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60th MPU Anniversary Special Section - Review

## Fungal trunk diseases of fruit trees in Europe: pathogens, spread and future directions

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**Summary.** Production from crops of pome, stone fruit, nut, berry fruit, citrus, grapevine, and olive is increasingly threatened by fungal trunk diseases (FTD). These diseases and the consequent production losses are major problems. Many fungi (including *Botryosphaeriaceae*, *Calosphaeriaceae*, *Diaporthaceae*, *Diatrypidae*, *Nectriaceae*, *Phaeomoniellaceae*, *Pleosporaceae*, *Togniniaceae*, *Valsaceae*) infect host wood, mainly through wounds and subsequent colonization of woody tissues, causing symptoms such as cankers, gummosis, wood rotting, blight and dieback. Propagative plant material, seedlings and fruit play a significant role in pathogen spread. Several abiotic factors (e.g. shifts in cultural practices and climate change) are involved in the disease development. This paper reviews recent literature on FTD of fruit crops, particularly focusing on the European status of pathogen occurrence. Case studies are described related to diseases of apple, citrus, grapevine, berry, nut and stone fruit, and olive trees. Aspects related to epidemiology and the increase in disease incidence along with the future perspectives on the FTD research are also discussed.

**Keywords.** Wood cankers, dieback, *Botryosphaeriaceae*, abiotic factors, epidemiology.

## INTRODUCTION

Trees cultivated in plantations are increasingly threatened by fungal trunk diseases (FTD) (van Niekerk *et al.*, 2004; Gramaje *et al.*, 2016). There is increasing evidence that trees share pathogens with plants of forestry environments and with woody hosts that are not considered to be trees (Crous and Wingfield, 2018). Examples are pathogens in the family *Botryosphaeriaceae*, which are polyphagous, being often involved in diseases affecting diverse crops and plants of forest importance (Van Niekerk *et al.*, 2004; Guarnaccia *et al.*, 2022). High incidence of FTD in fruit crops, such as pome and stone fruits, nut, berry fruit, citrus and olive, has been reported (Gramaje *et al.*, 2012; Úrbez-Torres *et al.*, 2013b; Carlucci *et al.*, 2015b; Guarnaccia and Crous, 2017), demonstrating a need for focus on this group of host plants. FTD have become major concerns for fruit industry stakeholders, and their occurrence in orchards and consequent production losses, is likely to have resulted from several causes, including shifts in cultural practices and climate change (Doll *et al.*, 2013).

Canker diseases of fruit crops are caused by a broad range of fungi that infect host wood, mainly through different kinds of wounds and subsequent colonization of vascular tissues (Crous and Wingfield, 2018). Wood pathogens cause symptoms such as cankers, gummosis, wood rotting, blight and dieback (Fig. 1; Gramaje *et al.*, 2012). Dieback of shoots, branches, and main trunks can lead to tree death in severe cases (Slippers and Wingfield 2007). Several FTD pathogens have been identified as species within *Botryosphaeriaceae*, *Calosphaeriaceae*, *Diaporthaceae*, *Diatrypaceae*, *Nectriaceae*, *Phaeomonilaceae*, *Pleosporaceae*, *Togniniaceae*, and *Valsaceae*, as well as *Basidiomycota* (Rumbos 1988; Moral *et al.*, 2010; Kaliterna *et al.*, 2012; Carlucci *et al.*, 2013; 2015; Úrbez-Torres *et al.*, 2013a; Guarnaccia *et al.*, 2018b).

Some of these fungal pathogens live as endophytes in hosts after entering through wounds or natural openings, and pathogen spread occurs through asymptomatic plant material, seedlings and fruit, frequently circumventing country and region quarantine measures (Slippers and Wingfield, 2007).

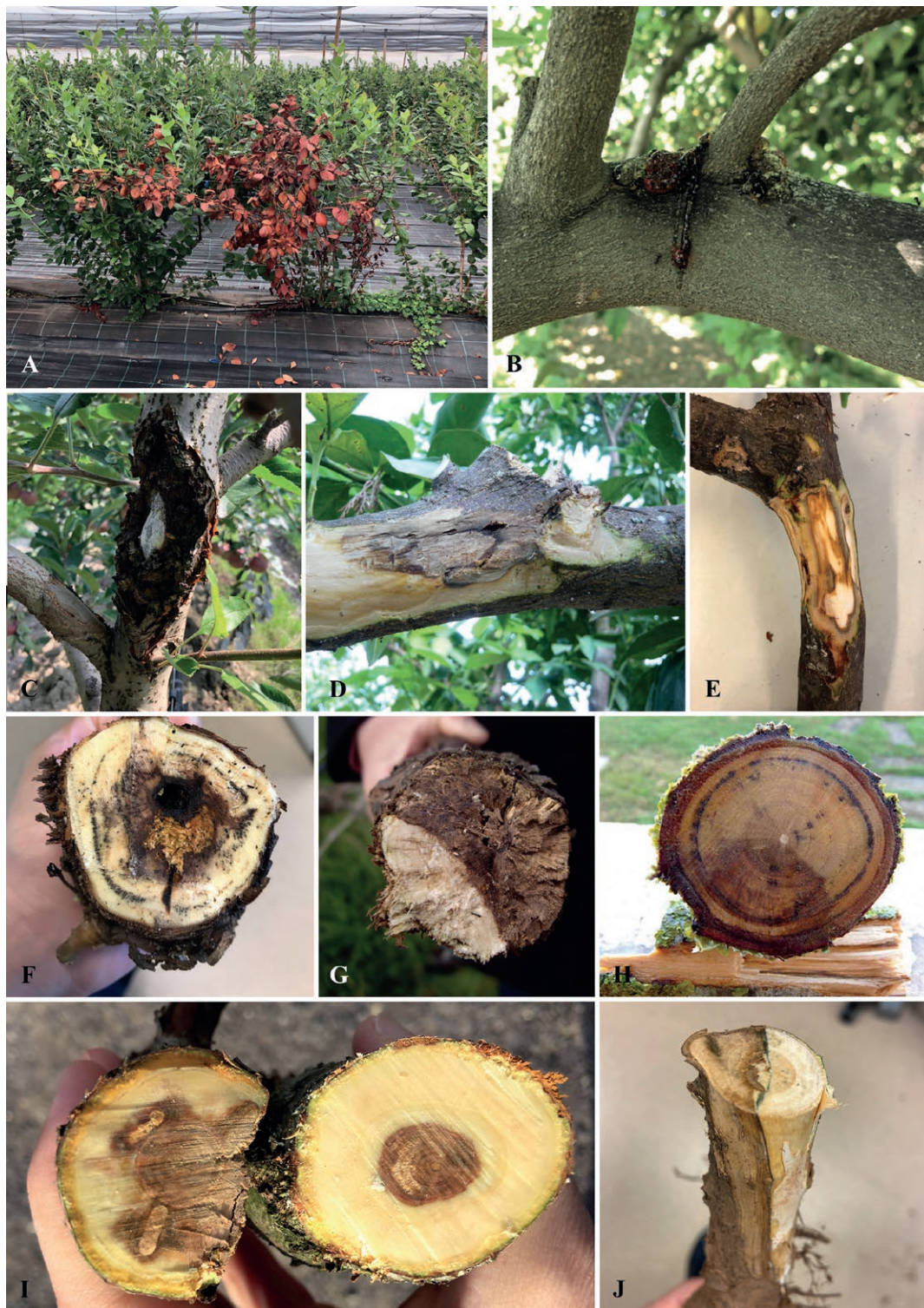
Abiotic factors are strongly involved with FTD. High planting densities are required to maximize production and land resources, and these are combined with plant nutrient programmes, giving stressed cultivated plants. For example, almond production in Spain has increased in recent years, and new agronomic practices were adopted to increase yields from new plantations (León *et al.*, 2020). However, incidence of almond associated FTD, such as twig cankers and shoot blight caused by *Dia-*

*porthe* spp., has also increased (León *et al.*, 2020). Abundant pruning wounds also promote chances of infections through possible airborne pathogen entry points (Henderson *et al.*, 2021). Similarly, wounds induced by mechanical shaking of trunks for fruit harvesting can increase host infection (Holland *et al.*, 2021a). Tree crop nurseries are important for meeting demands for plant material, and a lack of top-quality plants means greater incidence of FTD pathogens in the orchards. Global warming and climate change can increase plant stress and generate favourable conditions for the development of FTD, as for diseases caused by *Botryosphaeriaceae* (Pour *et al.*, 2020), which are serious threats to different crops (Slippers *et al.*, 2006).

The present paper aims to review recent literature on FTD, with a particular focus on the European situation of their causal agents, distribution and host associations, particularly relating to case studies on apple, citrus, grapevine, berry, nut and stone fruit, and olive trees. Moreover, epidemiology and hypotheses on the increase of FTD incidence are discussed, and future prospects and direction of trunk disease research are presented with the purpose of achieving sustainable disease management.

## PATHOGEN DISTRIBUTION AND HOST RANGE IN EUROPE

In Europe, the group of fungi causing FTD is diverse and expands as new reports demonstrate (Table 1). While some of these fungi are probably host-specific, others have broad host ranges, including members of the *Botryosphaeriaceae*. This family is the most prevalent, and members can infect many different fruit crops. For example, *B. dothidea* is ubiquitous in Europe, and has been associated with FTD of walnut, hazelnut, almond, stone fruit, grapevine, olive, pistachio, apple and blueberry (Moral *et al.*, 2010; Gramaje *et al.*, 2012; Akgül *et al.*, 2014; Fischer *et al.*, 2016; Baránek *et al.*, 2018; Hilário *et al.*, 2020a; López-Moral *et al.*, 2020a,b). In contrast, *Neofusicoccum luteum* has only been isolated from grapevines in Portugal and France (van Niekerk *et al.*, 2004). *Diplodia seriata* can also be found in different parts of Europe on many hosts, including walnut, grapevine, pear, quince, apple, apricot, plum, nectarine, almond and olive (Luque *et al.*, 2009; Gramaje *et al.*, 2012; Phillips *et al.*, 2012; Carlucci *et al.*, 2013; Kraus *et al.*, 2019; Bien and Damm 2020; Eichmeier *et al.*, 2020; López-Moral *et al.*, 2020a). *Diplodia mutila* is also common and infects grapevine, and trees of walnut, apricot, olive, plum, pear and apple (Phillips *et al.*, 2012; Carlucci *et al.*, 2013; Alves *et al.*, 2014; Gierl and Fischer,



**Figure 1.** FTD symptoms on different fruit trees. Natural dieback of *Vaccinium corymbosum* 'Blue Ribbon' in the field (A); branch canker on *Citrus sinensis* caused by *Diaporthe* spp. (B, from Guarnaccia *et al.*, 2020); trunk canker on apple caused by *Neonectria ditissima* (C); internal discoloration of *Citrus reticulata* branch affected by *Botryosphaeriaceae* (D, from Bezerra *et al.*, 2022); internal discoloration of avocado twig caused by *Neofusicoccum* spp. (E); cross-section showing a central white rot surrounded by black spots and sectorial necrosis of an esca infected vine (F), wedge-shaped canker in a *Eutypa* dieback affected vine (G), black spots and dark brown to black streaking of the xylem tissue in almond branches (H), sectorial necrosis of walnut affected trees (I), wood discoloration in pear branches (J).

Table 1. Distribution and host range of fungal pathogens associated with FTD on fruit crops in Europe based on literature research.

Division	Family	Genus	Species	Host	Country	References
Ascomycota	Bionectriaceae	<i>Acremonium</i>	<i>Acremonium sclerotigenum</i>	<i>Olea, Vitis</i>	Spain, Italy	Agusti-Brisach et al., 2021; Lorenzini et al., 2016
Ascomycota	Xylariaceae	<i>Biscogniauxia</i>	<i>Biscogniauxia nummularia</i>	<i>Prunus</i> (Plum), <i>Prunus</i> (Cherry)	Germany	Bien and Damm, 2020
Ascomycota	Xylariaceae	<i>Biscogniauxia</i>	<i>Biscogniauxia rosacearum</i>	<i>Cydonia, Prunus</i> (Plum), <i>Pyrus</i>	Italy	Raimondo et al., 2016
Basidiomycota	Phanerochaetales	<i>Bjerkandera</i>	<i>Bjerkandera adusta</i>	<i>Prunus</i> (Plum), <i>Prunus</i> (Cherry), <i>Vitis</i>	Germany	Bien and Damm, 2020; Kraus et al., 2018
Ascomycota	Botryosphaeriaceae	<i>Botryosphaeria</i>	<i>Botryosphaeria dothidea</i>	<i>Juglans, Prunus, Vitis, Prunus, Olea, Pistacia, Malus, Prunus</i> (Almond), <i>Vaccinium, Mangifera</i>	Spain, Switzerland, Portugal, Italy, Germany, Turkey, France, Czech Republic	López-Moral et al., 2020a,b; van Niekerk et al., 2004; Batista et al., 2020; Carlucci et al., 2013; Fischer et al., 2016, Akgül et al., 2014; Pintos et al., 2018; Turkolmez et al., 2016; Moral et al., 2010; Baránek et al., 2018; Gramaje et al., 2012; Hilário et al., 2019; Aiello et al., 2022
Ascomycota	Botryosphaeriaceae	<i>Botryosphaeria</i>	<i>Botryosphaeria lutea</i> (= <i>Neofusicoccum luteum</i> )	<i>Vitis</i>	Portugal	van Niekerk et al., 2004
Ascomycota	Ploetnerulaceae	<i>Cadophora</i>	<i>Cadophora fastigiata</i>	<i>Vitis</i>	Germany, Switzerland	Fischer et al., 2016; Casieri et al., 2009
Ascomycota	Ploetnerulaceae	<i>Cadophora</i>	<i>Cadophora luteo-olivacea</i>	<i>Vitis, Vaccinium, Olea, Prunus</i> (Plum)	Germany, Spain, France, Italy	Fischer et al., 2016; Pintos et al., 2018; Guarnaccia et al., 2020; Agusti-Brisach et al., 2021; Bien and Damm, 2020; Raimondo et al., 2019, Casieri et al., 2009
Ascomycota	Ploetnerulaceae	<i>Cadophora</i>	<i>Cadophora malorum</i>	<i>Malus, Actinidia</i>	Germany, Italy	Gierl and Fischer, 2017; Prodi et al., 2008
Ascomycota	Ploetnerulaceae	<i>Cadophora</i>	<i>Cadophora melinii</i>	<i>Vitis</i>	Spain	Gramaje et al., 2011
Ascomycota	Ploetnerulaceae	<i>Cadophora</i>	<i>Cadophora novi-eboraci</i>	<i>Juglans, Malus, Prunus</i> (Cherry)	Czech Republic, Germany	Eichmeier et al., 2020; Gierl and Fischer, 2017; Bien and Damm, 2020
Ascomycota	Ploetnerulaceae	<i>Cadophora</i>	<i>Cadophora prunicola</i>	<i>Prunus</i> (Plum), <i>Prunus</i> (Cherry)	Germany	Bien and Damm, 2020
Ascomycota	Ploetnerulaceae	<i>Cadophora</i>	<i>Cadophora ramosa</i>	<i>Prunus</i> (Cherry), <i>Juglans</i>	Germany, Czech Republic	Bien and Damm, 2020; Eichmeier et al., 2020
Ascomycota	Calosphaeriaceae	<i>Calosphaeria</i>	<i>Calosphaeria pulchella</i>	<i>Prunus</i> (Cherry)	Spain	Berbegal et al., 2014
Ascomycota	Glomerellaceae	<i>Colletotrichum</i>	<i>Colletotrichum fruticola</i>	<i>Persea</i>	Italy	Guarnaccia et al., 2016
Ascomycota	Glomerellaceae	<i>Colletotrichum</i>	<i>Colletotrichum gloeosporioides</i>	<i>Citrus, Persea</i>	Italy	Guarnaccia et al., 2016., 2017
Ascomycota	Glomerellaceae	<i>Colletotrichum</i>	<i>Colletotrichum karstii</i>	<i>Citrus</i>	Portugal	Ramos et al., 2016
Ascomycota	Typhariaceae	<i>Collophora</i>	<i>Collophora africana</i>	<i>Prunus</i> (Apricot), <i>Prunus</i> (Almond), <i>Prunus</i> (Plum)	Germany	Gierl and Fischer, 2017; Bien and Damm, 2020
Ascomycota	Typhariaceae	<i>Collophora</i>	<i>Collophora badensis</i>	<i>Prunus</i> (Plum)	Germany	Bien and Damm, 2020
Ascomycota	Typhariaceae	<i>Collophora</i>	<i>Collophora germanica</i>	<i>Prunus</i> (Cherry)	Germany	Bien and Damm, 2020

