

Supplementary Materials

Table S1. % GTDs (per OTUs) in graft unions as influenced by variety under nursery conditions in Catalonia, NE Spain. Results are grouped by homogenous group (determined from LS Means) and compared with previous groupings based on severity of grapevine trunk disease (GTD) symptoms related to actual disease presence in varieties under field conditions in La Mancha Designation of Origin (DO), Central Spain.

Group	Variety	LS Means	Homogenous group	Field Conditions*	Susceptibility
1	Carignan (tinta)	0.894	A		High 
2	Malvasia	0.672	AB	CD	
3	Sumoll	0.601	B		
4	Autumn Royal	0.509	BC		
5	Xarel.lo vermell	0.418	BCD		
6	Tempranillo	0.356	BCDE	CD	
7	Chardonnay	0.356	CD	D	
	Macabeu	0.351	CD	CD	
	Garnacha tinta	0.343	CD	D	
	Xarel.lo	0.318	CD		
8	Merlot	0.323	CDE	D	
9	Parellada	0.283	DE	D	
	Syrah	0.265	DE	BCD	
	Pinot Noir	0.233	DE	D	
	Caladoc	0.202	DE		
10	Cabernet Sauvignon	0.209	E	BCD	Low

* Reference Field Conditions data from Chacón-Vozmediano et al., 2021 [47].

Table S2. List of GTD-related fungi. All species that appeared in this study and that have been considered as GTD-related fungus, or that are of the same genus. Method of identification was either via isolation and sequencing the amplified region ITS 1-4 (Iso), or by metabarcoding and sequencing (MBC). All fungi belong to the Phylum *Ascomycota*.

GTD Species	Method	Family	# OTUs	Tissue	Life mode	Disease caused	References
<i>Acremonium alternatum</i>	MBC	<i>Bionectriaceae</i>	5	Both	E		47, 48
<i>Acremonium hansfordii</i>	MBC	<i>Bionectriaceae</i>	1	Root			49
<i>Acremonium sp.</i>	MBC	<i>Bionectriaceae</i>	12	Both	P,E	'Hoja de malvon' Botryosphaeria	33, 50-55, 147
<i>Botryosphaeria dothidea</i>	MBC	<i>Botryosphaeriaceae</i>	2	Both	P,E,S	dieback, Macrophoma rot	17,18, 33, 51, 52, 56-72
<i>Botryosphaeria sp.</i>	MBC/Iso	<i>Botryosphaeriaceae</i>	2	Both/Graft	P,E	dieback, Macrophoma rot	51, 61, 73-76
<i>Cadophora luteo-olivacea</i>	MBC	<i>Ploettnerulaceae</i>	7	Both	P	Petri disease	2, 65, 72, 77, 78
<i>Cadophora malorum</i>	MBC	<i>Ploettnerulaceae</i>	1	Both		Soft rot	79, 80
<i>Campylocarpon fasciculare</i>	MBC	<i>Nectriaceae</i>	2	Both	P	Wood canker, Black foot disease	2, 51, 81-86
<i>Campylocarpon sp.</i>	MBC	<i>Nectriaceae</i>	1	Both			87-89
<i>Cylindrocarpon sp.</i>	MBC	<i>Nectriaceae</i>	7	Both	P,S	Black foot	33, 51,74, 75, 77, 90, 91
<i>Dactylonectria alcacerensis</i>	Iso	<i>Nectriaceae</i>		Root	P	Black foot	86, 92
<i>Dactylonectria anthuriicola</i>	Iso	<i>Nectriaceae</i>		Root			88
<i>Dactylonectria sp.</i>	Iso	<i>Nectriaceae</i>		Both	P	Black foot	88, 89
<i>Diaporthe celeris</i>	Iso	<i>Diaporthaceae</i>		Graft	P	Canker and Arm swelling	93

