Chapter 6
Diversity of Pathogenic Fungi in Agricultural Crops

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Abstract Fungi constitute an important group of organisms that possess beneficial as well as negative traits against plants and animals. Association of fungi with plants is mostly saprotrophic and involves in decomposition. However, a multitude of fungal species are widely recognized as plant pathogens owing to many diseases in crops like potato, paddy, wheat, maize, pulses, oil-yielding plants, floricultural crops, horticultural crops, plantation crops, and so on. Over 70% percent of plant disease is due to fungal pathogens, and they are usually parasitic and exhibit disease symptoms. Biotrophic fungal pathogens exhibit long-term establishment by obtaining nutrients from live host tissues via specialized cells "haustoria" that develop inside the host. Necrotrophic pathogens fetch nutrients from the dead host tissues by killing the tissues with toxins or enzymes, whereas biotrophs have a narrow host range. However, necrotrophs are generalists with a wide host range or specialized with a narrow host range for their survival. Recent advances in molecular biology and sequencing platforms enable the exploration of diverse plant pathogenic fungi associated with crop plants. This chapter intends to summarize the diversity of plant pathogenic fungi on selected agriculturally important crops. It includes the detailed comprehension of plant disease concepts, classification of plant pathogenic fungi based on their lifestyle, fungal diseases of historical records, major fungal diseases of crop plants (rice, maize, and vegetables), and global perspectives of major pathogenic genera.

Keywords Cereals · Millets · Oilseeds · Pulses · Timbers · Vegetables · *Colletotrichum* · *Diaporthe* · *Fusarium* · *Pestalotiopsis* · *Phytophthora* · *Sclerotium rolfsii*

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6.1 Introduction

India is known for diverse agro-climatic zones such as tropical, subtropical, and temperate climates ranging from average to high in temperature, humidity, and rainfall. Thus, the Indian subcontinent is the home to rich flora and fauna in the world. India ranks second in the output of fruits, vegetables, cereals, pulses, oilseeds, fiber crops, sugarcane, spices, and ornamentals (Anonymous 2009). About 40% of the geographical area of the Indian subcontinent is utilized for agriculture, thus playing a crucial role in comprehensive socioeconomic development. India is a major producer of several crops; the major crops could be placed in four different categories:

1. Food grains (maize, millets, pulses, rice, and wheat)
2. Cash crops (fiber-yielding crops, cotton and jute; sugar-yielding crops, sugarcane and tobacco; oilseeds, soybean, castor, sesame, and others)
3. Plantations (coffee, coconut, rubber, and tea)
4. Horticultural crops (fruits and vegetables)

Even though India is producing a large number of agricultural products, it succumbs to substantial loss of production due to diseases caused by various biotic factors. These include diseases caused by bacteria, fungi, insect pests, nematodes, phytoplasma, viroids, viruses, and others. The extent of losses caused by such biological agents differs from crops as well as seasons. As per the data released by the Parliament on Agriculture and Farmers Welfare, loss of crop production up to 15–20% is due to diseases. Thus, India raises agricultural production to ensure food security and nutrition for the teeming population. A total of 68% net loss of global agricultural production is due to various pests and diseases (microbial diseases, 16%; animals and pests, 18%; weeds, 34%; pathogenic fungi, 70–80%) (Oerke 2006).

The overall loss of yield occurs by various pests, diseases, and weeds during growth and post-harvest are of paramount significance for raise in loss up to 10–30%. The economic loss could be up to 15.4 billion US$. The average crop loss (20%) by pests and diseases was up to 1.4 billion US$ (Kumar and Gupta 2012). The current situation is further worsening due to the appearance of new diseases, pathotypes, and variants (pathovars) of pathogens, as they can adapt in varying climates. The extent of losses incurring due to pests and diseases is higher than the extent of production via innovative programs (Kumar and Saxena 2009). Agricultural loss due to plant diseases may also be attributed to other direct or indirect economic failures by various factors: (1) reduced quality as well as quantity of crop production; (2) increased cost of production; (3) threat on animal health and environment; (4) limiting the type of crops/varieties grown; (5) loss of natural resources; and (6) less remunerative alternatives (Kumar 2014).

Fungi are well known for agricultural diseases; being eukaryotes, fungi are capable to fetch nutrients externally and absorb them through their cell walls. The majority of fungi reproduce via spores and possess thallus constituting microscopic tubular hyphae. Fungi as heterotrophs obtain carbon and energy through live organisms or detritus. Nutrition derivation by fungi from living hosts is referred to as biotrophs, while nutrition from dead plants or animals is called as saprotrophs. The process of infecting a living host and killing host cells for nutrition purposes are referred to as necrotrophs. However, organisms conventionally classified as kingdom “fungi” are divided into three unrelated groups such as true fungi (eumycota), the oomycetes, and the slime molds. As per the classification proposed by Alexopoulos et al. (1997) and subsequent literature, there are four major groups of true fungi, viz., *Ascomycota*, *Basidiomycota*, *Chytridiomycota*, and *Zygomycota* (Webster and Weber 2007). Members having different cell wall compositions and flagellated zoospores are placed under Oomycota. Recent inferences suggest the addition of *Glomeromycota* as a phylum, under *Zygomycota*, which is known to develop an association with the roots of most of the plant species as arbuscular mycorrhizae. To date, it is unclear how many species of fungi exist globally. A conservative estimate based on the angiosperm/fungus ratio will be between 2.2 and 3.8 million species, and so far only 3.7–6.4% of fungi were recorded (Hawksworth and Lücking 2017). This chapter addresses the diversity of plant pathogenic fungi in crops with major emphasis on diverse symptoms, diverse groups of pathogenic fungi, diversity among the individual groups, and current developments in the evaluation of the diversity of plant pathogenic fungi in crop plants.