(Continued)

Table 1. (Continued).

Division	Family	Genus	Species	Host	Country	References
Ascomycota	Tympanidaceae	<i>Collophorina</i>	<i>Collophorina hispanica</i>	<i>Prunus</i> (Apricot), <i>Prunus</i> (Almond)	Germany, Spain	Gierl and Fischer, 2017; Gramaje <i>et al.</i> , 2012
Ascomycota	Tympanidaceae	<i>Collophorina</i>	<i>Collophorina neorubra</i>	<i>Prunus</i> (Cherry)	Germany	Bien and Damm, 2020
Ascomycota	Tympanidaceae	<i>Collophorina</i>	<i>Collophorina paarla</i>	<i>Prunus</i> (Cherry)	Germany	Gierl and Fischer, 2017
Ascomycota	Diademaceae	<i>Comoclathris</i>	<i>Comoclathris incompta</i>	<i>Olea</i>	Spain, Croatia, Italy	Moral <i>et al.</i> , 2017; Ivic <i>et al.</i> , 2010; Carlucci <i>et al.</i> , 2013
Ascomycota	Contiochaetaceae	<i>Contiochaeta</i>	<i>Contiochaeta hoffmannii</i>	<i>Vitis</i>	Germany	Fischer <i>et al.</i> , 2016
Ascomycota	inertiae sedis	<i>Cryptovalsa</i>	<i>Cryptovalsa ampelina</i>	<i>Juglans</i> , <i>Vitis</i>	Czech Republic, Spain, Germany	Eichmeier <i>et al.</i> , 2020; Luque <i>et al.</i> , 2009, 2012; Martin <i>et al.</i> , 2009; Kraus <i>et al.</i> , 2018
Ascomycota	Nectriaceae	<i>Cylindrocarpon</i>	<i>Cylindrocarpon destructans</i>	<i>Olea</i> , <i>Vitis</i>	Italy, Spain	Carlucci <i>et al.</i> , 2013; Gonzalez and Tello, 2011
Ascomycota	Nectriaceae	<i>Cylindrocarpon</i>	<i>Cylindrocarpon pauciseptatum</i>	<i>Vitis</i> , <i>Prunus</i> (Peach), <i>Prunus</i> (Plum)	Slovenia, Portugal, Italy, Spain, Bulgaria, France	Cabral <i>et al.</i> , 2012; Yaseen <i>et al.</i> , 2012; Martin <i>et al.</i> , 2011; Piperkova <i>et al.</i> , 2017; Pintos <i>et al.</i> , 2018
Ascomycota	Nectriaceae	<i>Cylindrocarpon</i>	<i>Cylindrocarpon peruviana</i>	<i>Persea</i>	Italy	Aiello <i>et al.</i> , 2020
Ascomycota	Valsaceae	<i>Cytospora</i>	<i>Cytospora chrysoasperma</i>	<i>Prunus</i> (blackthorn), <i>Vitis</i>	Germany, Spain	Gierl and Fischer, 2017; Kraus <i>et al.</i> , 2018; González and Tello, 2011
Ascomycota	Valsaceae	<i>Cytospora</i>	<i>Cytospora oleina</i>	<i>Olea</i>	Greece, Italy	Rumbos, 1988; Carlucci <i>et al.</i> , 2013
Ascomycota	Valsaceae	<i>Cytospora</i>	<i>Cytospora pistaciae</i>	<i>Pistacia</i>	Italy	Aiello <i>et al.</i> , 2019
Ascomycota	Valsaceae	<i>Cytospora</i>	<i>Cytospora pruinosa</i>	<i>Olea</i>	Spain	López-Moral <i>et al.</i> , 2020b; Moral <i>et al.</i> , 2017
Ascomycota	Nectriaceae	<i>Dactylonectria</i>	<i>Dactylonectria hordeicola</i>	<i>Vitis</i>	France	Pintos <i>et al.</i> , 2018
Ascomycota	Nectriaceae	<i>Dactylonectria</i>	<i>Dactylonectria macrodidyma</i>	<i>Vitis</i>	France, Spain	Pintos <i>et al.</i> , 2018
Ascomycota	Nectriaceae	<i>Ilyonectria</i>	<i>Ilyonectria macrodidyma</i>	<i>Vitis</i>	Portugal, France, Turkey, Spain	Cabral <i>et al.</i> , 2012; Augusti-Brisach and Armengol, 2013
Ascomycota	Nectriaceae	<i>Dactylonectria</i>	<i>Dactylonectria pauciseptata</i>	<i>Vitis</i>	France, Spain	Pintos <i>et al.</i> , 2018
Ascomycota	Nectriaceae	<i>Dactylonectria</i>	<i>Dactylonectria torresensis</i>	<i>Vitis</i>	France, Spain	Pintos <i>et al.</i> , 2018
Ascomycota	Diaportheaceae	<i>Diaporthe</i>	<i>Diaporthe ampelina</i>	<i>Vitis</i>	France, Spain, Turkey, Czech Republic, Germany, UK, Croatia, Hungary	Pintos <i>et al.</i> , 2018; Akgül <i>et al.</i> , 2015; Baránek <i>et al.</i> , 2018; Kraus <i>et al.</i> , 2018; Guarnaccia <i>et al.</i> , 2018
Ascomycota	Diaportheaceae	<i>Diaporthe</i>	<i>Diaporthe amygdali</i>	<i>Prunus</i> (Almond), <i>Juglans</i> , <i>Vaccinium</i> , <i>Persea</i>	Portugal, Spain, Hungary, Italy	López-Moral <i>et al.</i> , 2020b; Varias <i>et al.</i> , 2017; Guarnaccia <i>et al.</i> , 2016, 2018
Ascomycota	Diaportheaceae	<i>Diaporthe</i>	<i>Diaporthe baccae</i>	<i>Vitis</i> , <i>Vaccinium</i> , <i>Citrus</i> , <i>Mangifera</i>	Spain, France, Italy, Croatia	Guarnaccia <i>et al.</i> , 2017, 2018; Aiello <i>et al.</i> , 2022
Ascomycota	Diaportheaceae	<i>Diaporthe</i>	<i>Diaporthe bohemiae</i>	<i>Vitis</i>	Czech Republic	Guarnaccia <i>et al.</i> , 2018
Ascomycota	Diaportheaceae	<i>Diaporthe</i>	<i>Diaporthe celeris</i>	<i>Vitis</i>	UK	Guarnaccia <i>et al.</i> , 2018
Ascomycota	Diaportheaceae	<i>Diaporthe</i>	<i>Diaporthe cinerascens</i>	<i>Ficus</i>	Bulgaria	López-Moral <i>et al.</i> , 2020a,b

(Continued)

Table 1. (Continued).

Division	Family	Genus	Species	Host	Country	References
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe eres</i>	<i>Malus, Vitis, Prunus</i> (Cherry), <i>Vaccinium, Juglans, Prunus</i> (Peach), <i>Pyrus</i>	Germany, France, Spain, Czech Republic, UK, Italy, Hungary, Croatia, Poland, the Netherlands, Lithuanian, Greece, Switzerland	Gierl and Fischer, 2017; Pintos <i>et al.</i> , 2018; Bien and Damm, 2020; Guarnaccia <i>et al.</i> , 2018; Lombard <i>et al.</i> , 2014; Eichmeier <i>et al.</i> , 2020; Thomidis <i>et al.</i> , 2009; Prencipe <i>et al.</i> , 2017; Bertetti <i>et al.</i> , 2018; Casieri <i>et al.</i> , 2009
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe foeniculina</i>	<i>Ficus, Vitis, Citrus, Persea, Pyrus, Vaccinium, Juglans, Prunus</i> (Almond), <i>Mangifera, Litchi</i>	Germany, France, Spain, Greece, Malta, Portugal, Italy	Gierl and Fischer, 2017; Pintos <i>et al.</i> , 2018; Vakalounakis <i>et al.</i> , 2019; Guarnaccia <i>et al.</i> , 2016., 2017; Mathioudakis <i>et al.</i> , 2020; Santos <i>et al.</i> , 2017; Hilario <i>et al.</i> , 2020; Lopez-Moral <i>et al.</i> , 2020; Gramaje <i>et al.</i> , 2012; Aiello <i>et al.</i> , 2022
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe hispaniae</i>	<i>Vitis</i>	Spain	Guarnaccia <i>et al.</i> , 2018
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe hungariae</i>	<i>Vitis</i>	Spain, Hungary	Guarnaccia <i>et al.</i> , 2018
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe limonicola</i>	<i>Citrus</i>	Malta	Guarnaccia <i>et al.</i> , 2017
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe malthocarpus</i>	<i>Prunus</i> (Cherry)	Germany	Bien and Damm, 2020
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe melitensis</i>	<i>Citrus</i>	Malta	Guarnaccia <i>et al.</i> , 2017
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe novem</i>	<i>Vitis, Citrus</i>	France, Spain, Italy	Pintos <i>et al.</i> , 2018; Guarnaccia <i>et al.</i> , 2017
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe phaeosporum</i>	<i>Vitis</i>	Spain, Switzerland	Pintos <i>et al.</i> , 2018; Casieri <i>et al.</i> , 2009
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe rudis</i>	<i>Vitis, Vaccinium, Prunus</i> (Plum), <i>Prunus</i> (Cherry), <i>Litchi</i>	France, Spain, Italy, Portugal, Germany, UK, Switzerland, the Netherlands	Pintos <i>et al.</i> , 2018, Guarnaccia <i>et al.</i> , 2018., (Plum), <i>Prunus</i> (Cherry), Germany, Portugal, 2020; Bien and Damm, 2020; Casieri <i>et al.</i> , 2009; Lombard <i>et al.</i> , 2014; Aiello <i>et al.</i> , 2022
Ascomycota	Diaporthaceae	<i>Diaporthe</i>	<i>Diaporthe vaccinii</i>	<i>Vaccinium</i>	the Netherlands, Lithuania, Latvia	Lombard <i>et al.</i> , 2014
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia bulgarica</i>	<i>Malus, Pyrus</i>	Bulgaria, Germany, Turkey	Phillips <i>et al.</i> , 2012; Hinrichs-Berger <i>et al.</i> , 2021; Eken, 2021
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia corticola</i>	<i>Vitis</i>	Italy	Carlucci <i>et al.</i> , 2015
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia pseudoseriata</i>	<i>Pistacia</i>	Italy	Batista <i>et al.</i> , 2020
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia juglandis</i>	<i>Juglans</i>	France	López-Moral <i>et al.</i> , 2020
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia malorum</i>	<i>Malus</i>	Portugal	Phillips <i>et al.</i> , 2012; Alves <i>et al.</i> , 2014
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia mutila</i>	<i>Vitis, Juglans, Prunus</i> (Apricot), <i>Olea, Prunus</i> (Plum), <i>Pyrus, Malus</i>	Portugal, Germany, Italy, Spain, France, Netherlands, England	López-Moral <i>et al.</i> , 2020, Gierl and Fischer, 2017; Carlucci <i>et al.</i> , 2013; Pintos <i>et al.</i> , 2018; Bien and Damm, 2020; Batista <i>et al.</i> , 2020; Phillips <i>et al.</i> , 2013; Alves <i>et al.</i> , 2014
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia olivarum</i>	<i>Olea, Prunus</i> (Almond), <i>Pistacia</i>	Italy, Spain	Phillips <i>et al.</i> , 2012; Gramaje <i>et al.</i> , 2012; Alves <i>et al.</i> , 2014; Linaldeddu <i>et al.</i> , 2016
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia sapinea</i>	<i>Malus, Vitis, Olea</i>	Portugal, France, Italy	Batista <i>et al.</i> , 2020; Comont <i>et al.</i> , 2016; Alves <i>et al.</i> , 2014; Phillips <i>et al.</i> , 2012

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Table 1. (Continued).

