

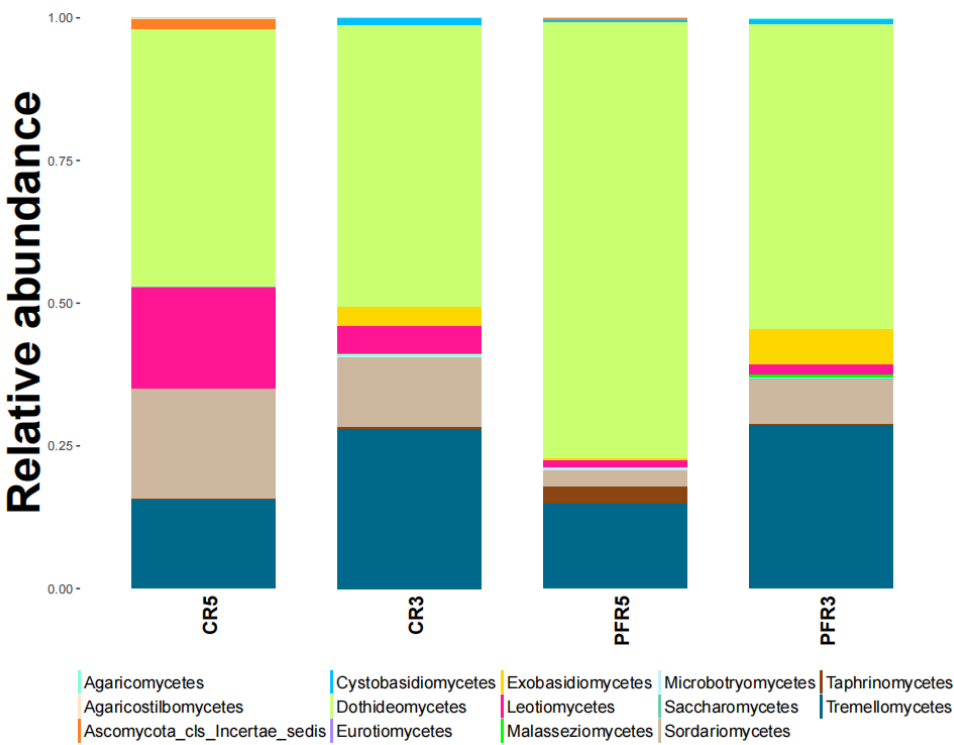
Variations in Community Structure of Fungal Microbiota Associated with Apple Fruit Shaped by Fruit Bagging-based practice

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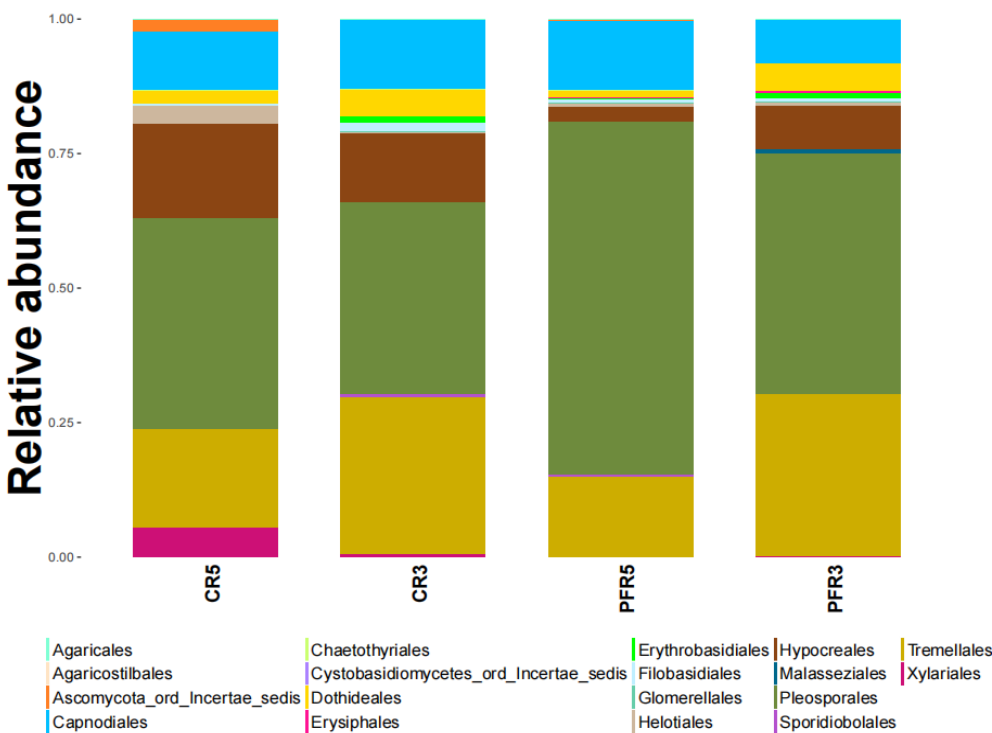
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a)



b)



c)

