	Study of genetic diversity analysis of isolates from plants and air	[91]
	<i>Colletotrichum graminicola</i>	Study of genetic diversity	[92]
	<i>Corollospora maritima sensu lato</i>	Study of genetic diversity in the marine arenicolous fungus	[93]

	<i>Sclerotium rolfsii</i>	Study of virulence and genetic diversity of isolates infecting groundnut	[94]
	<i>F. oxysporum f. sp. melongenae</i>	Characterization of isolates	[95]
	<i>Curvularia lunata</i>	Study of genetic diversity of indigenous and exotic isolates	[96]
	<i>Aspergillus spp.</i>	Molecular identification and differentiation of <i>Aspergillus</i> species and its implications in mycotoxins production	[97]
	<i>Pyricularia oryzae</i>	Study of genetic diversity of rice blast fungus	[98]
	<i>Trichoderma harzianum</i>	Study of antagonistic activity and molecular characterization of the biological control agent	[99]
	<i>Athelia rolfsii</i>	Study of genetic diversity	[100]
	<i>Botrytis cinerea</i>	Study of genetic diversity of isolates from different plant hosts and localities	[101]
Food and beverage	<i>Auricularia polytricha</i>	Study of genetic diversity among wild populations of edible mushrooms	[102]
	<i>Pleurotus eryngii</i>	Study of genetic diversity among Chinese edible mushrooms cultivars	[103,104]
	<i>Auricularia auricula-judae</i>	Study of genetic diversity of wild medicinal and edible mushrooms	[105]
	<i>A. bisporus</i> (Button) <i>A. bisporus</i> (Portobello) <i>P. eryngii</i> (King Oyster) <i>L. edodes</i> (shiitake) <i>H. tessellatus</i> (Brown Shimeji) <i>H. tessellatus</i> (White Shimeji) <i>F. velutipes</i> (Enoki) <i>P. ostreatus</i> (Oyster) <i>P. djamor</i> (Pink Oyster) <i>C. indica</i> (Milky) <i>P. florida</i> (Florida Oyster)	DNA fingerprinting of commercial mushrooms for genetic discrimination	[106]
	<i>Fusarium spp.</i>	Identification and characterization of isolated associated with sorghum seeds	[107]
	<i>A. flavus</i>	Study of genetic diversity of strains isolated from barley grains	[108]
	<i>A. flavus</i>	Molecular characterization of aflatoxigenic and non-aflatoxigenic isolates of fungal strains isolated from corn grains	[109]
	<i>Agaricus bisporus</i>	Identification and strain-typing of button mushroom	[110]
	<i>Aspergillus</i> section <i>Flavi</i>	Identification of members belonging to food-contaminating aflatoxigenic and non-aflatoxigenic species	[111]
	<i>Volvariella volvacea</i>	Phylogenetic analysis of high yielding strain of paddy straw mushroom	[112]
	<i>Pleurotus pulmonarius</i>	Study of the genetic diversity of edible mushrooms	[113]
	<i>Polyporus umbellatus</i>	Study of genetic diversity of edible mushrooms	[114]

	<i>Macrophomina phaseolina</i>	Study of genetic diversity of isolates associated with cowpea	[115]
	<i>Fusarium</i> spp.	Molecular identification and characterization of isolates from wheat grains	[116]
	<i>Pleurotus ostreatus</i>	Study of genetic diversity of different strains	[117]
	<i>Monascus</i> spp.	Comparative analysis of genetic polymorphisms among strains	[118]
	<i>Lepista nuda</i>	Study of genetic diversity	[119]
	<i>Colletotrichum falcatum</i>	Study of genetic diversity	[120]
	<i>Alternaria</i> spp.	Molecular identification and genetic variation of isolates from tomatoes	[121]
	<i>Grifola frondosa</i>	Study of genetic diversity of edible mushrooms	[122]
	<i>Phomopsis asparagi</i>	Study of genetic diversity of the etiological agent of asparagus stem blight	[123]
	<i>Tuber</i> spp	Genetic diversity in some of black and brown Iranian truffles	[124]
Medicinal products	<i>Wolfiporia cocos</i>	Study of genetic diversity of Chinese cultivars of medicinal mushrooms	[125]
	<i>Sanghuangporus sanghuang</i>	Study of genetic diversity of wild strains	[126]
	<i>Ganoderma lingzhi</i>	Identification of Lingzhi medicinal mushroom	[127]
Soil	<i>Aspergillus flavus</i>	Study of genetic diversity of isolates from peanut-cropped soils in China	[128]
	<i>Trichoderma viride</i>	Molecular characterization of isolates from rhizospheric soils of uttar pradesh	[129]
	<i>Hypocreales</i>	Study of genetic diversity of entomopathogenic fungi in soil and phylloplanes of five Mediterranean cropping systems	[130]

Supplementary Table S5. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using VNTR and similar techniques.

Importance	Molecular marker	Fungal identification	Purpose	Reference
Human health	Microsatellites	<i>Candida albicans</i> <i>Candida glabrata</i>	Analysis of isolates from recurrent vulvovaginal candidiasis	[1]
	Minisatellite	<i>Cryptococcus neoformans</i> <i>Cryptococcus gattii</i>	Molecular characterisation of the etiological agent of cryptococcosis in patients of a tertiary healthcare facility	[2]
	Microsatellites	<i>Cryptococcus neoformans</i>	Study of genetic diversity of the etiological agent of cryptococcosis	[3]
	Microsatellites	<i>Candida parapsilosis</i>	Study of the transmission in neonatal intensive care units	[4]
	VNTR	<i>Aspergillus flavus</i>	Tracing sources of the etiological agent of fungal sinusitis, keratitis, and endophthalmitis	[5]
	Microsatellites	<i>Candida parapsilosis</i> s. s.	Study of dominance and persistence of a particular epidemiological clone among neonatal intensive care unit patients	[6]
	Microsatellites	<i>Microsporum</i> spp. <i>Trichophyton</i> spp.	Identification and epidemiology of dermatophytes causing cutaneous mycosis	[7]
	Minisatellites	<i>Candida glabrata</i>	Study of genome structure and potential virulence factors of the yeast pathogen	[8]
	VNTR	<i>Aspergillus flavus</i>	Study of genetic diversity, relatedness and virulence of the etiological agent of invasive aspergillosis and cutaneous, sinus, nasal and nail infections	[9,10]
	VNTR	<i>Trichophyton interdigitale</i>	Study of population structure and genotype differentiation of the etiological agent of superficial fungal infections	[11]
	Minisatellites	<i>Cryptococcus gattii</i>	Identification of the etiological agent of cutaneous cryptococcosis in an immunocompetent patient	[12]
	Microsatellites	<i>Candida tropicalis</i>	Molecular typing of the etiological agent of nosocomial fungemia and hepatosplenic fungal infections in patients with cancer	[13]
	VNTR	<i>Rasamsonia argillacea</i>	Identification in cystic fibrosis patients	[14]
	Microsatellites	<i>Aspergillus terreus</i> species-complex	Study of genetic diversity of isolates of the etiologic agent of invasive aspergillosis in immunocompromised individuals	[15,16]

	Microsatellites	<i>Trichophyton rubrum</i>	Study of genetic diversity of the etiological agent of tinea unguium, tinea pedis, and tinea corporis	[17]
	Minisatellites	<i>Cryptococcus neoformans</i>	Study of genetic diversity and variation in antifungal susceptibility profiles	[18]
	Microsatellites	<i>Candida parapsilosis</i>	Genotyping of clinical isolates of the etiological agent of nosocomial infections	[19]
	VNTR	<i>Aspergillus fumigatus</i>	Study of clinical strains and environmental fungal aerocontamination to prevent invasive aspergillosis infections in hospital	[20]
	Minisatellites	<i>Candida parapsilosis</i> species-complex	Molecular identification of isolates for epidemiological studies and the establishment of appropriate therapies and prophylactic measures	[21]
	Minisatellites	<i>Cyberlindnera fabianii</i>	Study of a fungaemia outbreak in preterm neonates	[22]
	Minisatellites	<i>Enterocytozoon bieneusi</i>	Genotyping approach for potential common source of the etiological agent of <i>E. bieneusi</i> microsporidiosis in hematology unit	[23]
	Microsatellites	<i>Sporothrix globosa</i>	Study of genetic diversity and population structure	[24]
	VNTR	<i>Madurella mycetomatis</i>	Study the genetic diversity, susceptibility to antifungal agents monitor any potential outbreaks of the etiological agent of mycetoma	[25–27]
	VNTR	<i>Aspergillus fumigatus</i>	Investigation of the relationships between clinical and environmental isolates during major demolition work in a French hospital	[28]
	Minisatellites	<i>Candida kefyr</i>	Study of prevalence, antifungal drug susceptibility and genotypic heterogeneity	[29]
	Microsatellite	<i>Candida glabrata</i>	Study of pathogenicity, virulence, or drug resistance traits	[30]
	Microsatellite	<i>Pneumocystis jirovecii</i>	Genotyping of the etiological agent of severe respiratory infections in immunocompromised patients.	[31]
	Microsatellite	<i>Candida auris</i>	Microsatellite typing during a emergence of in Brazil in a COVID-19 intensive care unit	[32]
	VNTR	<i>Candida auris</i>	Study of the prevalence and emerging status of multidrug-resistant fungi and their mortality	[33]
	VNTR	<i>Aspergillus fumigatus</i>	Molecular epidemiology of in chronic pulmonary aspergillosis patients	[34]

	Microsatellite	<i>Candida auris</i>	Colonization and transmission dynamics among chronic respiratory diseases patients hospitalized in a chest hospital	[35]
	Microsatellite	<i>Candida parapsilosis</i>	Study of genetic diversity of the etiological agent of candidemia among hospitalized pediatric patients	[36]
Animal health	VNTR	<i>Trichoderma pseudokoningii</i>	Fungi detection on pulmonary infection in tuberculous dairy cattle	[37]
	VNTR	<i>Aspergillus</i> spp.	Study of genetic diversity and antifungal susceptibility of isolates from avian farms	[38]
	VNTR	<i>Aspergillus fumigatus</i>	Study of pathogenicity in aerosol-challenged chickens (<i>Gallus gallus</i>)	[39]
	Microsatellites	<i>Trichophyton mentagrophyton</i> <i>Microsporum gypseum</i> <i>Microsporum canis</i>	Detection for rabbit-derived dermatophytes	[40]
	Microsatellites	<i>Beauveria</i> spp. <i>Metarhizium</i> spp.	Specific diversity of the entomopathogenic fungi in Mexican agricultural soils	[41]
	Microsatellites	<i>Beauveria bassiana</i>	Microsatellite markers to monitor a commercialized isolate of the entomopathogenic fungus from different environments	[42]
	VNTR	<i>Aspergillus fumigatus</i>	Procedures and techniques for aspergillosis diagnosis of in birds	[43]
	Microsatellites	<i>Metarhizium</i> spp.	Community composition and population genetics of insect pathogenic fungi from soils of a long-term agricultural research system	[44,45]
	Minisatellites	<i>Malassezia pachydermatis</i>	Study of the genetic diversity of the etiological agent of otitis and dermatitis on pets	[46]
	Minisatellites	<i>Enterocytozoon bienersi</i>	Molecular detection of the etiological agent of microsporidiosis	[47,48]
	Minisatellites	Marine fungi	Study of the diversity of culturable mycobiota associated with the Mediterranean	[49]
	Microsatellites	<i>Pseudogymnoascus destructans</i>	Mating type determination of the etiological agent of white-nose disease in bats	[50]
	Minisatellites	<i>Beauveria bassiana</i> <i>Metarhizium anisopliae</i>	Efficacy of different entomopathogenic fungal isolates against four key stored-grain beetle species	[51]
Human and animal health	VNTR	<i>Aspergillus flavus</i>	Study of genetic structure of populations in human and avian isolates	[52]
	Microsatellite	<i>Microsporum canis</i>	Development and validation of method for tracing infections	[53]

Plant health	Microsatellite	<i>Macrophomina phaseolina</i>	Molecular identification of the phytopathogen	[54]
	Minisatellites	<i>Hymenoscyphus pseudoalbidus</i>	Study of population structure of and its genetic relationship to <i>H. albidus</i>	[55]
	VNTR	<i>Hypoxylon pulicicidum</i>	Characterization of a pantropical insecticide-producing endophyte	[56]
	Minisatellite	<i>Leptosphaeria maculans</i>	Migration patterns and changes in population biology associated with the worldwide spread of the oilseed rape pathogen	[57]
	Microsatellite	<i>Monilinia fructicola</i>	Study of genetic population structure of the etiological agent of brown rot in peach trees	[58]
	VNTR	<i>Mycosphaerella fijiensis</i>	Study of genetic diversity of the etiological agent of black sigatoka in banana	[59]
	Microsatellite	<i>Erysiphe necator</i>	Study of population structure in North America and Europe	[60]
	Microsatellite	<i>Geosmithia morbida</i>	Study of the genetic diversity of the etiological agent of thousand canker disease in black walnut (<i>Juglans nigra</i>)	[61]
	Minisatellites	<i>Ustilago scitaminea</i>	Study of the genetic diversity of the etiological agent of sugarcane smut	[62]
	Minisatellites	<i>Puccinia triticina</i>	Study of population structure, pathological and molecular characterization of the etiological agent of slow leaf rusting in wheat	[63,64]
	Microsatellite	<i>Plasmopara viticola</i>	Characterization of native and introduced populations of the etiological agent of grapevine downy mildew	[65]
	Microsatellite	<i>Ceratocystis fimbriata</i>	Analysis of microsatellite markers in the genome of the plant pathogen	[66,67]
	Microsatellite	<i>Peronospora tabacina</i>	Ten polymorphic microsatellite loci identified from a small insert genomic library for the tobacco pathogen	[68]
	Minisatellite	<i>Botrytis cinerea</i>	Comparison of populations isolated from two open-field cultivated host plants	[69,70]
	Microsatellite	<i>Puccinia</i> spp.	Rust fungi forming aecia on barberry (<i>Berberis</i> spp.)	[71]
	VNTR	<i>Bipolaris oryzae</i>	Study of genetic diversity, population structure, sexual state. And aggressiveness of the etiological agent of rice brown spot	[72]-[74]
	Microsatellite	<i>Anisogramma anomala</i>	Identification of the etiological agent of filbert blight disease on commercial European hazelnut	[75]