Division	Family	Genus	Species	Host	Country	References
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia scrobiculata</i>	<i>Olea</i>	Italy	Phillips <i>et al.</i> , 2012; Alves <i>et al.</i> , 2014
Ascomycota	Botryosphaeriaceae	<i>Diplodia</i>	<i>Diplodia seriata</i>	<i>Juglans</i> , <i>Vitis</i> , <i>Pyrus</i> , <i>Cydonia</i> , <i>Malus</i> , <i>Prunus</i> ( <i>Apricot</i> ), <i>Olea</i> , <i>Prunus</i> ( <i>Plum</i> ), <i>Prunus</i> ( <i>Nectarine</i> ), <i>Prunus</i> ( <i>Almond</i> ), <i>Prunus</i> ( <i>Plum</i> )	Czech Republic, Spain, Turkey, Spain, Germany, Germany, France, Italy, Bulgaria, Croatia, Portugal	Eichmeier <i>et al.</i> , 2020; López-Moral <i>et al.</i> , 2020; Kurbethli and Demirci, 2014; Moral <i>et al.</i> , 2010; Phillips <i>et al.</i> , 2012; Kaliterna <i>et al.</i> , 2012; Carlucci <i>et al.</i> , 2013; Ende <i>et al.</i> , 2016; Batista <i>et al.</i> , 2020; Kraus <i>et al.</i> , 2019; Akgül <i>et al.</i> , 2014; Luque <i>et al.</i> , 2009; Gramaje <i>et al.</i> , 2012; Bien and Damm, 2020
Ascomycota	Botryosphaeriaceae	<i>Dothiorella</i>	<i>Dothiorella iberica</i>	<i>Juglans</i> , <i>Prunus</i> ( <i>Apricot</i> ), <i>Corylus</i> ( <i>Hazelnut</i> ), <i>Malus</i> , <i>Vitis</i>	Spain, Germany, Italy	López-Moral <i>et al.</i> , 2020; Gierl and Fischer, 2017; Phillips <i>et al.</i> , 2005; Carlucci <i>et al.</i> , 2015
Ascomycota	Botryosphaeriaceae	<i>Dothiorella</i>	<i>Dothiorella omnivora</i>	<i>Juglans</i> , <i>Vitis</i>	Czech Republic, France, Hungary	Eichmeier <i>et al.</i> , 2020; Linaldeddu <i>et al.</i> , 2016; Vaczy <i>et al.</i> , 2018
Ascomycota	Botryosphaeriaceae	<i>Dothiorella</i>	<i>Dothiorella sarmentorum</i>	<i>Juglans</i> , <i>Malus</i> , <i>Prunus</i> ( <i>Almond</i> ), <i>Cydonia</i> , <i>Vitis</i> the Netherlands, Norway, Germany, Italy, Spain, Poland, Ukraine	Czech Republic, Italy, France	López-Moral <i>et al.</i> , 2020; van Niekerk <i>et al.</i> , 2004; Gierl and Fischer, 2017; Carlucci <i>et al.</i> , 2015; Dissanayake <i>et al.</i> , 2016
Ascomycota	Botryosphaeriaceae	<i>Dothiorella</i>	<i>Dothiorella viticola</i>	<i>Vitis</i>	Spain, France	López-Moral <i>et al.</i> , 2020; Batista <i>et al.</i> , 2020; Comont <i>et al.</i> , 2016
Ascomycota	Diatriypaceae	<i>Eutypa</i>	<i>Eutypa lata</i>	<i>Juglans</i> , <i>Cydonia</i> , <i>Vitis</i> , <i>Pistacia</i> , <i>Prunus</i> ( <i>Almond</i> ), <i>Prunus</i> ( <i>Plum</i> ), <i>Prunus</i> ( <i>Cherry</i> ), <i>Olea</i>	Czech Republic, Germany, Spain, Italy, France	Eichmeier <i>et al.</i> , 2020; Gierl and Fischer, 2017; Luque <i>et al.</i> , 2009; López-Moral <i>et al.</i> , 2020b; Baránek <i>et al.</i> , 2018; Gramaje <i>et al.</i> , 2012; Bien and Damm, 2020; Tosi and Natalini, 2009; Aiello <i>et al.</i> , 2019; Baranek <i>et al.</i> , 2018; Laveau <i>et al.</i> , 2009; Kraus <i>et al.</i> , 2022
Ascomycota	Diatriypaceae	<i>Eutypella</i>	<i>Eutypella citricola</i>	<i>Vitis</i>	Spain	Luque <i>et al.</i> , 2012
Ascomycota	Diatriypaceae	<i>Eutypella</i>	<i>Eutypella leptoplaca</i>	<i>Vitis</i>	Spain	Luque <i>et al.</i> , 2009
Ascomycota	Diatriypaceae	<i>Eutypella</i>	<i>Eutypella microtheca</i>	<i>Vitis</i>	Spain	Luque <i>et al.</i> , 2012
Ascomycota	Diatriypaceae	<i>Eutypella</i>	<i>Eutypella vitis</i>	<i>Vitis</i>	Spain	Luque <i>et al.</i> , 2009
Basidiomycota	Hymenochaetaeaceae	<i>Fomitiporia</i>	<i>Fomitiporia mediterranea</i>	<i>Olea</i> , <i>Vitis</i> , <i>Actinidia</i> , <i>Citrus</i> , <i>Prunus</i> ( <i>Almond</i> ), <i>Pyrus</i>	Italy, Spain, Turkey, Czech Republic, Germany, France, Greece, Austria, Portugal, Slovenia, Switzerland	Carlucci <i>et al.</i> , 2013; Luque <i>et al.</i> , 2009; Akgül <i>et al.</i> , 2015; Baránek <i>et al.</i> , 2018; Kraus <i>et al.</i> , 2022; Laveau <i>et al.</i> , 2009; Elena and Papolomatis, 2009; Elena <i>et al.</i> , 2006; Rumbos and Rumbou, 2001; Moretti <i>et al.</i> , 2021; Olmo <i>et al.</i> , 2017; Markakis <i>et al.</i> , 2017
Basidiomycota	Hymenochaetaeaceae	<i>Fomitiporia</i>	<i>Fomitiporia punctata</i>	<i>Vitis</i> , <i>Actinidia</i>	Italy, Greece, France	Cortesi <i>et al.</i> , 2000; Elena and Papolomatis, 2007; Jamaux-Desprésaux and Péros, 2003
Ascomycota	Nectriaceae	<i>Ilyonectria</i>	<i>Ilyonectria europa</i>	<i>Vitis</i> , <i>Actinidia</i>	Portugal, France	Cabral <i>et al.</i> , 2012
Ascomycota	Nectriaceae	<i>Ilyonectria</i>	<i>Ilyonectria liriiodendri</i>	<i>Vitis</i> , <i>Malus</i>	France, Spain, Portugal, Switzerland, Turkey	Pintos <i>et al.</i> , 2018; Cabral <i>et al.</i> , 2012; Alaniz <i>et al.</i> , 2009; Casieri <i>et al.</i> , 2009; Savas <i>et al.</i> , 2015

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Table 1. (Continued).

Division	Family	Genus	Species	Host	Country	References
Ascomycota	Nectriaceae	<i>Ilyonectria</i>	<i>Ilyonectria lusitanica</i>	Vitis	Portugal	Cabral et al., 2012
Ascomycota	Nectriaceae	<i>Ilyonectria</i>	<i>Ilyonectria pseudodestructans</i>	Vitis	Portugal, Spain	Cabral et al., 2012; Berlanas et al., 2020
Ascomycota	Nectriaceae	<i>Ilyonectria</i>	<i>Ilyonectria robusta</i>	Vitis	France, Portugal, Spain	Pintos et al., 2018; Cabral et al., 2012; Berlanas et al., 2020
Ascomycota	Nectriaceae	<i>Ilyonectria</i>	<i>Ilyonectria vitis</i>	Vitis	Portugal	Cabral et al., 2012
Ascomycota	Botryosphaeriaceae	<i>Lasiodiplodia</i>	<i>Lasiodiplodia citricola</i>	Vitis	Italy	Carlucci et al., 2015
Ascomycota	Botryosphaeriaceae	<i>Lasiodiplodia</i>	<i>Lasiodiplodia pseudotheobromae</i>	Olea, Prunus (Nectarine), Pistacia	Italy, Turkey, Spain	Carlucci et al., 2013; Endes et al., 2016; Akgül et al., 2014; Aroca et al., 2010; López-Moral et al., 2020b
Ascomycota	Botryosphaeriaceae	<i>Lasiodiplodia</i>	<i>Lasiodiplodia theobromae</i>	Olea, Prunus (Nectarine), Vitis, Vaccinium, Mangifera	Italy, Turkey, Spain	Carlucci et al., 2013, 2015; Endes et al., 2016; Akgül et al., 2014; Aroca et al., 2010; Martin et al., 2009; Borrero et al., 2019; Aiello et al., 2022
Ascomycota	Botryosphaeriaceae	<i>Lasiodiplodia</i>	<i>Lasiodiplodia viticola</i>	Vitis	France	Comont et al., 2016
Ascomycota	Phaeomontellaceae	<i>Minutiella</i>	<i>Minutiella pruni-avium</i>	Prunus (Cherry)	Germany	Bien and Damm, 2020
Ascomycota	Sclerotiniaceae	<i>Monilinia</i>	<i>Monilinia laxa</i>	Prunus (Plum)	Germany	Bien and Damm, 2020
Ascomycota	Nectriaceae	<i>Neocosmospora</i>	<i>Neocosmospora perseae</i>	Persea	Italy, Greece	Guarnaccia et al., 2018, 2022
Ascomycota	Botryosphaeriaceae	<i>Neofusicoccum</i>	<i>Neofusicoccum australe</i>	Mangifera, Prunus (Almond), Vitis, Olea, Vaccinium	Italy, Spain, Portugal	Ismail et al., 2013; Gramaje et al., 2012; Aroca et al., 2010; Lopes et al., 2016; Hilário et al., 2019
Ascomycota	Botryosphaeriaceae	<i>Neofusicoccum</i>	<i>Neofusicoccum hellenicum</i>	Pistacia	Greece, Italy	Lopes et al., 2016; Gusella et al., 2022
Ascomycota	Botryosphaeriaceae	<i>Neofusicoccum</i>	<i>Neofusicoccum luteum</i>	Olea, Vitis	Italy, Germany, Spain, France, Portugal	Carlucci et al., 2013; Fischer et al., 2016; Luque et al., 2009; Pintos et al., 2018; Lopes et al., 2016
Ascomycota	Botryosphaeriaceae	<i>Neofusicoccum</i>	<i>Neofusicoccum parvum mediterraneum</i>	Juglans, Vitis, Olea, Pistacia	Spain, Italy	López-Moral et al., 2020a,b; Moral et al., 2010, 2017; Brunetti et al., 2022
Ascomycota	Botryosphaeriaceae	<i>Neofusicoccum</i>	<i>Neofusicoccum parvum</i>	Juglans, Malus, Vitis, Castanea, Citrus, Ficus, Prunus (Nectarine), Persea (Peach), Pistacia, Mangifera, Vaccinium, Prunus (Almond), Persea, Olea	Spain, Portugal, Italy, Turkey, France, Greece, Croatia	López-Moral et al., 2020a,b; Moral et al., 2010; Batista et al., 2020; Mondello et al., 2013; Akgül et al., 2014; Luque et al., 2009; Pintos et al., 2018; Ciordia et al., 2022; Vakalounakis et al., 2019; Aiello et al., 2020; Thomidis et al., 2011; Kaliterna et al., 2013; Ismail et al., 2013; Guarnaccia et al., 2020; Gramaje et al., 2012; Guarnaccia, 2016; Ismail et al., 2013; Hilário et al., 2019; Castillo et al., 2013; Polizzi et al., 2022
Ascomycota	Botryosphaeriaceae	<i>Neofusicoccum</i>	<i>Neofusicoccum vitifusiforme</i>	Vitis	Italy, Spain	Mondello et al., 2013; Aroca et al., 2010
Ascomycota	Nectriaceae	<i>Neonectria</i>	<i>Neonectria ditissima</i>	Malus	Portugal	Cabral et al., 2012
Ascomycota	Sporocadaceae	<i>Neopestalotiopsis</i>	<i>Neopestalotiopsis rosae</i>	Persea	Italy	Fiorenza et al., 2022
Ascomycota	Sporocadaceae	<i>Neopestalotiopsis</i>	<i>Neopestalotiopsis siciliana</i>	Persea	Italy	Fiorenza et al., 2022

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Table 1. (Continued).

Division	Family	Genus	Species	Host	Country	References
Ascomycota	Botryosphaeriaceae	<i>Neoscytalidium</i>	<i>Neoscytalidium dimidiatum</i>	<i>Citrus</i> , <i>Juglans</i> , <i>Vitis</i> , <i>Prunus</i> (Cherry), <i>Prunus</i> (Almond)	Italy, Turkey	Polizzi <i>et al.</i> , 2009; Dervis <i>et al.</i> , 2019; Oksal <i>et al.</i> , 2019; Oren <i>et al.</i> , 2020, 2022
Ascomycota	<i>Didymeliaceae</i>	<i>Nothophoma</i>	<i>Nothophoma quercina</i>	<i>Olea</i>	Spain	Moral <i>et al.</i> , 2017
Ascomycota	<i>Diutrypaceae</i>	<i>Peroneutypa</i>	<i>Peroneutypa scoparia</i>	<i>Juglans</i> , <i>Vaccinium</i>	Czech Republic, Italy	Eichmeier <i>et al.</i> , 2020; Guarnaccia <i>et al.</i> , 2020
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium abiesii</i>	<i>Olea</i> , <i>Vitis</i>	Italy, Turkey	Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium amygdalinum</i>	<i>Prunus</i> (Almond)	Spain, Italy	Gramaje <i>et al.</i> , 2012; Raimondo <i>et al.</i> , 2021
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium angustius</i>	<i>Cydonia</i> , <i>Vitis</i>	Germany, Portugal, Spain	Gierl and Fischer, 2017; Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium cinereum</i>	<i>Vitis</i>	Spain	Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium croatiense</i>	<i>Vitis</i>	Croatia	Essakhi <i>et al.</i> , 2008
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium fraxinopennsylvanicum</i>	<i>Vitis</i> , <i>Actinidia</i>	Germany, Italy, Croatia, Hungary, Spain	Fischer <i>et al.</i> , 2016; Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium griseorubrum</i>	<i>Vitis</i>	Italy	Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium hispanicum</i>	<i>Vitis</i>	Spain	Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium hungaricum</i>	<i>Prunus</i> (Plum), <i>Prunus</i> (Cherry)	Germany, Hungary	Bien and Damm, 2020; Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium infatipes</i>	<i>Vitis</i>	Spain	González and Tello, 2011
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium iraniamum</i>	<i>Actinidia</i> , <i>Prunus</i> (Almond), <i>Prunus</i> (Plum), <i>Vitis</i>	Italy, Spain, Germany	Prodi <i>et al.</i> , 2008; Gramaje <i>et al.</i> , 2012; Bien and Damm, 2020
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium italicum</i>	<i>Olea</i> , <i>Vitis</i>	Spain, Italy	Agusti-Brisach <i>et al.</i> , 2021; Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium krajdenii</i>	<i>Vitis</i>	Spain	Gramaje <i>et al.</i> , 2011
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium minimum</i>	<i>Vitis</i> , <i>Olea</i> , <i>Actinidia</i> , <i>Prunus</i> (Cherry), <i>Pistacia</i>	Spain, France, Turkey, Italy, Austria, Greece, Germany, Portugal	Pintos <i>et al.</i> , 2018; Akgül <i>et al.</i> , 2015, Agusti-Brisach <i>et al.</i> , 2021; Carlucci <i>et al.</i> , 2013; Luque <i>et al.</i> , 2019; Prodi <i>et al.</i> , 2008; Di Marco <i>et al.</i> , 2000; Mostert <i>et al.</i> , 2006; Lopez-Moral <i>et al.</i> , 2020; Gramaje <i>et al.</i> , 2015
Ascomycota	<i>Togniniaceae</i>	<i>Phaeoacremonium</i>	<i>Phaeoacremonium oleae</i>	<i>Olive</i>	Italy	Raimondo <i>et al.</i> , 2022

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Table 1. (Continued).