6.2 Concepts of Plant Disease

Plants make up the majority of the earth’s living environment and provide necessary nutrition to humans as well as animals. Plants convert energy from sunlight into stored exploitable chemical energy, viz., carbohydrates, proteins, and lipids. Animals depend on plant substances for their survival (Agrios 2005). Plant growth is dependent on soil providing adequate moisture and nutrients and sufficient light reaching leaves, and temperature remains within the normal range. Sickness in plants leads to poor growth as well as poor production. The agents that cause infection in plants include bacteria, fungi, nematodes, protozoa, and viruses. Plants are also known to suffer from the competition with other plants (weeds) and also damages caused by insects.

Fungal plant pathogens cause a wide array of diseases in major crops globally and cause substantial loss of yield (Anderson et al. 2004; Strange and Scott 2005; Rossman et al. 2014). Many phytopathogenic fungi have devastating threats in the history of agriculture. So far, ancient knowledge recognized as major of rust infection in crops and also the smuts infecting monocot crops such as barley (*Ustilago hordei*), wheat (*Ustilago tritici*), and maize (*Ustilago maydis*). A historically known threatened fungal plant pathogen is *Claviceps purpurea* (ergot of rye, barley, oats, and wheat). The sclerotia of *C. purpurea* are known to have a broad range of toxic alkaloids and replace kernels in the heads of crops, thereby causing contamination of harvested grains and flours.

6.3 Diversity Based on Lifestyle

Fungal pathogens are collectively referred to as those that derive nutrients from plants and induce a negative impact on plants' health. Some pathogens completely depend on their host (as obligate parasites), and some others as facultative exist in close association with the hosts to compete with its life cycle (phenology). The facultative pathogens are capable to prosper in varied environments; thus, they are capable to cause diseases in several hosts successfully. The traditional classification of plant pathogens (necrotrophs, biotrophs, and hemibiotrophs) differentiates fungi based on their lifestyle and the strategies of dependence on host. The recent reports suggest that such division is less stringent than previously realized; however, such categorization defines basic denominators as those that are common to all in each class and simplifies the lifestyle of pathogens.

Plant pathogenic fungi are ubiquitous and exhibit varied lifestyles. Many of them display a range of lifestyles from biotrophy through necrotrophy and ultimately to saprotrophy. Biotrophism is dependent on host plant, whereas hemibiotrophs shift from the initial biotrophic phase to the necrotrophic phase. The necrotrophic life cycle involves the active killing of host cells by secretion of cell wall-degrading phytotoxins and enzymes. The biotrophic fungi develop a close relationship with the host by haustorium, a specialized structure for assimilation of nutrition. It is proposed that biotrophy could essentially modulate plant defense mechanisms. Therefore, biotrophs adopt diverse strategies to counter the host plant defenses (De Silva et al. 2016). Specific examples of biotrophic fungi as well as oomycetes and other lifestyles are presented in Table 6.1. The discussion proceeds on plant pathogenic fungi under three subheadings based on their lifestyles (biotrophs, necrotrophs, and hemibiotrophs).

6.3.1 Biotrophs

Biotrophic fungi are those dependent on a narrow range of hosts for deriving nutrition from host's living cells leading to the damage of host tissue. They produce structures such as haustoria and appressoria to penetrate and acquire nutrients from the host (De Silva et al. 2016). Plant pathogenic fungi adapted to biotrophic mode of lifestyle are either obligate or non-obligate parasites. The powdery mildews (*Ascomycota*) and rusts (*Basidiomycota*) are the best representatives of obligate biotrophs causing diseases on various economically important crops like cereals, millets, vegetables, and horticultural crops. The downy mildews and white rusts (except white rust on *Chrysanthemum*) are also obligate biotrophs that belonged to Oomycota (protozoa) (Schulze-Lefert and Panstruga 2003).

The obligate biotrophs like rusts and powdery mildews have developed their lifestyle to match with the phenology of the hosts to complete the life cycle. Specifically, rusts possess five varied spore stages (aeciospores, pycniospores,

Table 6.1 Examples of fungi with different lifestyles (including oomycetes)