	VNTR	<i>Colletotrichum lindemuthianum</i>	Molecular genetic characterization of fungal isolates of the etiological agent of anthracnose on common bean (<i>Phaseolus vulgaris</i>)	[76]
	Minisatellites	<i>Puccinia melanocephala</i>	Development and characterization of the etiological agent of sugarcane brown rust	[77]
	Microsatellite	<i>Phytophthora</i> spp.	Development of new polymorphic microsatellite markers for three closely related plant-pathogenic species	[78]
	Microsatellite	<i>Knoxdaviesia proteae</i>	Study of genetic diversity and dispersal of the ophiostomatoid fungus within <i>Protea repens</i> infructescences	[79]
	Minisatellites	<i>Erwinia amylovora</i>	Study of phylogeography and population structure of the etiological agent of fire blight	[80]
	Minisatellites	<i>Monilinia vaccinii-corymbosi</i>	Study of population structure, genetic diversity, and the reproductive biology of the Blueberry Pathogen. North Carolina State University.	[81]
	Minisatellites	<i>Melampsora larici-populina</i>	Microsatellite analysis of Icelandic populations of the poplar fungal pathogen	[82]
	Microsatellite	<i>Exserohilum turcicum</i>	Study of microsatellite and mating type primers for the maize and sorghum pathogen	[83]
	Microsatellite	<i>Lecanosticta acicola</i>	Development of microsatellite and mating type markers for the pine needle pathogen	[84]
	Microsatellite	<i>Fusarium verticillioides</i>	Genome distribution and validation of novel microsatellite markers and their transferability to other <i>Fusarium</i> species	[85]
	Microsatellite	<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	Analysis of SSR in the genome and development of microsatellite markers	[86]
	Microsatellite	<i>Colletotrichum</i> spp	Characterization for the etiological agent of anthracnose in blackberry	[87]
	Minisatellites	<i>Beauveria bassiana</i>	Study of the potential of the entomopathogenic fungus as an endophyte in grapevine	[88]
	Microsatellite	<i>Colletotrichum truncatum</i>	Study of genetic diversity of the etiological agent of chilli	[89]
	Microsatellite	<i>Alternaria brassicicola</i>	Assessment of cross-species transferability and utility of microsatellites as a diagnostic marker	[90]
	Microsatellite	<i>Magnaporthe grisea</i>	Study of genetic diversity of the etiological agent of rice blast	[91]
	Microsatellite	<i>Epichloë festucae</i>	Development and characterization of nuclear microsatellite markers in the endophytic fungus	[92]

	Microsatellites	<i>Blumeria graminis</i> f. sp. <i>Tritici</i>	Study of genetic diversity	[93]
	Microsatellite	<i>Sclerotinia sclerotiorum</i>	Study of genetic diversity and compatibility groups within and among populations of sunflower	[94]
	Microsatellite	<i>Stagonosporopsis</i> spp.	Study of genetic diversity and population structure of the etiological agent of cucurbit gummy stem blight	[95]
	Minisatellites	<i>Ralstonia solanacearum</i>	Study of genetic diversity of isolates from three different regions	[96]
	VNTR	<i>Sarocladium oryzae</i>	Molecular characterization and distribution of the etiological agent of sheath rot on rice	[97]
	Microsatellite	<i>Colletotrichum</i> spp.	Study of the genetic diversity of the endophytic fungi from <i>Phaseolus vulgaris</i>	[98]
	Microsatellite	<i>Villosiclava virens</i>	Study of population structure of the rice false smut fungus	[99]
	Microsatellite	<i>Ganoderma boninense</i>	Identification and of the etiological causal agent of oil palm basal stem rot disease	[100]
	Microsatellite	<i>Neofabraea</i> spp.	Identification and characterization of etiological agent of bull's eye rot on apple	[101]
	VNTR	<i>Pseudocercospora fijiensis</i>	Study of genetic diversity of the etiological agent of banana black Sigatoka	[102]
	Minisatellites	<i>Togninia minima</i>	Study of genetic diversity in Iranian populations of the etiological agent of leaf stripe disease on grapevines	[103]
	Minisatellite	<i>Trichaptum abietinum</i>	Study of population structure of the wood-decay fungus	[104]
	Microsatellite	<i>Fusarium oxysporum</i>	Evolution of nine microsatellite loci in the fungus	[105]
	Microsatellite	<i>Diaporthe</i> sp. <i>Diaporthe infecunda</i> <i>Diaporthe phaseolorum</i>	Identification of endophytic fungi isolated from common bean (<i>Phaseolus vulgaris</i> L.)	[106]
	Microsatellites	<i>Microbotryum saponariae</i>	Polymorphic microsatellite markers for the tetrapolar anther-smut fungus based on genome sequencing	[107]
	VNTR	<i>Bipolaris sorghicola</i>	Genetic diversity of fungal pathogen infecting <i>Sorghum bicolor</i>	[108]
	Microsatellites	<i>Stagonosporopsis</i> spp.	Study of genetic structure and population dynamics of gummy stem blight fungi in watermelon fields	[109]
	Microsatellites	<i>Colletotrichum gloeosporioides</i>	Study of genetic diversity and population structure	[110,111]
	VNTR	<i>Rhizoctonia solani</i>	Study of genetical diversity among isolates causing sheath blight on rice	[112]

	Microsatellites	<i>Fusarium virguliforme</i>	Development and characterization of microsatellite markers and their utility within clade 2 of the <i>Fusarium solani</i> species complex	[113]
	Microsatellites	<i>Ustilaginoidea virens</i>	Analysis of SSR and the development of microsatellite markers	[114]
	VNTR	<i>Fusarium culmorum</i>	Study of population structure and mycotoxin potential of the wheat crown rot and head blight pathogen	[115]
	Microsatellites	<i>Fusarium oxysporum</i> f. sp. <i>lentis</i>	Study of population genetic structure of the etiological agent of lentils wilt	[116]
	Minisatellites	<i>Zymoseptoria tritici</i>	Study of the population structure of the etiological agent of Septoria tritici blotch on wheat	[117]
	Microsatellites	<i>Microbotryum</i> spp.	Co-occurrence among three divergent plant-castrating fungi in the same <i>Silene</i> host species	[118]
	Microsatellites	<i>Thekopsora areolata</i>	Development of microsatellite markers for the etiological agent of cherry spruce rust	[119]
	Microsatellites	<i>Puccinia triticina</i>	Genetic variation between different populations of the etiological agent of wheat leaf rust from different geographic locations and hosts	[120]
	VNTR	<i>Rhizoctonia oryzaesativae</i>	Molecular characterization of etiological agent of aggregate sheath spot on rice	[121]
	Microsatellites	<i>Sclerotinia sclerotiorum</i>	Microsatellite loci for isolates collected from ten locations in Bangladesh and one in Ohio, USA	[122]
	Minisatellites	<i>Amylostereum areolatum</i>	Study of the genetic diversity of the fungal symbiont of the invasive woodwasp	[123]
	Microsatellites	<i>Verticillium dahliae</i>	Study of population structure in the clonal fungus	[124]
	Microsatellites	<i>Tilletia indica</i> <i>Ustilago segetum tritici</i>	Development and validation of microsatellite markers for Karnal bunt and loose smut of wheat from related fungal species	[125]
	Microsatellites	<i>Aspergillus flavus</i>	Use of microsatellite markers to assess the competitive ability of nontoxigenic strains in studies on biocontrol of aflatoxins in maize	[126]
	VNTR	<i>Podosphaera xanthii</i> <i>Golovinomyces cichoracearum</i>	Identification of fungal species causing powdery mildew on cucurbits, determination of the genetic and pathogenic variations of the fungi and their sensitivity to major powdery mildew fungicides	[127]
	Microsatellites	<i>Marssonina brunnea</i>	Identification and development of microsatellite markers and their applications in two populations	[128]

	Minisatellites	<i>Pyrenophora semeniperda</i>	Study of mating system complexity and cryptic speciation in the seed bank pathogen	[129]
	Microsatellites	<i>Cadophora luteo-olivacea</i> <i>Colletotrichum fioriniae</i> <i>Seimatosporium vitis-vinifera</i> <i>Truncatella angustata</i>	Identification and pathogenicity of lignicolous fungi associated with grapevine trunk diseases	[130]
	Microsatellites	<i>Alternaria alternata</i>	Study of the genetic diversity of the etiological agent of saffron corm rot	[131]
	Microsatellites	<i>Glutonomyces brunneus</i>	Recombination and local population structure of the root endophytic fungus	[132]
	Microsatellites	<i>Pyrenophora graminea</i>	Study of pathogenicity of the etiological agent of barley leaf stripe	[133]
	VNTR	<i>Phomopsis vexans</i>	Detection of the etiological agent of leaf blight and fruit rot on eggplant (<i>Solanum melongena</i> L.)	[134,135]
	Microsatellites	<i>Ustilago hordei</i>	Study of genetic diversity and population structure of the etiological agent of covered smut of barley	[136]
	Microsatellites	<i>Fusarium</i> spp. <i>Rhizoctonia solani</i> <i>Alternaria alternata</i> <i>Curvularia coatesiae</i>	Population structure and genetic diversity of the etiological agent of rice seedling blight	[137]
	Microsatellites	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	Development and characterization of novel microsatellite markers and their transferability in <i>Puccinia</i> species	[138]
	VNTR	<i>Erwinia amylovora</i>	Molecular characterization of strains and biocontrol efficacy of <i>Bacillus</i> spp. and <i>Pseudomonas brassicacearum</i> antagonists	[139]
	Minisatellites	<i>Beauveria bassiana</i> <i>Metarhizium anisopliae</i>	Identification of entomopathogenic fungi from agricultural and forestry crops	[140]
	Microsatellites	<i>Puccinia triticina</i> <i>Puccinia recondita</i> f. sp. <i>secalis</i>	Study if utility and informativeness in genetic studies of brown rust fungi on wheat, triticale, and rye	[141]
	Microsatellites	<i>Racodium therryanum</i>	New microsatellite markers for the population studies of the etiological agent of snow blight	[142]
Fungal diversity	Minisatellites	<i>Leptosphaeria maculans</i>	Study of population structure, reproductive behavior and virulence factors of a fungal phytopathogen	[143–147]

	Minisatellites	<i>Diversispora</i> sp	Study of inter-and intrasporal nuclear ribosomal gene sequence variation within one isolate of arbuscular mycorrhizal fungus	[148]
	Microsatellite	<i>Protoparmeliopsis muralis</i>	Development of microsatellite markers in a lichenized Ascomycete	[149]
	Microsatellite	<i>Fusarium oxysporum</i> <i>Fusarium udum</i>	Cross-species transferability and assessment of genetic diversity	[150]
	Minisatellite	<i>Saccharomyces cerevisiae</i>	Study of genetic diversity of isolates	[151]
	Minisatellites	<i>Verticillium albo-atrum</i>	Study of frequency and distribution of microsatellites in the whole genome	[152]
	Minisatellite	<i>Mycosphaerella fijiensis</i>	Study of genetic diversity and mating-type of the etiological agent of black leaf spot of bananas	[153]
	Minisatellites	<i>Orpinomyces</i> sp.	Study of the evolutionary history of a anaerobic fungus strain acting as a plant biomass degrader	[154]
	Minisatellites	<i>Magnaporthe oryzae</i>	Study of the genetic diversity of the fungal pathogen	[155,156]
	Microsatellite	<i>Valsa malicola</i>	Study of genetic diversity of isolates	[157]
	VNTR	<i>Aspergillus fumigatus</i>	Study of genetic diversity and susceptibility to itraconazole in isolated from avian farms	[158]
	Minisatellite	<i>Microbotryum lychnidis-dioicae</i>	Study of genetic diversity and mating-type of the etiological agent of anther-smut fungus	[159]
	Minisatellites	<i>Puccinia striiformis</i>	Molecular identification of somatic recombination of etiological agent of stripe rust	[160]
	Microsatellite	<i>Puccinia psidii</i>	Study of genetic population structure	[161]
	Minisatellite	<i>Colletotrichum lentis</i>	Study of genetic diversity and pathogenicity of the etiological agent of lentil anthracnose	[162]
	VNTR	<i>Pyrenophora semeniperda</i>	Characterization and variation of Mating-type Locus	[163]
	Microsatellite	<i>Aspergillus flavus</i>	Characterization of nonaflatoxigenic strains	[164]
	Microsatellite	<i>Epichloë typhina</i> <i>Epichloë clarkii</i>	Genetic evidence for reproductive isolation among sympatric endophytes	[165]
	Microsatellite	<i>Pyrenophora tritici-repentis</i>	Study of genetic structure of populations	[166]
	Minisatellite	<i>Ophiocordyceps sinensis</i>	Study of genetic diversity of the Chinese caterpillar fungus	[167]
	Minisatellites	<i>Chondrostereum purpureum</i>	Study of interfertility and genetic variability among European and North American isolates	[168]

	Minisatellite	<i>Epichloë</i> spp.	Identification, ecological evaluation and phylogenetic analysis of non-symbiotic endophytic fungi colonizing timothy grass and perennial ryegrass grown in adjacent plots	[169]
	VNTR	<i>Acremonium massei</i>	Identification of Insect-Deterrent Metabolites from a Saprophytic Fungus	[170]
	Microsatellite	<i>Fusarium oxysporum</i> <i>Fusarium avenaceum</i> <i>Fusarium poae</i>	Comparative analysis of polymorphism of microsatellite markers in several species of <i>Fusarium</i>	[171]
	Minisatellites	<i>Leptosphaeria maculans</i>	Study of the distribution of mating-type alleles and genetic variability in field populations	[172]
	Microsatellite	<i>Aspergillus flavus</i>	Study of genetic diversity and resistance mechanism analysis of voriconazole-resistant isolates	[173]
	Microsatellite	<i>Aspergillus fumigatus</i>	Clonal expansion of environmental triazole resistant	[174]
	Microsatellites	<i>Usnea florida</i> <i>Usnea subfloridana</i>	Differentiation between apotheciate between species	[175]
	Microsatellites	<i>Aspergillus fumigatus</i>	Molecular epidemiology of azole-resistant fungi in sawmills of eastern France by genotyping	[176]
	Microsatellites	<i>Ceratocystis</i>	Quantification of outcrossing events in haploid fungi	[177]
	Microsatellites	<i>Rhizopus arrhizus</i>	Study of population structure	[178]
	Minisatellites	<i>Colletotrichum lentils</i>	Study of mating incompatibility genes of the etiological agent of anthracnose in lentil	[179]
Food and beverage	Minisatellite	<i>Agaricus bisporus</i>	Study of repetitive DNA elements in the button mushroom	[180]
	Microsatellite	<i>Tuber aestivum</i>	Identification of polymorphic microsatellite markers in the Burgundy truffle	[181]
	Minisatellites	<i>Amanita ponderosa</i>	Molecular evaluation of fungal strains living in association with these mushrooms in the southwestern Iberian Peninsula	[182]
	Microsatellite	<i>Volvariella volvacea</i>	Microsatellites in the genome of the edible mushroom	[183]
	Minisatellites	<i>Torulaspora delbrueckii</i>	Study of molecular typing of yeast strains being applied in the winemaking process	[184]
	Microsatellite	<i>Lachancea thermotolerans</i>	Study of genetic diversity and population structure of wine-associated isolates	[185]
	Microsatellite	<i>Agaricus bisporus</i>	Study of genetic diversity among commercial and wild	[186]
	Minisatellites	<i>Saccharification fungi</i> <i>Makgeolli</i> yeasts	Distribution of Autochthonous Yeast Strains Isolated from Different Regional Makgeolli, a Korean Traditional Fermented	[187]