Division	Family	Genus	Species	Host	Country	References
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium parasiticum</i>	<i>Vitis</i> , <i>Olea</i> , <i>Actinidia</i> , <i>Prunus</i> (Cherry)	Spain, Italy, Greece	Aroca <i>et al.</i> , 2010; Agustí-Brisach <i>et al.</i> , 2021; Prodi <i>et al.</i> , 2008; Gramaje <i>et al.</i> , 2015
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium rubrigenum</i>	<i>Olea</i> , <i>Vitis</i> , <i>Actinidia</i>	Italy, Croatia	Gramaje <i>et al.</i> , 2015; Di Marco <i>et al.</i> , 2010
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium scolyti</i>	<i>Olea</i> , <i>Prunus</i> (Plum), <i>Vitis</i>	Spain, Germany, Italy, France, Turkey	Agustí-Brisach <i>et al.</i> , 2021; Bien and Damm, 2020; Carlucci <i>et al.</i> , 2015; Gramaje <i>et al.</i> , 2015; Ozben <i>et al.</i> , 2012
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium sicilianum</i>	<i>Olea</i> , <i>Vitis</i> , <i>Juglans</i>	Italy, Spain, Czech Republic	Carlucci <i>et al.</i> , 2015; Gramaje <i>et al.</i> , 2015; Eichmeier <i>et al.</i> , 2020
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium tuscianum</i>	<i>Vitis</i>	Italy	Gramaje <i>et al.</i> , 2015
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium venezuelense</i>	<i>Prunus</i> (Apricot)	Spain	Gramaje <i>et al.</i> , 2015
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium vibratile</i>	<i>Prunus</i> (Cherry)	Sweden	Gramaje <i>et al.</i> , 2015
Ascomycota	Togniniaceae	<i>Phaeoacremonium</i>	<i>Phaeoacremonium viticola</i>	<i>Vitis</i> , <i>Actinidia</i> , <i>Prunus</i> (Plum), <i>Prunus</i> (Cherry), <i>Olea</i>	Germany, Spain, Italy, France	Fischer <i>et al.</i> , 2016; Luque <i>et al.</i> , 2009; Prodi <i>et al.</i> , 2008; Bien and Damm, 2020; Mostert <i>et al.</i> , 2006; Gramaje <i>et al.</i> , 2015; Raimondo <i>et al.</i> , 2022
Ascomycota	Phaeomoniellaceae	<i>Phaeomoniella</i>	<i>Phaeomoniella chilamydospora</i>	<i>Vitis</i> , <i>Actinidia</i>	Spain, France, Turkey, Czech Republic, Portugal, Germany, Slovakia, Switzerland	Luque <i>et al.</i> , 2009; Pintos <i>et al.</i> , 2018; Akgül <i>et al.</i> , 2015; Baránek <i>et al.</i> , 2018; Agustí-Brisach <i>et al.</i> , 2021; Di Marco <i>et al.</i> , 2000; Chicau <i>et al.</i> , 2000; Fischer and Kassemeyer, 2003; Kakalikova <i>et al.</i> , 2006; Casieri <i>et al.</i> , 2009
Basidiomycota	Hymenochaetales	<i>Phellinus</i>	<i>Phellinus tuberosus</i>	<i>Prunus</i> (Plum), <i>Prunus</i> (Cherry)	Germany	Bien and Damm, 2020
Ascomycota	Nectriaceae	<i>Pleiocarpon</i>	<i>Pleiocarpon algeriense</i>	<i>Persea</i>	Italy	Aiello <i>et al.</i> , 2020b
Ascomycota	Pleurostomatales	<i>Pleurostoma</i>	<i>Pleurostoma richardsiae</i>	<i>Vitis</i>	Turkey, Spain	Ozben <i>et al.</i> , 2017; Pintos Varela <i>et al.</i> , 2016
Ascomycota	Phaeomoniellaceae	<i>Pseudophaeomoniella</i>	<i>Pseudophaeomoniella oleae</i>	<i>Olea</i>	Greece, Italy	Markakis <i>et al.</i> , 2022; Crous <i>et al.</i> , 2015
Ascomycota	Phaeomoniellaceae	<i>Pseudophaeomoniella</i>	<i>Pseudophaeomoniella oleicola</i>	<i>Olea</i>	Italy, Spain	Crous <i>et al.</i> , 2015; Agustí-Brisach <i>et al.</i> , 2021
Basidiomycota	Stereaceae	<i>Stereum</i>	<i>Stereum hirsutum</i>	<i>Prunus</i> (Almond), <i>Vitis</i>	Germany, Spain, France	Gierl and Fischer, 2017; Luque <i>et al.</i> , 2009; Larrignon and Dubos, 1997; Fischer and Kassemeyer, 2003
Basidiomycota	Polyporaceae	<i>Trametes</i>	<i>Trametes versicolor</i>	<i>Prunus</i> (Plum), <i>Vitis</i>	Germany	Bien and Damm, 2020; Fischer and Kassemeyer, 2003

2017; Pintos *et al.*, 2018; Batista *et al.*, 2020; Bien and Damm, 2020; López-Moral *et al.*, 2020a). Other *Diplodia* spp. occur rarely and share different hosts: *Dip. corticola* (grapevines), *Dip. juglandis* (walnut), *Dip. malorum* (apple), *Dip. prunicola* (almond), *Dip. pseudoseriata* (pistachio), *Dip. scrobiculata* (olive) (Phillips *et al.*, 2012; Alves *et al.*, 2014; Carlucci *et al.*, 2015b; López-Moral *et al.*, 2020a; Batista *et al.*, 2020).

*Neofusicoccum* is another common member of the *Botryosphaeriaceae*, which is a predominant FTD pathogen. The host range of *N. parvum* is broad, including walnut, grapevine, apple, chestnut, citrus, fig, nectarine, peach, pistacia, mango, blueberry, almond, avocado, and olive (Moral *et al.*, 2010; Gramaje *et al.*, 2012; Ismail *et al.*, 2013; Akgül *et al.*, 2014; Guarnaccia *et al.*, 2016; Aiello *et al.*, 2020a; Guarnaccia *et al.*, 2020; Hilário *et al.*, 2020a; López-Moral *et al.*, 2020a). To date, this pathogen has only been isolated from plants in Croatia, France, Greece, Italy, Portugal, Spain, and Turkey, indicating a preference for warm climates. Further *Neofusicoccum* spp. probably restricted to the Mediterranean area and associated with FTD mainly of grapevine and olive trees, are *N. australe*, *N. hellenicum*, *N. luteum*, *N. mediterraneum* and *N. vitifusiforme* (Gramaje *et al.*, 2012; Ismail *et al.*, 2013; Hilário *et al.*, 2020a; López-Moral *et al.*, 2020a; López-Moral *et al.*, 2020b; Gusella *et al.*, 2022).

*Lasiodiplodia* spp. were exclusively isolated from fruit crop plants in the south of Europe, including France, Italy, Spain, and Turkey. *Lasiodiplodia citricola* was isolated from grapevine, *L. pseudotheobromae* from olive, nectarine and pistachio, *L. theobromae* from olive, nectarine and grapevine, and *L. viticola* only from grapevine (Martin *et al.*, 2009; Aroca *et al.*, 2010; Carlucci *et al.*, 2013, 2015b; Akgül *et al.*, 2014; Comont *et al.*, 2016; Endes *et al.*, 2016; Borrero *et al.*, 2019; López-Moral *et al.*, 2020b). *Dothiorella sarmentorum*, however, was associated with FTD of walnut, apple, almond, pear and grapevine, mainly in areas with cool climates, such as the Czech Republic, Germany, the Netherlands, Norway, and Poland (van Niekerk *et al.*, 2004; Carlucci *et al.*, 2015b; Gierl and Fischer 2017; Dissanayake *et al.*, 2017; López-Moral *et al.*, 2020a). The closely related *Dip. omnivora* was also found in cool regions (the Czech Republic, France, Hungary) on walnut and grapevine (Linaldeddu *et al.*, 2016; Váczy *et al.*, 2018; Eichmeier *et al.*, 2020). *Dothiorella iberica* has been associated with FTD of walnut, apricot, hazelnut, apple and grapevine, in Spain, Germany and Italy (Phillips *et al.*, 2005; Carlucci *et al.*, 2015b; Gierl and Fischer 2017; López-Moral *et al.*, 2020a). *Neoscytalidium dimidiatum* has recently been related to canker and dieback of walnut, grapevine, cherry, almond and apricot in Turkey (Derviş *et al.*,

2019; Oksal *et al.*, 2019; Oksal *et al.*, 2020; Ören *et al.*, 2020; Ören *et al.*, 2022). This pathogen also caused shoot blight, canker and gummosis on citrus in Italy (Polizzi *et al.*, 2009).

Among *Diatrypaceae*, *Eutypa lata* has been commonly associated with FTD in Europe. This fungus was found on walnut, quince, grapevine, pistachio, almond, plum, cherry, blueberry, and olive, in the Czech Republic, France, Germany, Italy, and Spain (Prodorutti *et al.*, 2008; Laveau *et al.*, 2009; Luque *et al.*, 2009; Tosi and Natalini 2009; Wenneker *et al.*, 2011; Gramaje *et al.*, 2012; Gierl and Fischer, 2017; Baránek *et al.*, 2018; Aiello *et al.*, 2019; Bien and Damm 2020; Eichmeier *et al.*, 2020; Guarnaccia *et al.*, 2020; López-Moral *et al.*, 2020b; Kraus *et al.*, 2022). Other *Diatrypaceae* are less frequently associated with FTD in Europe; *Eutypella citricola*, *Eu. leptoplaca*, *Eu. microtheca* and *Eu. vitis* were found on grapevine in Spain (Luque *et al.*, 2009; Luque *et al.*, 2012). *Peroneutypa scoparia* was recently associated with dieback of walnut and blueberry in, respectively, the Czech Republic and Italy (Eichmeier *et al.*, 2020; Guarnaccia *et al.*, 2020). *Cryptovalsa ampelina* infected walnut and grapevine, in the Czech Republic, Germany, and Spain (Luque *et al.*, 2009; Martin *et al.*, 2009; Luque *et al.*, 2012; Kraus *et al.*, 2019; Eichmeier *et al.*, 2020).

*Diaporthaceae* is another diverse group of fungi causing FTD of fruit crops. Like some *Botryosphaeriaceae*, *Dia. eres* is ubiquitous in Europe, and affects a wide range of hosts including apple, blueberry, cherry, grapevine, peach, pear, and walnut (Casieri *et al.*, 2009; Thomidis and Michailides, 2009; Lombard *et al.*, 2014; Gierl and Fischer, 2017; Prencipe *et al.*, 2017; Bertetti *et al.*, 2018; Guarnaccia *et al.*, 2018; Pintos *et al.*, 2018; Bien and Damm, 2020; Eichmeier *et al.*, 2020). *Diaporthe foeniculina* caused FTD symptoms on almond, avocado, blueberry, chestnut, citrus, fig, grapevine, pear, and walnut, in France, Germany, Greece, Italy, Malta, Portugal, and Spain (Gramaje *et al.*, 2012; Annesi *et al.*, 2016; Guarnaccia *et al.*, 2016; Guarnaccia and Crous, 2017b; Gierl and Fischer, 2017; Santos *et al.*, 2017; Pintos *et al.*, 2018; Vakalounakis *et al.*, 2019; Mathioudakis *et al.*, 2020; Hilário *et al.*, 2020b; López-Moral *et al.*, 2020a). Other *Diaporthe* spp. have also been linked to FTD on many different crops, especially grapevine, but their occurrence is rare (Lombard *et al.*, 2014; Guarnaccia and Crous, 2017; Guarnaccia *et al.*, 2018; Pintos *et al.*, 2018), or some species such as *Dia. amygdali* are more host specific infecting mainly almond trees (León *et al.*, 2020).

Species of *Phaeoacremonium* are well known for their involvement in FTD of grapevine. This group of fungi is diverse, with *P. minimum* being the most prevalent in Europe affecting grapevine, olive, blueberry,

cherry and pistachio (Di Marco *et al.*, 2004; Mostert *et al.*, 2006; Prodi *et al.*, 2008; Luque *et al.*, 2009; Carlucci *et al.*, 2013; Gramaje *et al.*, 2015; Akgül *et al.*, 2015; Pintos *et al.*, 2018; López-Moral *et al.*, 2020b; Agustí-Brisach *et al.*, 2021). *Phaeoacremonium viticola*, *Pm. iraniana* and *Pm. parasiticum* are also common and have similar host ranges to *P. minimum*, including blueberry, grapevine, olive and *Prunus* trees (cherry, plum) (Mostert *et al.*, 2006; Prodi *et al.*, 2008; Luque *et al.*, 2009; Aroca *et al.*, 2010; Gramaje *et al.*, 2012; Gramaje *et al.*, 2015; Fischer *et al.*, 2016; Bien and Damm 2020; Agustí-Brisach *et al.*, 2021; Raimondo *et al.*, 2021). *Phaeoacremonium cinereum*, *Pm. croatiense*, *Pm. griseorubrum*, *Pm. hispanicum*, *Pm. infatipes*, *Pm. krajdienii* and *Pm. tuscanum* were only isolated from grapevine in Croatia, Italy, and Spain (Essakhi *et al.*, 2008; González and Tello, 2011; Gramaje *et al.*, 2011b, 2015). In contrast, *Pm. amygdalinum* (from almond), *Pm. hungaricum* (*Prunus* trees, plum and cherry), *Pm. olea* (olive), *Pm. venezuelense* (apricot), and *P. vibratile* (cherry) were only found on hosts other than grapevine (Gramaje *et al.*, 2012; Gramaje *et al.*, 2015; Bien and Damm, 2020; Raimondo *et al.*, 2021).