Lifestyle	Fungal pathogen	Host	Reference
Biotrophs	Rusts:		Oliver and Ipcho (2004), Meinhardt et al. (2014)
	Puccinia arachidis	Groundnut	
	Puccinia graminis	Wheat	
	Puccinia horiana	*Chrysanthemum*	
	Uromyces appendiculatus	Cowpea	
	U. fabae	Common beans	
	Smuts:		Mendgen and Hahn (2002), Latijnhouwers et al. (2003)
	Sphacelotheca sorghi	*Sorghum*	
	Ustilago maydis	Corn/maize	
	Ustilaginoidea virens	Rice	
	Powdery mildews:		Oliver and Ipcho (2004), Delaye et al. (2013)
	Blumeria graminis	Barley	
	Erysiphe cichoracearum	Cucurbits	
	Leveillula taurica	Chili and tomato	
	Podosphaera oxyacanthae	–	
	Podosphaera xanthii	Brinjal	
	Sphaerotheca mors-uvae	Gooseberry	
	Sphaerotheca pannosa	Rose	
Biotrophic oomycetes	*Albugo candida*	Crucifers	Latijnhouwers et al. (2003), Figueiredo et al. (2015)
	Peronospora parasitica	–	
	Plasmopara viticola	Grapes	
Hemibiotrophs	*Colletotrichum destructivum*	–	Damm et al. (2014)
	C. lindemuthianum	Common bean	Mendgen and Hahn (2002)
	Fusarium oxysporum	–	Krola et al. (2015)
	Gibberella zeae	Maize/corn	Kabbage et al. (2015)
	Magnaporthe oryzae	Rice	Oliver and Ipcho (2004), Kankanala et al. (2007), Kabbage et al. (2015)
	Moniliophthora roreri	–	Meinhardt et al. (2014)
	Mycosphaerella graminicola	–	Spanu (2012)
Hemibiotrophic oomycetes	*Phytophthora capsici*, *Phytophthora* sp., and *Pythium* sp.	Potato, tomato, beans, and vegetables	Meadows (2011)
Necrotrophs	*Alternaria brassicicola*	Crucifers	Spanu (2012), Pandey et al. (2016)
	Botrytis cinerea	Fruit crops	
	Leptosphaeria maculans	–	
	Sclerotinia sclerotiorum	Cabbage	

urediniospores, teliospores, and basidiospores) developed in specialized fruit bodies (aecidium, pycnium, uredenium, telium, and basidium); thus, they are capable to infect alternate hosts to complete the life cycle. But not all rusts have such mechanisms of completion of life cycles (Petersen 1974). Rust diseases are due to members of basidiomycetes of the order *Pucciniales* (earlier considered under the order *Uredinales*) (Duplessis et al. 2011). Usually, the urediniospores (dikaryotic) germinate on the leaf surface (on primary host) and produce penetration plug or haustorium, which invades the mesophyll tissue through stomata. The haustoria further differentiate to form sub-stomatal vesicles to develop the hyphae within the host tissue. On the contrary, the powdery mildews are caused by filamentous ascomycetous fungi (haploids) belonging to the order *Erysiphales*. The germination of conidia of these fungi occurs on the leaf surface, and appressoria helps in the penetration of the epidermal tissues (Spanu et al. 2010; Hückelhoven and Panstruga 2011). Following the penetration from the surface, the rusts cross the wall of mesophyll, and powdery mildews cross the wall of the epidermis and differentiate into haustoria, which are exclusive infection erections that help to survive inside the host tissues through the acquisition of nutrients. Usually, the haustoria are formed behind the plant cell wall without disrupting the cell membrane, and they push and invaginate the cell membrane establishing a maintainable "cell within cell" complex (Heath and Skalamera 1997). Once the fungi establish inside the host tissues, the haustoria secrete a broad varied array of transporters to derive the nutrition from the host (surrounding the living tissues where the obligate pathogen entered) into the haustorium which, in turn, nourishes the fungi to successfully colonize the tissues and extends its territory inside the host (Struck 2015; Voegele and Mendgen 2011; Voegele et al. 2001). They also synthesize effector molecules to suppress the host defense and keep the cells alive (Kemen et al. 2005, 2013; Petre et al. 2016). The obligate biotrophic fungi fully depend on their host for energy, and they are aptly designated as obligate parasites or energy parasites (Schulze-Lefert and Panstruga 2003).

Non-obligate biotrophs are capable to survive as true biotrophs in living tissues/host and capable to grow and survive without the presence of a host. The ergot disease caused by *Claviceps purpurea* acts as a true biotroph in the host, and it can also be grown in axenic culture (Tudzynski and Scheffer 2004). These non-obligate biotrophic fungal pathogens are taxonomically diversified throughout a wide range of genera, and important ones are the smuts belonging to the order *Ustilaginales* (*Basidiomycota*) and certain species in *Claviceps* (*Ascomycota*, *Clavicipitaceae*). In ergot disease, the wind-borne ascospores germinate on the pistil surface during anthesis and penetrate through the stigmatic hairs and colonize the ovarian tissue and launch a specific and persisting host-pathogen interface. A mycelial stroma develops in the ovary with the production of mass of conidiospores, and they exude sugar-rich fluid from the phloem sap. Sclerotia (overwintering structures) are formed after 10–15 days of post-infection. *Claviceps purpurea* does not produce classical haustoria and intracellular hyphae; instead, this fungus is completely covered by the host plasma membrane (Tudzynski and Tenberge 2003). The smut pathogen in maize *U. maydis* stands out among other smuts due to its acquiescence to molecular genetic manipulation and its small genome size (Brefort et al. 2009).

