Fusarium oxysporum: Genomics, Diversity and Plant–Host Interaction

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Abstract

Fusarium oxysporum is amongst the most important and diverse phytopathogenic fungi infecting almost 150 plant species, pathogen of each being specific and identified as formae speciales. It is a broad host range pathogen employing various infection strategies. Considering the economic importance and availability of sequenced genomes of several *Fusarium* species, its interaction with plant host is under intense investigation. Comparative genomics of four *Fusarium* species (*Fusarium graminearum*, *Fusarium oxysporum* f.sp. *lycopersici*, *Fusarium solani* and *Fusarium verticillioides*) have led to identification of basic and specialized/dynamic pathogenicity genes that confer host specialization. Fungal pathogenicity mechanisms, rapid emergence of pathogenic lineages and polyphyletic origins of host specialization have been identified but regulation of host and tissue specificity is still not known. Although comparative genomics, transcriptomics and proteomic analysis have greatly accelerated the identification of fungal functional genes, but assigning definitive roles is still a challenging task.

Keywords

Fusarium oxysporum · Diversity · Fungal–plant interactions · Genomics Pathogenicity genes · *Six* genes

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Fusarium: An Overview

Fusarium is a filamentous fungi (*Sordariomycetes: Hypocreales: Nectriaceae*) containing phytopathogenic and toxigenic species. The genus *Fusarium* wasfirst described by Link in 1809 as *Fusisporium* and is presently known as *Fusarium*, referred to as *Fusarium* sensu Wollenweber (Wollenweber 1931; Wollenweber and Reinking 1935). The genus is highly diverse with twenty monophyletic species complex and outgroups of nine species. Infestation of *Fusarium* coincides with that of the flowering plants nearly 91.3 million years ago (Fig. 10.1). *Fusarium* species are distributed on the plants, in soil and in water either as parasites, endophytes or saprophytes. Plant pathogenic *Fusarium* species cause wilts, blights, rots and cankers affecting field, horticultural, ornamental and forest crops in both agricultural and natural ecosystems. Fusaria also produce diversified toxic secondary metabolites (such as trichothecenes and fumonisins that can contaminate agricultural product, making them unsuitable for food and feed; trichothecenes can also act

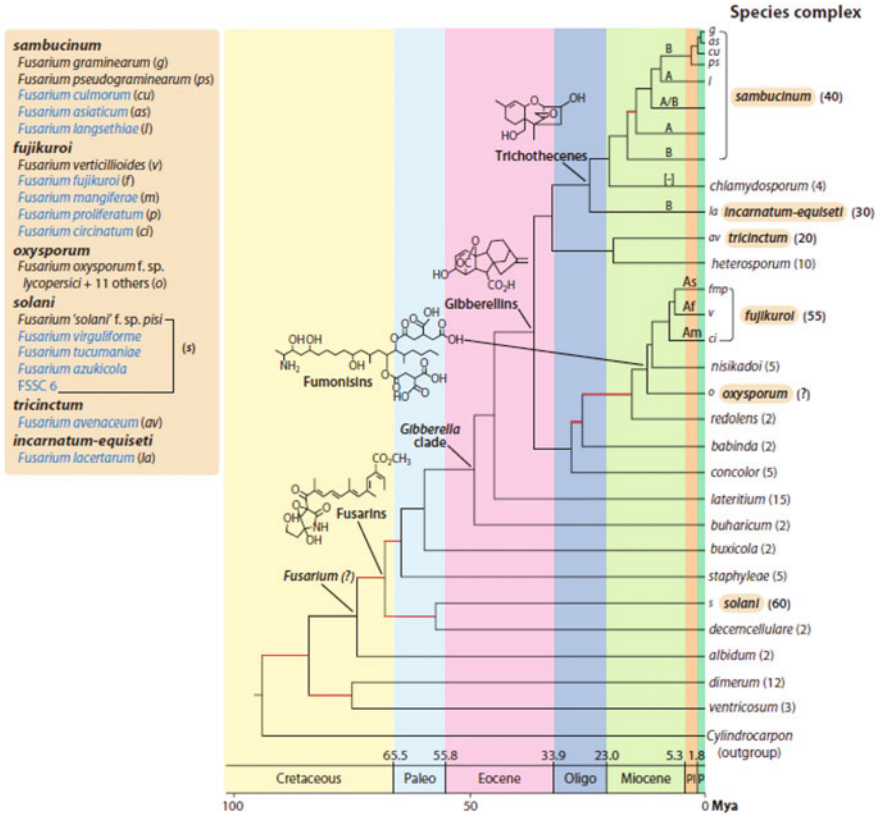

Fig. 10.1 Evolutionary diversification of the 20 *Fusarium* species. (reproduced from Ma et al. 2013, which was modified with permission from O'Donnell et al. 2013)

as virulence factor in plant diseases. A few *Fusarium* species are opportunistic human pathogens also causing corneal infections (O'Donnell et al. 2004).

Diversity Amongst *Fusarium* Species

Fusarium pathogens have diverse life cycles, niche specialization, host adaptation and specificity. *Fusarium graminearum* (Fg) and *Fusarium verticilloides* (Fv) are a narrow host range pathogens infecting predominantly the cereals, whereas *Fusarium oxysporum* (Fo) has a broad host range and infects both monocotyledonous and dicotyledonous plants (Armstrong and Armstrong 1981); besides, it is also an emerging pathogen on immuno compromised patients (O'Donnell et al. 2004) and other mammals (Ortoneda et al. 2004). *Fusarium* species vary in reproduction strategy; Fo is asexual, others are both asexual and sexual with either self-fertility (homothalism) or obligate out-crossing (heterothalism). *Fusarium* species produce meiotic (sexual) spores and at least three types of mitotic (asexual) spores. However, all *Fusarium* species do not produce all type of spores: Also, less than 20% of *Fusarium* species reproduce sexually (Fig. 10.2).

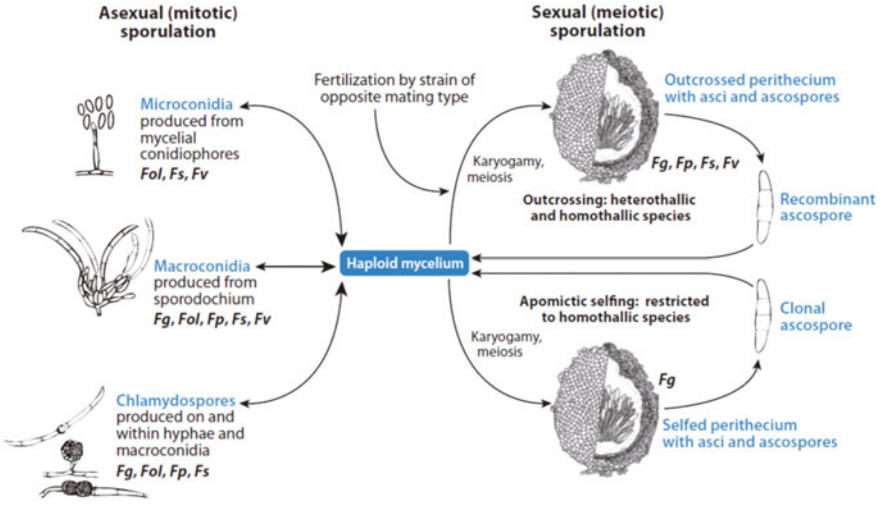

Fig. 10.2 Generalized life cycle of *Fusarium* depicting varying reproduction strategy (*Source* Ma et al. 2013) *Abbreviations* Fg, *F. graminearum*; Fol, *F. oxysporum* f. sp. *lycopersici*; Fp, *F. pseudograminearum*; Fs, *F. solani* f. sp. *pisi*; Fv, *F. verticillioides*

Fusarium oxysporum

Fusarium oxysporum Schlechtend, Fr. emended by Snyder and Hansen (1940) is an anamorphic species within the genus *Fusarium*. It is genetically heterogenous, polytypic morphospecies (O'Donnell and Cigelnik 1997; Waalwijk et al. 1996) which represents most abundant and ubiquitous soil-borne fungus; few strains have been reported from tundra soils as well (Stoner 1981) which exist as saprophytes and pervasive plant root endophytes. During saprophytism mode, *Fusarium* species degrade lignin (Rodriguez et al. 1996; Sutherland et al. 1983) and complex carbohydrates associated with soil debris (Christakopoulos et al. 1995, 1996). Root endophytic *Fusarium* species may be pathogenic or beneficial. A few strains are also pathogenic on gymnosperms. Pathogenic species within *F. oxysporum* have been differentiated into opportunistic, true pathogens and obligate pathogens based on the level/specialization of fungal–plant interactions (Scheffer 1991). Opportunistic parasites colonize weakened host plants or enter through wounds, have broad host range and exhibit low virulence. True pathogens require living plants for their growth; however, it can survive outside their hosts also, but are highly virulent on few host species. Obligate pathogens essentially require living host plant to complete their life cycle. They utilize host plant metabolism for their own growth, and in process alters plant growth pattern and morphology (Jackson and Taylor 1996). Members of *F. oxysporum* species complex are capable of causing vascular wilt diseases in over one hundred agronomically important plant species. However, individual *F. oxysporum* isolates are characterized by a high degree of host specificity; isolates that are pathogenic on single host are grouped into a forma specialis, e.g. *F. oxysporum* forma specialis *lycopersici* for tomato pathogens. Several *F.oxysporum* formae speciales consist of multiple independent lineages that have evolved polyphyletically. Interestingly, substantial genetic diversity has been revealed by molecular phylogenetic studies amongst isolates, supporting the present view that *F. oxysporum* represents a species complex (FOSC).

Reproduction

Fusarium oxysporum reproduces asexually, and its sexual state has never been observed (Booth 1971); it produces chlamydospores, microconidia and macroconidia (Nelson et al. 1983). Microconidia are uninucleate which germinate poorly with germination efficiency ranging from 1 to 20% (Ebbole and Sachs 1990). Macroconidia are multinucleate and germinate rapidly. Chlamydospores are resulting from the structural modification of vegetative hyphae or a thick-walled conidial cell and accessory spores (Schippers and van Eck 1981); *F. oxysporum* is diversified on shape of macroconidia, structure of micro-conidiophores, formation of chlamydospores (Beckman 1987).

Formae Speciales

Pathogenic and non-pathogenic *F. oxysporum* species cannot be distinguished morphologically unless pathogenic tests are performed. Pathogenic isolates of *F. oxysporum* (Fo) exhibit high level of host specificity which is directly linked to its pathogenicity to various plant species (Fravel et al. 2003). There are over 150 described formae speciales for Fo (Gordon 1965; Michielse and Rep 2009). Single forma specialis consist of isolates with the ability to cause wilt on a unique host or group of plant host species (Table 10.1). Thus, formae speciales is defined as an informal rank in classification scheme assigned on ability to cause disease in a unique host. Preliminarily, a forma specialis may be assigned to a strain based on the host from which a *F. oxysporum* isolate was recovered. It has been assumed that members of a forma specialis (f. sp.) are closely related and may have arisen from a common ancestor (Correll 1991; Kistler 1997). However, considerable genetic diversity has been reported within representative isolates of a forma specialis based on sequence comparisons in conserved regions of mitochondrial and nuclear DNA (Guadet et al. 1989; O'Donnell 1993). Kim et al. (1992, 1993) have analysed mt DNA of five formae speciales within cucurbitaceae, f. sp. *cucumerinum*, f.sp. *lagenaria*, f.sp. *luffae*, f.sp. *melonis* and f.sp. *niveum* that are pathogens of cucumber, calabash gourd, vegetable sponge, muskmelon and watermelon, respectively, and identified, fourteen mt DNA haplotypes within each forma specialis, out of which a few were common across formae speciales. Thus, all five formae speciales within cucurbitaceae are monophyletic (Kim et al. 1993). Similarly, Fo f. sp. *melonis* isolates were placed in two separate clusters, one closely related to Fo f. sp. *lagenaria* and other to Fo f. sp. *melonis* cluster. On the other hand, *F. oxysporum* isolates pathogenic to banana (f.sp. *cubense*) are more divergent than those of cucurbits. Koenig et al. (1997) identified 72 RFLP haplotypes in 165 isolates of f. sp. *cubense* and placed them into two major groups and seven lineages. Two lineages of Fo *cubense* were genetically similar to an isolate of f. sp. *niveum*, than to each other. Moreover, *F. oxysporum* f. sp. *cubense* strains from all over the world were placed in 10 clonal lineages. Thus, it is concluded that Fo *cubense* has polyphyletic origin, and pathogenicity to banana is acquired independently.

The isolates within forma specialis also have overlapping host ranges. Gerlagh and Blok (1988) reported that Fo causing wilt in cucumber was pathogenic to both muskmelon and watermelon and grouped it as f. sp. *cucurbitacearum*.

Pathogenic Races

Pathogenic races are sub-divisions of individual forma specialis based on differential virulence to various cultivars of the same host (Correll 1991). *F. oxysporum* forma specialis *cucumis* (Armstrong and Armstrong 1978) constitute, five races (0, 1, 2 and 1, 2), and their pathogenicity to different melon cultivars varies (Risser et al. 1976). All pathogenic races within a forma specialis might have a single

Table 10.1 List of *Fusarium oxysporum* formae speciales along with its host plant

S. no	Formae speciales (f.sp.)	Habitat/crop hosts	
		Botanical name	Common name
1.	*anoectochili*	*Anoectochilus formosanus*	Jewel orchid
2.	*aechemeae*	*Aechema fasciata*	
3.	*albedinis*	*Phoenix dactylifera*	*Date palm*
4.	*anethi*	*Anethum graveolens*	*Dill*
5.	*apii*	*Apium graveolens* *Tithonia rotundifolia*	*Delery* *Mexican sunflower*
6.	*asparagi*	*Asparagus officinalis*	*Asparagus*
7.	*batatas*	*Ipomoea batatas* *Nicontiana tabacum*	*Sweet potato* *Tobacco*
8.	*betae*	*Beta vulgaris*	*Beet root*
9.	*callistephi*	*Calistephuschinensis*	China aster
10.	*cannabis*	*Cannabis sativa* L.	Hemp
11.	*carthami*	*Carthamus tinctorium* L.	Safflower
12.	*cassiae*	*Cassia tora*L.	
13.	cattleyae	*Cattleya* spp.	Orchid
14.	*cepae*	*Allium* spp.	Onion
15.	*chrysanthemi*	*Chrysanthemum* spp.	
16.	*ciceris*	*Cicerarietinum*	Chickpea
17.	*coffeae*	*Coffea arabica* L.	Coffee
18.	*conglutinans*	*Brassicaoleracea* L. var.*capitat*	Cabbage
19.	*crassulae*	*Crassula ovata*	
20.	*cubense*	*Musa* spp.	Banana
21.	*Cucumerinum*	*Cucumis sativus* L.	Cucumber
22.	*Cyclaminis Gerlach* earlier known as *aurantiacum*	*Cyclamen persicum* Mill	Cyclamen
23.	*delphini* Laskaris	*Delphinium cardinale*	Forking larkspur
24.	*dianthi*	*Dianthus* spp. *Lychnis chalcedonica* L.	Carnation Maltese cross
25.	*echeveriae*	*Echeveria gavoides*	
26.	*elaeidis* Toovery	*Elaeis guineensis* Jacq.	Oil palm
27.	*eucalyptis* Arya & jain	*Eucalyptus gomphocephala D.C, E. rudis Endl.*	
28.	*fragariae*	Strawberry	
29.	*gerberae*	*Gerbera jamesonii* Hook	
30.	*gladioli*	*Gladiolus* spp., *Babina* spp. *Crocus* spp., *Freesia* spp., *Iris* spp., *Ixia* spp., *Sparaxis* spp., *Streptanthera* spp., *Tritonia* spp., *Watsonia* spp.	Gladioli and other flowers

(continued)

Table 10.1 (continued)