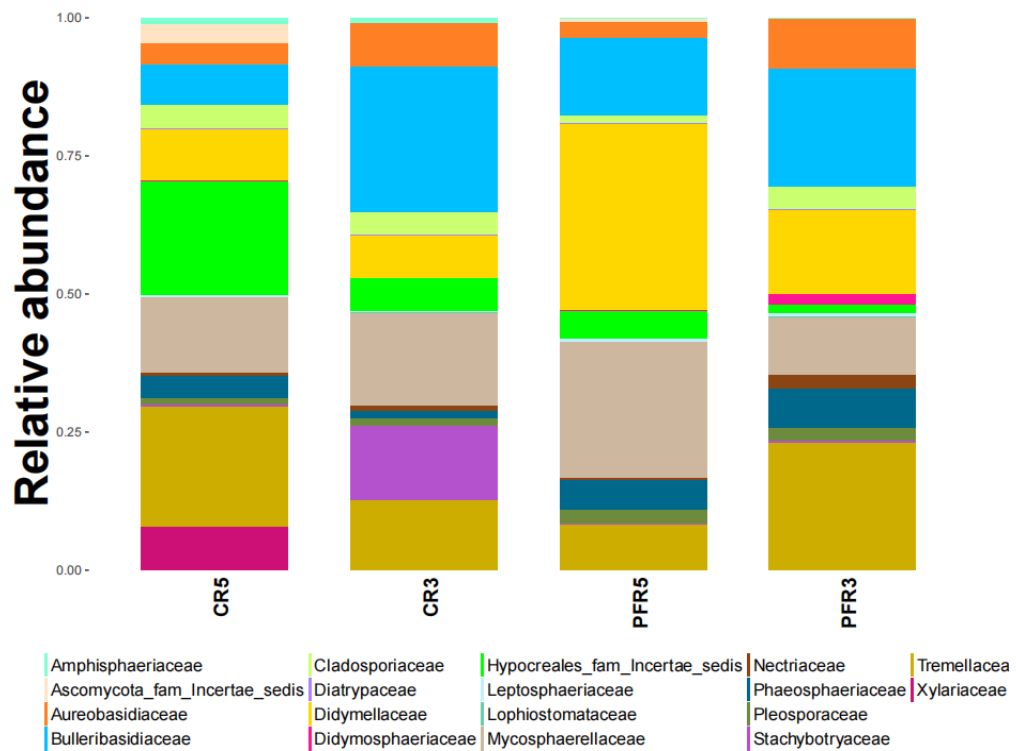


Figure S1: Bar charts showing the relative abundance of fungi distributed in class (a), order (b), and family (c) across all samples of the calyx-end and peel tissues derived from bagged (i.e., CR5, PFR5) and unbagged (i.e., CR3 and PFR3) fruit.