			Rice Wine and Their Biochemical and Genetical Characterization	
	VNTR	<i>Fusarium graminearum</i>	Study of population structure and trichothecene mycotoxin profiling from corn and wheat	[188]
	Microsatellite	<i>Tricholoma matsutake</i>	Study of genetic diversity and population structure of matsutake mushroom	[189]
	Minisatellites	<i>Tuber bellonae</i>	Morphological, physico-chemical and molecular investigations on truffle from Basilicata-Italy	[190]
	VNTR	<i>Lentinula edodes</i>	Study of mtDNA variation and their application as genetic marker	[191]
	Microsatellites	<i>Didymella pisi</i>	Study of genetic diversity and population structure of associated with ascochyta blight of dry pea	[192]
	Microsatellites	<i>Tuber magnatum</i>	Study of genetic diversity in white truffles	[193]
	Microsatellites	<i>Penicillium digitatum</i>	Microsatellite characterization and marker development for the etiological agent of green mold of citrus	[194]
	Microsatellites	<i>Agaricus bisporus</i>	Identification of commercial cultivars from China	[195]
	VNTR	<i>Saccharomyces cerevisiae</i>	Yeast inoculation practices influence the microbial communities of barrel-fermented Chardonnay wines	[196]
	Minisatellites	<i>Leccinum</i> sp.	Morphological and Molecular characterization of the ectomycorrhizal symbionts and edible mushrooms	[197]
Lichens	Microsatellites	<i>Lobaria pindarensis</i>	Study of genetic diversity of the lichen fungus in the Himalayas	[198]
	Microsatellites	<i>Lobarina scrobiculata</i>	Study of genetic diversity of the lichen fungus in the Iberian Peninsula and Europe	[199]
	Microsatellites	<i>Rhizoplaca melanophthalma</i>	Characterization of the cosmopolitan lichen-forming fungus	[200]
	Microsatellites	<i>Bactrospora dryina</i>	Study of population structure	[201]
	Microsatellites	<i>Usnea antarctica</i> <i>U. aurantiacoatra</i>	Species delimitation in Antarctic <i>Usnea</i> subgenus <i>Neuropogon</i>	[202]
	Microsatellites	<i>Usnea subfloridana</i>	Study of genetic diversity of the widespread epiphytic lichen and comparison of among different populations	[203]
	Microsatellites	<i>L. immixta</i> <i>L. macaronesica</i>	Deep divergence between island populations in lichenized fungi	[204]
Medicinal products	Microsatellite	<i>Agaricus subrufescens</i>	Development of polymorphic microsatellite markers for the medicinal mushroom	[205]

	Minisatellites	<i>Ganoderma applanatum</i> <i>Fomitopsis pinicola</i>	Study of intraspecies genetic variability, mating compatibility and clonality in two medicinal mushrooms	[206]
Extreme environments	Minisatellites	<i>Leucosporidium</i> spp. <i>Pseudogymnoascus</i> spp. non-identified Ascomycota NIA6 <i>Metschnikowia</i> sp. <i>Penicillium</i> spp.	Identification of fungi from admiralty bay (King George Island, Antarctica) soils and marine sediments	[207]
Soil	Microsatellites	<i>Rhizopogon</i>	Vertical partitioning between sister species on mesic and xeric sites in an interior Douglas-fir forest	[208]
	Minisatellites	<i>Hypholoma lateritium</i>	Identification of fungi isolated from coarse woody debris, the forest floor, and mineral soil in a deciduous forest	[209]
	Ministellites	<i>Rhizoscyphus</i>	Novel root-fungus symbiosis in Ericaceae: sheathed ericoid mycorrhiza formed by a hitherto undescribed basidiomycete with affinities to Trechisporales	[210]
	Microsatellites	<i>Rhizopogon vinicolor</i> <i>R. vesiculosus</i>	Study of population genetic structure between two sympatric sister-species of ectomycorrhizal fungi	[211]
	Microsatellites	<i>Tulasnella</i>	Phylogenetic and microsatellite markers for mycorrhizal fungi associated with Australian orchids	[212]
	Microsatellites	<i>Trichophyton ajelloi</i>	Study of intra-species genetic relatedness in strains isolated from various soil samples	[213]
	Microsatellites	<i>Rhizopogon kretzeriae</i> <i>R. salebrosus</i>	Microsatellite primers for the fungi for 454 shotgun pyrosequencing	[214]
	Microsatellites	<i>Laccaria</i> sp	Mitochondrial microsatellite markers for the Australian ectomycorrhizal fungus	[215]
	Microsatellites	<i>Laccaria amethystina</i> <i>Laccaria laccata</i>	Genetic dynamics and ecological functions of the pioneer ectomycorrhizal fungi in a volcanic desert on Mount Fuji	[216]
	Microsatellites	<i>Pisolithus tinctorius sensu stricto</i>	Study of the genetic structure in different populations	[217]
	Minisatellites	<i>Cenococcum geophilum</i>	Study of genetic diversity and pathogenicity genes of the symbiont of the mycorrhizal species	[218]
	Minisatellites	<i>Aspergillus flavus</i>	Study of diversity of isolates from corn and soil in three different Tuscany areas treated with the biological product AF-X1	[219]

	Microsatellites	<i>Phialocephala fortinii</i> s.l. <i>Acephala applanata</i> species-complex	Study of host preference of root endophytes of three european tree species	[220]
Fresh water ecosystems	Minisatellites	<i>Candida</i> spp. <i>Cryptococcus</i> spp. <i>Williopsis saturnus</i> <i>Hanseniaspora</i> spp. <i>Rhodotorula mucilaginosa</i> <i>Saccharomyces cerevisiae</i> <i>Torulaspora</i> spp. <i>Tricosporon</i> spp. <i>Yarrowia lypolitica</i>	Study of yeast diversity associated to sediments and water from two Colombian artificial lakes	[221]
	Microsatellites	<i>Blastomyces dermatitidis</i> <i>Blastomyces gilchristii</i>	Study of genetic diversity of fungi from freshwater drainage basins	[222]
Salt water ecosystems	Microsatellites	<i>Penicillium lusitanum</i>	Study of the diversity of fungi isolated from marine environments	[223]
	Microsatellites	<i>Neoscochyta fuci</i> <i>Paraconiothyrium salinum</i>	Study of the diversity of marine fungi	[224]
	Microsatellites	<i>Paralutworthia halima</i> <i>Remispora submersa</i> <i>Zalerion pseudomaritima</i> ,	Study of the diversity of marine fungi associated with wood baits in the estuary Ria de Aveiro	[225]
	Microsatellites	<i>Cladosporium rubrum</i> <i>Hypoxylon aveirense</i>	Study of the diversity of estuarine environment	[226]

Supplementary Table S6. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using SNP.

Importance	Fungal identification	Purpose	Reference
Human health	<i>Aspergillus fumigatus</i>	Detection, identification and genotyping of the fungi in patients with invasive aspergillosis	[1–3]
	<i>Blastomyces gilchristii</i>	Identification of the etiological agent of blastomycosis	[4]
	<i>Cladophialophora bantiana</i> <i>C. immunda</i> <i>C. devriesii</i>	Identification of the etiological agent of human infection	[5]
	<i>Exophiala dermatitidis</i> <i>E. oligosperma</i> <i>E. spinifera</i> <i>E. xenobiotica</i> <i>E. jeanselmei</i>	Detection and identification of opportunistic <i>Exophiala</i> species causing mycosis	[6]
	<i>Exserohilum rostratum</i>	Detection and identification of the etiological agent of an outbreak of fungal meningitis and other infections	[7]
	<i>Paracoccidioides spp.</i>	Study of the genetic diversity of the etiological agent of paracoccidioidomycosis	[8,9]
	<i>Rhizopus</i> <i>Mucor</i>	Identification of the etiological agent of mucormycosis	[10]
	<i>Sarocladium kiliense</i>	Determination of the origin of multinational outbreak of bloodstream infections	[11]
	<i>Aspergillus fumigatus</i>	Detection, identification and study of azole resistance in samples from patients with invasive aspergillosis	[12,13]
	<i>Aspergillus fumigatus</i>	Study of fungal natural product gene cluster	[14]
	<i>Candida auris</i>	Study of the genetic diversity and genomic epidemiology of the emerging human fungal pathogen	[15–17]
	<i>Candida glabrata</i>	Study of the genetic diversity of the etiological agent of candidiasis	[18]
	<i>Candida albicans</i> <i>Cryptococcus neoformans</i>	Study of population genetics in human pathogenic fungi	[19]
	<i>Trichophyton rubrum</i> <i>T. violaceum</i> <i>T. soudanense</i>	Study of the genetic diversity and genotyping of the etiological agent of skin, nail and hair infections	[20]

	<i>T. kuryangei</i> <i>T. megninii</i>		
Animal health	<i>Arthrobotrys oligospora</i>	Study of the genetic diversity and population structure of the nematode-trapping fungus	[21]
	<i>Grossmannia clavigera</i> <i>Leptographium longiclavatum</i> <i>Ophiostoma montium</i>	Study of the genetic diversity and relatedness in fungi associated with the mountain pine beetle	[22–24]
	<i>Pseudogymnoascus destructans</i> <i>Pseudogymnoascus spp.</i>	Distinction between <i>Pseudogymnoascus</i> species	[25]
	<i>Aspergillus fumigatus</i> <i>Aspergillus tubingensis</i> <i>Aspergillus uvarum</i>	Identification of the etiological agents of canine sino-nasal aspergillosis	[26]
	<i>Ophiomyces ophioidicola</i>	Detection of the fungus associated with snake fungal disease	[27]
	<i>Batrachochytrium dendrobatidis</i>	Study of the genetic diversity of the chytrid fungi causing global amphibian declines	[28]
	<i>Ophiocordyceps unilateralis</i>	Study of the genetic diversity of the entomopathogenic fungi responsible for zombie-ants	[29]
Human and animal health	<i>Pythium insidiosum</i>	Identification and genotyping etiological agent of pythiosis in humans and animals	[30]
Plant health	<i>Ophiognomonia clavignenti-juglandacearum</i>	Study of the population structure of the etiological agent of butternut canker	[31]
	<i>Leptosphaeria maculans</i>	Study of genetic diversity, virulence and reproductive behaviour of the an important phytopathogen	[32–34]
	<i>Podosphaera plantaginis</i>	Study of the genetic diversity of an obligate fungal pathogen of <i>Plantago lanceolata</i>	[35]
	<i>Heterobasidion annosum ss</i>	Study of virulence factors	[36]
	<i>Magnaporthe oryzae</i>	Study of the genetic diversity and virulence factors of the etiological agent of rice blast	[37–40]
	<i>Pyrenophora teres</i>	Study of the genetic diversity of the etiological agent of barley net blotch	[41,42]
	<i>Ganoderma</i> <i>Inonotus</i> <i>Phellinus</i> <i>Ceriporia</i> <i>Schizophyllum</i> <i>Phanerochaete</i> <i>Pleurotus</i> <i>Leucoagaricus</i>	Study of genetic diversity of wood-decay macro-fungi associated with declining arid zone trees	[43]

<i>Ustilaginoidea virens</i>	Study of the genetic diversity and population structure of the etiological agent of false smut on rice	[44]
<i>Verticillium longisporum</i>	Distinction between pathogen and apathogen species	[45]
<i>Rhizoctonia solani</i>	Study of the genetic diversity of a broad host-range pathogen	[46]
<i>Zymoseptoria tritici</i>	Study of the genetic diversity, virulence and antimicrobial resistance in the plant pathogenic fungus	[47–49]
<i>Alternaria solani</i>	Characterization and detection of mutations associated with resistance to succinate dehydrogenase-inhibiting fungicides	[50]
<i>Verticillium dahliae</i>	Study of genetic diversity, population structure and mating-type locus of a plant-pathogenic fungus	[51,52]
<i>Melampsora larici-populina</i>	Study of the genetic diversity and virulence factors of the poplar rust fungus	[53]
<i>Alternaria alternata</i>	Study of the genetic diversity of genes involved in toxin production in the etiological agent of black and brown spot diseases	[54]
<i>Pyrenophora teres</i> <i>Sphaerulina musiva</i>	Genotyping of plant-pathogenic fungi	[55]
<i>Pseudoperonospora cubensis</i> <i>Pseudoperonospora humuli</i>	Study of the genetic variation between obligate plant pathogens	[56]
<i>Melampsora lini</i>	Study of genetic diversity and virulence of the etiological agent of flax rust	[57]
<i>Parastagonospora nodorum</i>	Study of virulence factors in the etiological agent of septoria nodorum blotch on wheat	[58]
<i>Colletotrichum fructicola</i>	Study of genetic diversity of the fungal pathogen on tea-oil trees	[59]
<i>Calonectria pseudonaviculata</i>	Distinction of the etiological agent of sarcococca blight from two different plant species	[60]
<i>Rhynchosporium commune</i>	Study of multilocus resistance evolution to azole fungicides	[61]
<i>Fusarium graminearum</i> species complex	Distinction of closely related <i>Fusarium</i> species causing head blight fungi	[62]
<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	Study of genetic diversity, population structure, and virulence in the etiological agent of wheat stripe rust	[63,64]
<i>Monilinia yunnanensis</i> <i>Monilinia polystroma</i> <i>Monilinia fructicola</i>	Identification of species associated with brown rot of cultivated apple and pear fruit	[65]
<i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i>	Distinction of races in plant pathogenic fungi	[66]

	Diaporthaceae	Study of the genetic diversity of fungal families associated with grapevine	[67]
	Botryosphaeriaceae		
	<i>Phellinus noxius</i>	Study of the genetic diversity of the etiological agent of root rot in trees	[68]
	<i>Rhynchosporium commune</i>	Study of the genetic diversity	[69]
	<i>Fusarium graminearum</i>	Study of genetic diversity and host adaptation	[70]
	<i>Blumeria graminis</i> f. sp. <i>tritici</i>	Study of genetic diversity and virulence factors in the etiological agent of wheat and rye powdery mildew fungus	[71]
	<i>Fusarium proliferatum</i> <i>Fusarium solani</i> <i>Fusarium brachygibbosum</i> <i>Fusarium oxysporum</i> <i>Fusarium verticillioides</i>	Identification of species associated with date palm diseases (chlorosis, necrosis and whitening)	[72]
	<i>Microbotryum lychnidis-dioicae</i> <i>Microbotryum silenae-dioicae</i>	Study of the genetic diversity of castrating anther-smut fungi	[73,74]
	<i>Bipolaris sorokiniana</i>	Study of the genetic diversity and virulence factors of the etiological agent of multiple diseases on wheat and barley	[75]
	<i>Hymenoscyphus fraxineus</i>	Study of the structure of the etiological agent of ash dieback	[76]
	<i>Hemileia vastatrix</i>	Study of genetic diversity and recombination in the etiological agent of coffee leaf rust	[77]
	<i>Colletotrichum kahawae</i>	Study of genetic diversity and evolution of the etiological agent of coffee berry disease in Arabica coffee	[78]
	<i>Puccinia triticina</i>	Study of genetic diversity the etiological agent of leaf rust on wheat	[79]
	<i>Plasmopara viticola</i>	Study of mating-type locus in the etiological agent of grapevine downy mildew	[80]
	<i>Fusarium odoratissimum</i>	Study of the genetic diversity of the etiological agent of fusarium wilt in bananas	[81]
	<i>Tilletia indica</i>	Study of the genetic diversity of the etiological agent of karnal bunt on wheat	[82]
	<i>Setosphaeria turcica</i>	Study of the genetic diversity and population structure of the etiological agent of northern leaf blight in sorghum	[83]
Genetic diversity	<i>Neurospora crassa</i>	Study of the genetic diversity	[84]
	Glomeromycota	Study of vegetative compatibility, genetic diversity, and population structure in arbuscular mycorrhizal fungi	[85–90]
	<i>Fusarium fujikuroi</i>	Study of the ability to produce fumonisin	[91]
	Parasite fungi	Study of the genetic diversity	[92]

	<i>Armillaria cepistipes</i>	Study of the population genetic structure	[93]
	<i>Fusarium culmorum</i>	Study of virulence and comparison between species	[94]
	<i>Aspergillus</i> section <i>versicolores</i>	Detection of sterigmatocystin producing fungal strains	[95]
Food and beverage	<i>Lentinula edodes</i>	Genotyping and genetic linkage maps of the Shiitake mushroom	[96]
	<i>Aspergillus flavus</i>	Study of the genetic diversity and aflatoxin production	[97]
	<i>Tuber melanosporum</i>	Study of the genetic diversity of the Périgord black truffle	[98]
	<i>Penicillium digitatum</i>	Study of the genetic diversity in two postharvest pathogens from fruits	[99]
	<i>Penicillium expansum</i>		
	<i>Agaricus bisporus</i>	Study of the of genetic diversity and population structure in the germplasm of button mushroom	[100]
Lichens	<i>Xanthoparmelia</i> genera	Study of the evolution of the lichenized fungi	[101]
	<i>Letharia</i> spp.	Distinction between species included in the same species complex	[102]
	<i>Cetradonia linearis</i>	Study of population structure of a endangered, endemic lichen	[103]
	<i>Tremalla</i> spp.	Identification of fungi present in the cortex of wolf lichens	[104]
	<i>Rhizoplaca melanophthalma</i>	Study of the role of hybridization in lichen-forming fungi	[105]
Medicinal products	<i>Ophiocordyceps sinensis</i>	Study of the genetic diversity of an important medicinal fungus	[106,107]
Extreme environments	<i>Psychrophila</i> spp. <i>Tetracladium</i>	Identification of psychrophilic fungi from the world's roof (alpine glaciers)	[108]
	<i>Aspergillus fumigatus</i>	Study of the genetic diversity of isolates from air and surfaces of the international space station	[109]
	<i>Agaricus bisporus</i>	Study of genetic diversity, evolution and adaptation to extreme environment	[110]
Soil	<i>Rhizophagus irregularis</i>	Study of the genetic diversity of the mycorrhizal fungus	[111,113]
	<i>Tricholoma populinum</i>	Study of the genetic diversity of a ectomycorrhizal fungus	[114]
	<i>Suillus brevipes</i>	Distinction between populations of a symbiotic fungus	[115]
	<i>Rhizophagus irregularis</i>	Study of the genetic diversity of mycorrhizal fungi	[116]
	<i>Gigaspora margarita</i>		
	Arbuscular mycorrhizal fungi	Study of the genetic diversity and mating type	[117]
	Fungal community	Characterization of fungi from Arabidopsis root microbiome	[118]
Enzyme production	<i>Suillus luteus</i>	Study of adaptation in the mycorrhizal fungus driven by soil heavy metal contamination	[119]
	<i>Trichoderma reesei</i>	Identification of a hyper-cellulolytic mutant fungi	[120]

Supplementary Table S7. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using InDels.