S. no	Formae speciales (f.sp.)	Habitat/crop hosts	
		Botanical name	Common name
31.	*hebae* Raabe	*Hebe buxifolia* (=*Veronica buxifolia* Benth.)	
32.	*herbemontis*	*Vitis aestivatis* Michx. *V. cinerea* *V. vinifera* L. hybrids	Herbemont grapes
33.	*lathyri* Bhide & Uppal	*Lathyrus sativus* L.	Lantana
34.	*lentis*	*Lens esculenta* Moench.	Lentil
35.	*lilii* Imle	*Lilium spp.*	Lily
36.	*lini*	*Linumusitatissimum* L.	Flax
37.	*lupini*	*Lupinus luteus*, *L. albus*, *L. angustifolia, L. mutabilis*	Lupine varieties
38.	*luffae*	*Luffa cylindrica*	
39.	*lycopersici*	*Lycopersiconesculentum*	Tomato
40.	*mathioli* Baker	*Mathiola incana var annua L.*	Stock
41.	*medicaginis* Weimer	*Medicago sativus L.*	Alfalfa
42.	*melongenae*	*Solanum melongena* L.	Egg plant
43.	*melonis*	*Cucumis melo* L.	Muskmelon
44.	*momordicae*	*Momordica charantia*	Balsam pear
45.	*narcissus*	*Narcissus pseudo-narcissus* L.	Daffodil, trumpet narcissus
46.	*nelumbicolum*	*Nelumbo nucifera* Gaertn	Lotus
47.	*nicotianae* Johns.	*Nicotiana tabacum* L.	Tobacco
48.	*niveum*	*Citrullusvulgaris* Schrad.	Water melon
49.	*opuntiarum* Pettinari	*Opuntia fucus-indica* Mill.	Spine less cactus alongwith other cactus
50.	*passiflorae* Gordon apud Purss	*Passiflora edulis*	Passion flower
51.	*palmae*	*Syagrus romanzoffiana* *Washingtonia robusta*	(Queen palm) (Mexican fan palm)
52.	*papaveris*	*Papaver nudicaule*	Iceland poppy
53.	*perniciosum*	*Albizzia* spp.	Mimosa
54.	*phaseoli* Kend. & Snyd.	*Phaseolus vulgaris L.*	Kidney bean
55.	*pini*	*Coniferae*	Conifers
56.	*phormii*	*Phormium tenax Forst.*	New Zealand flax
57.	*pisi*	*Pisum* spp.	Pea
58.	*psidii* Prasad, Mehta & Lal	*Psidium guajava* L.	Guava

(continued)

Table 10.1 (continued)

S. no	Formae speciales (f.sp.)	Habitat/crop hosts	
		Botanical name	Common name
59.	*querci*	*Quercus* spp.	Oak
60.	*radici-lupini* Weiner	*Lupinus angustifolius* L., *L. luteus* L., *L. albus* L.	
61.	*raphani* Kendr, Snyd.	*Raphanus sativus* var. *longi pinnatus* Bailey	Radish
62.	*racini*	*Ricinus communis L.*	Castor bean
63.	*rhois*	*Rhus typhina L.*	Slaghorn sumac
64.	*sedi* Raabe	*Sedum amecamecanum*	
65.	*sesami* Castell.	*Sesamum indicum L.*	Sesame
66.	*sesbaniae* Singh	*Sesbania aegyptiaca*	
67.	*spinaciae* (Sherb.) S & H	*Spinacia oleracea L.*	Spinach
68.	*stachydis*	*Stachys sieboldii Miq.*	Japanese artichoke
69.	*tracheiphilum*	*Vigna sinensis* *Glycine max*	Cowpea Soybean
70.	*trifolii* Bilai	*Trifolium* spp.	Clover
71.	*tuberosi*	*Solanum tuberosum* L.	Potato
72.	*tulipae*	*Tulipa* spp.	Tulip
73.	*vanillae*	*Vanilla planifolia*	Vanilla
74.	*vasinfectum*	*Gossypium* spp.	Cotton

ancient ancestor (monophyletic forma specialis) or affiliated to distinct clades (polyphyletic forma specialis).

Vegetative Compatibility Groups (VCGs)

Vegetative compatibility group (VCG) comprises of isolates that undergo somatic fusion and form stable heterokaryons. They are genetically similar and represent a clonal population (Puhalla 1985; Kistler 1997; Gordon and Martyn 1997). Moreover, a VCG could also be correlated with virulence (Katan et al. 1989; Manicom et al. 1990).

There is a correlation between forma specialis, VCG and pathogenic races. Sometimes all isolates of a forma specials correspond to a single VCG (Puhalla 1985). Within certain formae speciales, vegetative compatibility could be used as a method for identifying and differentiating pathogenic races. For example, a large collection of isolates each of Fo *apii* race 2, a pathogen of celery and Fo *vasinfectum* race 3, a pathogen of cotton from diverse geographical locations correspond to a single VCG. FOX isolates pathogenic to crucifers are placed in three distinct VCGs, each containing isolates pathogenic to a specific host. All Fo *niveum* isolates

are placed in three VCGs. VCG1 consist of all race 2 isolates, VCG 2 comprises of race 1 isolates from USA (all areas except Florida), Australia and Taiwan. VCG3 includes isolates from Florida.

Vegetative compatibility cannot always be used to identify races within a forma specialis because more than one race has been reported in a single VCG; also, isolates of single race may as well belong to different VCGs, e.g. four VCGs have been identified in f.sp.*pisi*, races 1 and 6 constitute single VCG, race 5 another and race 2 isolates were placed in two VCGs. Eight VCGs are identified in Fo*melonis,* out of which one contains isolates of different pathogenic races (Jacobson and Gordon 1988). Eleven VCGs have been identified in Fo *cubense* isolates from all over the world (Ploetz 1990; Ploetz and Correll 1988); a single VCG comprises of multiple races and a given race may belong to multiple VCGs. Similarly, in Fo *lycopersici,* three known races form single VCG as well isolates of one race are placed in multiple VCGs viz., race1 isolates belong to 41 different VCGs (Elias and Schneider 1991) and 46 distinct VCGs have been identified amongst a collection of isolates pathogenic to asparagus during greenhouse assay for testing pathogenicity (Elmer and Stephens 1989).

The high degree of VCG diversity has been observed in pathogenic and non-pathogenic strains of *F. oxysporum*. The mutations amongst isolates of single VCG lead to changes in virulence, which could be strong, weak, or non-existent (Leslie 1993, 1996). In general, RFLP patterns of mitochondrial (mt) DNA are identical within a VCG but vary between different VCGs of same formae speciales. All 44 isolates of Fo *albedinis* recovered from entire geographical range of disease occurrence were represented by a single VCG because of similarity in mt and nuclear DNA (Tantaoui et al. 1996). Four different models have been proposed to explain evolutionary relationships between VCG-race diversity in *F. oxysporum* (Kistler and Momol 1990). The VCG-race diversity is supported by genomic DNA and mitochondrial DNA (mt DNA), restriction fragment length polymorphism (RFLP) profiles. In *F. oxysporum, f. sp. melonis*a single VCG is shown to be associated with multiple races, e.g. VCG 0134 is associated with all four known races race 0, race1 and race1, 2 within f.sp. *melonis*; these races have identical mt DNA (Jacobson and Gordon 1990a, b) and nuclear DNA haplotypes (Schroeder and Gordon 1993). Minor genetic variation results in one pathogenic race giving rise to another; for example, race 3 was first identified in a field where race 2 of f.sp. *lycopersici* was already present. Isolates of race 2 and 3 constitute a single VCG (Elias and Schneider 1991) with identical isozyme (Elias and Schneider 1992) and nuclear DNA profiles. Co-occuring pathogenic and non-pathogenic Fo strains have similar mt DNA haplotype (Gordon and Okamoto 1992) or IGS haplotype (Appel and Gordon 1995) and placed in single VCG.

At times, non-pathogenic and pathogenic isolates are vegetatively compatible owing to a coincidental sharing of alleles at the loci-governing vegetative compatibility. The inter-isolate transfer of mt DNA through hyphal anastomosis has been reported. For example, in California, eight non-pathogenic isolates from a single field exhibited identical mtDNA haplotype and varying nuclear DNA fingerprints. Similarly, Fo f.sp. *vasinfectum* (Katan and Katan 1988) and f.sp. *spinaciae*

(Fiely et al. 1995) were different from root colonizing non-pathogenic *F. oxysporum* isolates based on vegetative compatibility, whereas non-pathogenic isolates of *F. oxysporum* associated with cyclamen were similar to pathogenic isolates based on polymorphisms in the intergeneric spacer region (IGS) of nuclear rDNA (Woudt et al. 1995). Hence, VCGs are not markers for pathogenicity.

Diversity of Plant–Fungal Interactions

Fungal–plant interactions are complex, diverse and give rise to morphological and physiological alterations in both partners. Fungi produce species-specific signals and employ species-specific mechanisms during interactions with plant host. The outcome of plant–fungal interactions can be saprophytic, symbiotic and pathogenic based on receptors and expression pattern of defence-related plant proteins which interact with specific fungus-derived molecules (Grigoriev 2013). Fungal endophytes become pathogenic if they are able to evade the plant's innate immunity that comprises physical barriers, mechanism of programmed cell death and production of antimicrobial compounds (Dangl and Jones 2001; Brundrett 2004).

The interactions between plants and their pathogens are constantly evolving, wherein pathogens employ innovative strategies to cause vascular infection. The process of vascular infection by *F. oxysporum* is complex and requires a series of highly regulated processes, adhesion, penetration and colonization. Pathogenic fungi form feeding structures similar to symbiotic fungi to establish obligate relationships with plants (Corradi and Bonfante 2012). Fungal pathogens after adhesion gain access into plant interior through stomata and wounds in leaf and stem tissue. However, in several cases, cell wall degrading enzymes (CWDEs) and secondary metabolites secreted by fungus facilitate penetration. Once pathogen penetrates host, it secretes protein effectors that suppress plant defence responses and promotes invasion (Lo Presti et al. 2015). Moreover, several morphological and biochemical alterations occur so that pathogenic fungi take over and utilize host metabolic pathways for their growth and development (Zeilinger et al. 2015).

Plant pathogenic fungal species have been classified as biotrophs, hemibiotrophs and necrotrophs, each interacting differently with their host plants. Pathogenic fusarium employ various infection strategies like biotropic (pathogen that colonizes living plant tissue and obtains nutrient from them), necrotrophic (pathogen that kills host cell and obtains nutrient from dead cells) and hemibiotrophic (pathogens that are initially biotrophic and subsequently necrotrophic) varying in mode of interaction. Biotrophic pathogens interact with the host through specialized hyphae which secrete host-specific effectors that suppress host immunity at interfacial zone (Perfect and Green 2001; Yi and Valent 2013). For example, powdery mildews develop primary and appressorial germ tubes on the plant cuticle and breach the cell wall using a combination of mechanical force and CWDEs (Takahashi 1985; Pryce-Jones et al. 1999). After plant cell wall penetration, a close metabolic interaction between plant host and biotrophic pathogen is established

(Horbach et al. 2011). Subsequently, the aim of fungus is to block host defence and utilizes host processes for feeding and growth (Giraldo et al. 2013; Yi and Valent 2013). In necrotrophic pathogens, virulence has been correlated with toxin synthesis (Wang et al. 2014). A combination of CWDEs, reactive oxygen species (ROS) and or toxins destroys host cells, their nutrients are released (Kistler and Momol 1990) which results in colonization of plant host (Wolpert et al. 2002). Hemibiotrophic pathogens are initially biotrophic later switching to a necrotrophic lifestyle (Struck 2006; Gardiner et al. 2013). The biotroph–necrotroph switch in hemibiotrophs depends on molecular and physiological factors. Several hemibiotrophs require extended periods to establish infection while for others, the switch to necrotrophy is rapid (Kabbage et al. 2015). From evolutionary perspective, biotrophy is primitive while necrotrophy is a recent phenomenon (Pieterse et al. 2009); hemibiotrophy is a transitional infection strategy for pathogenic fungi (Horbach et al. 2011). The infection strategy of necrotrophic fungi is less complex than that of obligate biotrophs. Necrotrophs exhibit restricted physiological interaction with plant host on account of poorly developed infection structures and smaller number of biochemical compounds required for host penetration.

A mutation in either, fungal pathogen or host receptor genes alters pathogen–plant interactions from resistant to susceptible or vice versa (Stracke et al. 2002; Giraldo and Valent 2013).

Fusarium Pathogenicity and Pathogenicity Factors

Pathogenesis is the complete process describing disease development in the host, from initial infection to production of symptoms (Lucas 1998), and pathogenicity is the ability for pathogenesis. *F. oxysporum* initially penetrates roots asymptomatically; subsequently, it colonizes vascular tissue and triggers massive wilting, necrosis and chlorosis of aerial produce. Certain species-producing toxin, fusaric acid initially infect floral tissue during anthesis, spreads to flower through central axis of inflorescence, eventually damaging and contaminating grains with toxins (Gardiner et al. 2013).

Fusarium pathogens use both general and specific pathogenicity factors/mechanisms to invade their hosts (Fig. 10.3). Hydrolytic enzymes involved in plant cell wall degradation and components of cellular signalling pathways, which are often required for systemic pathogen invasion, comprise general pathogenicity factors, whereas production and secretion of effectors and host-specific toxin are specific pathogenicity factors. The counter defence mechanism of plants plays significant role in pathogenesis and categorised as general and specific (Poppenberger et al. 2003). General defence mechanisms encompass production of antifungal proteins and activation of defence signalling pathways, whereas pathogen-specific include recognition of specific pathogen effectors by plant resistance gene products and detoxification of pathogen-specific toxins (Proctor et al. 2007).The specific properties that discriminate endophytic strains

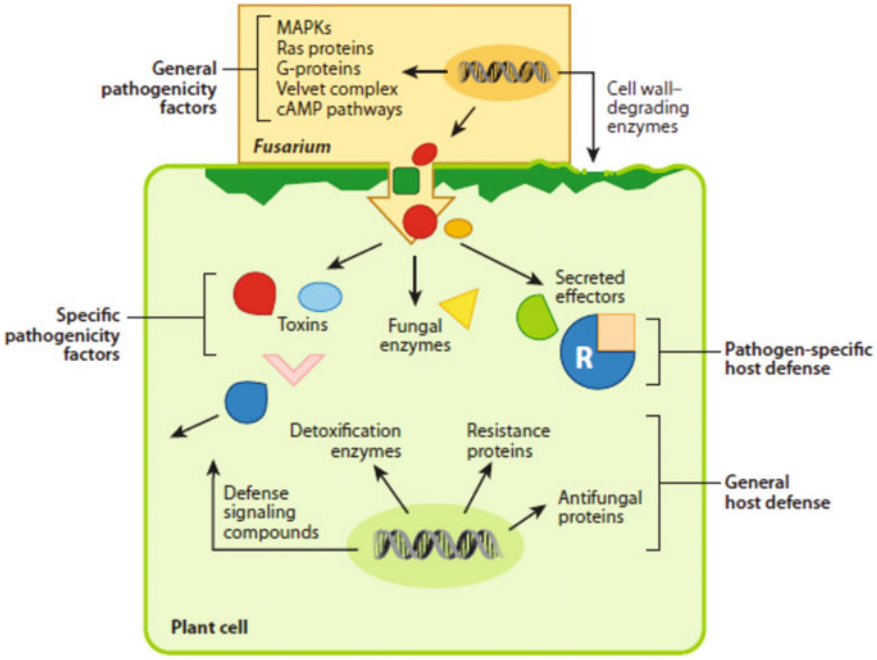

Fig. 10.3 Pathogenicity factors and host defence mechanisms during *Fusarium*–plant interactions (reproduced from Ma et al. 2013)

from closely related non-endophytic strains have been identified in several studies (Taghavi et al. 2010; Mitter et al. 2013; Amadou et al. 2008; Tisserant et al. 2013; Tian et al. 2012; Karpinets et al. 2014).

Comparative studies analysing genomic and metabolic network revealed major difference in cellular processes and metabolic capabilities of pathogenic ($n = 36$) and mutualistic ($n = 28$) plant microbes (Tian et al. 2012). Genes regulating biosynthetic processes and functions were enriched and more diversed amongst plant mutualists, while those controlling degradation and host invasion were detected in phytopathogens. Pathogens possess genes and regulons required for plant penetration and colonization (Wright et al. 2013). Moreover, mutualists utilize more stress-related compounds, whereas pathogens compound from plant cell wall. Genes encoding secretion systems, required to invade the host plant, were present in pathogen genome, while those encoding nitrogen fixation proteins and ribulose bisphosphate carboxylase/oxygenase (RuBisCO) proteins were specifically present in mutualistic bacteria (Karpinets et al. 2014). Bacteria with relatively large genomes often successfully colonize a wide range of unrelated plant hosts and soils, whereas strains with smaller genomes have a narrow host range (Mitter et al. 2013).

Fungi generally secrete a mixture of CWDEs to enter plant cells and secrete effectors, toxins or plant hormone-like compounds that manipulate the plants' physiology for its invasion and growth.

Cell Wall Degrading Enzymes

Fungal cell wall degrading enzyme (CWDE) system comprises of peroxidases and laccases for the degradation of lignin and glycoside hydrolases. Fungus secretes cellulases, hemicellulases and pectinases for degradation of cellulose, hemicellulose and pectin, respectively (Kubicek 2013). Genomics analysis of 103 fungi revealed that a large number of carbohydrate-active enzymes (CAZymes) such as carbohydrate esterase and pectate lyases (PL) are present in fungal pathogen compared to saprophytic fungi (Liao et al. 2013). Thus there is an upregulation of genes encoding CWDEs in *Fusarium graminearum,* the hemibiotrophic pathogen and *Magnaporthe oryzae* during infection of plant hosts (Kawahara et al. 2012; Zhao et al. 2013). In contrast, biotroph genomes possess few plant CWDEs encoding genes which completely lack glycoside hydrolase family 6(GH6) endoglucanase and cellobiohydrolase genes (Zhao et al. 2013).