<i>Diaporthe foeniculina</i>	MBC	<i>Diaporthaceae</i>	1	Both	P	Canker and Arm swelling	18, 94-97
<i>Diaporthe hispaniae</i>	Iso	<i>Diaporthaceae</i>		Graft			93
<i>Diaporthe rudis</i>	MBC	<i>Diaporthaceae</i>	1	Both	P,S	Canker	33, 64, 95, 96, 98-100
<i>Diaporthe sp.</i>	MBC/Iso	<i>Diaporthaceae</i>	1	Both/Both	P	Canker	18, 77, 94, 101-105
<i>Diplodia sp.</i>	MBC/Iso	<i>Botryosphaeriaceae</i>	4	Both/Both	P	Canker	77, 104, 106, 107
<i>Eucasphaeria capensis</i>	MBC	<i>Niessliaceae</i>	1	Both	P	Eutypa dieback	72
<i>Ilyonectria liriodendri</i>	Iso	<i>Nectriaceae</i>		Root	P	Black foot	51, 82, 85, 92, 108, 109
<i>Ilyonectria sp.</i>	Iso	<i>Nectriaceae</i>		Both	P,S	Black foot	33, 85, 108, 110
<i>Lasiopodia sp.</i>	MBC					Botryosphaeria die back	111
<i>Nectria sp.</i>	MBC	<i>Nectriaceae</i>	4	Both	S		112, 113
<i>Neofusicoccum parvum</i>	MBC/Iso	<i>Botryosphaeriaceae</i>	2	Both/Graft	P,E,S	Botryosphaeria die back	33, 52, 54, 60, 65, 83, 114-121, 147
<i>Neofusicoccum sp.</i>	MBC/Iso	<i>Botryosphaeriaceae</i>	2	Both/Both			107
<i>Paraphoma sp.</i>	MBC	<i>Phaeosphaeriaceae</i>	1	Both			
<i>Pestalotiopsis sp.</i>	MBC/Iso	<i>Sporocadaceae</i>	2	Both/Graft	P,E,S	Fruit rot	33, 51, 64, 122
<i>Phaeoacremonium minimum</i>	MBC	<i>Togniniaceae</i>	3	Both	P	Esca	64, 85, 108, 123, 124
<i>Phaeoacremonium parasiticum</i>	MBC	<i>Togniniaceae</i>	1	Both	P	Esca	50, 125, 126
<i>Phaeoacremonium sp.</i>	MBC	<i>Togniniaceae</i>	7	Both	P,S	Esca	33, 50, 53, 127, 128
<i>Phaeomoniella chlamydospora</i>	MBC	<i>Phaeomoniellaceae</i>	3	Both	P,E	Esca	129-136
<i>Phaeomoniella sp.</i>	MBC	<i>Phaeomoniellaceae</i>	2	Both		Esca	128
<i>Phoma sp.</i>	MBC	<i>Didymellaceae</i>	8	Both	P,E,S	Leaf and stem lesions	33, 54, 57, 77, 147
<i>Phomopsis ampelina</i>	MBC	<i>Diaporthaceae</i>	1	Both	P, S	Phomopsis cane and leaf spot/Deadarm/Phomopsis dieback	18, 57
<i>Phomopsis sp.</i>	MBC	<i>Diaporthaceae</i>	5	Both	P,E,S	Phomopsis cane and leaf spot/Deadarm/Phomopsis dieback	57
<i>Pleurostoma richardsiae</i>	MBC	<i>Pleurostomataceae</i>	1	Graft	P	Trunk disease	10, 71, 128
<i>Thelonectria sp.</i>	Iso	<i>Nectriaceae</i>		Root	P	Black foot disease	65
<i>Truncatella angustata</i>	MBC/Iso	<i>Sporocadaceae</i>	1	Root/Both	P,E		77, 128, 137, 138, 147, 150
<i>Truncatella sp.</i>	MBC	<i>Sporocadaceae</i>	1	Both			150

Table S3. Relative abundance (%) of GTD-related OTUs (species) in each tissue type. Abundances are calculated considering the totals for each tissue separately.