The *Nectriaceae* family includes diverse genera of FTD pathogens, currently named *Cylindrocarpon*-like asexual morphs, which are most known for their involvement in black foot of grapevine, mainly in France, Portugal and Spain (Alaniz *et al.*, 2011; González and Tello, 2011; Martin *et al.*, 2011; Cabral *et al.*, 2012; Agustí-Brisach and Armengol, 2013; Reis *et al.*, 2013; Pintos *et al.*, 2018; Berlanas *et al.*, 2020). However, these fungi have also been associated with decline of olive trees (in Italy), peach (Italy), plum (Bulgaria), apple (Portugal) and kiwifruit (Turkey) (Cabral *et al.*, 2012; Yaseen *et al.*, 2012; Carlucci *et al.*, 2013; Erper *et al.*, 2013; Piperkova *et al.*, 2017).

Investigation of wood necroses in crop trees often results in isolation of *Cadophora* spp., being *C. luteo-olivacea* the most common species in grapevine, but also occurs on olive, plum and blueberry, in Germany, Spain, France and Italy (Casieri *et al.*, 2009; Fischer *et al.*, 2016; Pintos *et al.*, 2018; Raimondo *et al.*, 2019; Bien and Damm, 2020; Guarnaccia *et al.*, 2020; Agustí-Brisach *et al.*, 2021). Furthermore, *C. fastigiata* (in Germany and Switzerland) and *C. viticola* (Spain) were exclusively found on grapevine (Casieri *et al.*, 2009; Gramaje *et al.*, 2015; Fischer *et al.*, 2016). More *Cadophora* spp., e.g. *Ca. malorum*, *Ca. viticola*, *Ca. novi-eboraci*, *Ca. prunicola* and *Ca. ramosa*, infected stone fruit trees (plum, cherry), walnut, apple and blueberry, in Germany, Italy and the Czech Republic (Prodi *et al.*, 2008; Gierl and Fischer, 2017; Eichmeier *et al.*, 2020; Bien and Damm, 2020).

Similar to *Cadophora* spp., *Collophorina* spp., including *Collop. australe*, *Collop. badensis*, *Collop. germanica*, *Collop. hispanica*, *Collop. neorubra*, and *Collop. paarla*, have been associated with wood necrosis, but mostly on stone fruit trees (apricot, almond, cherry, and plum) (Gramaje *et al.*, 2012; Gierl and Fischer 2017; Bien and Damm 2020). Only *Collop. hispanica* has also been linked to discolouration of chestnuts in Spain (Yurkewich *et al.*, 2017).

Besides the above-mentioned fungal families and genera, further species can cause FTD symptoms on different crops in Europe. For instance, *Phaeomoniella chlamydospora*, also associated with esca, appears in every European vineyard, and is probably host-specific for grapevine (Chicau *et al.*, 2000; Fischer and Kassemeyer, 2003; Kakalíková *et al.*, 2006; Casieri *et al.*, 2009; Luque *et al.*, 2009; Akgül *et al.*, 2015; Baránek *et al.*, 2018; Pintos *et al.*, 2018; Agustí-Brisach *et al.*, 2021). However, this fungus was also isolated from kiwifruit plants showing wood decay in Italy (Di Marco *et al.*, 2003). Relatives of *Pa. chlamydospora*, *Pseudophaeomoniella olea* and *Ps. oleicola*, are also host-specific, but for olive, and are linked to wood decay and shoot dieback in Greece, Italy and Spain (Crous *et al.*, 2015; Agustí-Brisach *et al.*, 2021; Markakis *et al.*, 2022). Species of *Colletotrichum*, such as *Col. fructicola*, *Col. gloeosporioides* and *Col. karstii*, have been related to canker and stem-end rot of avocado in Italy, and citrus disease in Italy and Portugal (Ramos *et al.*, 2016; Guarnaccia *et al.*, 2016, 2017). *Cytospora chrysosperma* affected grapevine and blackthorn (González and Tello, 2011; Gierl and Fischer, 2017; Kraus *et al.*, 2019). Its relatives *Cy. oleina*, *Cy. iistaciae* and *Cy. australe* were linked to dieback of olive and pistachio, in Greece, Italy and Spain (Rumbos 1988; Carlucci *et al.*, 2013; Moral *et al.*, 2017; Aiello *et al.*, 2019; López-Moral *et al.*, 2020b).

Several basidiomycetous fungi have been recorded as involved in FTD. *Fomitiporia mediterranea* is the predominant species in Europe, especially in vineyards, where it causes white rot in grapevine trunks (Rumbos and Rumbou 2001; Laveau *et al.*, 2009; Luque *et al.*, 2009; Akgül *et al.*, 2015; Baránek *et al.*, 2018; Moretti *et al.*, 2021; Kraus *et al.*, 2022). In addition, this fungus was also associated with decline symptoms on olive, kiwifruit, citrus, almond and pear (Elena *et al.*, 2006; Carlucci *et al.*, 2013; Markakis *et al.*, 2017; Olmo *et al.*, 2017). *Fomitiporia mediterranea* caused wood decay of kiwifruit, in Italy, Greece and France (Cortesi *et al.*, 2000; Elena and Paplomatas, 2002; Jamaux-Despréaux and Peros, 2003). *Stereum hirsutum*, was reported in Germany, Spain and France, where it was collected from decayed wood of grapevine, almond and chestnut

(Larignon and Dubos, 1997; Fischer and Kassemeyer, 2003; Luque *et al.*, 2009; Gierl and Fischer, 2017; Yurkewich *et al.*, 2017).

#### FUNGAL TRUNK DISEASES OF APPLE

Several pathogens infect trunks, branches and shoots of apple trees, causing cankers, twig blight, wood rot and, in severe cases, production losses and tree death (Sutton *et al.*, 2014). Symptoms on adult trees develop after long periods, while young plants can rapidly die (Marek *et al.*, 2013). Many Ascomycetes (approx. 36 species) have been associated with FTD of apple (Sutton *et al.*, 2014). Among these, *Neonectria ditissima* is the most serious threat as the cause of European canker, which has typical symptoms of elliptical, sunken areas of dark reddish-brown cankers. After the first year, the cankers become irregular and rough, with bark cracks and abundant production of perithecia (Sutton *et al.*, 2014; Weber and Børve, 2021). This disease has been reported in Germany, Ireland, Poland, and Portugal (Weber and Børve, 2021; Farr and Rossman, 2022).

The apple dieback syndrome is characterized by wood lesions, stunted plants, leaf chlorosis, bark discoloration and extensive cankers associated with wood decay, and progressive tree death (Sutton *et al.*, 2014; Mang *et al.*, 2022). Species in *Botryosphaeriaceae* and *Diaporthaceae* are considered the most relevant pathogens (Havenga *et al.*, 2019; Ali *et al.*, 2020; Diaz *et al.*, 2022). *Botryosphaeria dothidea* and *Dip. seriata* are the main pathogens found associated with dieback of apple trees in several countries (Havenga *et al.*, 2019; Diaz *et al.*, 2022; Ilyukhin *et al.*, 2022). Other *Diplodia* spp. recently reported as pathogenic on apple trees include *Dip. bulgarica* (Nourian *et al.*, 2021), *Dip. mutila* (Urbez-Torres *et al.*, 2016; Sessa *et al.*, 2017; Diaz *et al.*, 2019; Lodolo *et al.*, 2022), *Dip. intermedia* and *Dip. pseudoseriata* (Delgado-Cerrone *et al.*, 2016). Similarly, *Diaporthe* spp. were reported in association with dieback of apple, with *Dia. eres* dominating (Havenga *et al.*, 2019).

Considering the wide range of pathogens, apple dieback is considered as a disease complex (Mang *et al.*, 2022). However, only a few reports have been published on apple dieback in Europe. In Italy, *Dip. malorum*, *Phomopsis mali*, *Nectria* spp. and species in the *Botryosphaeriaceae* were reported as causing dieback, cracking and necrosis of trunks and from graft union sites of apple trees (Prodorutti *et al.*, 2012). Recently, Mang *et al.*, (2022) investigated apple orchards in Southern Italy, and characterized *N. parvum*, *Dia. eres*, *Dia. foeniculina*, *Pestalotiopsis australe*, *Trametes versicolor* and *Phomop-*

*sis* spp. The Basidiomycete *Inonotus hispidus* was also shown to be responsible for severe wood decay, canker and dieback symptoms on apple trees in southern Greece (Markakis *et al.*, 2017).

#### FUNGAL TRUNK DISEASES OF CITRUS

Twigs, branches and trunks of citrus plants affected by several FTD caused by diverse fungi have been reported in different continents (Timmer *et al.*, 2000; Mayorquin *et al.*, 2016; Bezerra *et al.*, 2021). *Colletotrichum* spp. are responsible of twig dieback in major producing areas in Asia and the USA (Huang *et al.*, 2013; Mayorquin *et al.*, 2019), and in Europe, where *Col. gloeosporioides* and *Col. karsti* were reported as dominant *Colletotrichum* spp. causing dieback of citrus twigs and shoots in Italy and Turkey (Aiello *et al.*, 2015; Uysal *et al.*, 2022).

Guarnaccia and Crous (2017) reported severe woody cankers of lemon trees caused by *Dia. limonicola* and *Dia. melitensis* in Malta, often showing gummous exudates and causing severe blight and dieback reported exclusively in Malta. Further *Diaporthe* species, including *Dia. baccae*, *Dia. foeniculina* and *Dia. novem*, are known as secondary pathogens causing wood diseases on citrus plants in Europe. *Diaporthe citri*, a key pathogen of citrus, was associated with shoot blight of *C. reticulata* in the Azores Islands, demonstrating for the first time the presence of a potential threat for citrus fruit production in Europe.

Several studies have recently revised species and genera of *Botryosphaeriaceae*, which include species largely distributed able to cause diseases of numerous plant species (Bezerra *et al.*, 2021; Zhang *et al.*, 2021). In particular, several studies have demonstrated the roles of *Diplodia*, *Dothiorella*, *Lasiodiplodia*, *Neofusicoccum*, and *Neoscytalidium* spp. as causal agents of FTD on *Citrus* spp. (Adesemoye *et al.*, 2011; Berraf-Tebbal *et al.*, 2020). Regarding European distribution, *Neoscytalidium dimidiatum* was reported to cause citrus branch canker in Italy (Polizzi *et al.*, 2009). A broad survey conducted by Bezerra *et al.*, (2021), through Greece, Italy, Portugal, Malta, and Spain, revealed the occurrence, genetic diversity, and pathogenicity of *Botryosphaeriaceae* species associated with symptomatic citrus cultivars. This study also demonstrated pathogenicity of *Botryosphaeriaceae* spp. in citrus-producing areas of these European countries. Phylogenetic multi-locus analyses identified four *Diplodia* species, with *Dip. pseudoseriata* being the most common, followed by three *Neofusicoccum* species, dominated by *N. parvum*, *Do. viticola* and *L. theobromae*.

Canker diseases of citrus are also caused by other fungal genera such as *Fusarium* and *Neocosmospora* (Sandoval-Denis *et al.*, 2018; Guarnaccia *et al.*, 2021), *Peroneutypa* (Timmer *et al.*, 2000), and *Phaeoacremonium* (Esparham *et al.*, 2020). Several *Fusarium* and *Neocosmospora* spp. were found in association with dry root rot, crown, trunk or twig cankers, or twig dieback, of citrus trees (Sandoval-Denis *et al.*, 2018).

#### FUNGAL TRUNK DISEASES OF GRAPEVINE

FTD of grapevine have become major problems in all grape producing countries, causing significant economic impacts from reduced production and vineyard longevity (AA.VV., 2022). Petri disease and black foot affect young grapevines while the diseases Eutypa, Botryosphaeria and Diaporthe diebacks, Cytospora canker and esca affect mature grapevines. These diseases are caused by a wide range of fungal pathogens producing diverse symptoms, including leaf and shoot distortion and discoloration, external wood cankers, internal wood necroses and staining, poor plant growth, mortality of roots, dieback and sudden grapevine collapse.

Petri disease is mainly caused by combinations of *Pa. chlamyospora* and 28 species of *Phaeoacremonium* (Gramaje *et al.*, 2018) with *Pm. minimum* being the most prevalent (Gramaje *et al.*, 2015). Other species associated with this disease include *Cadophora* spp. (Gramaje *et al.*, 2011a) and *Pleurostoma richardsiae* (Halleen *et al.*, 2007b). Up to 29 species of *Cylindrocarpon*-like asexual morphs belonging of *Campylocarpon*, *Cylindrocladiella*, *Cylindrodendrum*, *Dactylonectria*, *Ilyonectria*, *Neonectria*, *Pleiocarpon* and *Thelonectria* genera have been associated with black-foot of grapevine (Gramaje *et al.*, 2018; Aigoun-Mouhous *et al.*, 2019; Lawrence *et al.*, 2019; Akgül *et al.*, 2022). *Dactylonectria torresensis* is the most common species associated with this disease in Europe (Reis *et al.*, 2013; Carlucci *et al.*, 2017; Berlanas *et al.*, 2020) and Algeria (Aigoun-Mouhous *et al.*, 2019), while *Da. macrodidyma* has been considered the prevalent species in South Africa (Langenhoven *et al.*, 2018) and Canada (Úrbez-Torres *et al.*, 2014).

Eutypa dieback of grapevine is caused by 24 species of *Diatrypaceae* (Trouillas and Gubler 2010a; Luque *et al.*, 2012; Pitt *et al.*, 2013b; Rolshausen *et al.*, 2013), with *E. lata* being the most common and virulent fungus associated with this disease. Other genera of *Diatrypaceae* have been isolated from symptomatic wood, including *Anthostoma*, *Cryptosphaeria*, *Cryptovalsa*, *Diatrype*, *Diatrypella*, and *Eutypella* (Trouillas and Gubler 2010; Luque *et al.*, 2012).