Effector Proteins

Small effector proteins deregulate plant immune responses and facilitate pathogen in colonizing plant host (Rovenich et al. 2014). Fungal effectors are either apoplastic, those secreted into the plant extracellular component and cytoplasmic, those accumulated in plant membrane rich structure associated with invasive fungal hyphae (Giraldo et al. 2013). Apoplastic effectors include protease inhibitors that destroy host proteases. Plant proteases protect fungal cell walls against plant chitinase and small molecules minimising ROS levels. Host plant resistance (R) proteins recognize cytoplasmic effectors, thereby triggering the hypersensitive response (HR), a reaction characterized by rapid cell death in local infection region and thus blocks pathogen growth and spread (Giraldo and Valent 2013). Avirulence proteins are a type of cytoplasmic effectors. The interaction between an *avr* gene of pathogens and cognate resistance (R) gene of host leads to HR-mediated activation of host defence mechanism which prevents the pathogen invasion. This is an effector-triggered immunity (ETI) and is exemplified by C*f* 9 and *avr* 9 genes for the *Cladiosporum fulvum*-tomato pathosystem. The product of fungal race-specific *avr* 9 gene induces HR on tomato plants carrying the complementary resistance gene *Cf* 9. The fungal races virulent on *Cf* 9 tomato genotypes lack *avr* 9 gene. The genome analysis predicts that biotrophic maize pathogen *Ustilago maydis* encodes ~550 secreted proteins. Several of these are upregulated during host colonization (Djamei and Kahmann 2012). *U. maydis* secretes 'core' and organ-specific effectors. Core effectors suppress plant defence during the penetration stage and organ-specific effectors infect different plant tissue (Skibbe et al. 2010; Djamei and Kahmann 2012). *U. maydis* genome has effector-encoding gene clusters. There are 23 genes in the largest effector gene cluster, 19A. These are differentialy induced when different plant organs are colonized. It has been observed that deletion of complete 19A cluster abolished tumour formation in maize plants, whereas deletion of individual genes showed minor reduction in virulence (Kamper et al. 2006; Brefort et al. 2014).

Although, effectors are mostly proteins but a few are metabolites also. Fungal pathogens of genera *Cochliobolus*, *Alternaria* and *Pyrenspora* species secrete host-specific toxins (Tsuge et al. 2013), e.g. *Fusarium verticillioides* produces fumonisin (Arias et al. 2012) and *M. oryzae* pyrichalasin H and Ace 1 (avirulence conferring enzyme 1). Secondary metabolite-synthesized by *ace* 1 has not been identified yet (Collemare et al. 2008; Yi and Valent 2013). Pathogenic fungi deliver small non-coding RNAs into plant host cell to suppress plant immunity. *Botrytis cinerea* small RNAs silence genes confer immunity in *Arabidopsis* and tomato through hijacking host RNA machinery (Weiberg et al. 2013). Pathogens, e.g. *Cladosporium fulvum* and *M. oryzae* escape plant defence by secreting LysM effectors that bind to soluble chitin fragment and prevent them from detection by plant chitin receptors.

Signalling During Fungal–Plant Pathogen Interaction

The most critical step in fungal–plant interactions is the recognition of appropriate plant host. The process begins prior to direct contact between partners. Fungi detect chemical and physical signals and respond through differentiation, movement to an appropriate infection site, and/or formation of invasion-related structures (Kumamoto 2008; Bonfante and Genre 2010). The following section summarizes the current knowledge on the signals as well as signalling pathways involved in plant–fungal interactions with focus on fungal partner.

Signalling Mechanism

Root Exudates

Plant roots release both low and high molecular weight substances into rhizosphere. Amino acids, ion-free oxygen, sugars, phenolics and secondary metabolites are low molecular weight substances, whereas mucilage and proteins are high molecular weight substances (Bais et al. 2006). Root exudates can be produced both constitutively (so-called phytoanticipins) and in response to pathogen attack (so-called phytoalexins) (Baetz and Martinoia 2014). When soil-borne pathogen *F.graminearum* attacks barley, phenylpropanoids are released by its roots (Boddu et al. 2006). Similarly, the production of terpenes in barley roots is triggered by *Cochliobolus sativus* and *Fusarium culmorum* (Fiers et al. 2013).

Flavonoids also contribute towards signalling in plant–fungus interaction. They exert both positive and negative effect on fungal phytopathogens. On one hand, flavonoid inhibits spore germination and hyphal growth in several fungal pathogens, whereas on the other have a stimulatory effect. In case of *F. solani* f.sp. *pisi*, the isoflavonoid pisatin induces expression of *pda*1 encoding a pisatin demethylase, a virulence factor of this fungus (Khan et al. 2003). Recent studies revealed that class III peroxidase (POX) secreted by tomato roots function in chemotrophic

sensing by *F. oxysporum* via a pheromone receptor homologue and MAPK signalling (Turrà et al. 2015).

Oxylipins

Oxylipins are an oxygenated lipid secondary metabolites produced by plant and fungi. They are implicated in pathogenicity and promote disease progression. Fungal oxylipins act as endogenous signalling molecule that manipulates host lipid metabolism and alter its defence response (Tsitsigiannis and Keller 2007; Brodhagen et al. 2008). In contrast, plant oxylipins (jasmonates, JA) directly influence survival of invasive structures (Calvo et al. 1999), reproduction and production of secondary metabolites (Burow et al. 1997) in fungi.

Oxylipins act by inducing JA-responsive genes (Thatcher et al. 2009). JA signalling mediated by protein, coronatine insensitive (COL1) is responsible for susceptibility of *Arabidopsis thaliana* to *Fo* wilt. Oxylipins bind to G protein-coupled receptors (GPCRs) which induce cAMP signalling. Recently, it has been reported that cAMP signalling stimulated by plant oxylipin was absent in Gpr D (GPCR-encoding) mutant *Aspergillus nidulans* (Affedt et al. 2012). It was also reported that in the soil-borne plant pathogen *Aspergillus flavus*, endogenous oxylipins mediate, spore and sclerotia production and the biosynthesis of aflatoxin, which are regulated by Gpr C and Gpr D; Gpr C and Gpr D could be thus important for fungal–plant interactions.

Reactive Oxygen Species

Oxypilin-mediated signalling is linked to ROS-stimulated cell signalling during plant–fungus interaction, ROS interacts with phosphorylation cascades and controls transcription factors. Thus, mediating defence gene expression or oxypilins are generated through non-enzymatic oxygenation by ROS (Reverberi et al. 2012). In invading fungi nicotinamide adenine dinucleotide phosphate (NADPH) oxidase enzymes mediate production of superoxide. ROS accumulates at the plant–fungus interface and acts as signals for triggering attack and counterattack responses. In *M. grisea,* NOX1 and NOX2, NADPH oxidases trigger a local oxidative burst during plant infection (Egan et al. 2007). NOX1 and NOX2 are associated with appressorium formation. To establish infection, fungal pathogen must overcome plant's oxidative defense by employing ROS scavenging enzymes and modifying ROS accumulation in plant host, e.g. DES1 (defence suppressor 1) in *M. oryzae* (Chi et al. 2009), Leucine zipper (bzip) transcription factor and yes-associated protein (YAP1) in *U. maydis* (Molina and Kahmann 2007).

Plant Surface Signals

Plant signals, cutin monomers and leaf waxes trigger appresssorium formation in foliar rice pathogen *M.oryzae* (Liu et al. 2011; Perez-Nadales et al. 2014). Appressorium formation is mediated through multicopy suppression of budding defect2 (Msb2) signalling mucin and synthetic high osmolarity sensitive 1 (Sho1) tetraspanin protein (Lanver et al. 2014) present on fungus. Msb2 also plays an

important role in non-appressorium forming root-infecting, *F. oxysporum* by regulating plant infection and invasive growth through phosphorylating the Fmk1 MAPK in response to plant surface signals (Perez-Nadales and Di Pietro 2011). In pathogenic fungi, MAPK regulates the mechanical and enzymatic penetration of the host plant while the plant uses MAPK signalling for activation of immunity. In *M. oryzae*, cAMP-PKA signalling pathway controls plant surface recognition (Zhao and Xu 2007; Li et al. 2012) while Pmk1 (pathogenicity MAPK) stimulates appressorium formation and fungal growth in plant tissues (Xu and Hamer 1996). The membrane protein pth11 (aGPCR), that recognizes surface hydrophobicity, functions upstream of the cAMP-PKA pathway. It has been shown that although appressorium formation continues in PTH11 gene deletion mutant, they have reduced virulence (DeZwaan et al. 1999). This gives clear evidence of the overlapping roles of the Pth11 receptor and the signalling mucin Msb2 (which acts upstream of the Pmk1 MAPK cascade) in sensing surface hydrophobicity and regulation of appressorium formation (Xu and Hamer 1996; Liu et al. 2011).

In *U.maydis*, Kpp2 MAPK mediates virulence-related processes as filamentation and appressorium formation (Mendoza-Mendoza et al. 2009). Hence, there is a complex cross-talk of MAPK signalling with cAMP pathway. The two pathways appear to be connected at the Gpa3G protein subunit and the perforin 1 (Prf1) transcription factor. The Prf1 carries sequence motifs specific for PKA and MAPK-dependent phosphorylation, essential for its function (Bolker 2001). Similarly, proteins involved in calcium signalling are required for appressorium formation, turgor generation and host penetration in *M.oryzae* (Liu and Kolattukudy 1999). Hence, rice blast fungus is a model for deciphering the interplay of various signalling pathways in development of pathogenic potential.

Fungal Metabolic Diversity

The metabolic diversity of fungus determines whether fungus-plant interaction is beneficial or harmful (Zeilinger et al. 2015). Secondary metabolites enable fungus to colonize plant host systematically, survive in its niche and determines its virulence (Keller et al. 2005). Fungal species produce plant–specific secondary metabolites. The environmental changes affect the production of such secondary metabolites. Secondary metabolites associated with iron uptake govern the virulence potential of *A. brassicicola*, *C. heterostrophus, C. miyabeanus* and *F. graminearum* on their specific host plants (Oide et al. 2006).

Signalling Pathways

Plant distinguishes whether fungus is friend or a foe at multiple levels (Fig. 10.4). The first level is regulated by the receptor protein, pattern recognition receptors (PRRs) located in the plasma membrane. PRRs recognise microbial-associated molecular patterns (MAMPs) and pathogen-associated molecular patterns (PAMPs). These lead to activation of PAMP-triggered immunity (PT1) via calcium signalling and mitogen-activated protein kinase (MAPK) cascades. MAPK is

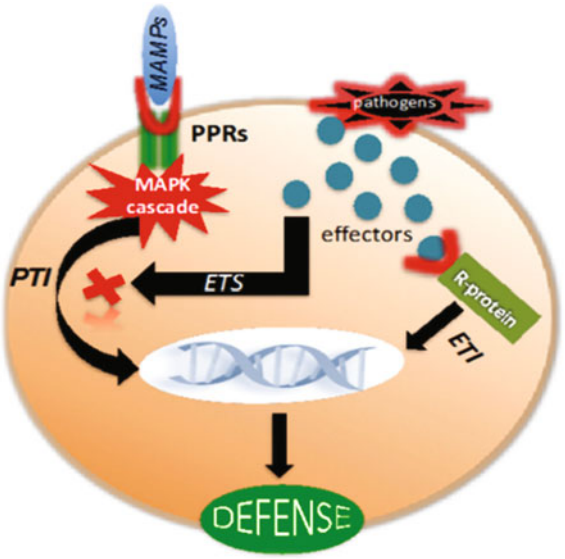

Fig. 10.4 Signalling in plant–fungal pathogen interactions. (reproduced from Zeilinger et al. 2015)

two-component system that regulates pathogenicity in fungal pathogens. It comprises of a membrane-bound histidine kinase which sense specific environmental stimuli and a response regulator that transmits the signal to a downstream pathway (Catlet et al. 2003). MAPK regulates stress responses and virulence in *C. heterotrophus* and *F. graminearum* (Oide et al. 2010) and in *Alternaria brassicicola* (Cho et al. 2009). Pathogens induce effector-triggered susceptibility (ETS) by blocking PTI response through effector proteins (Kazan and Lyons 2014). Calcium signalling is common cascade for plants to open a dialogue with their fungal partners because intracellular calcium levels are elevated during pathogenic as well as beneficial interactions (Navazio et al. 2007).

MAPK Cascade and Its Role in Virulence

The MAPK cascades of both partners help establish a molecular dialogue between plant and fungus (Hamel et al. 2012). MAPKs are organised as cascades consisting of three interlinked protein kinases, MAPK kinase (MAP3K), MAPK kinase (MAP2K) and MAPK, sequentially activated by phosphorylation (Widmann et al. 1999). The MAPK FmK1, an orthologue of the yeast Fus3/KSSI MAPKs, is essential for virulence of *F. oxysporum* on tamoto plants (Di Pietro et al. 2001). It is widely conserved and determines pathogenicity in all plant pathogenic fungi (Rispail et al. 2009). It is essentially required for all infection-related processes, invasive growth, fusion of vegetative hyphae and root adhesion (Di Pietro et al. 2001; Prados Rosales and Di Pietro 2008). Upstream and downstream components of this signalling cascade have been elucidated. The transcription factor Ste12 functions downstream of Fmk1 and regulates invasive growth of pathogen during plant infection (Rispail and Di Pietro 2009), and Msb2, a transmembrane protein is

an upstream component of this cascade (Perez-Nadales and Di Pietro 2011). In addition, *Saccharomyces cerevisae* high osmolarity (Hog 1) and cell integrity Mpk1 gene orthologues have been identified in *F. oxysporum* also. The GTPase Rho1, which function upstream of Mpk1, was essential for morphogenesis and pathogenicity (Martinez-Rocha et al. 2008).

Fusarium Genomics

The genomes of three economically important and phylogenetically diverse species, *Fusarium graminearum* (Fg) strain PH-1, *Fusarium verticilloides* (Fv) strain 7600 and *Fusarium oxysporum* f.sp. *lycopersici* (Fol) strain 4287 were compared and analysed. Fg strain H-1 causes head scab disease of small grain cereals, Fv strain 7600 is a maize pathogen-producing mycotoxin, fumonisin that contaminate grain and Fol strain 4287 is a tomato pathogen. The fully completed genome of *F. graminearum* PH-1 and its manually curated annotation is available at ensemble databank (King et al. 2015). Whole shot gun genome of Fol strain 4287 and Fv strain 7600 is available at BROAD Institute Website (Ma et al. 2010). The Fol genome (60 megabase) is about 44% larger to Fv (42 Mb), and 65% larger to Fg (36 Mb). Fol genome has a greater number of protein-encoding genes. 28% of the *F. oxysporum* genome corresponds to short interspersed elements (SINES) and class II transposable elements (Table 10.2). *Fusarium* genome is compartmentalized into core and accessory genomes. Core genome is identical in all *Fusarium* species and encodes for growth and survival, whereas accessory genome varies amongst formae speciales and characterizes host specialization, virulence and production of secondary metabolites. In *Fusarium solani* f. sp. *pisi*, the three

Table 10.2 Genome comparison amongst different *Fusarium species*

Species	*F. oxysporum*	*F. verticillioides*	*F. graminearum*
Strain	4287	7600	PH-1
Sequence coverage (fold)	6	8	10
Genome size (Mb)	59.9	41.7	36.2
Number of chromosomes	15	11[a]	4
Total scaffolds	114	31	36
N_{50} scaffold length (Mb)	1.98	1.96	5.35
Coding genes	17,735	14,179	13,332
Median gene length (bp)	1,292	1,397	1,355
Repetitive sequence (Mb)	16.83	0.36	0.24
Transposable elements (%)	3.98	0.14	0.03
NCBI accession	AAXH01000000	AAIM02000000	AACM00000000

N_{50} represents the size N such that 50% of the nucleotides is contained in scaffolds of size N or greater. Reprinted by permission from Macmillan Publishers Ltd: [Nature] (Ma et al. 2010), copyright (2010)

dispensible chromosomes have been linked to habitat specialization (Coleman et al. 2009) and pathogenicity towards pea (Han et al. 2001). In *Fusarium oxysporum* f. sp. *lycopersici*, chromosome 14 has been shown to convert a non-virulent strain into a virulent towards tomato via acquisition of the entire chromosome (Ma et al. 2010). In *F. graminearum*, regions of high single nucleotide polymorphism (SNP) density were found at the ends of chromosomes and in interstitial regions on three of the four chromosomes (Cuomo et al. 2007).