6.3.2 Necrotrophs

The necrotrophic fungi are those which feed on dead plant tissues (by killing the healthy tissues). However, there are two terminologies such as true necrotrophs and secondary necrotrophs. The true necrotrophs attack and kill the healthy plants, while the secondary necrotrophs are saprophytic but may occasionally infect the plants that have been previously weakened (Doehlemann et al. 2017). The basic definition of necrotrophy is "the mode of infection in which the pathogen kills the tissue before colonization" (Oliver and Solomon 2010; Doehlemann et al. 2017). This statement contradicts the fact since the initial contact of the pathogen is with a living tissue. There are two early stages following the first contact of the pathogen with the host. To survive, the pathogen needs to subvert the host defense and generate a necrotic zone where the pathogen can survive from the host defense spread the necrosis around the initial zone (Doehlemann et al. 2017). There will be initial and late reactions in biotrophic fungi which exist in two-phase strategy "survive or die," but the early stage has no direct fight with the host (defense), but it follows easy/simple "sneaking in" strategy, and further stages necessitate close contact with the living host, hence resulting in continuous conflict with the host defense. In biotrophic fungal pathogens, they observe a "survive or die" strategy at the first meeting with the plant defense. Further, biotrophs prosper to keep the host tissue alive, and host defense strategy at this stage is a morbid in the form of a hypersensitive response (HR), and the pathogen strategy is deterrence of this response (Doehlemann et al. 2017). The necrotrophic pathogens have to deal with the plant defense during the first contact and overcome the initiation of infection. Thus, the initial phase of necrotrophic fungi uses an array of effector molecules to cope with and operate the host defense during infection (Choquer et al. 2007). The true necrotrophic pathogens include several species that belong to diverse genera. It is convenient to divide all necrotrophic pathogens into narrow-host-range and broad-host-range species (Mengiste 2012). The host specificity of necrotrophs is due to the synthesis of host-specific toxins (HST); these pathogenicity factors are crucial for compatible host. For example, T-toxin (*Cochliobolus heterostrophus*), HSTs (*Pyrenophora tritici-repentis* and *Parastagonospora nodorum*), and HSTs from *Cochliobolus* sp. include HC-toxin (*Cochliobolus carbonum*), victorin (*Cochliobolus victoriae*), and ToxA toxins and specify the host range in spot and blotch diseases (Faris et al. 2010). These HSTs which interact with a specific gene from a host (similar to that of "Avr" or "effector proteins") interact with resistance proteins (R proteins). The HSTs are regarded as effectors as they share many of the characters of the avirulence gene. The HSTs share many characteristics with avirulence gene products similar to primary virulence function, they are specifically recognized by the host resistance counterparts, and they can be recognized by the immune system of plant as virulence factors.

The broad-host-range necrotrophs lack HSTs and may attack several host plants across the families. The best-represented broad-host-range necrotrophs is *Botrytis cinerea*, which is closely related to *Sclerotinia sclerotiorum*. Both of them have more than 300–500 host plants, and each causes severe economic losses pre- and post-harvest annual crop worldwide (Bolton et al. 2006; Williamson et al. 2007). The melanized sclerotia have a crucial role in germination (vegetatively or carpogenically) as well as production of apothecia to release ascospores (Doehlemann et al. 2017). The genetic basis of resistance against broad-host-range necrotrophic pathogens is more complex and typically quantitative (Oliver and Solomon 2010; Mengiste 2012). This is in contrast to R-gene-mediated resistance or HST-blocking genes, which provide complete resistance. For this reason, it is difficult to control broad-host-range necrotrophic pathogens, which might partially explain their growing economic importance.

Originally, the necrotrophy was inferred as toxin-assisted maceration of the tissue of host, and several studies showed the use of hydrolytic enzymes by necrotrophic pathogens (Smith 1900; Cole 1956). However, the recent literature and developments reveal that these enzymes do not function alone and they might have additional roles other than sheer hydrolysis of plant polymers. The large set of genes coding for cell wall-degrading and other hydrolytic enzymes present in the genomes of necrotrophic fungi support this strategy (Soanes et al. 2008; Amselem et al. 2011). The high redundancy of many of these enzymes (which is unusual in fungi) supports necrotrophic fungi. Recent transcriptome and secretome studies revealed that horde of these enzymes are produced and secreted at different stages of the infection (González et al. 2016; Kim et al. 2016; McCotter et al. 2016).

6.3.3 Hemibiotrophs

Hemibiotrophic pathogens are those that have combined biotrophic and necrotrophic lifestyles. Their life cycle has an initial biotrophic phase followed by the necrotrophic phase (Oliver and Ipcho 2004; Divon and Fluhr 2006). Hemibiotrophs are defined as species that have a flexible length of initial biotrophic stage before switching over to necrotrophy (Perfect et al. 1998; O'Connell et al. 2012; Yi and Valent 2013). This definition involves an initial true biotrophic phase mediated by special biotrophic organs. In the beginning, fungal pathogens secrete effectors to suppress the plant defense, and later (at the end of the brief biotrophic stage), the fungus undergoes a substantial developmental change that facilitates the transition from a biotrophic to a necrotrophic mode.

Two examples that fit very well as hemibiotrophic lifestyle are the rice blast fungus *M. oryzae* and species under the genus *Colletotrichum* (Yi and Valent 2013). Upon penetration into the sub-epidermal or epidermal cells, they develop specialized hyphae that establish close contact with the host and invaginate the host cell membrane, leading to true (temporary) biotrophic interphase. The true biotrophic phase may last from one to several days and then switches to the necrotrophic mode. This transition differentiates new types of hyphae, secretions (enzymes and toxins), and delivery of specialized effectors.