At least 26 different species of *Botryosphaeria*, *Diplodia*, *Dothiorella*, *Lasiodiplodia*, *Neofusicoccum*, *Neoscytalidium*, *Phaeobotryosphaeria*, or *Spencermartinsia* have been reported as causal agents of Botryosphaeria dieback of grapevines (Úrbez-Torres and Gubler 2011; Pitt *et al.*, 2013a,c; Rolshausen *et al.*, 2013; Yang *et al.*, 2017). *Diplodia seriata*, *N. parvum* and *B. dothidea* are the most frequently isolated species (Úrbez-Torres, 2011). Several studies have indicated that most rapidly infecting wood-colonizing fungi, and therefore the most virulent, are species of *Lasiodiplodia* and *Neofusicoccum* (van Niekerk *et al.*, 2004; Úrbez-Torres *et al.*, 2008; Úrbez-Torres and Gubler, 2009).

Several species of *Diaporthe* have been associated with Diaporthe dieback of grapevines (Baumgartner *et al.*, 2013; Úrbez-Torres *et al.*, 2013a; Dissanayake *et al.*, 2015; Guarnaccia *et al.*, 2018). Among these, the disease is primarily caused by *Dia. ampelina* (formerly *Phomopsis viticola*) (Úrbez-Torres *et al.*, 2013a; Dissanayake *et al.*, 2015), which has long been known as the causal agent of the grapevine disease named Phomopsis cane and leaf spot in the United States of America, or excoriosis in Europe (Phillips 2000; Úrbez-Torres *et al.*, 2013a).

Several *Cytospora* spp. have been associated with Cytospora canker in Iran (Fotouhifar *et al.*, 2010; Arzanlou and Narmani, 2015), Canada and United States of America (Lawrence *et al.*, 2017), although their pathogenicity on grapevine has only been evaluated for *Cy. viticola* and *C. vinacea*.

Regarding Basidiomycetes associated with esca disease in adult vineyards, these belong to the genera *Inocutis*, *Inonotus*, *Fomitiporella*, *Fomitiporia*, *Phellinus*, and *Stereum* (Cloete *et al.*, 2015; Gramaje *et al.*, 2018), being *F. mediterranea* the most frequent species in Europe.

#### FUNGAL TRUNK DISEASES OF BERRY FRUIT

Dieback, canker, and twig and stem blights are common diseases of berry fruit crops (e.g., blueberry, cranberry). These have been associated with diverse fungal pathogens, but most frequently with species of *Diaporthe* and several genera in the *Botryosphaeriaceae* (Lombard *et al.*, 2014; Guarnaccia *et al.*, 2020; Hilário *et al.*, 2020a; Hilário *et al.*, 2021a). Surveys of orchards have shown that dieback and blight are the most common symptoms, which affect plant longevity and fruit yields, and therefore represent threats to production (Lombard *et al.*, 2014; Cardinaals *et al.*, 2018; Guarnaccia *et al.*, 2020; Flor *et al.*, 2022). *Diaporthe vaccinii* (= *Phomopsis vaccinii*) has been regarded as the major species of *Diaporthe* occurring on *Vaccinium* spp. (until recently included in

the EPPO A2 list), causing Phomopsis canker and dieback, twig blight, leaf spots and viscid rot (fruit rot), mainly on highbush blueberry (*V. corymbosum*) and cranberry (*Vaccinium macrocarpon* and *V. oxycoccus*), and also known as upright dieback and viscid rot of cranberry (EPPO Bulletin 2009; Lombard *et al.*, 2014; Michalecka *et al.*, 2017). *Diaporthe vaccinii* is probably widespread in the United States of America and Canada, but there are only a few reports of this fungus in Europe (Germany, Latvia, Lithuania, the Netherlands, Poland, Romania, United Kingdom) (Lombard *et al.*, 2014; Michalecka *et al.*, 2017).

Several *Diaporthe* species have been reported from symptomatic blueberry plants rendering it questionable that *Dia. vaccinii* is a major pathogen of this crop. Its taxonomic status has also been the subject of debate, and Hilário *et al.*, (2021b) proposed that *Dia. vaccinii* is a synonym for *Dia. eres*. *Diaporthe eres* is emerging as the most common and widespread pathogen of highbush blueberry in Europe, being associated with dieback, twig and stem blight, and canker, in Croatia (Ivić *et al.*, 2018), Italy (Martino *et al.*, 2022), the Netherlands (Lombard *et al.*, 2014) and Portugal (as *Dia. vacucae*, a synonym of *Dia. eres*) (Hilário *et al.*, 2020b). This fungus has also been reported as causing cane blight of raspberry in Italy (Guarnaccia *et al.*, 2022b) and of blackberry in Croatia (Vrandecic *et al.*, 2011). In addition to *Dia. eres* and *Dia. vaccini* on *Vaccinium* spp. in different countries in Europe, Lombard *et al.* (2014) described three new species, *Dia. viticola* (= *Dia. rudis*) from the Netherlands, *Dia. baccae* and *Dia. sterilis* were from Italy, *Dia. rudis* has also been reported from symptomatic highbush blueberry plants in Italy (Guarnaccia *et al.*, 2020). A survey of highbush blueberry orchards in Portugal revealed the occurrence of ten *Diaporthe* species in symptomatic (dieback and twig blight) plants, namely *Dia. ambigua*, *Dia. amygdali*, *Dia. crousii*, *Dia. foeniculina*, *Dia. hybrida*, *Dia. leucospermi*, *Dia. phillipsii*, *Dia. malorum*, *Dia. rudis* and *Dia. vacucae* (= *Dia. eres*) (Hilário *et al.*, 2020b, 2021a). Inoculation trials showed that *Dia. amygdali* and *Dia. eres* were the most aggressive to blueberry plants (Hilário *et al.*, 2021a).

Species from at least four genera of *Botryosphaeriaceae*, namely *Botryosphaeria*, *Lasiodiplodia*, *Macrophomina* and *Neofusicoccum*, are known to cause disease on *Vaccinium* spp. *Botryosphaeria* stem canker is caused by *B. corticis*, a species considered an important pathogen of blueberry, but that has been reported only in the United States of America (Phillips *et al.*, 2006). *Botryosphaeria dothidea* is known to cause stem blight and dieback and has been reported from highbush blueberry in Portugal (Hilário *et al.*, 2020a). Of the 12 spe-

cies of *Neofusicoccum* associated with stem blight and dieback of blueberry plants, *N. parvum* and *N. australe* have been reported in Portugal and Spain (Castillo *et al.*, 2013; Hilário *et al.*, 2020a), and *N. eucalyptorum* in Portugal. From these three species, *N. parvum* was the most aggressive in inoculation trials with highbush blueberry plants (Castillo *et al.*, 2013; Hilário *et al.*, 2020a).

Species of *Lasiodiplodia*, mostly *L. theobromae*, are important pathogens of blueberry in tropical and subtropical climates (e.g., Rodríguez-Gálvez *et al.*, 2020), but have been also reported in Europe associated with canker and dieback of highbush blueberry in Spain (Borrero *et al.*, 2019) and the Czech Republic (Pečenka *et al.*, 2021). *Macrophomina phaseolina*, a common soil-borne fungus, has also been reported on highbush blueberry plants, causing charcoal rot in Spain (de los Santos *et al.*, 2019) and blight in Serbia (Popović *et al.*, 2018).

*Godronia cassandrae* f. sp. *vaccinii* (= *Topospora myrtilli*, syn. *Fusicoccum putrefaciens*) causes *Godronia* canker, also known as *Fusicoccum* canker. This fungus may cause severe stem dieback of highbush blueberry, especially in young plants. This pathogen has been reported in North America and Europe, as a cause of severe losses in commercial highbush blueberry production (Strømeng and Stensvand, 2011). However, there are no recent reports of this fungus, so its status in Europe is uncertain.

Although not representing major pathogens, pestalotioid fungi of the *Sporocadaceae* have also been reported from blueberry plants with canker, dieback, and blight symptoms (Rodríguez-Gálvez *et al.*, 2020; Santos *et al.*, 2022). *Neopestalotiopsis clavispora* was reported from canker and twig dieback of highbush blueberry in Spain (Borrero *et al.*, 2018). Also on this host in Portugal, Santos *et al.*, (2022) reported three species of *Pestalotiopsis* (*P. australis*, *P. biseriata*, *P. chamaeropsis*) and four species of *Neopestalotiopsis*, including *N. rosae* and the newly described *N. scalabiensis*, *N. vaccinii* and *N. vacciniicola*.

## FUNGAL TRUNK DISEASES OF NUT TREES

Trunk pathogens of nut trees are underestimated phenomena associated with decline, even where the plants have shown obvious symptoms of trunk diseases. The first comprehensive study of fungal trunk pathogens detected in the wood of almond trees in Mallorca was published in 2012 (Gramaje *et al.*, 2012). Pathogens detected were: the *Botryosphaeriaceae*, *B. dothidea*, *Dip. olivarum*, *Dip. seriata*, *N. australe*, and *N. parvum*, confirmed by Olmo *et al.* (2016) and Arzanlou *et al.* (2016);

the *Diatrypaceae E. lata*; the *Togniniaceae Phaeoacremonium amygdalinum* and *P. iranianum*, confirmed by Raimondo *et al.* (2021); and the *Diaporthaceae Diaporthe amygdali*, later confirmed by Varjas *et al.* (2017), León *et al.* (2020), and Beluzán *et al.* (2022). Almond wood is also invaded by *Pleurostoma richardsiae* (Olmo *et al.*, 2015) and *Calosphaeria pulchella* (Arzanlou *et al.*, 2013). Holland *et al.* (2021b) described detailed symptoms on the almond wood associated with pathogens. They observed *Botryosphaeriaceae* canker, *Ceratocystis* canker, *Cytospora* canker, *Diaporthe* canker, *Collophorina* canker, *Eutypa* and *Pallidophorina* canker. Severe stem canker of almond trees caused by *Fusarium solani* was also reported by Markakis *et al.* (2021).

Walnut woody parts are commonly invaded by trunk pathogens, including *Diatrypaceae*, *Diaporthaceae*, *Botryosphaeriaceae* and *Togniniaceae*. In general, the spread of these fungi is similar in regions and countries such as: California (*Diaporthe*, *Neofusicoccum*) (Trouillas *et al.*, 2010; Agustí-Brisach *et al.*, 2019), Chile (*Diaporthe*, *Diplodia*, *Neofusicoccum*) (Díaz *et al.*, 2018; Luna *et al.*, 2022), China (*Botryosphaeria*, *Lasiodiplodia*, *Neofusicoccum*) (Yu *et al.*, 2015; Li *et al.*, 2016), the Czech Republic (*Cadophora*, *Cryptovalsa*, *Diaporthe*, *Diplodia*, *Dothiorella*, *Eutypa*, *Eutypella*, *Peroneutypa*, *Phaeoacremonium*) (Eichmeier *et al.*, 2020), Italy (*Botryosphaeria*, *Neofusicoccum*) (Gusella *et al.*, 2021), Romania (*Diaporthe*) (Mihaescu *et al.*, 2020), Spain (*Botryosphaeria*, *Diaporthe*, *Diplodia*, *Dothiorella*, *Neofusicoccum*) (López-Moral *et al.*, 2020a; Moral *et al.*, 2010), and Turkey (*Botryosphaeria*, *Neofusicoccum*) (Kara *et al.*, 2021; Yildiz *et al.*, 2022). Walnut wood also hosts *Ca. spacidis* and *Ca. novi-eboraci* (*Incertae sedis*) and these pathogens were detected in most surveyed orchards in the Czech Republic (Eichmeier *et al.*, 2020).

Hazelnut plants can be hosts of *Diaporthe* as described for Turkey (Arciuolo *et al.*, 2020) and *Fomitiporia* in Italy (Pilotti *et al.*, 2010). Pistachio trunk pathogens are also known. Several pathogens were isolated in California, including *Col. karstii*, *Cy. californica*, *Cy. joaquinensis*, *Cy. parapistaciae*, *Cy. pistaciae*, *Dia. ambigua*, *Didymella glomerata*, *Dip. mutila*, *N. mediterraneum*, *Pm. canadense*, and *Schizophyllum commune* (Nouri *et al.*, 2019). Survey of FTD pathogens of pistachio in Iran revealed *Pm. parasiticum* as a dominant species, followed by *Pm. minimum*, *B. dothidea*, *N. parvum*, *Pm. cinereum*, *Pm. viticola* and *Do. viticola* (Mohammadi *et al.*, 2015). Chen *et al.* (2015) collected *L. americana* sp. nov. from blighted pistachio shoots in Arizona, United States of America, and *N. hellenicum* sp. nov. in Greece, while in Italy the new pathogen *Liberomyces pistaciae* sp. nov. was detected (Vitale *et al.*, 2018). Nut trees such as

almonds, pistachios and walnuts were described in Iran as hosts of *Botryosphaeria*, *Collophorina*, *Cryptosphaeria*, *Diatrype*, *Diplodia*, *Dothiorella*, *Eutypella*, *Lasiodiplodia*, *Neofusicoccum*, *Pleurostoma* by Sohrabi *et al.* (2020).

#### FUNGAL TRUNK DISEASES OF STONE FRUIT TREES

Stone fruit trees are commonly affected by numerous wood-invading pathogens causing cankers and dieback. *Eutypa lata* was first reported as the causal agent of gummosis or dieback of apricot in Australia (Carter, 1957), and has since been known to affect several types of stone fruit trees (Matthee *et al.*, 1974; Carter 1982, 1995; Munkvold and Marois 1994; Rumbos, 1997). To date, at least 19 distinct species of *Togniniaceae* (i.e. *Pm. scolyti*, *Pm. minimum*, *Pm. australiense*, *Pm. alvesii*, *Pm. parasiticum*, *Pm. infatipes*, *Pm. iranianum*, *Pm. italicum*, *Pm. griseorubrum*, *Pm. junior*, *Pm. longicollarum*, *Pm. pallidum*, *Pm. prunicolum*, *Pm. subulatum*, *Pm. fuscum*, *Pm. griseorubrum*, *Togninia africana*, *T. griseo-olivacea* and *T. fraxinopennsylvanica*) have been associated with necrotic wood of stone fruit trees (Hawksworth *et al.*, 1976; Rumbos, 1986; Hausner *et al.*, 1992; Damm *et al.*, 2008; Spies *et al.*, 2018). As well, four *Cytospora* species (*Cy. chrysoasperma*, *Cy. longispora*, *Cy. plurivora*, *Cy. sorbicola*) have been identified as canker and dieback-causing pathogens in stone fruit trees including *Persica vulgaris*, *Prunus armeniaca*, *P. avium*, *P. cerasus*, *P. domestica* and *P. persica*, in several countries (Lawrence *et al.*, 2017).