A total of over 9000 conserved syntenic orthologues were identified amongst Fol, Fv and Fg genomes (Ma et al. 2010). Fol and Fv orthologues display 91% nucleotide sequence identity within themselves and 85% with Fg orthologues. The orthologues of three species, Fol, Fv and Fg are enriched for predicted transcription factors ($P = 2.6 \times 10^{-6}$), lytic enzymes ($p = 001$) and transmembrane transporters ($p = 7 \times 10^{-9}$) when compared to other ascomycete genomes. In all three genomes, a total of 46 secondary metabolite synthesis (SMB) gene clusters have been identified. Microarray analysis confirmed that the genes in 14 of 18 Fg and 10 of 16 Fv SMB gene clusters were co-expressed. Ten out 14 Fg and eight out of the 10 Fv SMB gene clusters are co-expressed and novel (Ma et al. 2010).

Lineage-Specific (LS) Genomic Region

Lineage-specific (LS) genomic region, also known as supernumerary chromosome, constitutes accessory genome. They are usually small (<2 MB) and specific for forma specialis. They acquire foreign genes (i.e. xenologs) through horizontal transfer of an entire plasmid or chromosome from other *Fusarium* species and subsequent integration into the core chromosome. LS chromosomes are characterized by, (a) lack of housekeeping genes, (b) G + C content different than core chromosomal complement, (c) varying within related species and (d) 95% of transposable elements (TEs) present in an entire genome. The LS region harbours genes putatively related to host–pathogen interaction or pathogenicity (Ma et al. 2010). In all, 20% LS genes have been identified functionally. They encode for secreted effectors, transcription factors and virulence factors, involved in signal transduction. Analysis of genome sequence data suggests that *F. oxysporum* LS region differs considerably in strains with varying host specificities.

Comparisons amongst Fol, Fg and Fv genomes revealed the presence of four lineage-specific (LS) chromosomes. The genome assembly of Fol, Fv and Fg has 15, 11 and 4 chromosomes, respectively (Table 10.2).The number of chromosomes in Fg are less as compared to Fv and Fo due to chromosome fusion. The fusion occurs in high diversity regions (Cuomo et al. 2007). The genomic region in Fol is larger due to the presence of additional and unique sequences in extra chromosomes. All 11-mapped chromosomes, except for their telomere-proximal regions in the Fv assembly (41.1 Mb), correspond to 11 chromosomes in Fol (41.8 Mb). Syntenic region in Fol, Fg and Fv are 'core' region of genome. The core region of Fol has 80% similarity with that of Fg and 90% with that of Fv. About 40% of the Fol genome assembly is designated as Fol lineage-specific (Fol LS) region.

The Fol LS regions include four entire chromosome (3, 6, 14, and 15), parts of chromosome 1 and 2 (scaffold 27 and scaffold 31, respectively), and most of the small scaffolds not adhered to the optical map. The Fol LS region is 19 Mb, 28% of which is transposable elements (TEs). These are long interspersed nuclear elements (LINEs), retro elements copia-like and gypsy-like LTR retrotransposons, short interspersed nuclear elements (SINEs) and DNA transposons. DNA transposon classes like Pogo, hAT-like elements and MITEs are well represented in Fol. All in, about 74% TEs in Fol LS region are identifiable.

Fol genome has one intra-chromosomal and two inter-chromosomal segmental duplications, totalling approximately 7 Mb. Overall, these regions share 99% sequence identity indicating recent duplication events. Proteins encoded by 20% of Fol LS region are known. These are related to pathogenicity and include secreted effectors, transcription factors and virulence factors, involved in signal transduction and ethylene induction (Qutob et al. 2006). The enzymes that degrade or modify plant or fungal cell walls (Ma et al. 2010) are related to pathogenicity. Many of these enzymes have been reported to be expressed during early stages of infection on tomato root. It also harbours genes that encode for lipid metabolism and lipid-derived secondary messengers (Ma et al. 2010). These genes play important role in fungal pathogenicity. Fol LS region also has transcription factor sequences related to FTF 1 and specifically involved during early stages of *F. oxysporum* f. sp. *phaseoli* infection to its host (Ramos et al. 2007). The core genome in all *F. solani* isolates is well conserved (Coleman et al. 2009). Its accessory genome contains three LS regions distinct from its 'core' genome. *F. solani* LS region is distinct from that of Fol.

Therefore in conclusion, *Fusarium* species have similar core region and distinct LS regions. The LS regions are distinct in genes related to host–pathogen interactions.

Secondary Metabolite Gene Clusters

Fusarium species produce an array of bioactive secondary metabolites of which polyketides and non-ribosomal peptides are most abundant (Table 10.3). The comparative analyses of non-ribosomal peptide synthetases (NRPSs) and polyketide synthases (PKSs) from ten different *Fusarium* species, such as *F. avenaceum*, *F. acuminatum*, *F. culmorum*, *F. equiseti*, *F. fujikuroi*, *F. graminearum* (two strains), *F. oxysporum* (12 strains), *F. pseudograminearum*, *F. solani* and *F. verticillioides*, led to the identification of 52 NRPS and 52 PKSs orthology groups (Hansen et al. 2015). All NRPS and PKS were not functional in the strains analysed. A total of eight NRPSs (NRPS2-4, 6, 10-13) and two PKSs (PKS3, PKS7) were conserved in all the strains analysed. However, the products of the majority of PKSs and NRPSs are unknown. For example, in *F. graminearum*, the products of, only 8/15 PKSs and 3/19 NRPSs are known (Hansen et al. 2012b; Jørgensen et al. 2014; Sørensen et al. 2014). Some of the RPSs and PKSs genes have not been linked to metabolite production and may possibly represent pseudogenes.

Table 10.3 Different protein families including secondary metabolites produced in pathogenic and saprophytic fungi

Protein family	*Cochliobolus*	*Fusarium*	*Botrytis*	*Neurospora*	*Ashbya*	*Saccharomyces*
Peptide synthetases	30	37	29	7	0	0
Polyketide synthases	40	35	42	7	0	0
ABC transporters	51	54	46	39	17	29
Cytochrome P450s	63	40	33	44	ND	4
Protein kinases	112	94	70	120	ND	117

Source Yoder and Turgeon (2001)

Polyketide Synthases

Fungal pathogens synthesize polyketides from carboxylic acid derivatives (acetyl-CoA and malonyl-CoA) (Hopwood and Khosla 1992). Fungal PKSs contain five to eight functional domains and form two major groups based on their domain content: non-reducing PKSs (NR-PKSs) in which carbonyl groups are not reduced and reducing PKSs (R-PKS) in which carbonyl groups are partially or fully reduced. Fumonisin B, bikaverin, fusarubin and aurofusarin are examples of NR-PKS whereas fusaric acid and fusarielin are those of R-PKS. Fusarin C is NR-PKS with NRPS module. Zearalenone is both NR-PKS and R-PKS. Hansen et al. (2015) analysed the sequenced *Fusarium* strains through Blast P. The KS domains of PKS were extracted, phylogenetically analysed to identify PKS orthology group. Out of 52 different PKS genes, PKS3 and PKS7 were present in all the strains. In addition, PKS8 was also highly conserved amongst Fusarium strains although a part of KS domain was absent in *F. culmorum*, entire gene was absent in *F. oxysporum* f. sp. *melonis*. *F. graminearum* strain CS3005 shares 15 PKSs with Fg strain PH-1 which includes PKSs for biosynthesis of aurofusarin (PKS12), fusarubins PKS3, fusarins (PKS10), fusaristatin (PKS6 + NRPS7, and zearalenone (PKS4 + 13), (Sørensen et al. 2014) and a unique PKS (PKS52) which might have been acquired from *Colletotrichum* strains through horizontal gene transfer (HGT). *F. graminearum* and *F. culmorum* were closely related as there is overlap of 13 PKSs. PKS2 and PKS9 were absent in *F. culmorum*. Out of 14 putative PKSs identified in *F. pseudograminearum*, 13 have orthologue in *F. graminearum*, PKS40 was specific to *F. pseudograminearum* and encodes for W493A and B (a polyketide non-ribosomal peptide). Recently, PKSs and NRPS identified in *F. fujikuroi* earlier by Wiemann et al. (2013) have been renumbered (Hansen et al. 2015). Of the 17 PKSs identified in *F. fujikuroi*, 13 have orthologues in *F. verticillioides* and *F. oxysporum*, including bikaverin synthase (PKS16=BIKI) and hybrid PKS-NRPS (PKS18). PKSs ranging from 10 to 14 have been identified amongst completely sequenced 12 strains of different formae speciales. Six PKs were present in all 12 strains (PKS3, 7, 18, 20, 21 and 27), although the AT, KR, KS and MET domains are missing in *F. oxysporum* strain (F05176). The analysis

shows that *F. graminearum* had the highest number of species-specific PKSs followed by *F. solani, F. verticillioides* and *F. oxysporum*, respectively (Hansen et al. 2015). The polyketide synthase gene clusters in Fol, Fv, Fg and Fs have been characterized (Ma et al. 2010).

Non-ribosomal Peptide Synthetases (NRPSs)

These play a role in fungal pathogenesis because the products of several NRPSs are proven virulence factors, e.g. enniatin is essential for virulence of *Fusarium avenaceum* on potatoes (Herrmann et al. 1996), AM-toxin for *Alternaria alternata* on apple (Johnson et al. 2000) and HC-toxin for *Cochliobolus carbonum* race1 on corn (Walton 1996). The NRPS genes are up to 63 kb in size and form products in conjunction with other mega synthetases (Straight et al. 2007).

These are large multi-modular enzyme assembly lines (NRPSs) that synthesize non-ribosomal peptides (NRPs). The NRPSs consist of modules, each possessing catalytic domains in a specific order facilitating the sequential initiation and modification of the growing peptide chain. It has the adenylation domain (A) which recognizes the specific amino acid substrate, which is then transferred by the peptide acyl carrier domain (T or PCP) to the condensation domain (C) where the formation of the peptide bond takes place. These core domains are often supported by tailoring domains such as: thioesterase domains (TE) for cleavage or cyclization of the final peptide, reductase domain (R) for reducing the final peptide, epimerization domains (E) which can change the epimeric form of the amino acid substrate, cyclization domain (Cy) for modification of serines, and threonines and cysteines and N-methylation domains (NM) (Strieker et al. 2010). NRPSs were identified through Blast P analysis using a selected panel of variable A domains. The A domains were extracted from each NRPS and used for phylogenetic analyses. In all, six NRPS (NRPS2, 3, 6, 10, 11 and 12) were detected in all sequenced strains. NRPS 2 and NRPS6 are responsible for production of the siderophores ferricrocin and fusarinine, respectively (Oide et al. 2006; Tobiasen et al. 2007). NRPS6-produced fusarinine acts as an extracellular siderophore and is important for plant infection. NRPS4 was identified in all strains except *F. oxysporum* (Fo5176) and is reported to be involved in surface hydrophobicity in *F. graminearum* (Hansen et al. 2012a). In *F. graminearum*, a total of 16 NRPS genes were identified, of which NRPS32 was species-specific. In *F. culmorum*, 18 NRPS were identified. In *F. fujikuroi*, all except one (NRPS31) was common to those present in other sequenced *Fusarium* species. Out of a total of the 12 *F. oxysporum* strains, two *F. oxysporum* f. sp. *cubense* strain NRRL54006 and *F. oxysporum* f. sp. *pisi* strain HDV247 had identical distribution of NRPS genes. All *F. oxysporum* strains possess nine common NRPSs. These included two siderophore synthetases, NRPS2 and NRPS6 and the enniantin/beauvericin synthetase NRPS22. NRPS1 which encodes malonichrome, a type of siderophore is absent in *F. oxysporum* f. sp. *raphanin* and *F. oxysporum* Fo5156 and *F. fujikuroi*. Further, NRPS39, an orthologue of ferrirhodin synthatase, FNR1 was present in seven *F. oxysporum* species. Malonichrome (NRPS1), ferricrocin (NRPS2) and ferrirhodin (NRPS39) has similar domain structure (ATC-ATC-ATCTCTC).

Molecular Basis of Pathogenicity

Our understanding of molecular mechanisms involved in pathogenicity has improved through the genome sequencing and application of forward and reverse genetics. Michielse et al. (2009) identified more than 100 potential pathogenicity genes in *Fusarium oxysporum* f. sp. *lycopersici* upon analysis of 10,000 transformants for pathogenicity. With sequencing of more Fusarium genomes, similar genes have also been identified in *Fusarium* species other than f. sp. *lycopersici* (Kazan et al. 2012; Walter et al. 2010). A few with known functions have been listed (Table 10.4; Michielse et al. 2009; Sutherland et al. 2013). Functional characterization of putative genes indicates that those encoding for cell wall integrity, cell wall degrading enzymes, transcriptional regulators for carbon and nitrogen metabolism, cellular processes, such as amino acid and lipid metabolism, cell wall remodelling, protein translocation and degradation, seem to be important for complete pathogenicity of *F. oxysporum*. MAPK and cyclic AMP-protein kinase A (CAMP-PKA) cascade regulate virulence in Fo (Delgado-Jarana et al. 2005; Di Pietro et al. 2001; Jain et al. 2002, 2003, 2005). Cell wall integrity is necessary for invasive growth and resistance to plant defence compounds (Caracuel et al. 2005; Madrid et al. 2003; Martinez-Rocha et al. 2008; Martin-Udiroz et al. 2004, 2008). Cell wall degrading enzymes have been implicated in root penetration and colonization, but their role in infection process is not yet completely known. *F. oxysporum* f. sp. *lycopersici* virulence remains unaffected upon inactivation of individual genes, e.g. pectate lyase gene *plt*1, xylanase genes *xyl*3, *xyl*4 and *xyl*5, polygalacturase genes, *pg*1, *pg*5, *pgx*4 and subtilase gene *prt*1. Similarly, deletion of *xln*R did not affect virulence. However, targeted disruption of SNF1 reduced virulence as well as expression of various CWDEs indicating that central carbon metabolism plays key role in pathogenicity (Ospina-Giraldo et al. 2003). It has been reported that inactivation of Fnr1 (global nitrogen regulator) abolished the expression of nutrition genes, normally induced during early phase of infection, leading to reduction in pathogenicity. In addition, several plant degrading genes, pH-responsive transcription factors and regulators also play important role in pathogenicity. Moreover, the genes for peroxisome biosynthesis, ion homeostasis and toxin biosynthesis are also related to virulence. All the pathogenicity genes are categorized into basic and specialized pathogenicity genes.

Basic Pathogenicity Genes

The genes are common in *Fusarium* and other pathogenic fungi. These genes encode essential components of conserved pathways involved in sensing exogenous or endogenous signals. For example, mitogen-activated protein kinase (MAPK) signalling pathways in pathogens (Di Pietro et al. 2001; Hou et al. 2002; Urban et al. 2003), Ras protein (small GTPase) (Bluhm et al. 2007), G-protein signalling component and their downstream pathway (Jain et al. 2002; Park et al. 2012),

Table 10.4 Potential pathogenicity genes in *Fusarium oxysporum* f. sp. *lycopersici*

Category	Gene ID	Feature	Specific function
Chitin synthases	*chs*2, *chs*7, *chs*v, *chs*Vb	Cell wall integrity	Protect pathogen against host defences
GTPase	*rho*1	Cell wall integrity	Protects pathogen against host defences
β1,3-glucanosyltransferase	*gas*1	Cell wall integrity	
Pectate lyases	*plt*1	CWDEs	Pathogen entry into host
Xylanase genes	*xyl* 3, *xyl* 4 and *xyl* 5	CWDEs	Pathogen entry into host
Polygalacturonase Endo-polygalacturonase Exo-polygalacturonase	*pg*1, *pg*5, *pgx*4	CWDEs	Pathogen entry into host
Subtilase gene	*prt* 1		
FOL Frp1 gene	*frp1*	F-box protein	Assist pathogen to enter host xylem
FOX sucrose non-fermenting (SNF) gene	*snf1*	Expression of CWDEs through carbon catabolite repression	Assist pathogen to enter host xylem
Serine/threonine protein kinases	*ste*12		Regulate genes involved in MAPK cascade
FOX ste12 homologue	*fost*12		
FOL mitogen-activated protein kinase gene	*fmk*1		
Transcriptional regulator	*xlnR*		Expression of xylanolytic and cellulolytic genes
Global nitrogen regulator	*fnr*1		Expression of nutrition genes
FOX transcription factor	*fow*2	Zn(11) 2 Cys6 transcription factor	Rapid invasion of pathogen
FOX argininosuccinate lyase	*arg1*		
FOX plasmid pWB60S1 mitochondrial carrier protein gene	*fow1*		Mitochondrial carrier protein
FOX cyp55A1 gene	*cyp*55	*Cytochrome P450*	Regulate nitrogen respose pathway
CLC- voltage- gated Chloride channel gene	*clc1*		Regulate expression of laccase activity
Chloride conductance regulatory gene	*fpd 1*		Regulate expression of laccase activity
Cellular biosynthesis Mannose-6-phosphate isomerase			Mannose biosynthesis

(continued)

Table 10.4 (continued)

Category	Gene ID	Feature	Specific function
L-threo-3-deoxyhexlosonate aldolase			Catabolism of galacturonate
Catechol dehydrogenase			Catabolism of aromatic compounds
3-carboxy-cis,cis-muconate cyclase			
Succinate-semi aldehyde dehydrogenase (NADP+)			Enzyme involved in GABA-shunt
Peroxisome biogenesis	*pex* 1, *pex*10, *pex*12, *pex* 26		
Protein Translocation genes	*sec*61β, *sec*61α, *sec*62		
Major facilitator superfamily (MFS) multidrug transporter			Translocation of sugars, Kreb's cycle metabolites, aminoacids, osmolites, siderophores
Manganese superoxide dismutase	*mn* SOD		
Ion homeostatis		P type ATPase	
Redox balance NADH-ubiquinone oxido reductase			
G protein α subunit G protein β subunit	*fga*1 *fgb*1		

FOX, *Fusarium oxysporum*; FOL, *Fusarium oxysporum* f. sp. *lycopersici*

components of the velvet (LacA/veA/VelB) complex (Lee et al. 2012; Weimann et al. 2010) and cAMP pathway (Garcia-Martinez et al. 2012).