Colletotrichum and *Magnaporthe* are important plant pathogenic fungi, which could be cultured and amenable to genetic manipulations owing to their conventional hemibiotrophic mode of lifestyle. Other fungi that follow a hemibiotrophic mode of lifestyle include *Fusarium*, *Mycosphaerella*, *Verticillium*, and many others (Fradin and Thomma 2006; Churchill 2011; Goodwin et al. 2011; Ma et al. 2013; Ploetz 2015). The most common feature of these species is a latent stage that varies in length, but in most instances, they do not differentiate into the typical biotrophic specialized organs and do not form a close contact with the host cell, but remain in the apoplastic or intracellular sphere. However, the pathogenic lifestyle of these species includes symptomless, quiescent, latent, or endophytic stages, but they do not meet the criteria of hemibiotrophy as defined above and therefore should not be treated in the same fashion. To support, a list of representative fungi showing different lifestyles are given in Table 6.1 along with diseases caused by those fungi exhibiting different lifestyles (rusts, powdery mildews, *Choanephora* species, sooty bolds, and others) in Fig. 6.1.

6.4 Historically Known Major Fungal Diseases

Phytopathogenic fungi have caused devastating diseases on various crop plants throughout the history of agriculture. The Theophrastus botanical studies contributed for the first time a relevant scientific explanation to the knowledge on plant disease. So far, ancient knowledge recognized is rust infection in crops and also the smuts infecting monocot crops such as barley, wheat, and/or maize by *Ustilago hordei*, *U. tritici*, and *U. maydis*, respectively. Similarly, the rusts were also traditionally recognized as serious threats in agriculture. A fungal plant pathogen with vast agrarian and cultural influence in human history was *Claviceps purpurea* (associated with ergot of rye, barley, oats, and wheat). The sclerotia of *C. purpurea* are known to possess a broad range of toxic alkaloids and replace kernels in the heads of crops and thereby contaminate the harvested grains. Further, there are numerous epidemics of the plant diseases affected human life by causing diseases such as “devil’s curse” or “holy fire” (Agrios 2005).

In the history of plant pathology, the development of fungal diseases left bitter experiences on human life and was responsible for a large number of deaths. Important catastrophic events include (1) the Irish famine by *Phytophthora infestans*, which caused late blight of potato (1840–1845); (2) the Ceylon rust caused by *Hemileia vastatrix* which destroyed the coffee plantations in Sri Lanka; and (3) the Bengal famine contributed by *Helminthosporium oryzae* in rice. The impact caused by the occurrence of late blight of potato was the reason to initiate a new