Importance	Molecular marker	Fungal identification	Purpose	Reference
Human health	InDels	<i>Cryptococcus neoformans</i>	Study of the genetic diversity and virulence factors	[1–3]
	InDels	<i>Aspergillus fumigatus</i>	Study of the genetic diversity and recombination rates among of the etiological agent of invasive aspergillosis	[4–6]
	InDels	<i>Enterocytozoon bieneusi</i>	Study of the genetic diversity and population structure of the agent causing diarrhea and enteric disease	[7,8]
	InDels	<i>Candida albicans</i>	Study of the genetic diversity	[9]
	InDels	<i>Paracoccidioides brasiliensis</i> <i>Paracoccidioides lutzii</i>	Distinction of the etiological agents of paracoccidioidomycosis	[10]
	INdels	<i>Trichophyton</i> spp. <i>Microsporum</i> spp. <i>Epidermophyton</i> spp.	Identification of the etiological agents of superficial mycosis	[11]
	InDels	<i>Cryptococcus gattii</i>	Study of microevolutionary traits and comparative population genomics of the emerging pathogenic fungus	[12]
	InDels	<i>Malassezia arunalokei</i>	Study of the genetic diversity from isolates from seborrheic dermatitis patients and healthy individuals	[13]
	InDels	<i>Cryptococcus deuterogattii</i>	Study of genetic diversity and and drug resistance	[14]
	InDels	<i>Curvularia tamilnaduensis</i> <i>Curvularia coimbatorensis</i>	Identification of new etiological agents of fungal keratitis	[15]
	InDels	<i>Candida auris</i>	Diagnostic and identification of the pathogen	[16]
	InDels	<i>Trichophyton persicum</i> <i>Trichophyton spiraliforme</i>	Identification of new etiological agents of highly inflammatory tinea	[17]
	InDels	<i>Mucor irregularis</i> <i>Mucor hiemalis</i> <i>Lichtheimia corymbifera</i> <i>Rhizopus arrhizu</i>	Characterization of mitogenomes from Mucorales species and insights into pathogenicity	[18]
Animal health	InDels	<i>Batrachochytrium dendrobatidis</i>	Study of the genetic diversity and phylogeny of the etiological agent of the white-nose syndrome	[19,20]

	InDels	<i>Tritrichomonas foetus</i>	Study of the genetic diversity of the etiological agent of tritrichomonosis in different animal hosts	[21]
	InDels	<i>Sporothrix insectorum</i>	Study of the mitogenome of the entomopathogenic fungus and comparative mitogenomics in Ophiostomatales	[22]
	InDels	<i>Beauveria bassiana</i>	Study of the genetic diversity and virulence	[23]
	InDels	<i>Trichophyton benhamiae</i> species complex	Discrimination between the etiological agents of zoonotic tinea corporis and capitis	[24]
Human and animal health	InDels	<i>Trichophyton tonsurans</i> <i>Trichophyton equinum</i>	Discrimination between species	[25]
	InDels	<i>Enterocytozoon bieneusi</i>	Genotyping and study host specificity and its impacts on public health	[26,27]
Plant health	InDels	<i>Botrytis cinerea</i>	Study of the genome sequence, genetic diversity and resistance to fungicides	[28–30]
	InDels	<i>Phlebiopsis gigantea</i>	Study of the genetic diversity of the etiological agent of white rot of conifer logs and stumps	[31]
	InDels	<i>Colletotrichum gloeosporioides</i> species complex	Study of phylogeny and distinction between the species of the complex	[32,33]
	InDels	<i>Ceratocystis ss</i>	Distinction between the species of the complex	[34]
	InDels	<i>Phakopsora pachyrhizi</i>	Study of the genetic diversity of the etiological agent of soybean rust	[35]
	InDels	<i>Puccinia striiformis</i>	Study of the genetic diversity, evolution and virulence factors of the etiological agent of stripe rust	[36–38]
	InDels	<i>Blumeria graminis f. sp. hordei</i>	Study of the genetic diversity and comparison between populations	[39]
	InDels	<i>Pyrenophora tritici-repentis</i>	Detection of the wheat tan spot pathogen	[40]
	InDels	<i>Verticillium longisporum</i>	Study of the genetic diversity of the etiological agent of stem striping in oilseed rape	[41]
	InDels	<i>Epichloë spp.</i>	Study of the genetic diversity of a fungal endophyte	[42]
	InDels	<i>Fusarium graminearum</i>	Study of the genetic diversity and evolution	[43]
	InDels	<i>Coleosporium solidaginis</i> <i>Coleosporium asterum</i>	Study of the genetic diversity of the etiological agent of rust in <i>Solidago</i>	[44]
	InDels	<i>Magnaporthe oryzae</i>	Study of the phylogeny and population structure of the etiological agent of rice blast	[45]

	InDels	<i>Endoconidiophora resinifera</i>	Study of the genetic diversity of the etiological agent of blue-stain disease on sapwood	[46]
	InDels	<i>Pyrenophora semeniperda</i>	Study of the genetic diversity and mating system types of the seed bank pathogen	[47]
	InDels	<i>Ascochyta fabae</i>	Identification of a polyketide synthase gene responsible for Ascochitine biosynthesis	[48]
	InDels	<i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i>	Study of the genetic diversity, virulence, race profiling, and comparative genomic analysis of strains infecting cabbages	[49]
	InDels	<i>Parastagonospora nodorum</i>	Study of the genetic diversity of the etiological agent of septoria nodorum blotch on wheat	[50]
	InDels	<i>Fusarium culmorum</i> <i>Fusarium graminearum</i> ss	Distinction between closely related strains and its implication for diagnostic purposes	[51]
	InDels	<i>Fusarium asiaticum</i>	Study of the genetic diversity	[52]
	InDels	<i>Leptosphaeria maculans</i>	Study of the genetic diversity and population structure of the etiological agent of phoma stem canker in oilseed rape	[53]
	InDels	<i>Phomopsis longicolla</i>	Study of the genetic diversity of phomopsis seed decay in soybean	[54]
	InDels	<i>Podosphaera macularis</i>	Study of the population of the etiological agent of hop powdery mildew	[55]
	InDels	<i>Cryphonectria parasitica</i>	Study of the genetic diversity of the etiological agent of chestnut blight	[56]
Genomic diversity	InDels	<i>Neurospora crassa</i>	Study of the genetic diversity	[57]
	InDels	<i>Pyronemataceae</i>	Study of the genetic diversity, phylogeny and evolution	[58]
	InDels	<i>Bolbitiaceae</i>	Study of phylogenetic relationships in the mushroom family	[59]
	InDels	<i>Auricularia auricula-judae</i>	Identification of protoplast-regenerated monokaryotic isolates	[60]
	InDels	<i>Sclerotinia sclerotiorum</i>	Study of spontaneous and fungicide-induced genetic diversity	[61]
Food and beverage	InDels	<i>Zygosaccharomyces sapae</i>	Identification of new species isolated from Italian traditional balsamic vinegar	[62]
	InDels	<i>Lentinula edodes</i>	Construction of the genetic linkage map and mapping quantitative trait loci for vegetative mycelium growth rate, and architecture of fruiting body development	[63–66]
	InDels	<i>Aspergillus flavus</i>	Study of the genetic diversity of aflatoxin biosynthesis genes	[67]
	InDels	<i>Pleurotus eryngii</i>	Construction of the genetic linkage map and analysis of quantitative trait loci associated with the agronomically traits	[68]

	InDels	<i>Lentinula edodes</i>	Study of the genetic diversity and population structure of shiitake mushroom	[69–71]
	InDels	<i>Aspergillus section Flavi</i>	Study of the genetic diversity and aflatoxin biosynthesis cluster from isolates from nuts	[72–76]
	InDels	<i>Aspergillus oryzae</i>	Study of the genetic diversity of strains used in soy sauce koji fermentation	[77]
	InDels	<i>Auricularia species</i>	Study of the genetic diversity and evolution	[78]
	InDels	<i>Morchella importuna</i>	Construction of genetic linkage maps	[79]
Lichens	InDels	<i>Solenopsora spp.</i>	Study of the genetic diversity and phylogenetics	[80]
	InDels	<i>Peltigera spp</i>	Phylogenetic placement, species delimitation, and cyanobiont identity of endangered aquatic lichenized fungus	[81,82]
	InDels	<i>Umbilicaria decussata</i>	Study of the genetic diversity of the lichenized fungus collected in polar and non-polar regions	[83]
	InDels	<i>Strigula spp.</i>	Reallocation of foliicolous species into six genera	[84]
	InDels	<i>Sticta spp.</i>	Study of the evolutionary history of the lichenized fungus	[85]
Medicinal products	InDels	<i>Tolypocladium inflatum</i>	Study of genetic diversity of the cyclosporin-producing fungus	[86]
	InDels	<i>Cordyceps militaris</i>	Study of the genetic diversity of a medicinal fungus	[87]
	InDels	<i>Ganoderma lucidum</i>	Study of genetic diversity and phylogenetic relationships	[88]
	InDels	<i>Hypsizygus marmoreus</i>	Study of genetic diversity and phylogeny of a edible mushroom	[89]
	InDels	<i>Hericium erinaceus</i>	Study of the genetic diversity of an edible and medicinal mushroom	[90]
	InDels	<i>Gloeostereum incarnatum</i>	Construction of a genetic linkage map of an edible and medicinal mushroom	[91,92]
Riparian ecosystems	InDels	<i>Phytophthora spp.</i>	Characterization of hybrids	[93–95]
Soil	InDels	<i>Tricholoma populinum</i>	Study of the genetic diversity of the Populus-associated ectomycorrhizal fungus	[96]
	InDels	<i>Diversispora sp.</i>	Study of the genetic diversity of a arbuscular mycorrhizal fungus	[97]
	InDels	<i>Gigasporaceae</i> <i>Glomeraceae</i>	Sequencing and comparison of the mitochondrial COI gene from isolates of arbuscular mycorrhizal fungi belonging to different families	[98]
	InDels	<i>Sieverdingia tortuosa</i> <i>Diversispora peloponnesiaca</i>	Identification of new Diversisporaceae species of arbuscular mycorrhizal fungi	[99]
	InDels	<i>Dominikia bonfanteae</i>	Identification of new Glomeraceae species of arbuscular mycorrhizal fungi	[100]

		<i>Glomus atlanticum</i>		
	InDels	<i>Glomus chinense</i> <i>Dominikia gansuensis</i>	Identification of new Glomeraceae species of arbuscular mycorrhizal fungi from high altitude in the Tibetan Plateau	[101]
Enzyme production	InDels	<i>Lentinula edodes</i>	Study of the genetic diversity in genes involved in lignocellulose degradation in Shiitake mushroom	[102]
	InDels	<i>Arthrographis curvata</i> <i>Rhodospiridium babjevae</i>	Study of new potential fungal lipase producers	[103]
	InDels	<i>Aspergillus sydowii</i>	Genome analysis and characterization of two heterologous expressed, non-redundant xylanases	[104]
	InDels	<i>Trichoderma reesei</i>	Study of the genetic diversity of the workhorse strains used for industrial production of lignocellulosic enzymes and recombinant proteins	[105]

Supplementary Table S8. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using DNA Barcoding (ACT: actin, Btub: β -tubulin, CAL: calmodulin, COX1; cytochrome c oxidase subunit I, COX2; cytochrome c oxidase subunit II, GPDH: glyceraldehyde-3-phosphate dehydrogenase, ITS: internal transcribed spacer regions of the nrDNA operon, LSU: 28S nrDNA, PGK: phosphoglycerate kinase, RP60S: small ribosomal protein 60S L10, RPB2: RNA polymerase II second largest subunit, SSU: 18S nrDNA, TEF-1 α : translation elongation factor 1-alpha, TOP1: topoisomerase I).