Specialized Pathogenicity Genes

These genes determine the pathogenicity of individual *Fusarium* species on specific plant host. These include *avr* genes and *six* (secreted in xylem) genes, mycotoxin and gibberellins encoding genes. Of these, *six* are directly involved in host pathogen interaction and encode for hundreds of small secreted proteins that play significant role in determining host specificity. Mycotoxins are additional virulence factors and act in a host or pathogenic-specific manner. A few *Fusarium* species produce mycotoxin, trichothecene which promotes virulence towards wheat (*Triticuma estivum*) and maize (*Zea mays*) but not barley (*Hordeum vulgare*)

(Jansen et al. 2005). The complete gibberellin gene cluster is present in all species within *F. fujikuroi* species complex but expressed/detected in only three, *F. fujikuroi*, *F. sacchari* and *F. konzum*. During disease development, gibberellins alter host tissues. The genes that encode for CWDEs and hydrolytic enzymes and are significant in gaining access to nutrition during infection are present in all *Fusarium* genomes. However, very few of these genes have been directly connected to pathogenicity. One exception is FGLI, a secreted lipase gene, which is responsible for virulence of *F. graminearum* of barley, maize and wheat (Ilgen et al. 2008, Voigt et al. 2005). Further, if FGL1 gene is overexpressed, the virulence of non-pathogenic MAPK mutant on wheat is restored (Salomon et al. 2012).

Six Genes

Host specificity between different races of *F.oxysporum* f. sp. *lycopersici* and tomato cultivar is determined by genes encoding small cysteine-rich effector protein termed *six* (secreted in xylem) (Rep et al. 2004). One of these proteins Avr1 triggers a resistance response in tomato plant carrying resistance (R) gene I-1. Interestingly, Avr1 also functions as a virulence effector by suppressing disease resistance conferred by two other R gene, I-2 and I-3 (Houterman et al. 2007). In Fo, all *six* genes are located on lineage-specific chromosome 14, also called the pathogenicity chromosome (Ma et al. 2010). Expression of the *six* genes requires a transcription factor Sge1 located on a core chromosome (Michielse and Rep 2009). Most of six genes are induced *in planta*.

Fusarium Oxysporum as a Model for Fungal Trans-Kingdom Pathogenicity

F.oxysporum f sp *lycopersici* isolate FGSC 9935 was the first fungal strain reported to cause disease both on plant (tomato) and mammalian host (immuno-depressed mice) (Ortoneda et al. 2004). The fungal genes encoding Fmk1, MAPK or small G protein Rho1 are essential for its pathogenicity on tomato but not on mice (Di Pietro et al. 2001; Martinez-Rocha et al. 2008), whereas pH response factor Pac C (Caracuel et al. 2003) or the secreted pathogenesis-related 1(PR1) like protein Fpr1 (Prados Rosales et al. 2012) are required for virulence in mice but not on plants. Recently, Hapx, a transcription factor that governs iron homeostasis, was identified in the fungal strain virulent on both plant and animal (Lopez-Berges et al. 2012). Similarly, the velvet protein complex contributes to infection of plants and mammals, in part by promoting the biosynthesis of beauverin, a mycotoxin (Lopez-Berges et al. 2013). The fungal pathogenicity on plants and animals has fundamentally distinct evolutionary origins despite involvement of common virulence proteins.

Evolution of Pathogenicity

The genetic and evolutionary relationships within and amongst formae speciales of *F. oxysporum* are revealed by sequence analysis of DNA-directed RNA polymerase II subunit and elongation factor-1α (EF-1α) genes (O'Donnell et al. 1998; Baayen et al. 2000; Mbofung et al. 2007). It was revealed that *F. oxysporum* formae speciales viz.,*lili* and *tulipae* were monophyletic (Baayen et al. 2000) while f.sp. *asparagi*, *cubense*, *dianthi, lycopersici* and *vasinfectum* were polyphyletic (O'Donnell et al. 2000; Baayen et al. 2000; Skovgaard et al. 2001; Cai et al. 2003). The evolution of pathogenesis in FOX isolates can be traced by analysing formae speciales of closely related plant species assuming that pathogens of closely related plant species are also closely related. The phenomenon of gene duplication (GD) and horizontal gene transfer (HGT) are responsible for their constant/continuous diversification. Virulence genes are acquired through HGT and further diversify due to GD and gene loss (Joaramillo et al. 2015; Steindorff et al. 2015). *Fusarium* genome very well exemplifies the role of HGT in acquiring diversity. A non-pathogenic strain of *F. oxysporum* f.sp. *lycopersici* was transformed into a tomato pathogen subsequent to transfer of a pathogenicity chromosome to it (Ma et al. 2013).

Origin of LS Regions

LS region in Fol might have originated in three ways: (i) Fol LS region was present in the last common ancestor of four *Fusarium* species but lost in Fg, Fv and Fs during vertical transmission, (ii) LS regions arose from the core genome by duplication and divergence of Fol lineage and (iii) LS regions acquired as a result of horizontal transfer. In all, 90% of the Fol genes in core regions have homologues in Fg and Fv. About 50% of the genes on FOL LS regions lack homologues in either Fg or Fv. sequence divergence between Fol and Fv orthologues in core regions was less as compared to Fol and Fg orthologues. The LS genes that have homologues in the other *Fusarium* species are roughly equally distinct from both Fv and Fg genes indicating that the phylogenetic history of the LS genes differs from genes in the core region of the genome. The distinct evolutionary trend of the core and LS region is supported by the distinct codon usage in LS encoding genes compared to core/conserved genes. The most significant differences were observed for amino acids Ala, Cys, Gln, Glu, Gly, Thr and Val, with a preference for G and C over A and T amongst Fol LS regions. Their third codon positions have higher GC content. Nearly 93% of 1285 LS-encoded proteins are homologous to other ascomycetous fungi. Phylogenetic analysis of 362 proteins sharing homologues in seven ascomycete genomes—Fg, Fv, Fol, Fs, *Magnaporthe grisea* (Dean et al. 2005), *Aspergillus nidulans* (Galagan et al. 2005) and *Neurospora crassa* (Galagan et al. 2003) indicates that they originated within the genus *Fusarium* but were placed basal to the three most closely related *Fusarium* species Fg, Fol and Fv. Thus, it is

concluded that Fol LS regions originated through horizontal acquisition of genes or gene regions from other *Fusarium* species.

Host Specificity: Variations in LS Regions

F. oxysporum is a species complex, comprising of several different asexual lineages that are non-pathogenic or pathogenic towards different hosts. Fo strains with varying host specificities have different LS regions which has been determined by comparing sequences of Fo strain 5176, pathogen of *Arabidopsis* (Thatcher et al. 2009) and Fo f.sp *vasinfectum* (Dowd et al. 2004), a pathogen of cotton. Although overall sequence divergence between common sequences of Fol and Fo5176 is less than 2%, sequences in the Fo LS region do not have homologues in Fo5176. Fov EST sequences (Dowd et al. 2004) have 99% sequence identity to the Fol genome in core region only. These are large-scale genome polymorphism within Fo as karyotypes between strains vary (Teunissen et al. 2003). Small polymorphic and conditionally dispensable chromosomes confer host-specific virulence in the fungi *Nectria haematococca* (Miao et al. 1991) and *Alternaria alternata* (Harimoto et al. 2007). Small (<2.3 Mb) and variable chromosomes are absent in non-pathogenic *F. oxysporum* isolates indicating that Fol LS chromosomes are responsible for pathogenicity towards specific host. Chromosome 14 of Fol is probably responsible for its pathogenicity towards tomato; its transfer rates could increase the overall pathogenesis. Proteome analysis revealed that small proteins Six1 (Avr3), Six3 (Avr2) and in-planta oxidoreductase (Oxi1) are secreted during colonization of Fol in tomato xylem system (Houterman et al. 2007; van der Does et al. 2008) and are involved in virulence (Houterman et al. 2009; Rep et al. 2004). It was further revealed that genes encoding above proteins are present on chromosome 14 present in strains causing tomato wilt, but are generally not present in other strains (van der Does et al. 2008). Further, genome analysis identified that *six*5, *six*6, *six*7 are also present on chromosome 14. It has been demonstrated that entire LS chromosome 14 could be transferred through simple co-incubation between two, otherwise genetically separated members of Fo leading to the emergence of new pathogenic lineages. Horizontal transfer of host specificity factors between otherwise distant and genetically separated lineages of Fo explains the host specialization originated polyphyletically (Gale et al. 2003). Fol LS regions are enriched for genes regulating host-pathogenic interactions. These chromosomes could transfer an entire set of genes required for host compatibility to a new genetic lineage in a single event. If transferred to the recipient lineage with an environmental adaptation different from the donor, the overall incidence of disease in a host increases because pathogenicity is introduced in the genetic background pre-adapted to a local environment.

Conclusion and Future Prospectives

The establishment of *F. oxysporum* as plant and animal infection model, the use of molecular genetics approaches in this species, and the genomic characterization of different *Fusarium* f. sp. has advanced our understanding of several key aspects related to fungal pathogenicity and its evolutionary origins.

The availability of sequenced genomes, gene annotations and genome expression data of various *Fusarium* spp., has conclusively shown that pathogens harbour conserved as well as specialized pathogenicity genes. With the analysis of genome expression data, several conserved pathogenicity genes, such as those encoding MAPKs have been characterized (Ma et al. 2013), whereas specialised pathogenicity genes linked to host adaptation or evasion have remained largely undefined except, secreted in xylem (SIX) effectors in *F. oxysporum* f. sp. *lycopersici* and several mycotoxins in other *Fusarium* species. The multiple processes, e.g. population diversity in specific genomic regions, horizontal acquisition of whole pathogenicity chromosomes (Ma et al. 2010) or a few pathogenicity-related genes (Gardiner et al. 2014) have been involved in evolution of pathogenicity and host specificity in *Fusarium*. Diversifying selection studies in the three *Fusarium* pathogens Fg, Fv and Fol with distinct pathogenicity profiles have revealed that all *Fusarium* species have core group of genes under purifying selection to preserve their function and specialised group of genes as those encoding proteins with a N-terminal [SG]-P-C-[KR]-P sequence motif and pathogen-associated proteins evolve at a faster rate. These rapidly evolving gene groups are functionally associated with pathogenicity (Sperschneider et al. 2015). Further, diversifying selection acts strongly on accessory-/lineage-specific chromosomes. Moreover, diversifying selection studies combined with *in planta* expression data are useful for identifying pathogenicity genes involved in competition between pathogen and host. Future developments will be in the form of improved gene annotations, greater sequencing depth in the genus so that genes that show weak signal for diversifying selection during pathogen–host interactions are identified and generation of *in planta* expression data for other *Fusarium* species to detect effector production at early stages during infection. In future, *F. oxysporum* is likely to provide valuable new insights into molecular mechanisms of host specificity and pathogenicity in evolutionarily distant hosts.

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References

Affeldt KJ, Brodhagen M, Keller NP (2012) *Aspergillus* oxylipin signaling and quorum sensing pathways depend on G protein-coupled receptors. Toxins 4:695–717

Amadou C, Pascal G, Mangenot S, Glew M, Bontemps C, Capela D, Carrere S, Dossat C, Lajus A, Marchetti M, Poinsot V, Rouy Z, Servin B, Saad M, Schenowiyz C, Barbe V, Batuit J,

Medigue C, Masson-Boivin C (2008) Genome sequence of β-rhizobium *Cupriavidus taiwanensis* and comparative genomics of rhizobia. Genome Res 18:1472–1483

Appel DJ, Gordon TR (1995) Intraspecific variation within populations of *Fusarium oxysporum* based on RFLP analysis of the intergenic spacer (IGS) region of the rDNA. Exp Mycol 19:120–128

Arias SL, Theumer MG, Mary VS, Rubinstein HR (2012) Fumonisins: probable role as effectors in the complex interaction of susceptible and resistant maize hybrids and *Fusarium verticillioides*. J Agric. FoodChem 60:5667–5675

Armstrong GM, Armstrong JK (1978) *Formae speciales* and races of *Fusarium oxysporum* causing wilts of Cucurbitaceae. Phytopathology 68:19–28

Armstrong GM, Armstrong JK (1981) *Formae speciales* and races of *Fusarium oxysporum* causing wilt diseases. In: Nelson PE, Toussoun TA, Cook R (eds) *Fusarium* diseases, biology, and taxonomy. Penn State University Press, University Park, PA, pp 391–399

Baayen RP, O'Donnell K, Bonants PJM, Cigelnik E, Kroon LPNM, Roebroeck EJA, Waalwijk C (2000) Gene genealogies and AFLP analyses in the *Fusarium oxysporum* complex identify monophyletic and nonmonophyletic formae speciales causing wilt and rot disease. Phytopathology 90:891–900

Baetz U, Martinoia E (2014) Root exudates: the hidden part of plant defense. Trends Plant Sci 19:90–98

Bais HP, Weir TL, Perry LG, Gilroy S, Vivanco JM (2006) The role of root exudates in rhizosphere interactions with plants and other organisms. Annu Rev Plant Biol 57:233–266

Beckman CH (1987) The nature of wilt diseases of plants. American Phytopathology Society Press, University of California, St Paul, 175 pp

Bluhm BH, Zhao X, Flaherty JE, Xu JR, Dunkle LD (2007) *RAS2* regulates growth and pathogenesis in *Fusarium graminearum*. Mol Plant Microbe Interact 20:627–636

Boddu J, Cho S, Kruger WM, Muehlbauer GJ (2006) Transcriptome analysis of the barley-*Fusarium graminearum* interaction. Mol Plant-MicrobeInteract 19:407–417

Bolker M (2001) Ustilago maydis-a valuable model system for the study of fungal dimorphism and virulence. Microbiology 147:1395–1401

Bonfante P, Genre A (2010) Mechanisms underlying beneficial plant–fungus interactions in mycorrhizal symbiosis. Nat Commun 1:48

Booth C (1971) The genus *Fusarium*. Commonwealth Mycological Institute, Kew, Surrey, UK, p 237

Brefort T, Tanaka S, Neidig N, Doehlemann G, Vincon V, Kahmann R (2014) Characterization of the largest effector gene cluster of *Ustilago maydis*. PLoS Pathog 10:e1003866

Brodhagen M, Tsitsigiannis DI, Hornung E, Goebel C, Feussner I, Keller NP (2008) Reciprocaloxylipin-mediated cross-talk in the *Aspergillus*-seed pathosystem. Mol Microbiol 67:378–391

Brundrett M (2004) Diversity and classification of mycorrhizal associations. Biol Rev 79:473–495

Burow G, Nesbitt T, Dunlap J, Keller NP (1997) Seed Lipoxygenase products modulate *Aspergillus* mycotoxin biosynthesis. Mol Plant Microbe Interact 10:380–387

Cai G, Gale LR, Schneider RW, Kistler HC, Davis RM, Elias KS, Miyao EM (2003) Origin of race 3 of *Fusarium oxysporum* f. sp. *lycopersici* at a singlesite in California. Phytopathology 93:1014–1022

Calvo AM, Hinze LL, Gardner HW, Keller NP (1999) Sporogenic effect of polyunsaturated fatty acids on development of *Aspergillus* spp. Appl Environ Microbiol 65:3668–3673