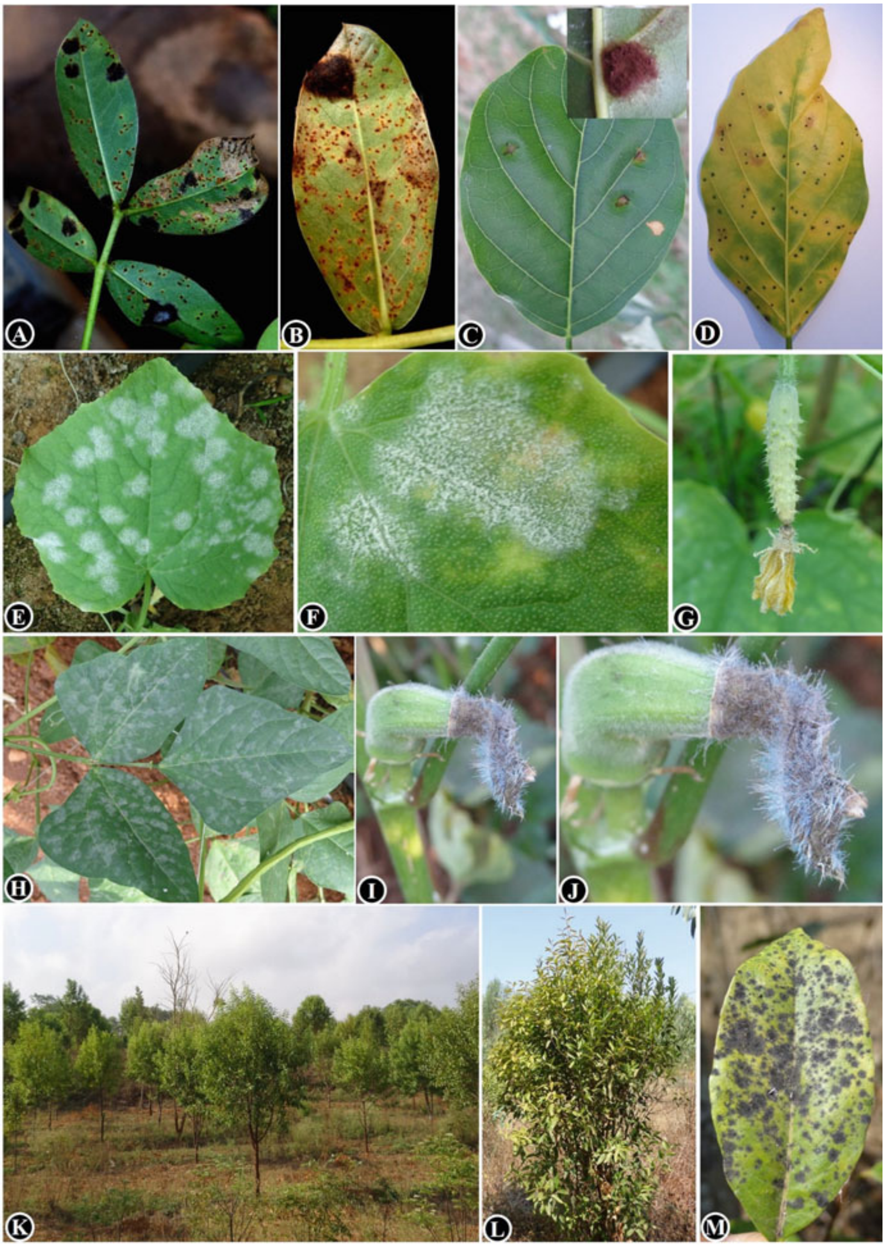

Fig. 6.1 Representative images of fungal diseases which explicate different mode of lifestyles: biotrophic lifestyle and groundnut rust (*Puccinia arachidis*) (**a**, **b**); rust on *Pongamia* tree (*Ravenelia* sp.) (**c**, **d**); powdery mildew of cucurbits (**e**–**g**); powdery mildew on cowpea (**h**); bud rot of okra by *Choanephora* sp. (**i**, **j**); dieback of sandalwood (**k**, **l**); and sooty mold on sandalwood (**m**)

discipline, the “plant pathology.” The following sections briefly discuss the three diseases which left their bitter impressions in the human history.

6.4.1 Phytophthora Infestans

Phytophthora infestans, the causative fungus of late blight of potato (Irish famine), occurs on many varieties of Solanaceae crops (potato, brinjal, tomato, and many other hosts) around the world. The genus *Phytophthora* placed under Oomycota has been a causative agent for diseases like blights, wilting, damping-off, chlorosis, root rot, and the rotting plant organs. The late blight of potato in the field is presented in Fig. 6.2. Although several species of *Phytophthora* are identified in different hosts causing different diseases, *P. infestans* find a place in the history for its infamous Irish potato famine in the 1840s (Fry 2008). At present, *P. infestans*, besides infecting potato, causes severe damage to other important Solanaceae crops like tomato (*Solanum lycopersicum*), brinjal (*Solanum melongena*), chili (*Capsicum annuum*), and many other vegetable crops.

The genus *Phytophthora* is capable to cause destructive and epiphytic diseases like blights, foot rots, wilts, cankers, seedling blights, damping-off, gummosis, and various rots in field and storage conditions. Therefore, it has the implicit role of a virulent pathogen owing to its capacity of zoosporangia to germinate by liberating zoospores as well as by germ tube. Diversity of *Phytophthora* spp. associated with crops is presented in Table 6.2 along with their hosts and other details. It is evident from the recent studies the existence of a complex nature or diverse population among the species *Phytophthora* or altogether a new species is present in the current agro-ecosystem, which needs to be deciphered by advanced molecular tools. Recently, Scanu et al. (2015) reported the occurrence of nine species of *Phytophthora* on the decline of Mediterranean maquis vegetation (a scrubland vegetation of the Mediterranean region) using multi-locus barcoding and phylogenomic analysis of the population. Thus, advanced molecular tools play a crucial role in deciphering the hidden diversity of *Phytophthora* (morphologically difficult to differentiate many of these species) and revealed for the first time the involvement of highly invasive pathogen with a wide host range *P. cinnamomi* and several species of *Phytophthora* (Scanu et al. 2015). The subsequent conventional and sequence analysis (ITS and Cox1 gene regions) revealed association of multiple *Phytophthora* spp. with two new species (Jung et al. 2011). Based on the morphological characters and molecular sequence analysis, the isolates were identified as *P. asparagi*, *P. bilorbang*, *P. cryptogea*, *P. cinnamomi*, *P. gonapodyides*, *P. melonis*, *P. syringae*, and the two new species (*P. crassamura* and *P. ornamentata*).

The genus *Phytophthora* is diversified, and variations are observed on mating types. The mating types vary from country to country and between the hosts. Different management strategies have been developed due to unsuccessful attempts of eradication. Even after 172 years of famine, the problem persists. Further, the