Importance	Barcode	Fungal identification	Purpose	Reference
Human health	β -TUB	<i>Wickerhamomyces anomalus</i>	Identification of an human opportunistic fungi	[1]
	ITS LSU	<i>Backusella</i> spp. <i>Cunninghamella</i> spp. <i>Mucor</i> spp. <i>Rhizomucor</i> spp. <i>Zygorhynchus moelleri</i>	Identification of clinical isolates	[2]
	LSU	<i>Fusarium</i> spp. <i>Neocosmospora</i> spp.	Study of the genetic diversity of fungi associated with chronic rhinosinusitis	[3]
	ITS TEF-1 α	<i>Cunninghamella</i> spp.	Identification the etiological agent of mucormycosis	[4]
	ACT β -TUB ITS TEF-1 α	<i>Exophiala jeanselmei</i>	Identification of black yeasts involved in opportunistic disease in humans	[5]
	PGK TOP1	<i>Fusarium</i> spp.	Identification of opportunistic pathogens	[6]
	ACT β -TUB RP60S TEF-1 α	<i>Scedosporium apiospermum</i> species-complex	Identification of species of the etiological agent of human infections	[7]
	β -TUB	<i>Aspergillus</i> spp.	Distinction between <i>Aspergillus</i> species.	[8]
	ITS	<i>Epidermophyton</i> spp. <i>Microsporum audouinii</i> <i>Nannizzia gypsea</i> <i>Trichophyton</i> spp.	Identification of clinical dermatophyte strains	[9]
	ITS TEF-1 α	<i>Candida</i> spp. <i>Diutina</i> spp.	Identification of the agents of invasive fungal infections	[10]

		<i>Pichia spp.</i> <i>Scedosporium spp.</i>		
	ITS	<i>Colletotrichum spp.</i> <i>Purpureocillium linacinum</i> <i>Aspergillus spp.</i> <i>Paracremonium spp.</i> <i>Phellinum spp.</i>	Identification of the etiological agents of fungal keratitis	[11]
	ITS	<i>Paracoccidioides spp.</i>	Identification of the etiological agents of paracoccidioidomycosis	[12]
	β -TUB ITS	<i>Scedosporium spp.</i> <i>Lomentospora spp.</i>	Identification of the etiological agents of invasive disease	[13]
	ITS	<i>Periconia spp.</i>	Identification of the etiological agent of corneal mycotic keratitis	[14]
	COX LSU	<i>Pythium Insidiosum</i>	Identification of the etiological agent of pythiosis	[15]
Animal health	β -TUB ITS LSU	<i>Phialophora spp.</i>	Identification of new species causing diseases in leaf-cutting ants	[16]
	ITS LSU	<i>Candida cetoniae</i> <i>Nematodospira valgi</i>	Identificaton of new species from the Lodderomyces clade	[17]
	ITS LSU	<i>Alternaria alternata</i> <i>Cladophialophora bantiana</i> <i>Curvularia lunata</i> <i>Exserohilum rostrata</i> <i>Flavodon flavus</i> <i>Fusarium solani</i> <i>Toxicocladosporium irritans</i>	Identification of the etiological agents of mycotic rhinitis and sinusitis in horses	[18]
	ITS	<i>Alternaria spp.</i> <i>Aspergillus spp.</i> <i>Cladosporium spp.</i> <i>Mucor indicus</i> <i>Penicillium spp.</i> <i>Pericornia sp.</i> <i>Sarocladium implicatum</i>	Identification of guanophilic fungi of bats	[19]

Human and animal health	ITS	<i>Acremonium spp.</i> <i>Alternaria spp.</i> <i>Arthrographis kalrae</i> <i>Arthrospira hispanica</i> <i>Aspergillus spp.</i> <i>Aureobasidium pullulans</i> <i>Bipolaris spp.</i> <i>Blastobotrys spp.</i> <i>Candida spp.</i> <i>Cryptococcus spp.</i> <i>Curvularia spp.</i> <i>Cyberlindnera spp.</i> <i>Debaryomyces hansenii</i> <i>Epidermophyton floccosum</i> <i>Exophiala spp.</i> <i>Filobasidium uniguttulatum</i> <i>Fonsecaea spp.</i> <i>Fusarium spp.</i> <i>Galactomyces candidus</i> <i>Hanseniaspora uvarum</i> <i>Histoplasma capsulatum</i> <i>Hormographiella aspergillata</i> <i>Hyphopichia burtonii</i> <i>Hypocrea orientalis</i> <i>Kazachstania pintolopesii</i> <i>Kluyveromyces spp.</i> <i>Kodamaea ohmeri</i> <i>Leptosphaeria sen</i> <i>Lichtheimia spp.</i> <i>Lomentospora prolificans</i> <i>Magnusiomyces capitatus</i> <i>Medicopsis romeroi</i>	Detection of human and animal pathogenic fungi	[20]
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		<i>Meyerozyma guilliermondii</i> <i>Meyerozyma</i> spp. <i>Microascus cirrosus</i> <i>Microsporum</i> spp. <i>Millerozyma farinosa</i> <i>Mucor circinelloides</i> <i>Neoscytalidium dimidiatum</i> <i>Paracoccidioides brasiliensis</i> <i>Penicillium brevicompactum</i> <i>Phialemonium atrogriseum</i> <i>Pichia</i> spp. <i>Pithomyces</i> spp. <i>Purpureocillium lilacinum</i> <i>Rasamsonia aegroticola</i> <i>Rhinocladiella similis</i> <i>Rhizomucor pusillus</i> <i>Rhizopus</i> spp. <i>Rhodotorula mucilaginosa</i> <i>Saccharomyces cerevisiae</i> <i>Sarocladium</i> spp. <i>Scedosporium</i> spp. <i>Scopulariopsis</i> spp. <i>Scytalidium cuboideum</i> <i>Sporothrix schenckii</i> <i>Torulaspora delbrueckii</i> <i>Trichoderma</i> spp. <i>Trichophyton</i> spp. <i>Trichosporon</i> spp. <i>Wickerhamomyces anomalus</i> <i>Yamadazyma</i> spp. <i>Yarrowia lipolytica</i>	
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Plant health	ACT β-TUB CAL ITS LSU RPB2 TEF-1α	<i>Lecanosticta acicola</i> species-complex <i>Mycosphaerella</i> spp.	Identification of species of quarantine importance	[21]
	AAC CDC48 Hsp90 TEF3	<i>Nectriaceae</i>	Identification of Nectriaceae species	[22]
	ITS	<i>Cronartium</i> spp. <i>Diaporthe</i> spp. <i>Fusarium</i> spp. <i>Gymnosporangium</i> spp. <i>Mycosphaerella</i> spp. <i>Peronosclerospora</i> spp. <i>Phoma</i> spp. <i>Phytophthora</i> spp. <i>Puccinia</i> spp. <i>Tilletia</i> spp.	Identification of species of quarantine importance	[23]
	ITS	<i>Ganoderma</i> spp. <i>Phellinus noxius</i> <i>Rigidoporus microporus</i>	Identification of basidiomycete fungi in hardwood plantations	[24]
	ITS LSU	<i>Fusarium fujikuroi</i> species-complex	Distinction of species within the complex	[25]
	ITS GPDH RPB1 TEF-1α	<i>Bipolaris oryzae</i> <i>Curvularia</i> spp. <i>Pyricularia oryzae</i>	Identification of fungal pathogens associated with foliar diseases of wild and cultivated rice	[26]
	ITS SSU	<i>Fusarium</i> spp.	Detection and identification of phytopathogens	[27]

	TEF-1 α			
	ITS	<i>Entyloma cosmi</i>	Identification and phylogenetic analysis of the etiological agent of garden cosmos	[28]
	ITS	<i>Alternaria longissima</i> <i>Curvularia</i> spp. <i>Epicoccum sorghinum</i> <i>Exserohilum rostratum</i> <i>Fusarium thapsinum</i>	Identification of ascomycetes in sorghum	[29]
	ITS LSU	<i>Coleosporium</i> spp.	Identification and phylogenetic analyses of the etiological agent of North American goldenrod rust	[30]
	β -TUB ITS	<i>Colletotrichum</i> spp.	Identification of fungal etiological agent of fruit rot	[31]
	β -TUB ITS LSU RPB2	<i>Allophoma</i> spp. <i>Alternaria</i> spp. <i>Arezzomyces</i> spp. <i>Brunneosphaerella</i> spp. <i>Elsinoe</i> spp. <i>Exserohilum</i> spp. <i>Globozamichloridium</i> spp. <i>Neosetophoma</i> spp. <i>Neostagonospora</i> spp. <i>Nothophoma</i> spp. <i>Parastagonospora</i> spp. <i>Phaeosphaeriopsis</i> spp. <i>Pleiocarpon</i> spp. <i>Pyrenophora</i> spp. <i>Ramichloridium</i> spp. <i>Seifertia</i> spp. <i>Seiridium</i> spp. <i>Septoriella</i> spp. <i>Setophoma</i> spp. <i>Stagonosporopsis</i> spp. <i>Stemphylium</i> spp.	Identification of species of phytopathogens	[32]

		<i>Tubakia spp.</i> <i>Wingfieldomyces spp.</i> <i>Zasmidium spp.</i>		
	ITS	<i>Uromyces erythronii</i>	Distribution, infection rates and identification	[33]
	ITS LSU	<i>Vishniacozyma alagoana</i>	Identification of a new yeast associated with plants from dry and rainfall tropical forests	[34]
	ITS	<i>Aspergillus spp.</i> <i>Fusarium spp.</i>	Identification of phytopathogens for disease diagnostics and bio-surveillance	[35]
	ITS	<i>Dothistroma spp.</i>	Identification of pathogens on <i>Pinus</i> species	[36]
	ITS	<i>Fusarium equiseti</i>	Identification of the etiological agent of chilli wilt	[37]
Genetic diversity	ITS	<i>Tomophagus cattienensis</i>	Identification of a new species	[38]
	B-TUB CAM ITS TEF 1- α	<i>Diaporthe spp.</i>	Study of the genetic diversity and phylogeny	[39]
	ITS	<i>Annulohypoxyton</i> <i>Hypoxyton</i>	Identification of species within the genera	[40]
	ITS LSU	<i>Mortierellales spp.</i>	Study of the genetic diversity and phylogeny of Mortierellomycotina	[41]
	ACT ITS TEF-1 α	<i>Rhizopus microsporus</i>	Study of fungal diversity and delimitation of the species	[42]
	ITS	<i>Sporothrix schenckii</i> species-complex	Study of fungal diversity	[43]
	ITS HSP RPB2 TEF-1 α	<i>Serpula species-complex</i>	Distinction of species within the complex	[44]
	ITS	<i>Cyathus stercoreus</i>	Study of the genetic diversity and distribution of the fungus	[45]
	β -TUB ITS TEF-1 α	<i>Neofusicoccum batangarum</i>	Identification of the etiological agent of scabby canker on <i>Opuntia ficus-indica</i>	[46]

	ITS	<i>Plenodomus biglobosus</i>	Identification of the etiological agent of blackleg on oilseed rape	[47]
	IGS RPB2 TEF-1 α	<i>Fusarium oxysporum f. sp. opuntiarum</i>	Identification of the etiological agent of stem rot on <i>Mammillaria painteri</i>	[48]
	LSU SSU ITS TEF-1 α	<i>Heterosporicola beijingense</i>	Identification of the etiological agent of leaf spots on <i>Chenopodium quinoa</i>	[49]
	β -TUB ITS TEF-1 α	<i>Cadophora luteo-olivacea</i> <i>Diaporthe rudis</i> <i>Neofusicoccum parvum</i> <i>Peroneutypa scoparia</i>	Identification of the etiological agent of stem blight and dieback on blueberry	[50]
	β -TUB CAM IGS TEF-1 α	<i>Fusarium incarnatum-equiseti</i> complex-species	Identification of the etiological agent of leaf spot in leafy vegetable crops	[51]
	ITS LSU	<i>Palmeiomyces chamaeropicola</i>	Identification of the etiological agent of leaf spot on <i>Chamaerops humilis</i>	[52]
	ITS LSU TEF1- α	<i>Codinaea</i> spp. <i>Codinaeella</i> spp. <i>Nimesporella</i> spp. <i>Stilbochaeta</i> spp. <i>Tainosphaeriella</i> spp. <i>Xyladelphia</i> spp.	Phylogenetic Reassessment, Taxonomy, and Biogeography of <i>Codinaea</i>	[53]
	β -TUB ITS LSU SSU RPB2 TEF1- α	<i>Achrochaeta</i> spp. <i>Tubulicolla</i> spp.	Study of the genetic diversity and phylogeny of <i>Dictyochoeta</i>	[54]

	CAM	<i>Aspergillus spp.</i>	Study of the genetic diversity and description of one new species from the Gcwihaba Cave (Botswana)	[55]
Food and beverage	LSU	<i>Candida spp.</i> <i>Isatchenkia spp.</i> <i>Kazachstania spp.</i> <i>Kluyveromyces spp.</i> <i>Pichia spp.</i> <i>Rhodotorula spp.</i> <i>Saccharomyces spp.</i>	Identification of yeasts from selected bulgarian food products	[56]
	ITS LSU BTUB TEF-1 α	<i>Aureobasidium pullulans</i> <i>Cladosporium oxysporum</i> <i>Eutypella scoparia</i> <i>Penicillium commune</i>	Identification of fungal species from Taleggio cheese	[57]
	ITS LSU BTUB	<i>Alternaria solani</i> <i>Aspergillus spp.</i> <i>Atrotriquata lineata</i> <i>Candida spp.</i> <i>Clavospora lusitaniae</i> <i>Colletotrichum gloesporioides</i> <i>Cryptococcus spp.</i> <i>Debaryomyces hansenii</i> <i>Euroticum amstelodami</i> <i>Exophiala spp.</i> <i>Funneliformis mosseae</i> <i>Galactomyces spp.</i> <i>Kluyveromyces marxianus</i> <i>Macrophomina phaseolina</i> <i>Ophiocordyceps oxysporioides</i> <i>Pachyphloeus virescens</i> <i>Peniophora cinerea</i> <i>Peronospora pulveracea</i> <i>Phoma spp.</i>	Identification of the fungal flora in raw milk from the Italian Alps in relation to pasture altitude	[58]

		<i>Pichia spp.</i> <i>Priceomyces carsonii</i> <i>Psathyrella lutensis</i> <i>Rhodotorula spp.</i> <i>Torulaspora delbrueckii</i> <i>Trichosporon spp.</i> <i>Wallemia sebi</i> <i>Yarrowia lipolytica</i>		
	ITS LSU	<i>Amanita spp.</i>	Distinction between edible and poisonous amanitas mushrooms	[59]
	ITS	<i>Gliophorus spp.</i>	Identification of new species of waxcap mushrooms	[60]
	ITS β-TUB CAL	<i>Alternaria spp.</i> <i>Aspergillus spp.</i> <i>Botrytis spp.</i> <i>Cladosporium spp.</i> <i>Mucor spp.</i> <i>Penicillium spp.</i> <i>Rhizopus spp.</i>	Identification of fungi in organic and conventional fruits and derived products	[61]
	SSU ITS RPB1 RPB2	<i>Albatrellus ellisii</i> <i>Cantharellus cibarius</i> <i>Clavulina cristata.</i> <i>Gomphus floccosus</i> <i>Inocybe aff. Sphaerospora</i> <i>Laccaria vinaceoavellanea</i> <i>Lactarius deliciosus</i> <i>Lactarius volemus</i> <i>Ramaria maculatipes</i> <i>Tricholoma viridiolivaceum</i>	Identification of wild edible mushrooms	[62]
	ITS	<i>Agaricus bisporus</i> <i>Armillaria spp.</i> <i>Boletus spp.</i> <i>Chalciporus piperatus</i>	Identification of wild and native mushrooms sold in the open-air markets of south-eastern Poland	[63]

		<i>Cortinarius caperatus</i> <i>Imleria badia</i> <i>Lactarius</i> spp. <i>Leccinum schistophilum</i> <i>Leucoagaricus nymphaeum</i> <i>Pleurotus cornucopiae</i> <i>Polyporus umbellatus</i> <i>Sparassis crispa</i> <i>Suillus</i> spp. <i>Tricholoma</i> spp. <i>Xerocomellus cisalpinus</i>		
	ITS LSU	<i>Candida</i> spp. <i>Clavispora lusitaniae</i> <i>Cyberlindnera fabianii</i> <i>Debaryomyces</i> spp. <i>Dipodascaceae</i> <i>Geotrichum</i> spp. <i>Hanseniaspora</i> spp. <i>Hypocreaceae</i> <i>Kazachstania</i> spp. <i>Kluyveromyces</i> spp. <i>Lachancea</i> spp. <i>Mucor</i> spp. <i>Nectriaceae</i> <i>Penicillium</i> spp. <i>Sarocladium</i> spp. <i>Sistotrema</i> spp. <i>Torulaspora delbrueckii</i> <i>Trichocomaceae</i> <i>Wickerhamomyces anomalus</i> <i>Yarrowia lipolytica</i>	Study of the fungal diversity in dairy products	[64]