Caracuel Z, Casanova C, Roncero MI, Di Pietro A, Ramos J (2003) pH response transcription factor PacC controls salt stress tolerance and expression of the P-Type Na^+-ATPase Ena1 in *Fusarium oxysporum*. Eukaryot Cell 2:1246–1252

Caracuel Z, Martinez-Rocha AL, Di Pietro A, Madrid MP, Roncero MI (2005) *Fusarium oxysporum gas1* encodes a putative beta-1, 3-glucanosyltransferaserequired for virulence on tomato plants. Mol Plant-Microbe Interact 18:1140–1147

Catlet NL, Yoder OC, Turgeon BG (2003) Whole-genome analysis of two-component signal transduction genes in fungal pathogens. Eukaryot Cell 2(6):1151–1161

Chi MH, Park SY, Kim S, Lee YH (2009) A novel pathogenicity gene is required in the rice blast fungus to suppress the basal defenses of the host. PLoS Pathog 5:e1000401

Cho Y, Kim KH, LaRota M, Scott D, Santopietro G, Callihan M, Mitchell TK, Lawrence CB (2009) Identification of novel virulencefactors associated with signal transduction pathways in *Alternaria brassicicola*. Mol Microbiol 72:1316–1333

Christakopoulos P, Kekos D, Macris BJ, Claeyssens M, Bhat MK (1995) Purification and mode of action of a low molecular mass endo-1, 4-β-D-glucanase from *Fusarium oxysporum*. J Biotechnol 39:85–93

Christakopoulos P, Nerinckx W, Kekos D, Macris B, Claeyssens M (1996) Purification and characterization of two low molecular mass alkaline xylanases from *Fusarium oxysporum* F3. J Biotechnol 51:181–189

Coleman JJ, Rounsley SD, Rodriguez-Carres M, Kuo A, Wasmann CC, Grimwood J, Schmutz J, Taga M, White GJ, Zhou S, Schwartz DC, Freitag M, Ma L-J, Danchin EGJ, Henrissat B, Coutinho PM, Nelson DR, Straney D, Napoli CA, Barker BM, Gribskov M, Rep M, Kroken S, Molnár I, Rensing C, Kennell JC, Zamora J, Farman ML, Selker EU, Salamov A, Shapiro H, Pangilinan J, Lindquist E, Lamers C, Grigoriev IV, Geiser DM, Covert SF, Temporini E, VanEtten HD (2009) The genome of *Nectria haematococca*: contribution of supernumerary chromosomes to gene expansion. PLoS Genet 5:e1000618

Collemare J, Pianfetti M, Houlle AE, Morin D, Camborde L, Gagey MJ, Barbisan C, Fudal I, Lebrun MH, Böhnert HU (2008) *Magnaporthe grisea* avirulence gene ACE1 belongs to an infection-specific gene cluster involved in secondary metabolism. New Phytol 179:196–208

Corradi N, Bonfante P (2012) The Arbuscular mycorrhizal symbiosis: origin and evolution of a beneficial plant infection. PLoS Pathog 8:8–10

Correll JC (1991) The relationship between formae speciales, races and vegetative compatibility groups in *Fusarium oxysporum*. Phytopathology 81(9):1061–1064

Cuomo CA, Güldener U, Xu JR, Trail F, Turgeon BG, Di Pietro A, Walton JD, Ma L-J, Baker SE, Rep M, Adam G, Antoniw J, Baldwin T, Calvo S, Chang YL, Decaprio D, Gale LR, Gnerre S, Goswami RS, Hammond-Kosack K, Harris LJ, Hilburn K, Kennell JC, Kroken S, Magnuson JK, Mannhaupt G, Mauceli E, Mewes HW, Mitterbauer R, Muehlbauer G, Münsterkötter M, Nelson D, O'Donnell K, Ouellet T, Qi W, Quesneville H, Roncero MI, Seong KY, Tetko IV, Urban M, Waalwijk C, Ward TJ, Yao J, Birren BW, Kistler HC (2007) The *Fusarium graminearum* genome reveals a link between localized polymorphism and pathogen specialization. Science 317:1400–1402

Dangl J, Jones J (2001) Plant pathogens and integrated defense responses to infection. Nature 411:826

Dean RA, Talbot NJ, Ebbole DJ, Farman ML, Mitchell TK, Orbach MJ, Thon M, Kulkarni R, Xu J-R, Pan H, Read ND, Lee Y-H, Carbone I, Brown D, Oh YY, Donofrio N, Jeong JS, Soanes DM, Djonovic S, Kolomiets E, Rehmeyer C, Li W, Harding M, Kim S, Lebrun M-H, Bohnert H, Coughlan S, Butler J, Calvo S, Ma L-J, Nicol R, Purcell S, Nusbaum C, Galagan JE, Birren BW (2005) The genome sequence of the rice blast fungus *Magnaporthe grisea*. Nature 434:980–986

Delgado-Jarana J, Martinez-Rocha AL, Roldan-Rodriguez R, Roncero MI, Di Pietro A (2005) *Fusarium oxysporum* G-protein beta subunitFgb1 regulates hyphal growth, development, and virulencethrough multiple signalling pathways. Fungal Genet Biol 42:61–72

DeZwaan TM, Carroll AM, Valent B, Sweigard JA (1999) *Magnaporthe grisea* pth11p is a novel plasma membrane protein that mediates ppressorium differentiation in response to inductive substrate cues. Plant Cell 11:2013–2030

Di Pietro A, Garcia-MacEira FI, Meglecz E, Roncero MI (2001) A MAP kinase of the vascular wilt fungus *Fusarium oxysporum* is essential for root penetration and pathogenesis. Mol Microbiol 39:1140–1152

Djamei A, Kahmann R (2012) *Ustilago maydis*: dissecting the molecular interface between pathogen and plant. PLoS Pathog 8:e1002955

Dowd C, Wilson IW, McFadden H (2004) Gene expression profile changes incotton root and hypocotyl tissues in response to infection with *Fusarium oxysporum f.* sp. *vasinfectum*. Mol Plant-Microbe Interact 17:654–667

Ebbole D, Sachs MS (1990) A rapid and simple method for isolation of Neurospora crassa homokaryons using microconidia. Fungal Genetic Newslett 37:17–18

Egan MJ, Wang ZY, Jones MA, Smirnoff N, Talbot NJ (2007) Generation of reactive oxygen species by fungal NADPH oxidases is required for rice blast disease. Proc Natl Acad Sci USA 104:11772–11777

Elias KS, Schneider RW (1991) Vegetative compatibility groups in *Fusarium oxysporum* f. sp. *lycopersici*. Phytopathology 18:159–162

Elias KS, Schneider RW (1992) Geneticdiversity within and among vegetativecompatibility groups of *Fusarium oxysporum* f. sp. *lycopersici* as determined by isozyme analysis. Phytopathology 82:1421–1427

Elmer WH, Stephens CT (1989) Classification of *Fusarium oxysporum* f.sp. *asparagi* into vegetatively compatible groups. Phytopathology 79:88–93

Fiely MB, Correll JC, Morelock TE (1995) Vegetative compatibility, pathogenicity, and virulence diversity of *Fusarium oxysporum* recovered from spinach. Plant Dis 79:990–993

Fiers M, Lognay G, Fauconnier M-L, Jijakli MH (2013) Volatile compoundmediated interactions between barley and pathogenic fungi in the soil. PloS One 8:e66805

Fravel D, Olivain C, Alabouvette C (2003) *Fusarium oxysporum* and its biocontrol. New Phytol 157:493–502

Galagan JE, Calvo SE, Borkovich KA, Selker EU, Read ND, Jaffe D, FitzHugh W, Ma L-J, Smirnov S, Purcell S, Rehman B, Elkins T, Engels R, Wang S, Nielsen CB, Butler J, Endrizzi M, Qui D, Ianakiev P, Bell-Pedersen D, Nelson MA, Werner-Washburne M, Selitrennikoff CP, Kinsey JA, Braun EL, Zelter A, Schulte U, Kothe GO, Jedd G, Mewes W, Staben C, Marcotte E, Greenberg D, Roy A, Foley K, Naylor J, Stange-Thomann N, Barrett R, Gnerre S, Kamal M, Kamvysselis M, Mauceli E, Bielke C, Rudd S, Frishman D, Krystofova S, Rasmussen C, Metzenberg RL, Perkins DD, Kroken S, Cogoni C, Macino G, Catcheside D, Li W, Pratt RJ, Osmani SA, DeSouza CPC, Glass L, Orbach MJ, Berglund JA, Voelker R, Yarden O, Plamann O, Seiler S, Dunlap J, Radford A, Aramayo A, Natvig DO, Alex DO, Mannhaupt G, Ebbole DJ, Freitag DJ, Paulsen I, Sachs MS, Lander ES, Nusbaum C, Birren B (2003) The genome sequence of the filamentous fungus *Neurospora crassa*. Nature 422:859–868

Galagan JE, Calvo SE, Cuomo C, Ma L-J, Wortman JR, Batzoglou S, Lee S-I, Bastürkmen M, Spevak CC, Clutterbuck J, Kapitonov V, Jurka J, Scazzocchio C, Farman M, Butler J, Purcell S, Harris S, Braus GH, Draht O, Busch S, D'Enfert C, Bouchier C, Goldman GH, Bell-Pedersen D, Griffiths-Jones S, Doonan JH, Yu J, Vienken K, Pain A, Freitag M, Selker EU, Archer DB, Penālva MA, Oakley BR, Momany M, Tanaka T, Kumagai T, Asai K, Machida M, Nierman WC, Denning DW, Caddick M, Hynes M, Paolett M, Fischer R, Miller B, Dyer P, Sachs MS, Osmani SA, Birren BW (2005) Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigatus* and *A. oryzae*. Nature 438:1105–1115

Gale LR, Katan T, Kistler HC (2003) The probable center of origin of *Fusarium oxysporum* f. sp. lycopersici VCG 0033. Plant Dis 87:1433–1438

Garcia-Martinez J, Adam AL, Avalos J (2012) Adenylyl cyclase plays a regulatory role in development, stress resistance and secondary metabolism in *Fusarium fujikuroi*. PLoS ONE 7: e28849

Gardiner DM, Kazan K, Manners JM (2013) Cross-kingdom gene transfer facilitates the evolution of virulence in fungal pathogens. Plant Sci 210:151–158

Gardiner DM, Stiller J, Kazan K (2014) Genome sequence of *Fusarium graminearum*isolate CS3005. Genome Announce 2:5–8

Gerlagh M, Blok WJ (1988) *Fusarium oxysporum* f. sp. *cucurbitacearum* n. f. embracing all formae speciales of *F. oxysporum* attacking Cucurbitaceous crops. Neth J Plant Pathol 94:17–31

Giraldo MC, Dagdas YF, Gupta YK, Mentlak TA, Yi M, Martinez-Rocha AL, Saitoh H, Terauchi R, Talbot NJ, Valent B (2013) Two distinct secretion systems facilitate tissue invasion by the rice blast fungus *Magnaporthe oryzae*. Nat Commun 4:1996. https://doi:10.1038/ncomms2996

Giraldo MC, Valent B (2013) Filamentous plant pathogen effectors in action. Nat Rev Microbiol 11:800–814

Gordon TR, Martyn RD (1997) The evolutionary biology of *Fusarium oxysporum*. Annu Rev Phytopathol 35:111–128

Gordon TR, Okamoto D (1992) Variationin mitochondrial DNA among vegetatively compatible isolates of *Fusarium oxysporum*. Exp Mycol 16:245–250

Gordon WL (1965) Pathogenic strains of *Fusarium oxysporum*. Can J Bot 45:1309–1318

Grigoriev I (2013) Fungal genomics for energy and environment. In: Horwitz B, Mukherjee P, Mukherjee M (eds) Genomics of soil- and plant-associated fungi: soil biology, vol 36. Springer, Berlin, pp 11–27

Guadet J, Julien J, Lafay JF, Brygoo Y (1989) Phylogeny of some *Fusarium* species, as determined by large-subunit rRNA sequence comparison. Mol Biol Evol 6:227–242

Hamel LP, Nicole MC, Duplessis S, Ellis BE (2012) Mitogen-activated protein kinase signaling in plant-interacting fungi: distinct messages from conserved messengers. Plant Cell 24:1327–1351

Han Y, Liu X, Benny U, Kistler HC, VanEtten HD (2001) Genes determining pathogenicity to pea are clustered on a supernumerary chromosome in the fungal plant pathogen *Nectria haematococca*. Plant J 25:305–314

Hansen FT, Gardiner DM, Lysøe E, Feurtes PR, Tudzynski B, Weimann P, Sondergaard TE, Giese H, Brodersen DE, Sørensen JL (2015) An update to polyketide synthase and non-ribosomal synthetase genes and nomenclature in *Fusarium* Fungal Genet. Biology 75:20–29

Hansen FT, Sørensen JL, Giese H, Sondergaard TE, Frandsen RJ (2012a) Quickguide to polyketide synthase and nonribosomal synthetase genes in *Fusarium*. Int J Food Microbiol 155:128–136

Hansen FT, Droce A, Sørensen JL, Fojan P, Giese H, Sondergaard TE (2012b) Overexpression of NRPS4 leads to increased surface hydrophobicity in *Fusarium graminearum*. Fungal Biol 116:855–862

Harimoto Y, Hatta R, Kodama M, Yamamoto M, Otani H, Tsuge T (2007) Expression profiles of genes encoded by the supernumerary chromosome controlling AM-toxin biosynthesis and pathogenicity in the applepathotype of *Alternaria alternata*. Mol Plant Microbe Interact 20:1463–1476

Herrmann M, Zocher R, Haese A (1996) Effect of disruption of the enniatinsynthetase gene on the virulence of *Fusarium avenaceum*. Mol Plant Microbe Interact 9:226–232

Hopwood DA, Khosla C (1992) Genes for polyketide secondarymetabolic pathways in microorganisms and plants. In: Chadwick DJ, Whelan J (eds) Secondary metabolites: their functionand evolution. Wiley, Chichester, pp 88–112

Horbach R, Navarro-Quesada AR, Knogge W, Deising HB (2011) When and how to kill a plant cell: infection strategies of plant pathogenic fungi. J Plant Physiol 168:51–62

Hou Z, Xue C, Peng Y, Katan T, Kistler HC, Xu JR (2002) A mitogen-activated protein kinase gene (*MGV1*) in *Fusarium graminearum* is required for female fertility, heterokaryon formation, and plant infection. Mol. Plant-Microbe Interact 15:1119–1127

Houterman PM, Ma L, van Ooijen G, de Vroomen MJ, Cornelissen BJ, Takken FL, Rep M (2009) The effector protein Avr2 of the xylem colonizing fungus *Fusarium oxysporum* activates the tomato resistance protein I-2 intracellularly. Plant J 58:970–978

Houterman PM, Speijer D, Dekker HL, de Koster CG, Cornelissen BJC, Rep M (2007) The mixed xylem sap proteome of *Fusarium oxysporum* infected tomato plants. Mol. Plant Pathol. 8:215–221

Ilgen P, Maier F, Schäfer W (2008) Trichothecenes and lipases are host-induced and secreted virulence factors of *Fusarium graminearum*. Cereal Res Commun 36:421–428

Jackson AO, Taylor CB (1996) Plant-microbe interactions: life and death at the interface. Plant Cell 8:1651–1668

Jacobson DJ, Gordon TR (1988) Vegetative compatibility and self-incompatibility within *Fusarium oxysporum f. sp. melonis*. Phytopathology 78:668–672

Jacobson DJ, Gordon TR (1990a) Furtherinvestigations of vegetative compatibilitywithin *Fusarium oxysporum* f. sp. *melonis*. Can J Bot 68:1245–1248

Jacobson DJ, Gordon TR (1990b) Variabilityof mitochondrial DNA as an indicator of relationships between populations of *Fusarium oxysporum* f. sp. *melonis*. Mycol Res 94:734–744

Jain S, Akiyama K, Mae K, Ohguchi T, Takata R (2002) Targeted disruption of a G protein alpha subunit gene results in reduced pathogenicity in *Fusarium oxysporum*. Curr Genet 41:407–413

Jain S, Akiyama K, Kan T, Ohguchi T, Takata R (2003) The G protein beta subunit *FGB1* regulates development and pathogenicity in *Fusarium oxysporum*. Curr Genet 43(2):79–86

Jain S, Akiyama K, Takata R, Ohguchi T (2005) Signaling via the G protein alpha subunit *FGA2* is necessary for pathogenesis in *Fusarium oxysporum*. FEMS Microbiol Lett 243(1):165–172

Jansen C, VonWettstein D, Schäfer W, Kogel K-H, Felk A, Maier FJ (2005) Infection patterns in barley and wheat spikes inoculated with wild-type and trichodiene synthase gene disrupted *Fusarium graminearum*. Proc Natl Acad Sci USA 102:16892–16897