OTU	Graft union	Root collar
<i>Acremonium alternatum</i>	11.52%	0.33%
<i>Botryosphaeria dothidea</i>	0.55%	0.11%
<i>Cadophora luteo-olivacea</i>	30.44%	4.61%
<i>Campylocarpon fasciculare</i>	-	0.15%
<i>Cylindrocarpon sp.</i>	0.01%	0.13%
<i>Diplodia sp.</i>	0.55%	0.11%
<i>Neofusicoccum parvum</i>	1.25%	0.04%
<i>Phaeoacremonium minimum</i>	1.28%	0.44%
<i>Phaeomoniella chlamydospora</i>	2.09%	1.21%
<i>Phomopsis ampelina</i>	0.69%	0.02%
<i>Phomopsis sp.</i>	0.21%	0.01%
Total	48.6%	7.2%

Table S4. Relative abundance (%) of GTD-related isolates (species) in each tissue type. Abundances are calculated considering the totals for each tissue separately.

Isolate	Graft	
	union	Root collar
<i>Botryosphaeria sp.</i>	3.39%	-
<i>Dactylonectria alcacerensis</i>	-	4.18%
<i>Dactylonectria anthuriicola</i>	-	0.52%
<i>Dactylonectria sp.</i>	0.26%	2.35%
<i>Diaporthe celeris</i>	0.78%	-
<i>Diaporthe hispaniae</i>	1.31%	-
<i>Diaporthe sp.</i>	1.04%	0.52%
<i>Diplodia sp.</i>	3.13%	0.78%
<i>Ilyonectria liriodendra</i>	-	0.78%
<i>Ilyonectria sp.</i>	0.26%	5.22%
<i>Neofusicoccum parvum</i>	1.31%	-
<i>Neofusicoccum sp.</i>	6.01%	1.31%
<i>Pestalotiopsis sp.</i>	0.26%	-
<i>Thelonectria sp.</i>	-	2.09%
<i>Truncatella angustata</i>	0.52%	0.52%
Total	18.28%	18.28%

Table S5. Indicator species in (A) graft unions and (B) root collars. Graft unions were analyzed by variety and root crowns by rootstock. For each species (OTU), we indicate the community habitat that had the highest correlation with the species. Correlation values (stat) and the statistical significance of the correlation (p-values) are reported. GTD-related indicator species are marked in bold, biocontrol species are marked with an asterisk. Annotation next to the numbers indicates significance level: *** < 0.001, ** < 0.01, * < 0.05, n.s. = not significant (> 0.05).

A. Graft unions

OTU	Community habitat	stat	p-value
<i>Coniochaeta sp.</i>	Autumn Royal	0.528	0.0214 *
<i>Robillarda sessilis</i>	Caladoc	0.408	0.0486 *
<i>unknown_42</i>	Caladoc	0.833	0.0007 ***
<i>Coprinellus sp.</i>	Carignan	0.446	0.0262 *
<i>Diplodia sp.</i>	Carignan	0.698	0.0032 **
<i>Lasiodiplodia sp.</i>	Carignan	0.572	0.0084 **
<i>Phaeoacremonium sp.</i>	Carignan	0.502	0.0333 *
<i>Phaeomoniella chlamydospora</i>	Carignan	0.729	0.0013 **
<i>Thelebolus ellipsoideus</i>	Carignan	0.444	0.0196 *
<i>unknown_1218</i>	Carignan	0.447	0.0226 *
<i>unknown_Ascomycota_94</i>	Carignan	0.447	0.0125 *
<i>unknown_382</i>	Carignan	0.427	0.0427 *
<i>Erysiphe sp.</i>	Malvasia	0.546	0.0123 *