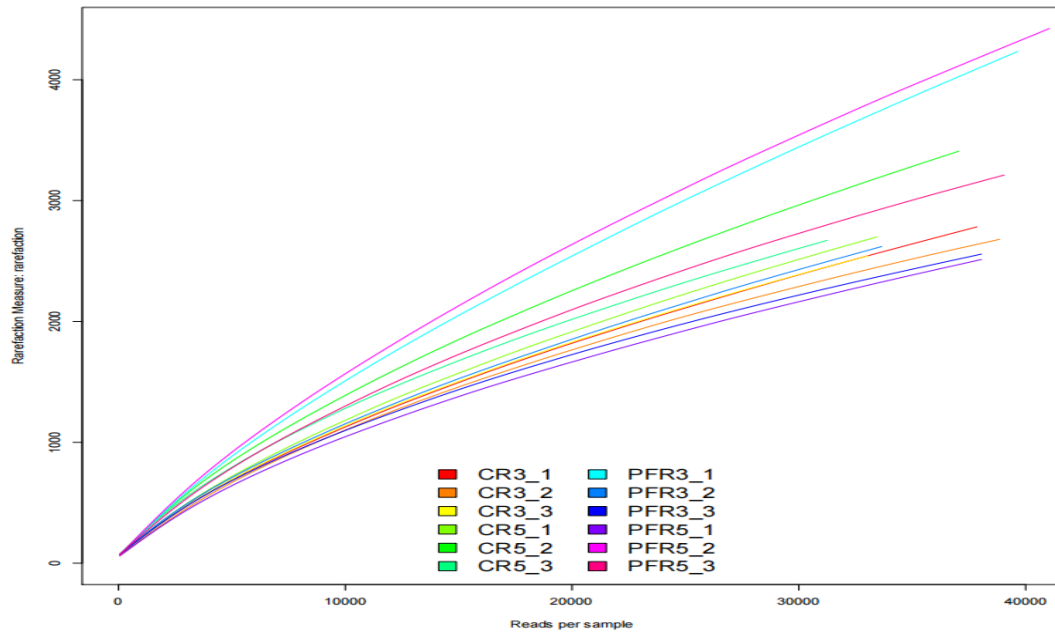


Figure S2: Rarefaction curves of fungi derived from different samples of apple fruit (calyx-end and peel tissues from bagged (i.e., CR5, PFR5) and unbagged (i.e., CR3 and PFR3) fruit). The x-axis shows the number of valid sequences per sample, and the y-axis shows the observed OTUs.

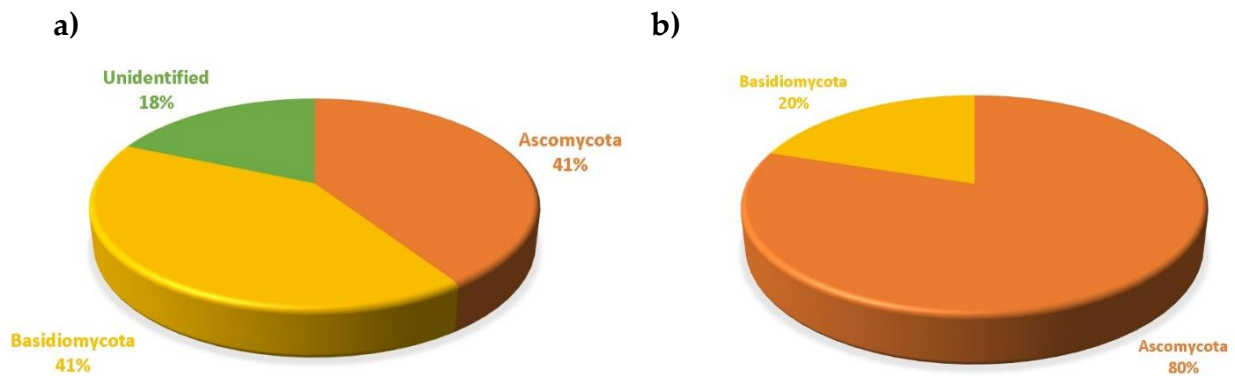


Figure S3: Pie charts showing the percentage of significant members (number of fungal taxa) of Ascomycota, Basidiomycota, and an unidentified phylum represented in the linear discriminant analysis (LDA) histogram of bagged (a) and unbagged (b) samples.

Table S1: Analysis data of apple fruit microbiome showing forty-seven genera and forty species with their most abundant OTUs, trophic modes, growth morphology, and the percentage of relative abundances of fungal genera in the CR5, CR3, PFR5, and PFR3 samples, as well as putative genus functions detected from barcode-type next-generation sequencing.