Joaramillo VD, Sukno SA, Thon MR (2015) Identification of horizontally transferred genes in the genus *Colletotrichum* reveals a steady tempo of bacterial to fungal gen etransfer. BMC Genom 16:2

Johnson RD, Johnson L, Itoh Y, Kodama M, Otani H, Kohmoto K (2000) Cloning and characterization of a cyclic peptide synthetase gene from *Alternaria alternata* apple pathotype whose product is involved in AM-toxin synthesis and pathogenicity. Mol Plant Microbe Interact 13:742–753

Jørgensen SH, Frandsen RJN, Nielsen KF, Lysøe E, Sondergaard TE, Wimmer R, Giese H, Sørensen JL (2014) *Fusarium graminearum* PKS14 is involved in orsellinicacid and orcinol synthesis. Fungal Genet Biol 70:24–31

Kabbage M, Yarden O, Dickman MB (2015) Pathogenic attributes of *Sclerotinia sclerotiorum*: switching from a biotrophic to necrotrophic lifestyle. Plant Sci 233:53–60

Kamper J, Kahmann R, Bolke M, Ma L-J, Brefort T, Saville BJ, Banuett F, Kronstad JW, Gold SE, Müller O, Perlin MH, Wösten HAB, de Vries R, Ruiz-Herrera J, Reynaga-Peña CG, Snetselaar K, McCann M, Pérez-Martín J, Feldbrügge M, Basse CW, Steinberg G, Ibeas JI, Holloman W, Guzman P, Farman M, Stajich JE, Sentandreu R, González-Prieto JM, Kennell JC, Molina L, Schirawski J, Mendoza-Mendoza A, Greilinger D, Münch K, Rössel N, Scherer M, Vraneš M, Ladendorf O, Vincon V, Fuchs U, Sandrock B, Meng S, Ho ECH, Cahill MJ, Boyce KJ, Klose J, Klosterman SJ, Deelstra HJ, Ortiz-Castellanos L, Li W, Sanchez-Alonso P, Schreier PH, Häuser-Hahn I, Vaupel M, Koopmann E, Friedrich G, Voss H, Schlüter T, Margolis J, Platt D, Swimmer C, Gnirke A, Chen F, Vysotskaia V, Mannhaupt G, Güldener U, Münsterkötter M, Haase D, Oesterheld M, Mewes H-W, Mauceli EW, DeCaprio D, Wade CM, Butler J, Young S, Jaffe DB, Calvo S, Nusbaum C, Galagan J, Birren BW (2006) Insights from the genome of the biotrophic fungal plant pathogen *Ustilago maydis*. Nature 444:97–101

Karpinets TV, Park BH, Syed MH, Klotz MG, Uberbacher EC (2014) Metabolic enviroment and genomic feature associated with pathogenic and mutualistic interaction between bacteria and plants. Mol. Plant-Microbe Interact. 27:664–667

Katan T, Hadar E, Katan J (1989) Vegetative compatibility of *Fusarium oxysporum* f. sp. *dianthi* from carnation in Israel. Plant Pathol 38:376–381

Katan T, Katan J (1988) Vegetativecompatibilitygroupings of *Fusariumoxysporum* f. sp. *vasinfectum* from tissueand the rhizosphere of cotton plants. Phytopathology 78:852–855

Kawahara Y, Oono Y, Kanamori H, Matsumoto T, Itoh T, Minami E (2012) Simultaneous RNA-seq analysis of a mixed transcriptome of rice and blast fungus interaction. PLoS ONE 7: e49423

Kazan K, Gardiner DM, Manners JM (2012) On the trail of a cereal killer: recent advances in *Fusarium graminearum* pathogenomics and host resistance. Mol Plant Pathol 13(4):399–413

Kazan K, Lyons R (2014) Intervention of phytohormone pathways by pathogen effectors. Plant Cell 26:2285–2309

Keller NP, Turner G, Bennett JW (2005) Fungal secondary metabolism from biochemistry to genomics. Nat Rev Microbiol 3:937–947

Khan R, Tan R, Mariscal AG, Straney D (2003) A binuclear zinc transcription factor binds the host isoflavonoid-responsive element in a fungal cytochrome p450 gene responsible for detoxification. Mol Microbiol 49:117–130

Kim DH, Martyn RD, Magill CW (1992) RFLP groups and physical map of themtDNA from *Fusarium oxysporum* f. sp.*niveum*. Phytopathology 82:346–353

Kim DH, Martyn RD, Magill CW (1993) Mitochondrial DNA (mt-DNA) relatednessamong formae speciales of *Fusarium oxysporum* in the Cucurbitaceae. Phytopathology 83:91–97

King R, Urban M, Hammond-Kosack MCU, Hassani-Pak K, Hammond-Kosack KE (2015) The completed genome sequences of pathogenic ascomycete fungus *Fusarium graminearum*. BMC Genom 16:544–564

Kistler HC (1997) Genetic diversity in theplant pathogenic fungus, *Fusarium oxysporum*. Phytopathology 87:474–479

Kistler HC, Momol EA (1990) Molecular genetics of plant pathogenic *Fusarium oxysporum*. In: Ploetz RC (ed) *Fusarium* wilt of banana. American Phytopathological Society, St. Paul, pp 49–54

Koenig RL, Ploetz RC, Kistler HC (1997) *Fusarium oxysporum* f. sp. *cubense* consists of a small number of divergent andglobally distributed clonal lineages. Phytopathology 87:915–923

Kubicek CP (2013) Fungi and Lignocellulosic Biomass. Wiley, New York

Kumamoto CA (2008) Molecular mechanisms of mechano-sensing and their roles in fungal contact sensing. Nat Rev Microbiol 6:667–673

Lanver D, Berndt P, Tollot M, Naik V, Vranes M, Warmann T, Münch K, Rössel N, Kahmann R (2014) Plant surface cues prime *Ustilago maydis* for biotrophic development. PLoS Pathog 10: e1004272

Lee J, Myong K, Kim JE, Kim HK, Yun SH, Lee YW (2012) FgVelBglobally regulates sexual reproduction, mycotoxin production and pathogenicity in the cereal pathogen *Fusarium graminearum*. Microbiology 158:1723–1733

Leslie JF (1993) Fungal vegetative compatibility. Ann Rev Phytopathol 31:127–150

Leslie JF (1996) Fungal vegetative compatibility promises and prospects. Phytoparasitica 24:3–6

Li G, Zhou X, Xu JR (2012) Genetic control of infection-related development in *Magnaporthe oryzae*. Curr Opin Microbiol 15:678–684

Liao X, Fang W, Lin L, Lu H-L, St. Leger RJ (2013) *Metarhizium robertsii* produces an extracellular invertase (MrINV) that plays a pivotal role in rhizospheric interactions and root colonization. PloS One 8:e78118

Link HF (1809) Observationes in ordines plantarum naturales, dissertatioprima, complectens anandrarum ordines Epiphytas, Mucedines. Gastromycosed Fungos, Der Gesellschaft Naturforschender Freunde zu Berlin, Berlin, Germany

Liu W, Zhou X, Li G, Li L, Kong L, Wang C, Zhang H, Xu JR (2011) Multiple plant surface signals aresensed by different mechanisms in the rice blast fungus forappressorium formation. PLoS Pathog 7: e1001261

Liu ZM, Kolattukudy PE (1999) Early expression of the calmodulin gene, which precedes appressorium formation in *Magnaporthe grisea*, is inhibited by self-inhibitors and requires surface attachment. J Bacteriol 181:3571–3577

Lo Presti L, Lanver D, Schweizer G, Tanaka S, Liang L, Tollot M, Zuccaro A, Reissmann S, Kahmann R (2015) Fungal effectors and plant susceptibility. Annu Rev Plant Biol 66:513–545

Lopez-Berges MS, Capilla J, Turra D, Schafferer L, Matthijs S, Jochl C, Cornelis P, Guarro J, Haas H, Di Pietro A (2012) HapX-mediated iron homeostasis isessential for rhizosphere competence and virulence of the soilborne pathogen *Fusarium oxysporum*. Plant Cell 24:3805–3822

Lopez-Berges MS, Hera C, Sulyok M, Schafer K, Capilla J, Guarro J, Di Pietro A (2013) The velvet complex governs mycotoxin production and virulence of*Fusarium oxysporum* on plant and mammalian hosts. Mol Microbiol 87:49–65

Lucas JA (1998) Plant pathology and plant pathogens, 3rd edn. Blackwell Science, p 274

Ma L-J, Geiser DM, Proctor RH, Rooney AP, O'Donnell K, Trail F, Gardiner DM, Manners JM, Kazan K (2013) *Fusarium* pathogenomics. Annu Rev Microbiol 67:399–416

Ma L-J, van der Does HC, Borkovich KA, Coleman JJ, Daboussi M-J, Di Pietro A, Dufresne M, Freitag M, Grabherr M, Henrissat B, Houterman PM, Kang S, Shim W-B, Woloshuk C, Xie X, Xu J-R, Antoniw J, Baker SE, Bluhm BH, Breakspear A, Brown DW, Butchko RAE, Chapman S, Coulson R, Coutinho PM, Danchin EGJ, Diener A, Gale LR, Gardiner DM, Goff S, Hammond-Kosack KE, Hilburn K, Hua-Van A, Jonkers W, Kazan K, Kodira CD, Koehrsen M, Kumar L, Lee Y-H, Li L, Manners JM, Miranda-Saavedra D, Mukherjee M, Park G, Park J, Park S-Y, Proctor RH, Regev A, Ruiz-Roldan MC, Sain D, Sakthikumar S, Sykes S, Schwartz DC, Turgeon BG, Wapinski I, Yoder O, Young S, Zeng Q, Zhou S, Galagan J, Cuomo CA, Kistler HC, Rep M et al (2010) Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*. Nature 464:367–373

Madrid MP, Di Pietro A, Roncero MI (2003) Class V chitin synthase determines pathogenesis in the vascular wilt fungus *Fusarium oxysporum* and mediates resistance to plant defence compounds. Mol Microbiol 47:257–266

Manicom BQ, Bar-Joseph M, Kotze JM (1990) Molecular methods of potential use in the identification and taxonomy of filamentous fungi, particularly *Fusarium oxysporum*. Phytophylactica 22:233–240

Martinez-Rocha AL, Roncero MI, Lopez-Ramirez A, Marine M, Guarro J, Martinez-Cadena G, Di Pietro A (2008) Rho1 has distinct functionsin morphogenesis, cell wall biosynthesis and virulenceof *Fusarium oxysporum*. Cell Microbiol 10:1339–1351

Martin-Udiroz M, Madrid MP, Roncero MI (2004) Role of chitin synthase genes in *Fusarium oxysporum*. Microbiol. 150:3175–3187

Martin-Urdiroz M, Roncero MI, Gonzalez-Reyes JA, Ruiz-Roldan C (2008) ChsVb, a class VII chitin synthase involved in septation, iscritical for pathogenicity in *Fusarium oxysporum*. Eukaryot Cell 7:112–121

Mbofung GY, Hong SG, Pryor BM (2007) Phylogeny of *Fusarium oxysporum*f. sp. *lactucae* inferred from mitochondrial small subunit, elongation factor-1 and nuclear ribosomal intergenic spacer sequence data. Phytopathology 97:87–98

Mendoza-Mendoza A, Berndt P, Djamei A, Weise C, Linne U, Marahiel M, Vranes M, Kämper J, Kahmann R (2009) Physical–chemical plant-derived signals induce differentiation in *Ustilago maydis*. Mol Microbiol 71:895–911

Miao VP, Covert SF, VanEtten HD (1991) A fungal gene for antibiotic resistanceon a dispensable (''B'') chromosome. Science 254:1773–1776

Michielse CB, van Wijk R, Reijnen L, Cornelissen BJC, Rep M (2009) Insight into the molecular requirements for pathogenecity of *Fusarium oxysporum* f. sp. *lycopersici* through large-scale insertional mutagenesis. Genome Biol 10:R4. https://doi.org/10.1186/gb-2009-10-1-r4

Michielse CB, Rep M (2009) Pathogen profile update: *Fusarium oxysporum*. Mol Plant Pathol 10:311–324

Mitter B, Brader G, Afzal M, Compant S, Naveed M, Trogitnz F, Sessitsch A (2013) Advances in eluciadating beneficial interaction between plant soil and bacteria. In: Sparks DL (ed) Advances in agronomy, vol 121. Elesvier, San Diego, pp 381–445

Molina L, Kahmann R (2007) An *Ustilago maydis* gene involved in H_2O_2 detoxification is required for virulence. Plant Cell 19:2293–2309

Navazio L, Baldan B, Moscatiello R, Zuppini A, Woo SL, Mariani P, Lorito M (2007) Calcium-mediated perception and defence responses activated in plant cells by metabolite mixtures secreted by the biocontrol fungus *Trichoderma atroviride*. BMC Plant Biol 7:41

Nelson PE, Toussoun TA, Marasas WFO (1983) Fusarium species: an illustrated manual for identification. Pennsylvania State University Press, University Park

O'Donnell K (1993) *Fusarium* and its nearrelatives. In: Taylor JW, Reynolds DR (eds) The fungal holomorph. CAB International, England, pp 225–233

O'Donnell K, Kistler HC, Cigelnik E, Ploetz RC (1998) Multiple evolutionary originsof the fungus causing Panama disease of banana: concordant evidence fromnuclear and mitochondrial gene genealogies. Proc Natl Acad Sci USA 95:2044–2049

O'Donnell K, Rooney AP, Proctor RH, Brown DW, McCormick SP, Todd JW, Frandsen RJ, Lysøe E, Rehner SA, Aoki T, Robert VARG, Crous PW, Groenewald JZ, Kang S, Geiser DM (2013) Phylogeneticanalyses of *RPB1* and *RPB2* support a middle Cretaceous origin for a clade comprising all agriculturally and medically important fusaria. Fungal Genet Biol 52:20–31

O'Donnell K, Sutton DA, Rinaldi MG, Magnon KC, Cox PA, Revankar SG, Sanche S, Geiser DM, Juba JH, van Burik J-AH, Padhye AA, Anaissie EJ, Francesconi A, Walsh TJ, Robinson JS (2004) Genetic diversity of human pathogenic members of the *Fusarium oxysporum* complex inferred from multilocus DNA sequence data and amplified fragment length polymorphism analyses: evidence for the recent dispersion of a geographically widespread clonal lineage and nosocomial origin. J Clin Microbiol 42:5109–5120

O'Donnell K, Kistler HC, Tacke BK, Casper HH (2000) Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab. Proc Nat Acad Sci USA 95:7905–7910

O'Donnell K, Cigelnik E (1997) Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. Mol Phylogenet Evol 7:103–116

Oide S, Liu J, Yun SH, Wu D, Michev A, Choi MY, Horwitz BA, Turgeon BG (2010) Histidine kinase two-component response regulator proteins regulate reproductive development, virulence, and stress responses of the fungal cereal pathogens *Cochliobolus heterostrophus* and *Gibberella zeae*. EukaryotCell 9:1867–1880

Oide S, Moeder W, Krasnoff S, Gibson D, Haas H, Yoshioka K, Turgeon BG (2006) NPS6, encoding a nonribosomal peptide synthetase involved in siderophore mediated iron metabolism, is a conserved virulence determinant of plant pathogenic ascomycetes. Plant Cell 18:2836–2853

Ortoneda M, Guarro J, Madrid MP, Caracuel Z, Roncero MIG, Mayayo E, Di Pietro A (2004) *Fusarium oxysporum* as a multihost model for the genetic dissection of fungal virulence in plants and mammals. Infect Immun 72:1760–1766

Ospina-Giraldo MD, Mullins E, Kang S (2003) Loss of function of the *Fusarium oxysporum SNF1* gene reduces virulence on cabbage and *Arabidopsis*. Curr Genet 44:49–57

Park AR, Cho AR, Seo J-A, Min K, Son H, Lee J, Choi GJ, Kim J-C, Lee Y-W (2012) Functional analyses of regulators of G protein signaling in *Gibberella zeae*. Fungal Genet Biol 49:511–520

Perez-Nadales E, Nogueira MF, Baldin C, Castanheira S, El Ghalid M, Grund E, Lengeler K, Marchegiani E, Mehrotra PV, Moretti M, Naik V, Oses-Ruiz M, Oskarsson T, Schäfer K, Wasserstrom L, Brakhage AA, Gow NA, Kahmann R, Lebrun MH, Perez-Martin J, Di Pietro A, Talbot NJ, Toquin V, Walther A, Wendland J (2014) Fungal model systems and the elucidation of pathogenicity determinants. Fungal Genet Biol 70C:42–67

Perez-Nadales E, Di Pietro A (2011) The membrane mucin Msb2 regulates invasive growth and plant infection in *Fusarium oxysporum*. Plant Cell 23:1171–1185