	ITS LSU	<i>Aspergillus spp.</i> <i>Cladosporium spp.</i> <i>Eurotium spp.</i> <i>Hyphopichia spp.</i> <i>Lichtheimia spp.</i> <i>Millerozyma spp.</i> <i>Monascus spp.</i> <i>Mucor spp.</i> <i>Paecilomyces spp.</i> <i>Penicillium spp.</i> <i>Pichia spp.</i> <i>Rhizomucor spp.</i> <i>Rhizopus spp.</i> <i>Saccharomycopsis spp.</i> <i>Syncephalastrum spp.</i> <i>Wickerhamomyces spp.</i>	Identification of fungal species and enzyme activity in nuruk, a Korean fermenting starter	[65]
	ITS TEF-1 α RPB1 RPB2	<i>Pleurotus ostreatus</i> complex-species	Distinction between species of oyster mushrooms	[66]
	ITS	<i>Agaricus bisporus</i> <i>Boletus edulis</i> <i>Cantharellus cibarius</i> <i>Craterellus comucopioides</i> <i>Grifola frondosa</i> <i>Hericium erinaceous</i> <i>Inonotus obliquus</i> <i>Lentinula edodes</i> <i>Tremetes versicolor</i> <i>Wolfiporia cocos</i>	Identification of consumer-relevant mushrooms	[67]
	ITS	<i>Clitopilus prunulus</i> <i>Coprinus comatus</i>	Identification of wild mushrooms samples	[68]

		<i>Craterellus cornucopioides</i> <i>Cyclocybe cylindracea</i> <i>Hymenopellis radicata</i> <i>Infundibulicybe gibba</i> <i>Lactarius deterrimus</i> <i>Laetiporus sulphureus</i> <i>Lepista nuda</i> <i>Leucoagaricus leucothites</i> <i>Lycoperdon perlatum</i> <i>Macrolepiota procera</i> <i>Paralepista flácida</i> <i>Pleurotus dryinus</i> <i>Psathyrella spp.</i>		
	ITS	<i>Fomitopsis spp.</i> <i>Ganoderma spp.</i> <i>Hexagonia spp.</i> <i>Lentinus spp.</i> <i>Lenzites spp.</i> <i>Leucoagaricus spp.</i> <i>Leucocoprinus spp.</i> <i>Lycoperdon spp.</i> <i>Microporus spp.</i> <i>Panus spp.</i> <i>Physisporinus spp.</i> <i>Pleurotus spp.</i> <i>Polyporus spp.</i> <i>Trametes spp.</i>	Identification of wild mushrooms	[69]
Lichens	ITS	<i>Rhizoplaca melanophthalma</i> species-complex	Distinction of species within the complex	[70,71]
	ITS	<i>Cladia aggregata</i> species-complex	Distinction of species within the complex	[72]
	COX	<i>Cladonia spp.</i>	Identification of species	[73,74]

	ITS IGS RPB2 TEF-1 α			
	ITS	<i>Parmelia sensu stricto</i>	Study of the diversity in Parmeliaceae (Ascomycota)	[75]
	ITS	<i>Usnea spp.</i>	Identification of lichen-forming fungi	[76]
	ITS	<i>Cora spp.</i> <i>Corella spp.</i>	Identification of lichen-forming Basidiomycetes belonging to different genera	[77]
Medicinal products	ITS	<i>Ophiocordyceps sinensis</i>	Identification of the medicinal mushroom	[78,79]
	ITS	<i>Lignosus cameronensis</i> <i>Lignosus tigris</i>	Identification of two new species of tiger milk mushroom	[80]
	ITS	<i>Fomes fomentarius</i>	Study of the genetic variability of the medicinal tinder bracket polypore	[61]
Extreme environments	ITS SSU	<i>Ascotricha sp.</i> <i>Aspergillus sp.</i> <i>Cerrena sp.</i> <i>Chaetomium sp.</i> <i>Cladosporium sp.</i> <i>Eurotium sp.</i> <i>Hortaea sp.</i> <i>Penicillium sp.</i> <i>Pleospora sp.</i> <i>Sagenomella sp.</i> <i>Trametes sp.</i>	Identification of fungal species in deep-sea sediments	[82]
	ITS	<i>Melanelia spp.</i>	Identification and discrimination of the lichen-forming genus from Icelandic	[83]
	ACT B-TUB CAM GAPDH ITS TEF-1 α	<i>Alternaria spp.</i> <i>Aspergillus spp.</i> <i>Aureobasidium spp.</i> <i>Candida spp.</i> <i>Cladosporium spp.</i> <i>Debaryomyces spp.</i> <i>Fusarium spp.</i> <i>Hortaea spp.</i>	Identification and discrimination of fungal species of the hypersaline Inland Sea	[84]

		<i>Hyphozyma spp.</i> <i>Knufia spp.</i> <i>Kondoa spp.</i> <i>Naganishia spp.</i> <i>Papiliotrema spp.</i> <i>Penicillium spp.</i> <i>Rhodotorula spp.</i> <i>Sarocladium spp.</i> <i>Symmetrospora spp.</i> <i>Tremellales spp.</i> <i>Trichoderma spp.</i> <i>Ulocladioides spp.</i> <i>Zalaria obscura</i>		
	ITS	<i>Dothideomycetes</i> <i>Eurotiomycetes</i> <i>Lecanoromycetes</i> <i>Leotiomycetes</i> <i>Pezizomycetes</i> <i>Sordariomycetes</i>	Study of the endophytic and endolichenic fungal diversity in maritime Antarctica	[85]
Saltwater ecosystems	ITS	<i>Ascomycota</i> <i>Basidiomycota</i>	Study of the diversity of marine-derived fungal cultures	[86]
	ITS RPB2 TEF-1 α	<i>Trichoderma arenarium</i>	Identification of fungal bioeffectors for biosaline agriculture in salt marshes	[87]
	ITS	<i>Aspergillus</i> <i>Penicillium</i> <i>Phialemoniopsis</i> <i>Purpureocillium</i> <i>Trametes</i>	Identification of culturable marine fungi from coastal region	[88]
Freshwater ecosystems	ITS	<i>Hyphomycete</i>	Identification of fungal species	[89]
	ITS	<i>Capnodiales</i> <i>Eurotiales</i>	Identification of fungal species in Dukan Freshwater Lake	[90]

		<i>Helotiales</i> <i>Hypocreales</i> <i>Mortierellales</i> <i>Onygenales</i> <i>Pezizales</i> <i>Pleosporales</i> <i>Xylariales</i>		
Soil	ITS TEF-1 α	<i>Trichoderma spp.</i>	Study of the diversity in soil and litter	[91]
	ITS	<i>Cortinarius spp.</i>	Study of the diversity and geographic distribution of the ectomycorrhizal fungi	[92,93]
	ITS LSU RPB1 RPB2 SSU TEF-1 α	<i>Russula spp.</i>	Identification of species of the ectomycorrhizal mushrooms	[94]
	ITS LSU	<i>Gongronella eborensis</i>	Identification of a new fungal species from vineyard soil	[95]
	B-TUB	<i>Exophiala pseudooligosperma</i>	Identification of a new black yeast from soil	[96]
Enzyme production	ITS	<i>Aspergillus spp.</i> <i>Colletotrichum gloeosporioides</i> <i>Fusarium oxysporum</i> <i>Penicillium echinulatum</i>	Identification of leaf litter fungi potential for cellulose degradation	[97]
	ITS	<i>Trichoderma spp</i>	Identification of fungal species and screening for cellulolytic activity	[98]
	ITS	<i>Aspergillus fischeri</i> <i>Cosmospora viridescens.</i> <i>Curvularia spicifera</i> <i>Fusarium spp.</i> <i>Humicola grisea</i> <i>Mucor spp.</i> <i>Paecilomyces sp.</i> <i>Penicillium spp.</i>	Identification of ligno-cellulolytic fungi	[99]

		<i>Trichoderma atroviride</i>		
	ITS TEF-1 α	<i>Aspergillus nidulans</i> <i>Stemphylium lucomagnoense</i> <i>Trichoderma asperellum</i>	Screening of marine fungal strains for their potential to produce oxidases with laccase activities	[100]
Monument degradation	LSU	<i>Alternaria spp.</i> <i>Aspergillus spp.</i> <i>Aureobasidium spp.</i> <i>Cladosporium spp.</i> <i>Fusarium spp.</i> <i>Mucor spp.</i> <i>Penicillium spp.</i> <i>Pestalotiopsis spp.</i> <i>Trichoderma spp.</i>	Identification of culturable fungi associated with urban stone surfaces	[101]
	β -TUB ITS LSU TEF1- α	<i>Bionectria cf. ochroleuca</i> <i>Chaetomium murorum</i> <i>Cladosporium spp.</i> <i>Epicoccum nigrum</i> <i>Fusarium proliferatum</i> <i>Mucor racemosus</i> <i>Penicillium crustosum</i> <i>Rhizopus stolonifer</i> <i>Trichoderma harzianum</i>	Identification and biodeteriorative potential of fungal dwellers on ancient stone stela	[102]
	ITS LSU	<i>Aspergillus spp.</i> <i>Bjerkandera adusta</i> <i>Cladosporium spp.</i> <i>Penicillium spp.</i>	Identification of contaminant fungi at different coloured materials in ancient Egypt tombs and mosques	[103]
	ITS LSU	<i>Acremonium spp.</i> <i>Lecanicillium sp.</i> <i>Parengyodontium album</i> <i>Purpureocillium lilacinum</i> <i>Sarocladium kiliense</i>	Micromycetes as colonizers of mineral building materials in historic monuments and museums	[104]
	ITS	<i>Alternaria spp.</i>	Identification of fungi associated with building materials biodeterioration	[105]

		<i>Arthothelium spectabile</i> <i>Arthrinium spp.</i> <i>Aspergillus sp.</i> <i>Aureobasidium pullulans</i> <i>Cladosporium sp.</i> <i>Geomyces sp.</i> <i>Lasiodiplodia theobromae</i> <i>Moniliella sp.</i> <i>Mucor sp.</i> <i>Penicillium sp.</i>		
	ACT β -TUB ITS LSU RPB1 RPB2 SSU TEF-1 α	<i>Anthraccina spp.</i> <i>Bradymyces spp.</i> <i>Cladophialophora spp.</i> <i>Cyphellophora spp.</i> <i>Exophiala spp.</i> <i>Knufia spp.</i> <i>Lithohypha spp.</i> <i>Trichomerium spp.</i>	Identification of rock-inhabiting Chaetothyriales fungi	[106]
Effluents	ITS LSU	<i>Wickerhamiella shivajii</i>	Identification of a thermotolerant yeast isolated from distillery effluent	[107]
	β -TUB CAM ITS RPB2	<i>Aspergillus spp.</i> <i>Fusarium spp.</i> <i>Penicillium spp.</i> <i>Trichoderma spp.</i>	Identification and phylogeny of fungi isolated from industrial wastewater	[108]
Bioremediation	ITS	<i>Acremonium sp.</i> <i>Alternaria sp.</i> <i>Aspergillus spp.</i> <i>Beauvaria sp.</i> <i>Chaetomium spp.</i> <i>Cladosporium cladosporoides</i> <i>Cryptococcus spp.</i> <i>Cunninghamella elegans</i>	Identification and phylogeny of fungi associated with tarballs	[109]

		<i>Epicoccum purpurascens</i> <i>Fusarium</i> sp. <i>Graphium</i> sp. <i>Humicola fuscoatra</i> <i>Microascus cinereus</i> <i>Mucor</i> sp. <i>Paecilomyces</i> sp. <i>Passalora</i> sp. <i>Penicillium</i> spp. <i>Pseudallescheria ampullus</i> <i>Rhizopus</i> spp. <i>Rhodotorula</i> sp. <i>Saccharomyces estuary</i> <i>Sarocladium</i> spp. <i>Scopulariopsis brevicaulis</i> <i>Sordaria</i> spp. <i>Syncephalastrum racemosum</i> <i>Tetracoccusporium</i> sp.		
	β-TUB ITS	<i>Acremonium</i> spp. <i>Alternaria</i> spp. <i>Aspergillus</i> spp. <i>Beauveria</i> spp. <i>Curvularia</i> spp. <i>Emericellopsis</i> spp. <i>Exophiala</i> spp. <i>Fusarium</i> spp. <i>Sarocladium</i> spp. <i>Stachybotrys</i> spp. <i>Stemphylium</i> spp. <i>Trichoderma</i> spp. <i>Ulocladium</i> spp.	Study of the diversity of culturable fungi inhabiting petroleum-contaminated soils	[110]
	ITS	<i>Trichoderma</i> spp.	Identification of the fungus	[111]

	RPB2 TEF-1 α			
	ITS	<i>Aspergillus spp.</i> <i>Cladosporium spp.</i> <i>Exophiala spp.</i> <i>Flavodon spp.</i> <i>Hypocreales</i> <i>Nectriaceae</i> <i>Penicillium spp.</i> <i>Peniophora spp.</i> <i>Trichoderma spp.</i>	Identification of culturable petroleum-degrading fungi from petroleum-contaminated sites	[112]
	β -TUB ITS TEF-1 α	<i>Aspergillus</i> <i>Chaetomella</i> <i>Cladosporium</i> <i>Cochliobolus</i> <i>Diaporthe</i> <i>Epicoccum</i> <i>Eutypella</i> <i>Fusarium</i> <i>Gongronella</i> <i>Microsphaeropsis</i> <i>Myrothecium</i> <i>Neosascochyta</i> <i>Neocosmospora</i> <i>Oudemansiella</i> <i>Paraconiothyrium</i> <i>Paraphaeosphaeria</i> <i>Penicillium</i> <i>Perenniporia</i> <i>Periconia</i> <i>Phanerochaete</i> <i>Phoma</i>	Diversity and oil degradation potential of culturable fungi isolated from chronically contaminated soils	[113]

		<i>Phytophthora</i> <i>Pyrenochaetopsis</i> <i>Rhizopus</i> <i>Roussoella</i> <i>Saccharicola</i> <i>Scedosporium</i> <i>Sydowia</i> <i>Talaromyces</i> <i>Trichoderma</i> <i>Westerdykella</i>		
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Supplementary Table S9. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using Metagenomics (COX2; cytochrome c oxidase subunit II, ITS1: internal transcribed spacer regions of the nrDNA operon (region 1), ITS2: internal transcribed spacer regions of the nrDNA operon (region 2), LSU: 28S nrDNA, SSU: 18S nrDNA, TEF-1 α : translation elongation factor 1-alpha,).