Genera/ most abundant OTUs	Identified species/ most abundant OTUs	Trophic modes	Growth morphology	Relative abundance (%)				Putative genus functions		References
				CR5	CR3	PFR5	PFR3	Biocontrol agent (BCA)	Pathogen	
<i>Acremonium</i> OTU_15289 (0.6639)	<i>Acremonium alternatum</i> OTU_91310 (0.0079), <i>Acremonium fusidioides</i> OTU_1203 (0.0031), <i>Acremonium hyalinulum</i> OTU_113180 (0.0033), <i>Acremonium rutilum</i> OTU_69035 (0.0021)	E, P, S	Filamentous fungi	1.1430	0.1256	1.8852	0.1125	√	√	[1–6]
<i>Alternaria</i> OTU_3861 (0.001578)		E, P, S	Filamentous fungi	0.0005	0.0003	0.0019	0.0019	√	√	[6–11]
<i>Articulospora</i> OTU_57849 (0.0558)	<i>Articulospora proliferata</i> OTU_57849 (0.0558)	E, S	Filamentous fungi	0.0005	0.0062	0.1785	0.0379	√		[12]
<i>Aureobasidium</i> OTU_45119 (0.0012)	<i>Aureobasidium pullulans</i> OTU_45119 (0.0012)	E, P, S	Yeast-like fungi	0.0012	0.0050	0.0000	0.0019	√	√	[13–15]
<i>Biappendiculispora</i> OTU_8962 (0.0066)	<i>Biappendiculispora japonica</i> OTU_8962 (0.0066)	S	Filamentous fungi	0.0000	0.0028	0.0000	0.0237			
<i>Blumeria</i> OTU_36017 (0.0057)	<i>Blumeria graminis</i> OTU_36017 (0.0057)	P	Filamentous fungi	0.0003	0.0001	0.0024	0.0199		√	[16,17]
<i>Buckleyzyma</i> OTU_4088 (0.0056)	<i>Buckleyzyma aurantiaca</i>	S	Yeast	0.0073	0.0053	0.0212	0.0106	√		[6]

OTU_4088 (0.0056)										
<i>Bullera</i> OTU_17277 (0.0455)		E, P, S	Yeast	0.0068	0.0180	0.1031	0.0648	√		[18,19]
<i>Candida</i> OTU_10908 (0.0073)	<i>Candida</i> <i>hyderabadensis</i> OTU_10908 (0.0073)	E, P, S	Yeast	0.0005	0.0087	0.0078	0.0122	√		[6,15,20]
<i>Cercospora</i> OTU_24918 (0.0053)		E, P, S	Filamentous fungi	0.0029	0.0002	0.0163	0.0019		√	[21,22]
<i>Coniothyrium</i> OTU_14646 (0.0410)	<i>Coniothyrium sidae</i> OTU_14646 (0.0410)	E, P, S	Filamentous fungi	0.0553	0.0149	0.0175	0.1140	√	√	[6,23–26]
<i>Cryptococcus</i> OTU_17375 (4.9685)	<i>Cryptococcus laurentii</i> OTU_17375 (4.9685), <i>Cryptococcus</i> <i>stutzelliae</i> OTU_20854 (0.0010), <i>Cryptococcus</i> <i>uniguttulatus</i> OTU_12263 (0.0064)	E, P, S	Yeast	7.6804	5.0146	3.2410	7.8437	√		[6,14,27]
<i>Cystobasidium</i> OTU_10867 (0.0034)		E, P	Yeast	0.0023	0.0003	0.0019	0.0091	√		[28]
<i>Didymella</i> OTU_18485 (0.0098)		E, P, S	Filamentous fungi	0.0432	0.0025	0.0129	0.0132	√	√	[6,29–33]
<i>Dinemasporium</i> OTU_7667 (0.0341)		E, P, S	Null	0.0004	0.0000	0.0000	0.1417			
<i>Dioszegia</i> OTU_4020 (0.0855)	<i>Dioszegia</i> <i>changbaiensis</i> OTU_3401 (0.0039), <i>Dioszegia hungarica</i> OTU_22919 (0.0121)	E, P, S	Yeast	0.0352	0.1204	0.3091	0.0470	√		[34]
<i>Epicoccum</i> OTU_14212 (0.8266)	<i>Epicoccum nigrum</i> OTU_14212 (0.8266)	E, P, S	Filamentous fungi	0.2622	1.6004	0.3745	1.4080	√	√	[6,26,35]
<i>Erythrobasidium</i> OTU_8827 (0.0361)	<i>Erythrobasidium</i> <i>hasegawianum</i> OTU_8827 (0.0361)	S	Yeast	0.0246	0.8484	0.2807	0.5126	√		[15]