Perfect SE, Green JR (2001) Infection *structures* of biotrophic and hemibiotrophic fungal plant pathogens. Mol Plant Pathol 2:101–108

Pieterse CMJ, Leon-Reyes A, Van der Ent S, Van Wees SCM (2009) Networking by small-molecule hormones in plant immunity. Nat Chem Biol 5:308–316

Ploetz RC (1990) Variability in *Fusarium oxysporum* f. sp. *cubense* Can. J. Bot. 68:1357–1363

Ploetz RC, Correll JC (1988) Vegetative compatibility among races of *Fusarium oxysporum* f. sp. *cubense*. Plant Dis 72:325–328

Poppenberger B, Berthiller F, Lucyshyn D, Sieberer T, Schuhmacher R, Krska R, Kuchler K, Glössl J, Luschnig C, Adam G (2003) Detoxificationof the *Fusarium* mycotoxin

deoxynivalenol by a UDP-glucosyltransferase from *Arabidopsis thaliana*. J Biol Chem 278:47905–47914

Prados Rosales RC, Di Pietro A (2008) Vegetative hyphal fusion is not essential forplant infection by *Fusarium oxysporum*. Eukaryot Cell 7:162–171

Prados Rosales RC, Roldan-Rodriguez R, Serena C, Lopez-Berges MS, Guarro J, Martinez-del-Pozo A, Di Pietro A (2012) A PR-1-like protein of *Fusarium oxysporum* functions in virulence on mammalian hosts. J Biol Chem 287:21970–21979

Proctor RH, Butchko RAE, Brown DW, Moretti A (2007) Functionalcharacterization, sequence comparisons and distribution of a polyketidesynthase gene required for perithecial pigmentation in some *Fusarium* species. Food Addit Contam 24:1076–1087

Pryce-Jones E, Carver TIM, Gurr SJ (1999) The roles of cellulase enzymes and mechanical force in host penetration by *Erysiphe graminis* f.sp. *hordei.* Physiol Mol Plant P 55:175–182

Puhalla JE (1985) Classification of strain of *Fusarium oxysporum* on the basis of vagetative compatibility Can. J Bot 63:179–183

Qutob D, Kemmerling B, Brunner F, Küfner I, Engelhardt S, Gust AA, Luberacki B, Seitz HU, Stahl D, Rauhut T, Glawischnig E, Schween G, Lacombe B, Watanabe N, Lam E, Schlichting R, Scheel D, Nau K, Dodt G, Hubert D, Gijzen M, Nürnberger T (2006) Phytotoxicity and innate immune responses induced by Nep1-likeproteins. Plant Cell 18:3721–3744

Ramos B, Alves-Santos FM, Garcia-Sanchez MA, Martin-Rodrigues N, Eslava AP, Diaz-Minguez JM (2007) The gene coding for a new transcription factor (ftf1) of *Fusarium oxysporum* is only expressed during infection of common bean. Fungal Genet Biol 44:864–876

Rep M, van der Does HC, Meijer M, van Wijk R, Houterman PM, Dekker HL, de Koster CG, Cornelissen BJ (2004) Asmall, cysteine-rich protein secreted by *Fusarium oxysporum* duringcolonization of xylem vessels is required for I-3-mediated resistance in tomato. Mol Microbiol 53:1373–1383

Reverberi M, Fabbri AA, Fanelli C (2012) Oxidative stress and oxylipins in plant–fungus interaction. In: Guenther W (ed) Biocommunicationof Fungi. Springer, The Netherlands, pp 273–290

Rispail N, Soanes DM, Ant C, Czajkowski R, Grünler A, Huguet R, Perez-Nadales E, Poli A, Sartorel E, Valiante V, Yang M, Beffa R, Brakhage AA, Gow NA, Kahmann R, Lebrun MH, Lenasi H, Perez-Martin J, Talbot NJ, Wendland J, Di Pietro A (2009) Comparative genomics ofMAP kinase and calcium-calcineurin signalling componentsin plant and human pathogenic fungi. Fungal Genet Biol 46:287–298

Rispail N, Di Pietro A (2009) *Fusarium oxysporum* Ste12 controls invasive growthand virulence downstream of the Fmk1 MAPK cascade. Mol Plant MicrobeInteract 22:830–839

Risser G, Banihashemi Z, Davis DW (1976) A Proposed Nomenclature of*Fusarium oxysporum* f. sp. *melonis* races and resistance genes in *Cucumis melo*. Phytopathology 66:1105–1106

Rodriguez A, Perestelo F, Carnicero A, Regalado V, Perez R, De la Fuente G, Falcon MA (1996) Degradation of natural lignins and lignocellulosic substrates by soil-inhabiting fungi imperfecti. FEMS Microbiol Ecol 21:213–219

Rovenich H, Boshoven BPHJ, Thomma JC (2014) Filamentous pathogen effector functions: of pathogens, hosts and microbiomes. Curr Opin Plant Biol 20C:96–103

Salomon S, Gácser A, Frerichmann S, Kröger C, Schäfer W, Voigt CA (2012) The secreted lipase FGL1 is sufficient to restore the initial infection step to the apathogenic *Fusarium graminearum* MAP kinase disruption mutant Δgpmk1. Eur J Plant Pathol 134:23–37

Scheffer RP (1991) Role of toxins in evolution and ecology of plant pathogenic fungi. Experientia 47:804–811

Schippers B, van Eck WH (1981) Formation and survival of chlamydospores in Fusarium: In: Nelson PE, Toussoun TA, Cook RJ (eds) Fusarium: diseases, biology and taxonomy. Penn State University Press, University Park, pp 250–260

Schroeder DT, Gordon TR (1993) An assessment of the relatedness of subpopulations within *Fusarium oxysporum* f.sp.*melonis* based on DNA fingerprinting. Phytopathology 83:1346–1347

Skibbe D, Doehlemann G, Fernandes J, Walbot V (2010) Maize tumors caused by *Ustilago maydis* require organ-specific genes in host and pathogen. Science 328: 89–92

Skovgaard K, Nirenberg HI, O'Donnell K, Rosendahl S (2001) Evolution of *Fusarium oxysporum* f. sp. *vasifectum* races inferred from multigene genealogies. Phytopathology 91:1231–1237

Snyder WC, Hansen HN (1940) The species concept in Fusarium. Am J Bot 27:64–67

Sørensen JL, Sondergaard TE, Covarelli L, Fuertes PR, Hansen FT, Frandsen RJN, Saei W, Lukassen MB, Wimmer R, Nielsen KF, Gardiner DM, Giese H (2014) Identification of the biosynthetic gene clusters for the lipopeptidesfusaristatin A and W493 B in *Fusarium graminearum* and *F.pseudograminearum*. J Nat Prod 77:2615–2619

Sperschneider J, Gardiner DM, Thatcher LF, Lyons R, Singh SB, Manners JM, Taylor JM (2015) Genome-wide analysis of three Fusarium pathogens identifies rapidly evolving chromosomes and genes associated with pathogenicity. Genome Biol Evol 7(6):1613–1627

Steindorff AS, Persinoti GF, Monteiro VN, Silva RN (2015) Fungal metabolic diversity. In: Gupta VK, Mach RL, Sreenivasaprasad S (eds) Fungal biomolecules: sources, applications and recent developments. Wiley, Chichester, pp 239–262

Stoner MF (1981) Ecology of *Fusarium* in non-cultivated soils. In: Nelson PE, Toussoun TA, Cook RJ (eds) *Fusarium*: diseases, biology, and taxonomy. The Pennsylvania State University Press, University Park, pp 276–286

Stracke S, Kistner C, Yoshida S, Mulder L, Sato S, Kaneko T, Tabata S, Sandal N, Stougaard J, Szczyglowski K, Parniske M (2002) A plant receptor-like kinase required for both bacterial and fungal symbiosis. Nature 417:959–962

Straight PD, Fischbach MA, Walsh CT, Rudner DZ, Kolter R (2007) A singular enzymaticmega-complex from *Bacillus subtilis*. Proc Natl Acad Sci USA 104:305–310

Strieker M, Tanovic A, Marahiel MA (2010) Nonribosomal peptide synthetases:structures and dynamics. Curr Opin Struct Biol 20:234–240

Struck C (2006) Infection strategies of plant parasitic fungi. In: Cooke BM, Jones DG, Kaye B (eds) The epidemiology of plant diseases. Springer, The Netherlands, pp 117–137

Sutherland JB, Pometto AL, Crawford DL (1983) Lignocellulose degradation by *Fusarium species*. Can J Bot 61:1194–1198

Sutherland R, Viljoen A, Myburg AA, Van den Berg N (2013) Pathogenicity associated genes in *Fusarium oxysporum* f. sp. *cubense* race 4. S Afr J Sci 109(5/6), Art. #0023, 10 p. https://doi.org/10.1590/sajs.2013/20120023

Taghavi S, van der Lelie D, Hoffman A, Zhang YB, Walla MD, Vangronsveld J, Newman L, Monchy S (2010) Genome sequence of the plant growth prmoting endophytic bacterium *Enterobacter species* 638. PLoS Genet 6:e100943

Takahashi K (1985) Distribution of hydrolytic enzymes at barley powdery mildew encounter sites: implications for resistance associated with papilla formation in a compatible system. Physiol Plant Pathol 27:167–184

Tantaoui A, Ouinten M, Geiger JP, Fernandez D (1996) Characterization of asingle lineage of *Fusarium oxysporum* f.sp. *albedinis* causing Bayoud disease ofdate palm in Morocco. Phytopathology 86:787–792

Teunissen HAS, Rep M, Houterman PM, Cornelissen BJC, Haring MA (2003) Construction of a mitotic linkage map of *Fusarium oxysporum*based on Foxy-AFLPs. Mol Genet Genomics 269:215–226

Thatcher LF, Manners JM, Kazan K (2009) *Fusarium oxysporum* hijacks COI1-mediated jasmonate signaling to promote disease development in Arabidopsis. Plant J. 58:927–939

Tian CF, Zhou YZ, Zhang YM, Li Q, Zhang YZ, Li DF, Wang S, Wang J, Gilbert LB, Li YR, Chen WX (2012) Comperative genomics of rhizobia nodulating soybean suggests extensive recruitment of lineage specific gene in adaptation. Proc Natl Acad Sci USA 109:8629–8634

Tisserant E, Malbriel M, Kuo A, Kohler A, Symeonidi A, Balestrini R, Charron P, Duensing N, Frey NFD, Gianinazzi-Pearson V, Gibert LB, Handa Y, Herr JR, Hijri M, Koul R, Kawaguchi M, Krajinski F, Lammers PJ, Masclauxm FG, Murat C, Morin E, Ndikumana S, Pagni M, Petipuerre D, Requena N, Rosikiewhicz P, Riley R, Saito K, Clemente HS, Shapiro H, Van Tuinen D, Becard G, Bonfante P, Paszkowski U, Shacha-Ahaill AYY, Atuskan GA, Young PW, Sanders IR, Henrissat B, Rensing SA, Grigoriev MN, Roux C, Martin F (2013) Genome of an arbuscular mycohrrizal fungus provides insight into the oldest plant symbiosis. Proc Natl Acad Sci USA 110:20117–20122

Tobiasen C, Aahman J, Ravnholt KS, Bjerrum MJ, Grell MN, Giese H (2007) Nonribosomalpeptide synthetase (NPS) genes in *Fusarium graminearum*, *F. culmorum* and *F.pseudograminearium* and identification of NPS2 as the producer of ferricrocin. Curr Genet 51:43–58

Tsitsigiannis DI, Keller NP (2007) Oxylipins as developmental and host-fungal communication signals. Trends Microbiol 15:109–118

Tsuge T, Harimoto Y, Akimitsu K, Ohtani K, Kodama M, Akagi Y, Egusa M, Yamamoto M, Otani H (2013) Host-selective toxins produced by the plant pathogenic fungus *Alternaria alternata*. FEMS Microbiol Rev 37:44–66

Turrà D, El Ghalid M, Rossi F, Di Pietro A (2015) Fungal pathogen uses sex pheromone receptor for chemotropic sensing of host plant signals. Nature 527:521–536

Urban M, Mott E, Farley T, Hammond-Kosack K (2003) The *Fusarium graminearum MAP1* gene is essential for pathogenicity and development of perithecia. Mol. Plant Pathol. 4:347–359

Van der Does HC, Duyvesteijn RG, Goltstein PM, van Schie CC, Manders EM, Cornelissen BJ, Rep M (2008) Expression of effector gene SIX1 of *Fusarium oxysporum* requires living plant cells. Fungal Genet Biol 45:1257–1264

Voigt CA, Schäfer W, Salomon S (2005) A secreted lipase of *Fusarium graminearum* is a virulence factor required for infection of cereals. Plant J. 42:364–375

Waalwijk C, De Koning JRA, Baayen RP, Gams W (1996) Discordant groupings of *Fusarium* spp. from section Elegans, Liseola and Dlaminia based on ribosomal ITS1 and ITS2 sequences. Mycologia 88:361–368

Walter S, Nicholson P, Doohan FM (2010) Action and reaction of host and pathogen during *Fusarium* head blight disease. New Phytol 185:54–66

Walton JD (1996) Host-selective toxins: agents of compatibility. Plant Cell 8:1723–1733

Wang X, Jiang N, Liu J, Liu W, Wang GL (2014) The role of effectors and host immunity in plant–necrotrophic fungal interactions. Virulence 5:722–732

Weiberg A, Wang M, Lin FM, Zhao H, Zhang Z, Kaloshian I, Huang HD, Jin H (2013) Fungal small RNAs suppress plant immunity by hijacking host RNA interference pathways. Science 342:118–123

Weimann P, Brown DW, Kleigrewe K, Bok JW, Keller NP, Humpf H-U, Tudzynski B (2010) FfVel1 and FfLae1, components of a velvet—like complex in *Fusarium fujikuroi*, affect differentiation, secondary metabolism and virulence. Mol Micribiol 77(4):972–994

Widmann C, Gibson S, Jarpe MB, Johnson GL (1999) Mitogen-activated protein kinase: conservation of a three-kinase module from yeast to human. Physiol Rev 79:143–180

Wiemann P, Sieber CMK, von Bargen KW, Studt L, Niehaus EM, Espino JJ, Huß K, Michielse CB, Albermann S, Wagner D, Bergner SV, Connolly LR, Fischer A, Reuter G, Kleigrewe K, Bald T, Wingfield BD, Ophir R, Freeman S, Hippler M, Smith KM, Brown DW, Proctor RH, Münsterkötter M, Freitag M, Humpf H-U, Güldener U, Tudzynski B (2013) Deciphering the cryptic genome: genome-wideanalyses of the rice pathogen *Fusarium fujikuroi* reveal complex regulationof secondary metabolism and novel metabolites. PLoS Pathog 9:e1003475

Wollenweber HW (1931) *Fusarium*-Monographie. Fungi parasitici et saprophytici. Zeitschrift für Parasitenkunde 3:269–516

Wollenweber HW, Reinking OA (1935) Die Fusarien, ihre Beschreibung. Schadwirkung und Bekampfung. P, Parey, Berlin, p 365

Wolpert TJ, Dunkle LD, Ciuffetti LM (2002) Host-selective toxins and avirulence determinants: What's in a name? Annu Rev Phytopathol 40:251–285

Woudt LP, Neuvel A, Sikkema A, VanGrinsven MQJM, de Milliano WAJ, Campbell CL, Leslie JF (1995) Genetic variation in *Fusarium oxysporum* from cyclamen. Phytopathology 85:1348–1355

Wright KM, Chapman S, McGeachy K, Humphris S, Campbell E, TothI K, Holden NJ (2013) The endophytic lifestyle of *Escherichia coli* O157:H7: quantification and internal localization in roots. Phytopathology 103:333–340

Xu JR, Hamer JE (1996) MAP kinase and cAMP signaling regulate infection structure formation and pathogenic growth in the rice blast fungus *Magnaporthe grisea*. Genes Dev 10:2696–2706

Yi M, Valent B (2013) Communication between filamentous pathogens and plants at the biotrophic interface. Annu Rev Phytopathol 51:567–611

Yoder OC, Turgeon BG (2001) Fungal genomics and pathogenicity. Curr Opin Plant Biol 4:315–321

Zeilinger S, Gupta VK, Dahms TES, Silva RN, Singh HB, Upadhyay RS, Gomes EV, Tsui CKM, Nayak SC (2015) Friends or Foes? Emerging insights from fungal interactions with plants. FEMS Microbiol Rev https://doi.org/10.1093/femsre/fuv045

Zhao X, Xu JR (2007) A highly conserved MAPK-docking site in Mst7is essential for Pmk1 activation in *Magnaporthe grisea*. MolMicrobiol 63:881–894

Zhao Z, Liu H, Wang C, Xu JR (2013) Comparative analysis of fungalgenomes reveals different plant cell wall degrading capacityin fungi. BMC Genome 14:274