Importance	Metabarcoding	Purpose	Reference
Human health	ITS1 / ITS2	Identification of fungal species in the gut of HIV-infected patients	[1]
	SSU	Mosquito vector-associated microbiota across habitat endemic for dengue and other arthropod-borne diseases	[2]
	ITS2	Mycobiome in the middle ear cavity with and without otitis media with effusion	[3]
	ITS	Oral microbiome in down syndrome and its implications on oral health	[4]
	ITS	Comparison of fungal species from the oral microbiome in cystic fibrosis patients and controls	[5]
	ITS2	Identification of the human oral mycobiome in tissue and saliva	[6]
	ITS	Global distribution of the emerging pathogenic fungus <i>Scedosporium aurantiacum</i>	[7]
	ITS	Changes in the oral microbiome through age and lifestyle factors	[8]
Animal health	ITS LSU	Identification of saprophytic Polyporales mutualists of <i>Ambrosiodmus ambrosia</i> beetles	[9]
	ITS	Identification of fungal communities from bark beetles	[10]
	ITS2	Identification of the fungal microbiota associated to the olive fruit fly	[11]
	ITS1	Study of endomycobiome associated with females of the planthopper <i>Delphacodes kuscheli</i>	[12]
	ITS2	Identification of mixed strongyle infections in horses	[13]
	ITS2	Study of fungal diversity from feces of small mammals	[14]
	ITS2	Identification of fungal entomopathogens from <i>Aedes albopictus</i> larvae	[15]
	ITS2 LSU	Identification of insect-associated fungal communities	[16]
Plant health	ITS2	Identification of fungal diversity in the phyllosphere and carposphere of olive (<i>Olea europaea</i>)	[17]
	ITS1	Identification interactions of the etiological agent of oak powdery mildew from pedunculate oak	[18]
	ITS1 / ITS2 LSU	Identification of grapevine trunk pathogens in planta	[19,20]
	ITS	Identification of fungal community diversity associated with Norway spruce	[21]
	TEF-1 α	Assessment of <i>Fusarium</i> diversity on cereals	[22]
	ITS	Identification of the fungal community in leaves of <i>Acanthus ilicifolius</i> var. <i>xiamenensis</i>	[23]

	ITS TEF-1 α	Identification of <i>Fusarium</i> communities in maize stalks	[24]
	ITS1	Fungicides have complex effects on the wheat phyllosphere mycobiome	[25]
	ITS1	Identification of soil fungal and oomycete communities in holm oak declined	[26]
	COX2	Identification of oak rhizosphere-associated oomycetes	[27]
	ITS1	Identification of fungal species from wheat ears across a topographically heterogeneous field	[28]
	ITS1 ITS2	Identification of Botryosphaeriaceae fungal endophytes in grapevines and adjacent forest trees	[29]
	ITS	Identification of fungal endophyte communities in <i>Theobroma cacao</i> leaves	[30]
	ITS1	Identification of endophytic fungal community from <i>Olea europaea</i>	[31]
	ITS2	Identification of the fungal endophytic assemblage of <i>Brachypodium rupestre</i> growing in a range of anthropized disturbance regimes	[32]
	ITS2	Identification of fungal endophytes within wood of cultivated Proteaceae	[33]
	ITS2	Study of fungal endophyte diversity in the phyllosphere of a barley crop	[34]
	ITS1 / ITS2	Detection and surveillance of emerging and recurrent plant pathogens	[35]
	ITS2	Identification of fungal assemblages in fallen Norway spruce trunks	[36]
	ITS2	Detection and identification of rust fungal pathogens in environmental samples	[37]
	ITS2	Identification of fungal communities in Heshouwu (<i>Polygonum multiflorum</i> Thunb.)	[38]
	ITS2	Identification of endophytic fungal communities in <i>Vaccinium myrtillus</i> plant organs	[39]
	ITS1 / ITS2	Identification of weed-colonizing fungi	[40]
	ITS1	Study of <i>Phytophthora</i> diversity using genus-specific primers	[41]
	ITS1	Study of <i>Phytophthora</i> diversity in anthropized and natural ecosystems	[42]
Food and beverage	ITS1 / ITS2	Identification of fungal communities in brined Aloreña de Málaga green olive fermentations	[43]
	ITS	Identification of fungal species associated with spontaneous wine fermentation	[44]
	ITS	Identification from fungal species from dairy products and Mayonnaise	[45]
	ITS2	Identification of fungal species from traditionally prepared starters for alcoholic beverages in India	[46]
	ITS	Identification of fungal species from spontaneous fermentation of Chinese pu-erh tea	[47]
	ITS2	Identification of fungal species in honey samples from local beekeepers and markets	[48]
	ITS2	Identification of fungal species of barley grain	[49]
	ITS2	Identification of fungal contaminants in nutmeg	[50]
	ITS1 / ITS2	Identification of fungal species from Doushen with different flavors	[51]

	ITS2	Identification of fungal species associated with gwell	[52]
	LSU	Identification of fungal species associated with the Algerian traditional date product “Btana”	[53]
	ITS	Identification of fungal species from apple fruit after harvest and implications for fruit quality	[54]
	ITS	Identification of fungal species from French fermented sausages and mycotoxin risk evaluation during storage	[55]
	ITS1	Authentication of “wild mushrooms” in food products	[56]
	ITS1	Identification of fungal species from artisanal colonial salami-type dry-fermented sausages	[57]
	ITS	Identification of fungal species from kombucha tea	[58,59]
	ITS2	Identification of natural fungal contaminants in bee pollen	[60]
	ITS1	Identification of fungal communities from Greek PDO cheeses	[61]
	ITS2	Identification of desirable and spoilage fungi sources during black olive fermentations	[62]
	ITS2	Study of seasonal changes in the fungal species from an Australian Winery	[64]
	ITS1	Identification of truffles	[65]
	ITS2	DNA traces the origin of honey by identifying fungi	Wirta et al., [2021]
	ITS	Identification of fungal species from Mexican tepache fermented beverage	[66]
	ITS1 / ITS2	Identification of fungal species from flaxseed	[67]
Lichens	ITS2	Identification of fungal species in lichens	[68–70]
	ITS1	Identification of fungal species of lichen forming-fungi at a local scale	[71]
	ITS1 / ITS2	Identification of fungal species in photobiont lichens	[72]
	ITS	Identification of lichen-forming fungi from herbarium specimens	[73,74]
	ITS1 / ITS2	Study of the biodiversity of lichen-forming fungi	[75]
	ITS1	Identification of endolichenic fungal community of <i>Parmotrema tinctorum</i>	[76]
Medicinal products	LSU	Identification of yeasts and fungi from kombucha probiotic beverage	[77,78]
	ITS TEF-1 α	Identification the “mushroom of immortality”: assessing the <i>Ganoderma</i> species composition in commercial Reishi products	[79]
	ITS2	Identification of fungal communities in medicinal and edible <i>Cassia</i> Semen	[80]
	ITS2	Identification of biological ingredient from traditional herbal medicine Fuke Desheng Wan	[81]
Extreme environments	ITS	Fungal paleo-diversity from arctic permafrost	[823]
	ITS1	Identification of cryptoendolithic fungal communities in Antarctica	[83–85]

	ITS	Identification of fungal communities from Castaño Overa glacier–Mount Tronador, Patagonia, Argentina	[86]
	SSU	Study of fungal diversity of a shallow-water hydrothermal vent field at Kueishan Island, Taiwan	[87]
	ITS1	Identification of fungal communities from rock and soil substrates on a maritime antarctic glacier forefield	[88]
	ITS2	Identification of fungal diversity in soils from Antarctica	[89,90]
	ITS1 / ITS2	Identification of fungal communities from the continental solar saltern in Añana Salt Valley	[91]
	ITS2	Identification of fungal diversity present on rocks from a polar desert from Antarctica	[92]
	ITS2	Identification of fungal species present in lakes of Maritime Antarctica	[93,94]
	ITS	Identification of fungal communities present in Antarctic deep-sea sediments	[95]
	ITS2	Identification of fungal communities from permafrost in the South Shetland Islands, maritime Antarctic	[96]
	ITS	Identification of fungal communities from Arctic paleoecosystems	[97]
Marine ecosystems	ITS2	Diversity assessment of fungi from protected coastal <i>Salix repens</i> communities	[98]
	SSU	Identification of fungal communities from estuaries.	[99]
	SSU	Identification of fungal species from sediments of marine canyons	[100]
	ITS	Identification of fungal communities in sediments of subtropical Chinese seas	[101]
	SSU	Identification of fungal communities in marine sediments	[102]
	ITS2	Identification of fungal communities in unflooded and tidal flat soil in coastal saline ecosystem	[103]
	ITS SSU	Identification OF fungal species from sediments from Stellwagen Bank National Marine Sanctuary	[104]
	ITS2	Identification of fungal communities on the Swedish west coast	[105]
	SSU	Study of the diversity of endolithic fungi in coral skeletons and other reef substrates	[106]
	ITS2	Study of fungal diversity in deep-sea sediments from the Magellan seamounts	[107]
Freshwater ecosystems	SSU	Identification of fungal diversity on coarse and fine particulate organic matter in a first-order stream	[108]
	ITS	Identification of aquatic fungi on deciduous leaves	[109]
	ITS1	Study of spatial structure of fungal DNA assemblages of a forest river network	[110]
	ITS	Identification of fungal airborne communities from rice paddy	[111]
	ITS1	Study of seasonal dynamics of fungal communities in a flow-regulated stream in a restored forest	[112]
	ITS	Identification of fungal species from microplankton in lower reaches of Qiantang River	[113]
Built environment	ITS	The metagenomics and metadesign of the subways and urban biomes	[114]
	ITS1	Changes in fungal species associated with urban stress	[115]

	ITS	A global metagenomic map of urban microbiomes and antimicrobial resistance	[116]
	ITS	Urban environments harbor greater oomycete and <i>Phytophthora</i> diversity, creating a bridgehead for potential new pathogens to natural ecosystems	[117]
	ITS1 / ITS2	Identification of fungal community and potential pathogen identification across the PM size fractions and seasons in the urban atmosphere	[118]
Pollution	ITS2	Identification of belowground fungal communities in pioneer Scots pine stands growing on heavy metal polluted and non-polluted soils	[119]
	ITS SSU	Identification of plastic-associated species in the Mediterranean Sea	[120]
	ITS1 / ITS2	Identification of fungal communities in microplastics from terrestrial ecosystems	[121]
	SSU	Identification of fungal species and tolerance to contaminants in an urban brownfield site	[122]
	ITS	Identification of fungal communities at differential polluted sites of Rome	[123]
Soil	SSU	Identification of fungi in communities from a decommissioned gold mine	[124]
	ITS	Identification of fungal communities from poplar at a Hg phytomanagement site	[125]
	ITS1	Identification of mycorrhizal and pathogenic fungi from the soil of a Eucalyptus plantation	[126]
	ITS	Study of the diversity of mycorrhizal fungi in forest soils	[127]
	ITS1	Identification of soil mycobiota of the upper Andean Colombian agro-environment	[128]
	ITS	Identification of the diversity of woody host-associated <i>Phytophthora</i> spp. in soils at public gardens and amenity woodlands	[129]
	ITS	Fungal communities decline from the air and soil associated with urbanization	[130]
	ITS1 / ITS2	Identification of soil fungal communities in metropolitan green spaces across a vegetation biodiversity gradient	[131]
	ITS	Study of soil microbial communities in diverse agroecosystems exposed to the herbicide glyphosate	[132]
	ITS1	Study of soil fungal communities differ between shaded and sun-intensive coffee plantations	[133]
	SSU	Identification of arbuscular mycorrhizal fungal communities colonising the roots of indigenous legumes	[134]
	ITS1 / ITS2 LSU	Identification of soil fungi from different urban greenspaces	[135]
	ITS2	Identification of soil fungal communities associated with alpine field-grown saffron (<i>Crocus sativus</i> L.) inoculated with AM fungi	[136]
	SSU	Study in changes of fungal communities associated with the conversion of a High-Altitude temperate forest to agriculture fields or husbandry	[137]

	ITS	Identification of plant pathogenic oomycetes in soil from internationally traded plants	[138]
	ITS1 / ITS2	Identification of multiple mycetoma pathogens from soil	[139]
	ITS2	Identification of the soil fungal community to aid the conservation of underexplored church forests	[140]
	ITS2	Identification of cryptic diversity in forest soils on the isolated Brazilian Trindade Island	[141]
	ITS2	Identification of fungal communities among Amazonian Canga formations	[142]
Outdoor air aerobiology	ITS2	Identification of fungal spores from mixed airborne samples	[143]
	SSU	Identification of fungal species from the Red Sea Sector of the Global Dust Belt's Microbiome	[144]
	ITS2	Assessment of airborne fungal seasonal diversity	[145]
	SSU	Identification of the aerobiome and potential drivers of turn-over in the full microbial community in the air	[146]
	ITS2	Spatio-temporal patterns of airborne fungal spores	[147]
Indoor air aerobiology	ITS2	Climate change impact on fungi in the atmospheric microbiome	[148]
	ITS2	Identification of indoor fungi	[149,152]
	ITS2	Identification of fungal species of sawmills	[153]
	ITS	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment	[154]
	ITS1 / ITS2	The diversity and seasonality of the indoor mycobiome	[155]
	ITS2	Indoor mycobiome of daycare centers	[156]
Forensic Sciences	ITS2	Identification of fungal species from school classrooms surrounded by a forest	[157]
	SSU	Predicting the origin of soil evidence: high throughput eukaryote sequencing applied to a crime scene scenario	[158]
	ITS2	Predicting provenance of forensic soil samples	[159]
	ITS	Identification of fungal succession during mammalian cadaver decomposition and potential forensic implications	[160]
	ITS1 / ITS2	Identification of soil fungal communities investigated in simulated forensic burial contexts	[161]
	ITS1 / ITS2	Identification of fungal species from forensic samples	[162,164]
Compost	ITS1	Link between evidence and crime scene through soil fungal microbiome	[165]
	ITS1 / ITS2	Identification of fungal species from home composts	[166]
	ITS	Biodiversity and succession of mycobiota associated to agricultural lignocellulosic waste-based composting	[167]

Monument degradation	ITS1	Identification of fungal communities in pressmud composting harbour beneficial and detrimental fungi for human welfare	[168]
	SSU	Fungal community in the composting process of Chinese medicinal herbal residues	[169]
	ITS	Identification of epilithic and endolithic fungi associated with deterioration on stone church facades subject to urban pollution in a sub-tropical climate	[170]
	ITS	Identification of fungal species from the dark crusts on the church of Nossa Senhora do Carmo, Rio de Janeiro, Brazil	[171]
	ITS	Identification of fungal species in the first Portuguese King tomb	[172]
	ITS2	Study of biodeterioration of ancient wall paintings in an Italian cave	[173]
	ITS1	Identification of fungal communities from darkened white marble of Florence cathedral	[174]

Supplementary Table S10. Molecular markers in fungi: an overview of manuscripts published in the last 10 years using Whole Genome Sequencing.