<i>Filobasidium</i> OTU_103350 (0.1041)	<i>Filobasidium</i> <i>floriforme</i> OTU_103350 (0.1041), <i>Filobasidium</i> <i>wieringae</i> OTU_8749 (0.0018)	E, S	Yeast	0.0072	0.4244	0.0028	0.0124	√		[27]
<i>Fonsecazyma</i> OTU_31843 (0.0009)	<i>Fonsecazyma</i> <i>mujuensis</i> OTU_31843 (0.0009)	U	Yeast	0.0036	0.0000	0.0000	0.0000			
<i>Fusarium</i> OTU_19844 (0.0051)		E, P, S	Filamentous fungus	0.0064	0.0194	0.0037	0.0089	√	√	[6,26,36]
<i>Genolevuria</i> OTU_8344 (0.1461)	<i>Genolevuria</i> <i>amylolytica</i> OTU_8344 (0.1461), <i>Genolevuria</i> <i>armeniaca</i> OTU_5316 (0.0009)	U	Yeast	0.0218	0.3115	0.2406	0.0359			
<i>Knufia</i> OTU_55479 (0.0077)	<i>Knufia aspidiotus</i> OTU_55479 (0.0077)	E, P	Filamentous fungi	0.0446	0.0002	0.0017	0.0067	√	√	[28,37]
<i>Lachnum</i> OTU_129208 (0.0048)	<i>Lachnum fuscescens</i> OTU_129208 (0.0048)	E, S	Filamentous fungi	0.0005	0.0001	0.0000	0.0184	√		[38]
<i>Latorua</i> OTU_81530 (0.0064)	<i>Latorua caligans</i> OTU_81530 (0.0064)	S	Yeast	0.0000	0.0011	0.0000	0.0244			
<i>Lecanicillium</i> OTU_94854 (0.0050)	<i>Lecanicillium</i> <i>primulinum</i> OTU_94854 (0.0050)	E, P	Filamentous fungi	0.0001	0.0000	0.0000	0.0201	√		[6,39]
<i>Monocillium</i> OTU_134549 (0.0058)	<i>Monocillium indicum</i> OTU_134549 (0.0058)	E, P, S	Null	0.0000	0.0000	0.0000	0.0023	√		[40]
<i>Murilentithecium</i> OTU_88928 (0.0139)	<i>Murilentithecium</i> <i>clematidis</i> OTU_88928 (0.0139)	S	Null	0.0003	0.0005	0.0000	0.0588			

<i>Mycosphaerella</i> OTU_26248 (0.0599)	<i>Mycosphaerella</i> <i>ellipsoidea</i> OTU_26248 (0.0599)	E, P, S	Filamentous fungi	0.0241	0.0055	0.0475	0.1656	√	[41–43]
<i>Occultifur</i> OTU_24507 (0.0016)		P, S	Yeast	0.0000	0.0063	0.0000	0.0001		
<i>Paraconiothyrium</i> OTU_62952 (0.0025)		E, P, S	Filamentous fungi	0.0098	0.0000	0.0000	0.0000	√	√ [44–47]
<i>Paraphaeosphaeria</i> OTU_94126 (0.0192)	<i>Paraphaeosphaeria</i> <i>verruculosa</i> OTU_94126 (0.0192)	E, P, S	Null	0.0768	0.0000	0.0000	0.0000	√	[48]
<i>Phacidiella</i> OTU_90178 (0.0135)	<i>Phacidiella eucalypti</i> OTU_90178 (0.0135)	P, S	Null	0.0699	0.0046	0.0000	0.0003	√	[49]
<i>Rachicladosporium</i> OTU_91428 (0.0015)	<i>Rachicladosporium</i> <i>inconspicuum</i> OTU_91428 (0.0015)	E, P, S	Filamentous fungi	0.0057	0.0001	0.0000	0.0000	√	[50]
<i>Radulidium</i> OTU_5956 (0.3486)	<i>Radulidium</i> <i>subulatum</i> OTU_5956 (0.3486)	E, S	Null	1.2310	0.0052	0.2925	0.0379		
<i>Rhodosporidiobolus</i> OTU_24032 (0.0167)		P, S	Filamentous fungi	0.0000	0.0630	0.0038	0.0001		
<i>Rhodotorula</i> OOTU_125338 (0.0050)		E, P, S	Yeast	0.0005	0.0161	0.0000	0.0034	√	√ [13,51]
<i>Sarocladium</i> OTU_17877 (0.0207)	<i>Sarocladium</i> <i>bactrocephalum</i> OTU_17877 (0.0207)	E, P, S	Filamentous fungi	0.0007	0.0111	0.0000	0.0994	√	√ [5,6,52]
<i>Setomelanomma</i> OTU_83222 (0.0106)		P, S	Filamentous fungi	0.0000	0.0423	0.0000	0.0000	√	[53]
<i>Spegazzinia</i> OTU_68436 (0.0005)		E, S	Null	0.0020	0.0000	0.0000	0.0000		
<i>Sporobolomyces</i> OTU_11547 (0.0408)	<i>Sporobolomyces</i> <i>bannaensis</i> OTU_7177 (0.0030), <i>Sporobolomyces phaffii</i> OTU_11547 (0.0408),	E, P, S	yeast	0.0024	0.0401	0.1856	0.0118	√	[15,27]