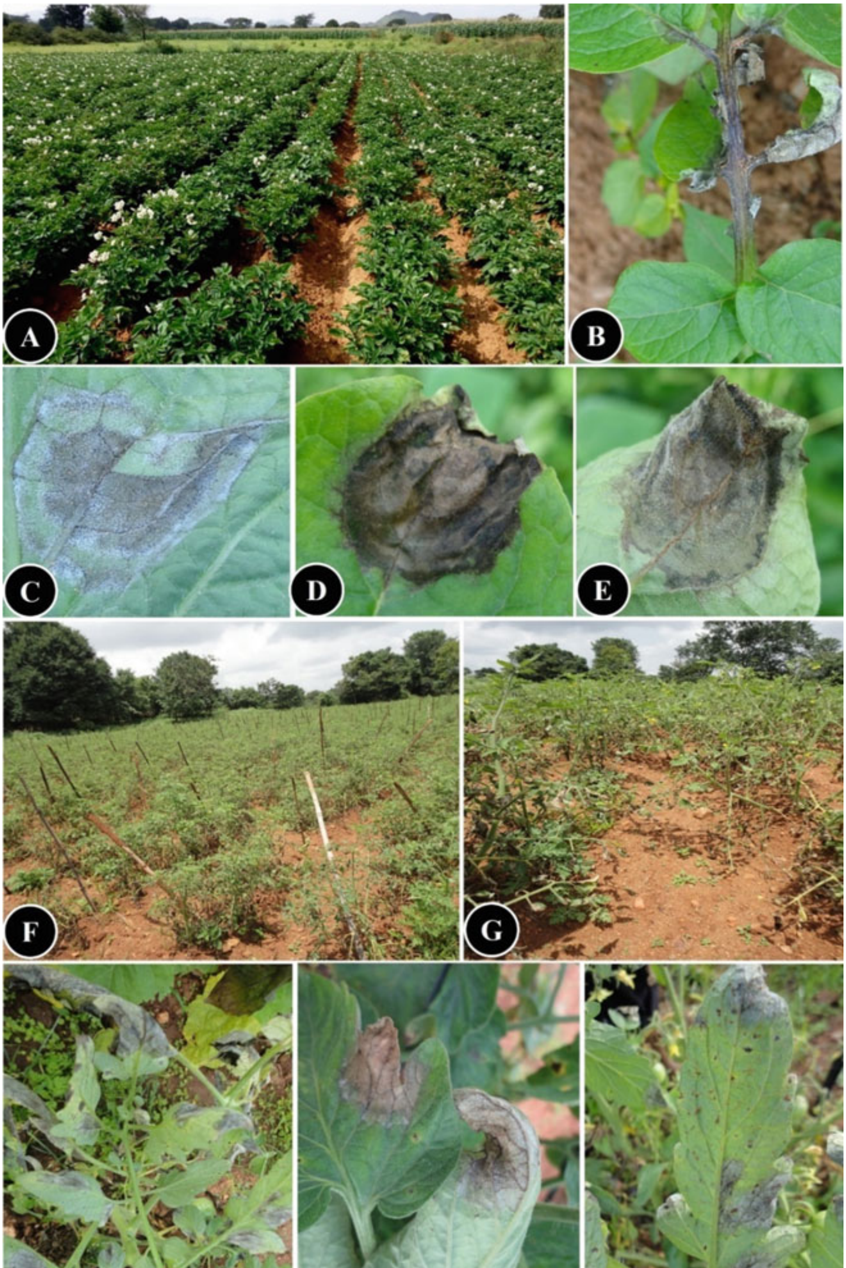

Fig. 6.2 *Phytophthora* blight observed in potato and tomato from Karnataka: field view of potato (**a**); leaf blight caused due to *P. infestans* (**b**–**e**); severe late blight affected tomato field view from Mysore region, Karnataka (**f**, **g**); and blight symptoms on individual leaves showing presence of sporangiospores on lower leaf surface of tomato (**h**–**j**)

Table 6.2 Diversity of *Phytophthora* species associated with diseases of crops

Phytophthora species	Crop plants and their disease	Reference
P. alni	Collar rot of alder	Hansen (2015)
P. boehmeriae	Wide host range (forest tree pathogen) and cotton	Elena and Paplomatas (1998)
P. cactorum	*Rhododendron*	Yang et al. (2018)
P. cambivora	Ink disease on chest nut	Vannini and Vettraino (2011)
P. capsici	Bell pepper, chili, eggplant, and tomato	Granke et al. (2012)
P. cinnamomi	Dieback of *Eucalyptus*	Hansen (2015)
P. citricola	Citrus orchards	Jung and Burgess (2009)
P. citrophthora	Citrus	Jung and Burgess (2009)
P. colocasiae	Black pepper and *Piper betel*	Shrestha et al. (2017)
P. cryptogea	Several floricultural crops	Ampuero et al. (2008)
P. erythroseptica	Potato (pink rot)	Jiang et al. (2019)
P. europea	European oak	Vettraino et al. (2005)
P. fragariae	Raspberry	Koprivica et al. (2009)
P. fragariae rubi	Root rot of red raspberry	Koprivica et al. (2009)
P. ilicis	Holly (ilicis leaf blight and spots)	Scanu et al. (2014)
P. infestans	Brinjal (eggplant), chili, potato, and tomato	Dey et al. (2018)
P. inundata	Tree pathogen	Brasier et al. (2003)
P. kernoviae	European beach and *Rhododendron*	Brasier et al. (2005)
P. lateralis	Cedar root disease	Hansen (2015)
P. medicaginis	Root rot of *alfalfa* and chickpea	Vandemark and Barker (2003)
P. melonis	Fruit rot of cucurbits	Guharoy et al. (2006)
P. nemorosa	Foliar and bole pathogen of various evergreen hardwood trees	Hansen et al. (2003)
P. nicotianae	*Citrus*, pepper, *Piper betel*, and tobacco	Meng et al. (2014)
P. palmivora	Bud rot of palms, fruit rot (or koleroga) of coconut and areca nut	Carella et al. (2018)
P. parasitica	Eggplant and tomato	Meng et al. (2014)
P. pinifolia	Radiata pine	Hansen (2015)
P. plurivora		