<i>Neofusicoccum sp._391</i>	Malvasia	0.549	0.014 *
<i>Neofusicoccum sp._398</i>	Malvasia	0.458	0.0443 *
<i>unknown_604</i>	Malvasia	0.577	0.008 **
<i>unknown_Basidiomycota_281</i>	Malvasia	0.569	0.0086 **
<i>unknown_1250</i>	Malvasia	0.566	0.0048 **
<i>unknown_1230</i>	Malvasia	0.456	0.0336 *
<i>Septoria sp.</i>	Pinot Noir	0.55	0.014 *
<i>unknown_Ascomycota_141</i>	Pinot Noir	0.469	0.0282 *
<i>Acremonium alternatum</i>	Sumoll	0.396	0.0091 **
<i>Pyrenophora dictyoides</i>	Sumoll	0.406	0.0391 *
<i>unknown_554</i>	Sumoll	0.528	0.0274 *
<i>unknown_683</i>	Sumoll	0.485	0.0337 *
<i>unknown_1582</i>	Sumoll	0.479	0.0228 *
<i>Cadophora malorum</i>	Tempranillo	0.499	0.0234 *
<i>Leptosphaeria sp.</i>	Tempranillo	0.544	0.0106 *
<i>unknown_Ascomycota_12</i>	Tempranillo	0.595	0.019 *
<i>unknown_Ascomycota_303</i>	Tempranillo	0.53	0.013 *
<i>unknown_1559</i>	Tempranillo	0.459	0.033 *
<i>Mortierella hyalina</i>	Xarel.lo vermell	0.544	0.0143 *

B. Root collars

OTU	Community habitat	stat	p-value
<i>Fusarium sp.</i>	R-110	0.628	0.0112 *
<i>Acremonium sp._1286</i>	41B	0.272	0.0218 *
<i>Acremonium sp._812</i>	41B	0.199	0.0493 *
<i>Cercophora sp.</i>	41B	0.201	0.0233 *
<i>Circinotrichum maculiforme</i>	41B	0.529	0.0143 *
<i>Coprinellus radians</i>	41B	0.204	0.0497 *
<i>Cryptococcus sp.</i>	41B	0.271	0.0031 **
<i>Exidia sp.</i>	41B	0.277	0.0225 *
<i>Harposporium sp.</i>	41B	0.293	0.01 **
<i>Lasiodiplodia sp.</i>	41B	0.199	0.0274 *
<i>Leptosphaeria sp.</i>	41B	0.203	0.0317 *
<i>Lophiostoma sp._839 *</i>	41B	0.391	0.0046 **
<i>Lophiostoma sp._1100 *</i>	41B	0.231	0.0497 *
<i>Lophiostoma sp._390 *</i>	41B	0.191	0.0396 *
<i>Massarina sp.</i>	41B	0.286	0.0078 **
<i>Mortierella hyalina</i>	41B	0.281	0.0048 **
<i>Radulidium subulatum</i>	41B	0.19	0.0297 *
<i>Seimatosporium sp.</i>	41B	0.204	0.0276 *
<i>Talaromyces amestolkiae</i>	41B	0.241	0.0221 *
<i>Tilletiopsis washingtonensis</i>	41B	0.266	0.0206 *
<i>Truncatella sp.</i>	41B	0.254	0.0158 *

<i>unknown_Ascomycota_99</i>	41B	0.378	0.017 *
<i>unknown_Basidiomycota_219</i>	41B	0.368	0.0202 *
<i>unknown_1174</i>	41B	0.319	0.0032 **
<i>unknown_Ascomycota_925</i>	41B	0.283	0.0131 *
<i>unknown_360</i>	41B	0.275	0.0069 **
<i>unknown_Ascomycota_581</i>	41B	0.262	0.0465 *
<i>unknown_666</i>	41B	0.253	0.0208 *
<i>unknown_Ascomycota_189</i>	41B	0.204	0.0451 *
<i>Meira nashicola</i>	RU-140	0.225	0.0359 *
<i>Thanatephorus cucumeris</i>	RU-140	0.386	0.0286 *
<i>unknown_21</i>	RU-140	0.517	0.0465 *
<i>Alternaria sp. *</i>	SO4	0.303	0.0268 *
<i>Colletotrichum sp.</i>	SO4	0.299	0.0484 *
<i>Oidiodendron cereale</i>	SO4	0.258	0.0232 *
<i>Podospora sp.</i>	SO4	0.264	0.0426 *
<i>Sarocladium kiliense</i>	SO4	0.355	0.0472 *
<i>unknown_Ascomycota_48</i>	SO4	0.318	0.0464 *
<i>unknown_771</i>	SO4	0.266	0.0333 *
<i>unknown_Basidiomycota_188</i>	SO4	0.248	0.0473 *