<i>Sporobolomyces symmetricus</i> OTU_7042 (0.0032)									
<i>Stagonospora</i> OTU_93157 (0.0034)		E, P, S	Filamentous fungi	0.0137	0.0000	0.0000	0.0000	√	[54]
<i>Stagonosporopsis</i> OTU_32562 (0.0069)		E, P, S	Null	0.0031	0.0131	0.0000	0.0115	√	[54]
<i>Strobilurus</i> OTU_122869 (0.0011)		S	Filamentous fungi	0.0043	0.0002	0.0000	0.0000		
<i>Taphrina</i> OTU_125697 (0.0311)		E, P	Filamentous fungi	0.0017	0.2385	2.3320	0.0147	√	√ [15,55]
<i>Trichometasphaeria</i> OTU_109962 (0.0013)		S	Null	0.0049	0.0002	0.0000	0.0000	√	[56]
<i>Vishniacozyma</i> OTU_30022 (3.1662)	<i>Vishniacozyma carnescens</i> OTU_29813 (1.1911), <i>Vishniacozyma victoriae</i> OTU_30022 (3.1662)	E, P, S	Yeast	2.6284	10.3875	5.1955	7.1629	√	[57]

Note: life mode —P (Pathogen), E (Endophyte), S (saprotroph), and U (Unknown)

Table S2: Functions/activities of fungal genera detected in apple fruit determined by next-generation sequencing. Information is presented based on the functions of putative biological control agent (BCA) and pathogenic agent associated with apples.

Genus	Functions/Activities		References
	Categories of function	Description	
<i>Acremonium</i>	Putative BCA	<ul style="list-style-type: none"> <i>Acremonium strictum</i> has been proposed to serve as biocontrol agents against <i>Venturia inaequalis</i>, the causal agent of apple scab. <i>Acremonium alternatum</i> can inhibit powdery mildew of cucumber caused by <i>Sphaerotheca fuliginea</i>. <i>Acremonium</i> sp. exhibit a potential biological control of brown rot of <i>Nectarine Janisiewicz</i>. 	[1–3]
	Apple pathogen	<ul style="list-style-type: none"> <i>Acremonium</i> spp. causes brown and black spot disease in apple fruit. 	[3,5,52]
<i>Alternaria</i>	Putative BCA	<ul style="list-style-type: none"> <i>Alternaria alternata</i> inhibits sporulation of <i>Plasmopara viticola</i>, the causal agent of grapevine downy mildew disease. 	[9]
	Apple pathogen	<ul style="list-style-type: none"> <i>Alternari</i> spp. causal agent of moldy core of apple. <i>Alternaria alternata</i> f. sp. <i>mali</i> the causal agent Alternaria leaf blotch and fruit spot of apple. 	[7,26,58]
<i>Articulospora</i>	Putative BCA	<ul style="list-style-type: none"> <i>Articulospora</i> can produce antibiotic compound which can inhibit bacterial growth 	[12]
	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
<i>Aureobasidium</i>	Putative BCA	<ul style="list-style-type: none"> <i>Aureobasidium pullulans</i> can be used as potential biocontrol agents in controlling the post-harvest decay of apples caused by <i>Botrytis cinerea</i>. <i>Aureobasidium pullulans</i> can control brown rot of nectarine fruit caused by <i>Monilinia fructicola</i>. 	[3,12]
	Apple pathogen	<ul style="list-style-type: none"> <i>Aureobasidium pullulan</i> is the causal agent of russet of apple fruit. 	[13]
<i>Biappendiculispora</i>	Putative BCA	<ul style="list-style-type: none"> Neutral 	-
	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
<i>Blumeria</i>	Putative BCA	<ul style="list-style-type: none"> Neutral 	-
	Apple pathogen	<ul style="list-style-type: none"> Neutral 	-
<i>Buckleyzyma</i>	Putative BCA	<ul style="list-style-type: none"> <i>Buckleyzyma aurantiaca</i> impeded pathogen growth and reproduction. 	[59]
	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
<i>Bullera</i>	Putative BCA	<ul style="list-style-type: none"> <i>Bullera elba</i> can secrete a killer toxin that inhibits the growth of some pathogenic yeasts and is most active against <i>Cryptococcus neoformans</i>. 	[18]
	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
<i>Candida</i>	Putative BCA	<ul style="list-style-type: none"> <i>Candida</i> is found to have potential for biocontrol of brown rot of nectarines <i>Candida</i> is applied as a biocontrol of gray mold on grapes caused by <i>Botrytis cinerea</i> <i>Candida sake</i> against <i>Penicillium expansum</i> is significantly enhanced L-Serine and L-Aspartic on apples. 	[15,20,60]