Importance	Fungal identification	Purpose	Reference
Human health	<i>Apophysomyces trapeziformis</i>	Sequence of the etiological agent of necrotizing cutaneous mucormycosis	[1]
	<i>Exserohilum rostratum</i>	Detection of the etiological agent of fungal meningitis and other infections	[2,3]
	<i>Sporothrix schenckii</i>	Sequence of the etiological agent of sporotrichosis	[4]
	<i>Scedosporium apiospermum</i>	Sequence of the pathogenic fungus	[5]
	<i>Candida auris</i>	Sequence of the etiological agent of candidiasis with multi-drug resistances	[6–12]
	<i>Aspergillus fumigatus</i>	Comparison of strains isolated from patients with pulmonary aspergilloma and chronic necrotizing pulmonary aspergillosis	[13]
	<i>Aspergillus lentulus</i>	Sequence of the etiological agent of aspergillosis	[14]
	<i>Penicillium capsulatum</i>	Sequence of the potential pathogenic fungus	[15]
	<i>Histoplasma capsulatum</i>	Sequence of the etiological agent of lung infections	[16]
	<i>Mucor circinelloides f. circinelloides</i>	Sequence of the etiological agent of invasive wound mucormycosis in a burn unit	[17]
	<i>Trichophyton rubrum</i>	Sequence of an ubiquitous dermatophyte pathogen	[18]
	<i>Candida inconspicua</i>	Sequence of the etiological agent of candidiasis	[19]
	<i>Aspergillus terreus complex-species</i>	Sequence of the etiological agent of invasive infection and chronic respiratory disease	[20]
Animal health	<i>Leptographium longiclavatum</i>	Sequence of a mountain pine beetle-associated symbiotic fungus	[21]
	<i>Metarhizium anisopliae</i>	Sequence of the fungus used as biocontrol agent of insect pests	[22]
	<i>Purpureocillium lilacinum</i>	Comparative genomic of bio-control fungus against nematodes	[23]
	<i>Aschersonia badia</i>	Sequence and comparative analysis of two insect-pathogenic fungus	[24]
	<i>Metarhizium spp.</i>		
	<i>Beauveria bassiana</i>	Sequence of an entomopathogenic fungus	[25]
	<i>Herpomyces periplanetae</i>	Sequence of a cockroach-infecting fungus	[26]
	<i>Sarocladium terricola</i>	Sequence of an endophytic fungus with potential biocontrol activity against <i>Meloidogyne incognita</i>	[27]
Human and animal health	<i>Geomyces pannorum sensu lato</i>	Sequences of human pathogenic fungus and bat white nose syndrome pathogen	[28]
	<i>Geomyces destructans</i>		
	<i>Aspergillus udagawae</i>	Genome sequence of the pathogenic filamentous fungus	[29]
	<i>Malassezia pachydermatis</i>	Sequence of the animal and human pathogen strain	[30]
	<i>Lomentospora prolificans</i>	Sequence of an opportunistic fungal pathogen causing infections in immunocompromised and immunocompetent people and animals	[31]
Plant health	<i>Eutypa lata</i>	Sequence of the etiological agent of grapevine dieback	[32]

<i>Neofusicoccum parvum</i>	Sequence of the etiological agent of grapevine cankers	[33]
<i>Rhizoctonia solani</i>	Sequence of the phytopathogenic fungus	[34,35]
<i>Sporisorium scitamineum</i>	Sequence of the etiological agent of smut from sugarcane	[36]
<i>Fusarium virguliforme</i>	Sequence of the etiological agent of sudden death syndrome in soybean	[37]
<i>Diplodia sapinea</i> <i>Ceratocystis manginecans</i> <i>Ceratocystis moniliformis</i>	Sequences of phytopathogenic fungal species	[38]
<i>Trichoderma harzianum</i>	Sequence of the fungus used as biostimulants and biopesticides agent	[39]
<i>Neonectria ditissima</i>	Comparison of two isolates of the plant-pathogenic fungus that differ in virulence	[40]
<i>Phytophthora fragariae</i> var. <i>fragariae</i>	Sequence of a quarantine plant-pathogenic fungus	[41]
<i>Fusarium graminearum</i>	Sequence of the pathogenic ascomycete fungus	[42]
<i>Dactylonectria macrodidyma</i>	Sequence of a plant-pathogenic fungus	[43]
<i>Ceratocystis eucalypticola</i> <i>Chrysosporthe cubensis</i> <i>Chrysosporthe deuterocubensis</i> <i>Davidsoniella virescens</i> <i>Fusarium temperatum</i> <i>Graphilbum fragrans</i> <i>Penicillium nordicum</i> <i>Thielaviopsis musarum</i>	Sequences of phytopathogenic fungal species	[44]
<i>Trametes hirsuta</i>	Sequence of the etiological agent of white-rot	[45]
<i>Sporisorium scitamineum</i>	Sequence of and biotrophic interaction transcriptome with sugarcane	[46]
<i>Ceratocystis fagacearum</i> <i>Ceratocystis harringtonii</i> <i>Grosmannia penicillate</i> <i>Huntia bhutanensis</i>	Sequences of important phytopathogenic fungi	[47]
<i>Diaporthe aspalathi</i>	Sequence of the etiological agent of stem canker in soybean	[48]
<i>Calonectria pseudonaviculata</i>	Diagnosis of Sarcococca blight	[49]
<i>Fusarium graminearum</i> <i>Fusarium meridionale</i> <i>Fusarium asiaticum</i>	Comparative genomics of closely related Fusarium head blight fungus	[50]
<i>Postia placenta</i>	Sequence of the etiological agent of brown-rot	[51]
<i>Fomitopsis palustris</i>	Sequence of wood rot fungus with cellulolytic and ligninolytic enzyme system	[52]

	<i>Athelia rolfsii</i>	Whole genome sequence of groundnut stem rot fungus	[53]
	<i>Sclerotinia sclerotiorum</i>	Sequence of the phytopathogenic fungus	[54]
	<i>Tilletia indica</i>	Sequence of Karnal bunt pathogen of wheat	[55]
	<i>Polyporus brumalis</i>	Sequence of the wood rot fungus	[56]
	<i>Diplocarpon rosae</i>	Sequence of the etiological agent of rose black spot	[57]
	<i>Colletotrichum truncatum</i>	Sequence of the etiological agent of anthracnose in chilli	[58]
	<i>Monilinia spp.</i>	Sequence of the etiological agent of brown rot	[59]
	<i>Ganoderma boninense</i>	Sequence of the etiological agent of basal stem rot on oil palm	[60]
	<i>Alternaria solani</i>	Sequence of the etiological agent of early blight from potato and tomato	[61]
	<i>Venturia inaequalis</i> <i>Venturia pirina</i> <i>Venturia aucupariae</i> <i>Venturia asperata</i>	Sequence of the scab fungal species	[62]
	<i>Didymella segeticola</i>	Sequences of the etiological of leaf spot from tea	[63]
	<i>Paraphaeosphaeria sporulosa</i>	Sequence of a plant pathogen, biocontrol, bioremediator, and endophytic fungus	[64]
	<i>Cryphonectria parasitica</i>	Sequence of the etiological agent of blight on chestnut	[65]
	<i>Diaporthe capsici</i>	Sequence of the etiological agent of blight from walnut	[66]
	<i>Puccinia striiformis f. sp. tritici</i>	Sequence of the etiological agent of stripe rust from wheat	[67]
	<i>Stagonosporopsis cucurbitacearum</i>	Analyses of putative pathogenicity genes of the etiological agent of pumpkin gummy stem blight fungus	[68]
	<i>Colletotrichum lupini</i>	Sequence of a plant-pathogenic fungus	[69]
	<i>Schizophyllum commune</i>	Sequence of the etiological agent of white-rot	[70]
	<i>Trichoderma virens</i> <i>Trichoderma asperellum</i> <i>Trichoderma atroviride</i>	Sequences of fungal species used as biocontrol agents or biofertilizers	[71]
	<i>Calonectria ilicicola</i>	Sequence of the etiological agent of red crown rot from soybean	[72]
	<i>Botryosphaeria dothidea</i>	Sequence of the etiological agent of trunk canker from Chinese hickory	[73]
	<i>Ganoderma lucidum</i>	Sequence of the etiological agent of white	[74]
	<i>Nigrospora oryzae</i>	Sequence of an pathogenic fungus	[75]
	<i>Claviceps spp.</i>	Comparisons of ergot fungi	[76]
	<i>Fusarium meridionale</i>	Sequence of the etiological agent of Fusarium head blight in rice	[77]
	<i>Fusarium oxysporum</i>	Sequence Resource of a plant growth promoting endophytic fungus from <i>Tetrastigma hemsleyanum</i>	[78]

	<i>Arthrinium rasikravindrae</i>	Sequence of a phytopathogen	[79]
	<i>Albifimbria verrucaria</i>	Sequence of a biocontrol fungal pathogen	[80]
Food and beverage	<i>Penicillium digitatum</i>	Sequence of the necrotrophic fungus considered as the main postharvest pathogen of citrus	[81]
	<i>Agaricus bisporus</i>	Sequence of the button mushroom reveals mechanisms governing adaptation to a humic-rich ecological niche	[82]
	<i>Volvariella volvacea</i>	Sequence and comparative genome analysis of the straw mushroom	[82]
	<i>Brettanomyces</i> spp.	Sequence of yeasts associated with spoilage from beer and wine	[83]
	<i>Aspergillus nomius</i>	Sequence of the aflatoxigenic filamentous fungus	[84]
	<i>Aspergillus flavus</i>	Sequence of a strain that causes aflatoxin contamination of food and feed	[85]
	<i>Lentinula edodes</i>	Sequence of the edible cultivated mushroom	[86]
	<i>Aspergillus flavus</i>	Sequences of strains isolated from peanut seeds	[87]
	<i>Aspergillus parasiticus</i>		
	<i>Aspergillus westerdijkiae</i>	Sequence of a fungus contaminating several food products	[88]
	<i>Flammulina velutipes</i>	Sequence of the edible mushroom	[89]
	<i>Listeria monocytogenes</i>	Detection of a listeriosis outbreak of caused by cold-smoked salmon	[90]
	<i>Cordyceps guangdongensis</i>	Sequence of an edible and potential medicinal fungus	[91]
	<i>Penicillium citrinum</i>	Sequence of the fungus responsible for citrinin production	[92]
	<i>Penicillium expansum</i>	Comparisons of species with different secondary metabolic gene clusters and candidate genes	[93]
	<i>Penicillium solitum</i>	associated with fungal aggressiveness during apple fruit decay	
	<i>Auricularia heimuer</i>	Sequence of the third most important cultivated mushroom	[94]
	<i>Hericium erinaceus</i>	Sequence of an edible-medicinal mushroom	[95]
	<i>Russula griseocarnosa</i>	Sequence of a wild edible mushroom	[96]
Genomic diversity	<i>Naematelia aurantialba</i>	Sequence of an edible-medicinal fungi	[97]
	<i>Stropharia rugosoannulata</i>	Sequence of the edible mushroom Daqiugaigu	[98]
	<i>Stachybotrys</i> spp.	Identification of chemotype-specific gene clusters	[99]
	<i>Aspergillus fumigatus</i>	Sequence data uncover azole resistance mutations	[100]
	<i>Helicobacter pylori</i>	Study of sequence diversity within single strains	[101]
	<i>Aspergillus flavus</i>	Comparison of L-morphotype strain NRRL 3357 (type) and S-morphotype strain AF70	[102]
	<i>Aspergillus ochraceus</i>	Comparative genomic analysis of ochratoxin A biosynthetic pathway	[103]
	<i>Lecanoromycetes</i>	Sequence data uncover heterothallism in lichen-forming fungi	[104]
Lichens	<i>Aspergillus fumigatus</i>	Study of the virulence potential of clinical and environmental isolates	[105]
	<i>Caloplaca flavorubescens</i>	Sequence of the lichen-forming fungus	[106]

	<i>Cladonia macilenta</i>	Sequence of the lichen-forming fungus producing biruloquinone	[107]
	<i>Umbilicaria muehlenbergii</i>	Sequence of the lichen-forming fungus	[108]
	<i>Cladonia metacorallifera</i>	Sequence of the lichen-forming fungus	[109]
	<i>Endocarpon pusillum</i>	Sequence of the lichen-forming fungus	[110]
	<i>Arthonia radiata</i>	Sequence of the lichen-forming fungus	[111]
	<i>Lasallia hispanica</i>	Sequence of the lichen-forming fungus	[112]
	<i>Ramalina intermedia</i>	Sequence of the lichen-forming fungus	[113]
	<i>Bacidia gigantensis</i>	Sequence of the lichen-forming fungus	[114]
Medicinal products	<i>Ganoderma lucidum</i>	Sequence of the model medicinal mushroom	[115]
	<i>Cordyceps militaris</i>	Sequence of the insect pathogenic fungus valued in traditional Chinese medicine	[116]
	<i>Phellinus gilvus</i>	Sequence of a medicinal fungus	[117]
	<i>Sanghuangporus sanghuang</i>	Sequence of a medicinal fungus	[118]
	<i>Amauroderma rugosum</i>	Sequence of a traditional medicinal mushroom	[119]
	<i>Ganoderma leucocontextum</i>	Sequence of a fungus with potential pharmacological activities	[120]
	<i>Keithomyces neogunnii</i>	Sequence of a medicinal fungus	[121]
Extreme environments	<i>Hortaea werneckii</i>	Genome of the extremely halotolerant black yeast	[122]
	<i>Wallemia ichthyophaga</i>	Sequence of the halophilic fungus	[123]
	<i>Rhizomucor miehei</i>	Sequence of the thermophilic zygomycete fungus	[124]
	<i>Cryomyces antarcticus</i>	Sequence of the most extremophilic fungus from Antarctica	[125]
	<i>Rachicladosporium antarcticum</i>	Sequences of the Antarctic endolithic fungi	[126]
	<i>Rachicladosporium sp.</i>		
	<i>Aspergillus niger</i> <i>Aspergillus terreus</i> <i>Aureobasidium pullulans</i> <i>Beauveria bassiana</i> <i>Cladosporium cladosporioides</i> <i>Cladosporium sphaerospermum</i> <i>Fusarium solani</i> <i>Trichoderma virens</i>	Effects of exposure to microgravity at the International Space Station in radiation-tolerant microorganisms	[127]
Marine ecosystems	<i>Candida auris</i>	Sequence from isolates from the coastal wetlands of Andaman Islands	[128]
Built environment	<i>Trichoderma atroviride</i>	Sequence of a cosmopolitan fungus	[129]

Soil	<i>Rhizophagus irregularis</i>	Sequence of the arbuscular mycorrhizal fungus	[130]
	<i>Russula griseocarnosa</i>	Sequence of an edible and medicinal mushroom and its association with mycorrhizal characteristics	[131]
Bioremediation	<i>Scopulariopsis brevicaulis</i>	Fungal degradation of polycyclic aromatic hydrocarbons (PAHs) by and its application in bioremediation of PAH-contaminated soil	[132]
	<i>Arthrobacter alpinus</i>	Sequence of a fungus potentially used for bioremediation	[133]
	<i>Lenzites elegans</i>	Sequence of a Lignolytic mushroom used for the bioremediation of synthetic dyes	[134]
	<i>Rhodotorula taiwanensis</i>	Sequence of a potential fungal species used for the bioremediation of acidic radioactive waste sites	[135]
	<i>Rhodotorula sp.</i>	Sequence of an acidophilic strain and its phenol-degrading capability under acidic conditions	[136]
Monument degradation	<i>Knufia petricola</i>	Sequence of the black rock fungus isolated from marble	[137]
Enzyme production	<i>Thermomyces lanuginosus</i>	Sequence of a compost-loving thermophilic fungus considered as a xylanase super-producer:	[138]
	<i>Flammulina velutipes</i>	Sequence of a mushroom with high capacity for lignocellulose degradation	[139]
	<i>Chaetomium globosum</i>	Sequence of the cellulolytic fungus	[140]
Industrial production	<i>Glarea lozoyensis</i>	Sequence of the pneumocandin producing fungus	[141,142]
	<i>Pseudozyma aphidis</i>	Genome sequence of an efficient producer of biosurfactant mannosylerythritol lipids	[143]
	<i>Umbelopsis isabellina,</i>	Genome sequence of an effective producer of lipids	[144]
	<i>Shiraia sp.</i>	Analysis of the huperzine A and hypocrellin A producing fungus	[145]
	<i>Monascus purpureus</i>	Pigment biosynthesis and regulatory mechanisms in an industrial strain	[146]
	<i>Aspergillus terreus</i>	Sequence of a producing lovastatin fungus	[147]
	<i>Aspergillus terreus</i> <i>Diaporthe ampelina</i>	Comparative study of the two lovastatin producing fungus	[148]