Canker and branch dieback of sweet cherry trees caused by *Calosphaeriophora pulchella* has also been reported in California, Chile, South Australia and Spain (Trouillas *et al.*, 2012; Berbegal *et al.*, 2014; Auger *et al.*, 2021).

Studies conducted primarily in South Africa demonstrated the diversity of indigenous flora and the occurrence of newly identified fungi causing trunk diseases in adult stone fruit trees and propagation material (Damm *et al.*, 2007, 2010). The pathogenic potential of most of these species has been confirmed in pathogenicity trials. Damm *et al.* (2007) isolated several *Botryosphaeriaceae* species (*Dip. seriata*, *N. vitifusiforme*, *N. australe*, *Do. viticola*, *Dip. pinea*, *Dip. mutila*, *L. plurivora* and *Dip. africana*) from plum, peach, nectarine and apricot trees showing wood necrosis in South Africa. In another study on *Prunus* trees showing wood necrosis (Damm *et al.*, 2010), identified species of *Coniochaeta* (*C. velutina* and the two new species, *C. africana* and *C. prunicola*) and *Phaeomoniellales* (*Pa. zymoides* on *Prunus salicina*, and the new species *Pa. dura*, *Pa. effusa*, *Pa. prunicola*



and *Pa. tardicola* mainly in plum wood). The new genus *Collophorina* was also proposed, comprising *Colloph. africana*, *Colloph. capensis*, *Colloph. pallida* and *Colloph. rubra* that occurred frequently in necrotic peach and nectarine wood. Also in South Africa, apricot and plum trees were inhabited by five *Diatrypaceae* species with *E. lata* the most dominant, followed by *Cryptovalsa ampelina*, *E. cremea*, *Eutypella citricola* and *Eu. microtheca*, whereas no *Diatrypaceae* were found on peach and nectarine (Moyo *et al.*, 2018).

In a similar study conducted in Germany, *Pallidophorina paarla*, *Colloph. africana* and the two new species *Colloph. badensis* and *Colloph. germanica*, were associated with wood necroses on *Prunus* trees (Bien and Damm, 2020). Here, *Cadophora* was reported for the first time from *Prunus*, with *Ca. luteo-olivacea* and *Ca. novi-eboraci* dominating (Bien and Damm, 2020). *Cadophora prunicola*, *Ca. ramosa* and *Minutiella pruni-avium* were also described as new species.

A study in the western cape of South Africa (van der Merwe *et al.*, 2021) showed that stone fruit propagation material and nursery plants had latent infections of canker- and wood rot-associated fungi, with *Ca. luteo-olivacea* and *Dip. seriata* as the most frequently isolated. Sampled nursery trees were 22% infected, ungrafted rooted rootstock plants, 11%, dormant rootstock shoots, 6%, dormant buds, 1%, and green buds were 0.4% infected. Van der Merwe *et al.* (2021) also made 22 new records of fungal species on stone fruit, including (among others), three species of *Coniochaeta*, two of *Cadophora* and *Cytospora*, and one species of *Biscogniauxia*, *Eutypella* and *Peniophora*.

## FUNGAL TRUNK DISEASES OF OLIVE TREES

FTD of olive have been considered as emerging problems for olive cultivation. Several studies have shown many wood-inhabiting fungi in diverse groups as causal agents of discrete diseases in adult and nursery olive plants. Numerous *Botryosphaeriaceae* species (i.e. *B. dothidea*, *B. obtusa*, *Dip. mutila*, *Dip. seriata*, *Do. iberica*, *L. theobromae*, *N. australe*, *N. stellenboschiana*, *N. luteum*, *N. mediterraneum*, *N. parvum* and *N. vitifusiforme*) have been shown as causing olive twig and branch dieback in California, Croatia, Italy, Tunisia, South Africa and Spain (Moral *et al.*, 2010, 2017; Carlucci *et al.*, 2013; Kaliterna *et al.*, 2013a; Úrbez-Torres *et al.*, 2013b; Spies *et al.*, 2020; van Dyk *et al.*, 2021b).

Several *Togniniaceae* (i.e. *Pm. africanum*, *Pm. alvesii*, *Pm. italicum*, *Pm. minimum*, *Pm. oleae*, *Pm. parasiticum*, *Pm. prunicola*, *Pm. rubrigenum*, *Pm. sco-*

*lyti*, *Pm. sicilianum*, *Pm. spadicum* and *Pm. viticola*), *Phaeomoniellales* (i.e. *Neophaeomoniella niveniae*, *Pa. chlamydospora*, *Pseudophaeomoniella globose*, *Ps. oleae* and *Ps. oleicola*) and *Acremonium sclerotigenum*, *Ca. luteo-olivacea*, *Comoclathris incompta*, *Paracremonium* sp. and *Pleurostoma richardsiae* have also been indicated as causal agents of olive wood streaking, wilting, dieback and decline in California, Croatia, Greece, Italy, South Africa and Spain (Ivic *et al.*, 2010; Nigro *et al.*, 2013; Carlucci *et al.*, 2015; Markakis *et al.*, 2017, 2022; Spies *et al.*, 2020; Agustí-Brisach *et al.*, 2021; Lawrence *et al.*, 2021; van Dyk *et al.*, 2021b; Raimondo *et al.*, 2022).

The Basidiomycetes *F. mediterranea* (Fig. 2), *Fomitiporella viticola*, *Ganoderma lucidum*, *Phellinus linteus*, *P. robiniae*, *Schizophyllum commune* and *Trametes versicolor* have also been reported to be involved in olive wood rot and decay, in California, Greece and South Africa (Crous *et al.*, 2000; Úrbez-Torres *et al.*, 2013b; Markakis *et al.*, 2017, 2019; Lawrence *et al.*, 2021; van Dyk *et al.*, 2021b). Members of *Diatrypaceae* (i.e. *Diat. oregonensis*, *Diat. stigma*, *E. lata*), and species of *Cytospora* (i.e. *Cy. oleina*, *Cy. oleicola*, *Cy. olivarum*, *Cy. plurivora*, *Cy. pruinosa* and *Cy. sorbicola*) and *Diaporthe* (i.e. *Dia. viticola*, *Dia. rubis*, *Dia. foeniculina*) were associated with canker and twig and branch dieback diseases of olive trees in California, Greece, South Africa and Spain (Rumbos, 1988, 1993; Moral *et al.*, 2017; Lawrence *et al.*, 2017; van Dyk *et al.*, 2021b).

A recent survey by van Dyk *et al.* (2021b), in the Western Cape Province, South Africa, and coupled with pathogenicity tests, showed *Ps. globosa* as a major olive trunk pathogen, and several lesser-known fungi were also associated with olive trunk disease symptoms. These included *Biscogniauxia rosacearum*, *Celerioriella umnquma*, *Coniochaeta velutina*, *Coniothyrium ferrisianum*, *Didymocyrtis banksiae*, *Punctularia atropurpurascens*, *Vredendaliella oleae*, an undescribed *Cytospora* sp., *Geosmithia* sp., two undescribed *Neofusicoccum* spp., and four *Xenocylindrosporium* spp. Van Dyk *et al.* (2021a) also surveyed trunk pathogens in South African olive nurseries, and found several pathogens in *Nectriaceae*, *Diaporthaceae*, *Botryosphaeriaceae*, *Togniniaceae*, *Phaeomoniellaceae* and *Pleurostomataceae*, with *N. australe*, *Pleurostoma richardsiae* and *Pm. parasiticum* the most common fungi in propagating plant material.

## EPIDEMIOLOGY OF TRUNK DISEASES

Most FTD pathogens can infect planting material during propagation processes in nurseries. Several studies have shown evidence to support non-pathogenic



**Figure 2.** Wood decay (Esca) symptoms in olive trees in Thrace, Northeastern Greece, infected by *Fomitiporia mediterranea*. Canker in the trunk (A); white rot appeared after removing a trunk sector due to incorrectly adjusted irrigation sprinklers which created conducive conditions for fungal infection (B); carpophore of *F. mediterranea* formed on the trunk surface (C); trunk cross section revealing light-coloured wood rot surrounded by a brown necrotic zone (D).

endophytic phases for these fungi, as they have been isolated from asymptomatic mother plants and propagation material (Halleen *et al.*, 2003; Aroca *et al.*, 2010; Berlanas *et al.*, 2020; van der Merwe *et al.*, 2021). Several studies have confirmed that plant propagation stages are potential infection points in grapevine nurseries (Edwards and Pascoe 2004; Aroca *et al.*, 2010; Halleen *et al.*, 2003; 2007a; Agustí-Brisach *et al.*, 2013), and recent studies indicate the role of infected planting material in the dissemination of fungal trunk pathogens in stone fruit trees (Marín-Terrazas *et al.*, 2016; van Dyk *et al.*, 2021a; van der Merwe *et al.*, 2021; Capote *et al.*, 2022) and apple (Havenga *et al.*, 2019).

*Cylindrocarpon*-like asexual morphs are soil-borne. These fungi are commonly found in nursery fields and soils, so inoculum may already exist in soils before planting (Agustí-Brisach *et al.*, 2013; Berlanas *et al.*, 2017). However, most FTD pathogens are primarily spread through the dispersion of airborne spores. Depending on the fungal species, conidia or ascospores are released from pycnidia or perithecia embedded in the surfaces of dead wood and/or in bark tissues (Eskalen and Gubler, 2001; Rooney-Latham *et al.*, 2005; Úrbez-Torres *et al.*, 2014; van Niekerk *et al.*, 2010; Kraus *et al.*, 2020). This inoculum is released under favourable environmental conditions, which have been mostly associated with rain events and/or high relative humidity along with temperatures above freezing, which also favour spore germination (Úrbez-Torres *et al.*, 2010a; van Niekerk *et al.*, 2010). Spores then land on susceptible pruning wounds and/or natural openings to germinate and start colonization of xylem vessels and pith parenchyma cells (Mostert *et al.*, 2006).

Jiménez-Luna *et al.* (2022) showed the presence and diversity of air-borne spores of FTD pathogens in almond and walnut orchards in California, where incidence was influenced by host, age of the plants and precipitation. Arthropod-mediated dispersal of FTD pathogens has also been demonstrated in vineyards, indicating potential roles for arthropods in trunk diseases epidemiology (Moyo *et al.*, 2014; Kalvelage *et al.*, 2021, 2022). Agustí-Brisach *et al.* (2015) showed that pruning equipment can spread FTD pathogens under controlled conditions. They also found that high inoculum concentrations of FTD pathogens were required to produce successful infection. In grapevine, studies have shown that high risk infection periods may vary throughout each host growing season, and from year to year, but these periods can also overlap with host dormancy seasons in the Northern and Southern Hemispheres (Larignon and Dubos, 2001; Eskalen and Gubler, 2001; Amponsah *et al.*, 2009; Kuntzmann *et al.*, 2009; Quaglia *et al.*, 2009;

Úrbez-Torres *et al.*, 2010; van Niekerk *et al.*, 2010; Cloete *et al.*, 2015; Valencia *et al.*, 2015; González-Domínguez *et al.*, 2020; Billones-Baaijens *et al.*, 2018). An epidemiological equation model for *Pa. chlamydospora* was developed by González-Domínguez *et al.* (2020) in Spanish vineyards. They showed that dispersal dynamics of this fungus was best explained by hydro-thermal time which takes account of effects of temperature and rainfall.

FTD fungi are cosmopolitan, and can colonize a range of hosts as saprotrophs or plant pathogens, infecting natural ecosystems and cultivated crops. Patterns of multiple host infections have been reported for *Botryosphaeriaceae* (Damm *et al.*, 2007; Slippers and Wingfield, 2007; Mojeremane *et al.*, 2020), *Diatrypaceae* (Moyo *et al.*, 2019), and *Togniniaceae* (Damm *et al.*, 2008). This is also the case for *F. mediterranea*, a lignicolous fungus that has been found as the causal agent of wood decay in several woody hosts (Markakis *et al.*, 2017). The overlap of trunk disease pathogens between agricultural systems and native plant ecosystems has also been indicated (Damm *et al.*, 2007, 2008; Moral *et al.*, 2010; Trouillas *et al.*, 2010; Markakis *et al.*, 2017; Moyo *et al.*, 2019). The discovery of a single fungal species on multiple hosts has important epidemiological implications, giving circumstantial evidence that inocula travel between different woody hosts, so those hosts occurring in close proximity can provide inoculum to each other.

#### HYPOTHESES FOR INCREASED INCIDENCE OF TRUNK DISEASES

##### *Crop intensification*

Crop intensification can increase FTD incidence in the field. Intensive cropping systems provide favourable environments for infection, since microclimate resulting from high plant densities can increase wetness duration and decrease sunlight entry into tree canopies (Kraus *et al.*, 2018). Modern super-high-density systems also demand mechanization of cultural practices (e.g. pruning and harvesting), with consequential injuries that create conducive conditions to wound-penetrating fungi such as Basidiomycetes, *Botryosphaeriaceae*, *Diatrypaceae* and *Togniniaceae* (Moral *et al.*, 2010; Úrbez-Torres *et al.*, 2013b; Markakis *et al.*, 2017; Agustí-Brisach *et al.*, 2021). In viticulture, intensive pruning schemes (e.g. spur or cane pruning), can cause more frequent external FTD symptoms than minimal pruning schemes (Lecomte *et al.*, 2018, 2022; Kraus *et al.*, 2019). It was also assumed that intensive pruning causes more and larger pruning wounds on grapevine trunks, leading

to increased infections by wood degrading fungi, and consequent interruption of host vascular systems and increased symptoms (Travadon *et al.*, 2016; Kraus *et al.*, 2022).

Intensive crop production with high yields elevates plant water demand and in combination with the ongoing climate warming provokes drought stress, which enhances FTD development. For almond trees in southern Spain, water deficiency leads to increased dieback severity compared to well-watered trees (Agustí-Brisach *et al.*, 2020). In addition, under drought stress, grapevines were more susceptible to infection and colonization by FTD pathogens (Sosnowski *et al.*, 2016, 2021; Galarneau *et al.*, 2019; Hrycan *et al.*, 2020). The exact role of climate/environmental conditions (e.g. drought, rainfall, water availability) in FTD incidence is not completely clear and requires further investigation (Fischer and Peighami Ashnaei, 2019; Songy *et al.*, 2019).