	Apple pathogen	• Neutral	
<i>Cercospora</i>	Putative BCA	• Neutral	
	Apple pathogen	• <i>Cercospora</i> , the causal agent of leaf spot disease on apple.	[61]
<i>Coniothyrium</i>	Putative BCA	• <i>Coniothyrium minitans</i> can control <i>Sclerotinia sclerotiorum</i> , the causal agent of the disease of lettuce and other plants.	[23,62,63]
	Apple pathogen	• <i>Coniothyrium</i> spp. the causal agent of moldy core and core rot of apple.	[64]
<i>Cryptococcus</i>	Putative BCA	• <i>Cryptococcus flavescentis</i> can be used as potential biocontrol agents in controlling the post-harvest decay of apples caused by <i>Botrytis cinerea</i> . • <i>Cryptococcus humicola</i> can control gray mold caused by <i>Botrytis cinerea</i> in apple.	[27,65,66]
	Apple pathogen	• Neutral	
<i>Cystobasidium</i>	Putative BCA	• <i>Cystobasidium</i> spp. increases the resistance of <i>Ulmus minor</i> to Dutch elm disease by increasing the concentration of flavonoids and phenolic compounds in xylem tissue.	[28]
	Apple pathogen	• Neutral	
<i>Didymella</i>	Putative BCA	• <i>Didymella pomorum</i> (<i>Phoma pomorum</i>) have been reported as biological control of damping-off disease of <i>Trifolium alexandrinum</i> L. caused by <i>Pythium</i> .	[33]
	Apple pathogen	• <i>Didymella pomorum</i> , the canker and wood rot pathogen of young apple tree.	[67]
<i>Denemasporium</i>	Putative BCA	• Neutral	
	Apple pathogen	• Neutral	
<i>Dioszegia</i>	Putative BCA	• <i>Dioszegia</i> plays an important role as biocontrol agent by supporting plant growth.	[34]
	Apple pathogen	• Neutral	
<i>Epicoccum</i>	Putative BCA	• <i>Epicoccum nigrum</i> , biological control agent of peach twig blight caused by <i>Monilinia laxa</i> . • <i>Epicoccum layuense</i> , a potential biological control agent of esca-associated fungi in grapevine.	[68,69]
	Apple pathogen	• <i>Epicoccum</i> spp. the causal agent of moldy and core rot of apple.	[26,64]
<i>Erythrobasidium</i>	Putative BCA	• <i>Erythrobasidium</i> exhibits the potential as biological control agent of brown rot of nectarine.	[15]
	Apple pathogen	• Neutral	
<i>Filobasidium</i>	Putative BCA	• <i>Filobasidium</i> spp. have been reported their function as biological control of <i>Botrytis cinerea</i> in apple.	[27]
	Apple pathogen	• Neutral	
<i>Fonsecazyma</i>	Putative BCA	• Neutral	
	Apple pathogen	• Neutral	
<i>Fusarium</i>	Putative BCA	• <i>Fusarium equiseti</i> enhances plant growth and reduces severity of anthracnose and damping-off diseases in cucumber (<i>Cucumis sativus</i>).	[36]

Genolevularia	Apple pathogen	<ul style="list-style-type: none"> <i>Fusarium</i> spp. have been reported as the causal agent of apple core rot. 	[26]
	Putative BCA	<ul style="list-style-type: none"> Neutral 	
Knufia	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> <i>Knufia</i> spp. enhance <i>Ulmus minor</i> resistance to Dutch elm disease by increasing concentration of flavonoids and phenolic compounds in xylem tissues. 	[28]
Lachnum	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> <i>Lachnum</i> isolates have the potential to enhance the growth of selected blueberry. 	[38]
Latorua	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> Neutral 	
Lecanicillium	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> There has been reported potential of <i>Lecanicillium</i> spp. in controlling of insects, nematodes and plant diseases. 	[39]
Monocillium	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> <i>Monocillium gamsii</i> and <i>M. bulbillosum</i> are parasites of nematode eggs. This genus has been reported as candidates for nematode biocontrol. 	[70]
Murilentithecium	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> Neutral 	
Mycosphaerella	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> Neutral 	
Occultifur	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> Neutral 	
Paraconiothyrium	Apple pathogen	<ul style="list-style-type: none"> There have been reported ability of <i>Paraconiothyrium</i> as the antagonistic fungi against <i>Sclerotinia sclerotiorum</i> associated with <i>Brachiaria</i> grasses. 	[47]
	Putative BCA	<ul style="list-style-type: none"> <i>Paraconiothyrium</i> is the causal agent of moldy core and core rot of apple. 	[44]
Paraphaeosphaeria	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> <i>Paraphaeosphaeria minitans</i> (<i>Coniothyrium minitans</i>) control <i>Verticillium dahliae</i> the causal agent of Verticillium wilt of olive. 	[48]
Phacidiella	Apple pathogen	<ul style="list-style-type: none"> <i>Phacidiella discolor</i> was reported as pathogenic strain associated with a dieback and canker disease of apple trees in England. 	[49]
	Putative BCA	<ul style="list-style-type: none"> Neutral 	
Rachicladosporium	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
Radulidium	Putative BCA	<ul style="list-style-type: none"> Neutral 	
Rhodosporidiobolus	Apple pathogen	<ul style="list-style-type: none"> Neutral 	
	Putative BCA	<ul style="list-style-type: none"> Neutral 	

<i>Rhodotorula</i>	Putative BCA	<ul style="list-style-type: none"> • <i>Rhodotorula</i> shows its putative mechanisms of antagonism against <i>Botrytis cinerea</i>, the causative agent of apple disease. • <i>Rhodotorula glutinis</i> can control postharvest pathogens on apple. • <i>Rhodotorula</i> can control brown rot of nectarine fruit caused by <i>Monilinia fructicola</i>. • <i>Rhodotorula rubra</i> presented antimicrobial activity and increase the growth stimulating property on the cotton seed, and protect the plant from diseases. 	[15,27,71,72]
	Apple pathogen	<ul style="list-style-type: none"> • <i>Rhodotorula glutinis</i> the causal agent of russet on apple 	[13]
<i>Sarocladium</i>	Putative BCA	<ul style="list-style-type: none"> • <i>Sarocladium implicatum</i> potential biocontrol agent of Ascochyta blight of chickpea disease caused by <i>Ascochyta rabiei</i>. 	[73]
	Apple pathogen	<ul style="list-style-type: none"> • <i>Sarocladium</i> causes brown spot associated with bagged apple. 	[5]
<i>Setomelanomma</i>	Putative BCA	<ul style="list-style-type: none"> • Neutral 	
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Spegazzinia</i>	Putative BCA	<ul style="list-style-type: none"> • Neutral 	
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Sporobolomyces</i>	Putative BCA	<ul style="list-style-type: none"> • <i>Sporobolomyces</i> has ability of biological control agent against brown rot of nectarine. 	[15]
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Stagonospora</i>	Putative BCA	<ul style="list-style-type: none"> • Neutral 	
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Stagonosporopsis</i>	Putative BCA	<ul style="list-style-type: none"> • Neutral 	
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Strobilurus</i>	Putative BCA	<ul style="list-style-type: none"> • Neutral 	
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Taphrina</i>	Putative BCA	<ul style="list-style-type: none"> • <i>Taphrina</i> can control brown rot of nectarine fruit caused by <i>Monilinia fructicola</i>. 	[15]
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Trichometasphaeria</i>	Putative BCA	<ul style="list-style-type: none"> • Neutral 	
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	
<i>Vishniacozyma</i>	Putative BCA	<ul style="list-style-type: none"> • <i>Vishniacozyma victoriae</i> shows biocontrol activity against <i>Penicillium expansum</i> and <i>Botrytis cinerea</i>, the causal agents of postharvest diseases such as blue and grey mold on pear fruit. 	[74]
	Apple pathogen	<ul style="list-style-type: none"> • Neutral 	

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