Different woody crops (e.g. olive, grapevine and almonds) that are affected by the same fungal pathogens are commonly grown in neighbouring orchards in several Mediterranean countries (Fig. 3). This is likely to allow inoculum proliferation and flow among the orchards (Markakis *et al.*, 2017). Crop intensification is also likely to disturb microflora balances in agro-ecosystems, promoting transfer of trunk pathogens and their adaptation to new woody hosts. In recent years, emergence of new FTD has been shown for several woody crops (Damm *et al.*, 2010; Markakis *et al.*, 2017; van der Merwe *et al.*, 2021; van Dyk *et al.*, 2021a; b).

#### *Planting material and nursery practices*

Plant propagation in fruit crop and grapevine nurseries includes complex systems in which pathogen management is challenging. Infected nursery stock can be important long-distance vectors for FTD pathogens (Gramaje and Armengol, 2011). Studies in Europe on death of young or newly established fruit crop trees have shown that latent infections occurring during nursery propagation are important for development of cankers observed in the orchards (Brown *et al.*, 1994; Smit *et al.*, 1996; Marek *et al.*, 2013). Certified nursery trees are not commonly surveyed for latent fungal infections, which can lead to severe symptoms in newly established stone fruit orchards (Mostert *et al.*, 2016; van der Merwe *et al.*, 2021). McCracken *et al.* (2003) found that cankers caused by *N. ditissima* on scion shoots of 1-year-old commercial apple trees, developed after infections that occurred during the final stages of propagation. Marek *et al.* (2013) found that latent infections, occurring in nurseries, caused wood cankers during cold stor-



**Figure 3.** Typical landscape of adjacent vineyards and olive orchards in Crete, Southern Greece, which allows the inoculum flowing.

age of propagation material or after planting. Havenga *et al.* (2019), in South Africa, showed presence of fungal pathogens causing FTD on the 65% of assessed certified apple tree nurseries. The pathogens isolated from 1-year-old diseased commercial trees were also recovered from latent infections in nursery trees, confirming the roles of rootstock wounds and bud unions as infection sites.

Van Dyk *et al.* (2021a) reported the presence of eight known FTD pathogens of olive and other woody host from plant portions which were in direct contact with perlite/soil and water. Infected grapevine propagation material is considered to have a major role for disease occurrence in the field (Halleen *et al.*, 2003; Gramaje and Armengol, 2011). Stone fruit nursery trees have also been investigated. Isolations conducted from scions and rootstocks have highlighted the importance of these materials as sources of latent infections for nursery trees, showing the presence of FTD pathogens on the 22% of 1080 trees tested (van der Merwe *et al.*, 2021).

This information emphasizes the importance of incorporating integrated disease management that combines different preventative control measures throughout the nursery propagation processes, storage, and during crop establishment, in order to reduce incidence and severity of FTD in orchards (Gramaje *et al.*, 2018). Cultural practices such as the removal of dead and affected material, which often bring fungal fruiting bodies and spores, is important in all phases of propagation and plant establishment (Van Zyl 2011). Authorized fungicides and biological control agents should be used to protect pruning wounds throughout plant propagation to reduce infections in nurseries (Fourie and Halleen 2004). For grapevine, hot water treatments of scions/

rootstocks before grafting, and of the dormant grafted nursery grapevines are recommended practices to reduce pathogen inocula (Fourie and Halleen 2004; Halleen *et al.*, 2007b; Bleach *et al.*, 2013; Eichmeier *et al.*, 2018).

### Climate change

Increased incidence of FTD on woody hosts can be attributed to climate change (Chakraborty and Newton 2011; Kaliterna *et al.*, 2013a; Markakis *et al.*, 2017). Climate change prediction models foresee more frequent extreme weather conditions, along with increases in summer air temperature and drought stress for many crops in the Mediterranean region (Lung *et al.*, 2013). In California, Allen and Luptowitz (2017) predicted significant rainfall increases in response to warming climate. Alterations of wet and dry cycles, and extremely low and/or high temperature events will probably be more frequent, as consequences of the climate change. These phenomena may favour pathogen dispersal and adaptation to hosts other than their primary hosts, and this has been suggested for the extended host range of *F. mediterranea* (Elena *et al.*, 2006; Markakis *et al.*, 2017, 2019). This was also the case for the epidemic caused by *Dip. seriata* (a weak pathogen) that occurred in summer 2010 in Croatia, when severe dieback occurred in young olive trees previously exposed to low winter temperatures (Kaliterna *et al.*, 2013a). *Botryosphaeriaceae*-incited diseases are commonly more severe in years with high rainfall, when inoculum increases are followed by drought periods and host susceptibility increases (Ma *et al.*, 2001; Michailides and Morgan 2004; Marsberg *et al.*, 2017).

### Microbiome balance

All plants contain microorganisms as parts of their holobionts (Berg *et al.*, 2020). These microbiota and their activities, the so-called microbiome, have been shown to change for all diseases, and as conditions alter (Bettenfeld *et al.*, 2020). There are functional core microbiota playing central roles in plant physiology and health. Increased numbers of (latent) pathogens in the core microbiota and detrimental effects on other microorganisms, which can take place when the plants are weakened by other biotic or abiotic factors, can lead to increase virulence and visible plant symptoms (Bettenfeld *et al.*, 2020). “Satellite microbiota” (i.e. not occurring in every plant) can be also be affected.

For FTD, Bruez *et al.* (2020) suggested that fungal microbiota from non-necrotic woody tissues were similar in healthy and esca diseased grapevines. In non-necrotic

woody tissues, fungal and bacterial microbiota varied according to organs and seasons, but not according to disease status. *Phaeoemoniella chlamydospora*, was the most abundant fungus in non-necrotic tissues from healthy plants. The only difference between healthy and diseased young grapevines was the presence of white rot necrotic tissues in cordons that were dominated by *F. mediterranea*, associated with *Pa. chlamydospora* and a few bacterial taxa. Increased numbers of pathogens, and changes in mycobiomes, were recorded in different plant tissues.

Meta barcoding studies of grapevines in Portugal (Del Frari *et al.*, 2019) and Greece (Bekris *et al.*, 2021) have assessed the mycobiomes of grapevine trunks with esca, and cultivar and biogeography-dependent patterns were identified that could be used as to distinguish between healthy and diseased grapevines. By analyzing the microbiomes of healthy and diseased grapevines, strong interactions between the bacterial and fungal wood microbiomes in asymptomatic grapevines could be used for discovery of novel biocontrol agents (Cobos *et al.*, 2022). However, specific bacteria isolated from healthy or diseased host tissues have been described as potentially increasing wood degradation by esca pathogens. This has been shown for *F. mediterranea* (Haidar *et al.*, 2021). Some bacterial strains that degrade grapevine wood components (cellulose and hemicellulose) did not inhibit *F. mediterranea* growth *in vitro*, but had synergistic interactions with *F. mediterranea* by enhancing the degradation of wood structures (Haidar *et al.*, 2021). One of these strains has been described as belonging to a new species, *Paenibacillus xylinteritus* sp. nov. (Haidar *et al.*, 2022). Analyzing the microbiomes of healthy and diseased plants can pinpoint balance/imbalance that could lead to discovery of new types of interaction, such as other microorganisms that increase or decrease pathogen virulence.

### Limited availability of fungicides

Chemical control using fungicides has been the main strategy for FTD management both in propagation material produced in nurseries and adult plants in orchards, for which pruning wound protection is essential to reduce FTD incidence. Nevertheless, limited products are currently registered to effectively control FTD in Europe and worldwide. Thus, future research should be focused on expanding the range of chemical and alternative options for this purpose (Gramaje *et al.*, 2018). Available management strategies against FTD on grapevines have been widely investigated in the last decades and, for instance, many new biological control agents have been evaluated and registered to control FTD both in nurseries and vineyards, including fungi, bacteria and oomycetes

es, being *Trichoderma* spp. based products the most frequent (Gramaje *et al.*, 2018; Mondello *et al.*, 2018a,b). In the same way, it is necessary to progressively expand the range of treatments available for all types of fruit trees.

#### FUTURE DIRECTION OF FTD RESEARCH

Over the last years, fungal trunk pathogens incidence has globally increased in woody crops. The etiology is still complex, as many pathogens have been recently described associated with FTD symptoms. Disease management implies the adoption of precision farming technologies and alternative strategies to the use of synthetic fungicides (i.e., microbial biocontrol agents, plant defense elicitors and possible microbiome manipulations). This will provide a new scenario to understand the role of trunk pathogens in the whole cropping system. The integration of plant pathology concepts and methodologies with those of other disciplines will be needed to deliver new disease management strategies in a wider context. Here, we discuss the future direction of FTD research and identify some key issues that, we anticipate, must be faced to overcome the losses caused by these diseases.

A key challenge in this complex pathosystem is to develop tools and methodology that enable the rapid detection of FTD fungi in asymptomatic plants, especially in planting material, and the accurate diagnosis of the causal agents. High throughput sequencing (HTS) diagnostics is revolutionizing plant pathology. HTS methods are probably the most significant advances in molecular biology since the advent of the PCR process. Microbial/fungal genome sequencing or metagenomics/metabarcoding become a routine analysis and using the latest technology it is possible to generate near complete genomes (Robert-Siegwald *et al.*, 2017; Eichmeier *et al.*, 2022) or whole spectra of microbial/fungal communities (Eichmeier *et al.*, 2018; Bruez *et al.*, 2020; Gramaje *et al.*, 2022). There are also other applications of HTS technology which can serve understanding of the plant pathogen interaction as transcriptomics (Romeo-Oliván *et al.*, 2022) or small RNA sequencing (Eichmeier *et al.*, 2019).

The advent of precision farming technologies coupled with remote sensing methods opens entire new fields of research, where the performance of cultural practices for FTD management can be addressed. Imaging analysis is one promising method for a non-invasive detection of FTD. For grapevine, with hyperspectral- or multispectral imaging analysis, esca symptomatic and asymptomatic plants can be diagnosed even before clear foliar-symptoms appear (Junges *et al.*, 2018; Bendel *et al.*, 2020; Pérez-Roncal *et al.*, 2022). Even with

unmanned aerial vehicles, whole vineyards could be monitored this way for FTD, which facilitates the assessment of the vineyard's health status (Di Gennaro *et al.*, 2016). Furthermore, for Laurel wilt disease on avocado, it was possible to distinguish between healthy and asymptomatic trees based on hyperspectral analysis of the leaves (Hariharan *et al.*, 2019, Abdulridha *et al.*, 2016). In a trial with potted olive trees artificially infected with *F. mediterranea*, the uninfected population could be differentiated from the infected population with a good accuracy also by hyperspectral analysis of the leaves (Zapolska *et al.*, 2020). These examples show that spectral imaging analysis of leaves are convenient diagnostic tools to detect FTD in different perennial crops. In the future, this tool could be implemented into the plant protection management process for an early detection of the disease. With that, proper curative countermeasures can be applied and, thus, preventing the plant from becoming symptomatic.

For many IPM programs, including the management of FTD, there is a crucial need of decision-support tools to determine disease risk and the best moments for any intervention (Rossi *et al.*, 2012). Mathematical models that establish relationships between the amount of inoculum and disease development, integrating knowledge on the host-pathogen interactions and environmental data, are key components of any decision-support tool for plant disease management (Ojiambo *et al.*, 2017), and have been consistently incorporated in decision support systems (DSSs) to assist users in operational and tactical decision-making in crop protection. Model-based forecasting has the potential to improve the timeliness, effectiveness, and foresight for managing crop diseases, while minimizing economic costs and environmental impacts (Newlands, 2018). For instance, improving our knowledge about the dispersal patterns of FTD spores and its relation to environmental conditions is essential for identifying periods with a high risk of spore dispersal and for adopting management strategies, such as pruning wound protection.

Regulatory changes are reducing the availability of fungicide options, as the health and ecological hazards of the chemicals are increasingly raising concerns. The consumer demand for residue free products have stimulated research into new tools for pest management. Alternatives to synthetic fungicides are mainly represented by a number of microbial active ingredients. Agronomic practices, i.e., reduction of the inoculum in the field, should be combined with biological control in order to reduce the input of synthetic fungicides on the crop.

Nanoparticles (NPs) in size 1–100 nm have demonstrated activity in suppressing plant diseases. These

NPs are mainly metalloids, metallic oxides, nonmetals, and carbon nanomaterials. NPs have been integrated into disease management strategies as fungicides or as nanofertilizers to enhance plant health. Although there are reports of different NPs of single element and carbon nanomaterials affecting plant pathogens. Mainly Ag, Cu, and Zn have received much attention thus far. Some NPs act directly as antimicrobial agents but others work more in altering the nutritional status of the host and they activate various defense mechanisms (Elmer *et al.*, 2018). A recent study about the use of nanomaterials against selected FTD pathogens showed that AgSe nanoparticles (NPs), CuSe NPs, Ag NPs, Cu NPs and Se NPs can serve a significant inhibitory activity against *Dia. eres*, *Dip. seriata* and *E. lata* (Štůsková *et al.*, 2022). Little information is still available on the use of NPs against FTD pathogens. In addition, more research is needed to evaluate the impact of these treatments on the microbiome and the environment.

Other alternatives to synthetic fungicides are the substances of botanical origin. Recently, several authors described the antimicrobial ability of wood extracts against various fungal species (Kawamura *et al.*, 2011; Minova *et al.*, 2015; Salem *et al.*, 2015; Vek *et al.*, 2021). Špetík *et al.* (2022) demonstrated that lignans extract from knotwood of Norway spruce function against *Cad. luteo-olivacea*, *Da. torresensis*, *Dia. ampelina*, *Dia. bohemiae*, *Dip. seriata*, *E. lata* and *Pm. minimum* affecting grapevine. Further research is needed to test the efficacy of these products under field conditions.

Over the last few years, the importance of the plant microbiome, the potential role of endophytes in disease control and/or development, and the interactions among microorganisms has been postulated (Blundell *et al.*, 2022). The use of the most advanced technologies will contribute to the discovery of the next generation of microbial biofungicides. In recent years, designing microbial consortia (SynComs – synthetic microbial communities) has received a great deal of interest to overcome the variable results of bioncontrol agents under field conditions. SynComs are expected to be more robust to environmental changes than single-microbiome inoculants and are designed to mimic the natural microbiome function and structure. However, research is still needed to validate the consortia functionality at field scale.

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