(continued)

Table 6.2 (continued)

Phytophthora species	Crop plants and their disease	Reference
	Infecting roots of: *Acer platanoides*, *Aesculus hippocastanum*, *Alnus glutinosa*, *Fagus sylvatica*, *Quercus robur*, *Tilia* spp., and conifer species	Jung and Burgess (2009)
P. psis	Causes root rot in: *Cicer arietinum* (chickpea) and *Lens culinaris* (lentil), *Lathyrus* spp. (pea), *Pisum sativum*; *Vicia faba*, *V. sativa* (garden vetch), and *V. benghalensis* (purple vetch)	Heyman et al. (2013)
P. ramorum	Sudden oak death and *Phytophthora ramorum* blight (also infects members of Ericaceae, Fagaceae, Larix, and others)	Elliott et al. (2009), Hansen (2015)

mystery surrounding the Irish famine was resolved by Yoshida et al. (2013). Until the 1970s, there was very low diversity of *P. infestans* confined only to Mexico and the USA. But, it later dominated the globe for a period of 150 years. However, Yoshida et al. (2013) concluded that the nineteenth-century epidemic was due to the HERB-1 unique genotype which persisted over 150 years. The HERB-1 genotype was distinct from modern strains, but closely related to the US-1 genotype that was replaced outside the Mexico in the twentieth century. It was proposed that HERB-1 and US-1 could have emerged from metapopulation established in the early 1800s outside of epicenter (Yoshida et al. 2013). This scenario holds good for many species of *Phytophthora*, which are causing devastating diseases in horticultural, floricultural, and other vegetable crops.

6.4.2 Hemileia vastatrix

One of the historical examples of disease is the coffee rust (or Ceylon coffee rust) caused by *Hemileia vastatrix*. Until the 1870s, Sri Lanka was one of the world's greatest coffee producers. This dramatically changed after *H. vastatrix* reached Ceylon in 1875. From 1870 to 1885, coffee production drastically dropped to 95%, the fungus destroyed the coffee plantations, and now Sri Lanka is known mainly for tea. Even today, the coffee rust is a significant threat to coffee productions with recent outbreaks in Central and South American regions (Avelino et al. 2015). The coffee leaf rust threat by *H. vastatrix* is one of the major diseases occurring in coffee plantations affecting commercial coffee species *Coffea arabica* (arabica coffee) and *Coffea canephora* (robusta coffee). This rust caused multiple outbreaks in several coffee-growing regions resulting in heavy loss of yield. The new races are constantly evolving as evidenced by the presence of fungus in plants that were previously resistant (Mahadevakumar and Sridhar 2020).

H. vastatrix is a hemicyclic fungus, and its source of inoculum is by the urediniosporic life cycle. The disease appears as chlorotic spots initially (can be visualized through naked eyes), followed by the development of differentiation of suprastomatal, bouquet-shaped, and orange-colored uredinia (Fig. 6.3). The disease has resulted in 35% loss of yield and caused polyetic epidemiological impact. Although *H. vastatrix* is the only fungus causing rust on coffee, there exists variation in population structure and genotype composition, which plays an important role in determining the virulence of the isolate/pathogen at different ecological and environmental conditions (Talhnihas et al. 2017). Despite exhibiting low genetic polymorphism, the large genomes of *H. vastatrix* (c797 Mbp) cover up great pathological diversity (>50 physiological races). The gene expression studies conducted, which suggested the activation of signaling pathways for the production of putative effectors, suggest the plant-fungus dialogue starts as early as the germ tube stage, which provides clues for the identification of avr genes (Talhnihas et al. 2017).

6.4.3 Helminthosporium oryzae

Pathogenic fungi associated with rice are important historically and economically as the diseases caused by them lead to severe economic loss as well as an acute shortage of staple food. Historically, the rice brown spot disease is very important as it witnessed famine in two instances. The first famine was during 1769–1770, and the second was during 1943 (called the great Bengal famine). The 1943 famine resulted in mortality of more than two million people due to 10–58% seedling mortality. The diseases are associated with all stages of growth and development of rice (from seedbed to harvest and post-harvest).

6.5 Global Perspectives of Major Fungal Diseases

The main sources of staple food for the majority of the globe include maize, rice, and wheat. These crops are not only serving as staple diets for humans but also used as livestock feeds, thus indirectly contributing toward the production of meat, dairy, and other animal-derived products. Soya bean is the fourth important crop, which is grown primarily as feed for livestock. The trade-in four crops constitute a major share of food system of 7% (rice), 12% (maize), 19% (wheat), and 30% (soya beans) being traded internationally between 1995 and 2010 (Dowlah 2015). All these four crops are susceptible to fungal infections. In a recent review, Fisher et al. (2012) detailed the major fungal pathogens of each species responsible for the reduction in yield.

The rice blast (*Magnaporthe oryzae*) is a widely distributed disease, potentially found wherever rice is grown (Fig. 6.2). This blast can cause up to 10–35% loss depending on crop variety and environmental conditions (Talbot 2003). Infection in wheat is associated with the stem rust *Puccinia graminis* (and other *Puccinia* spp.), and *Puccinia tritici* cause crop loss up to 70% (Leonard and Szabo 2005). The

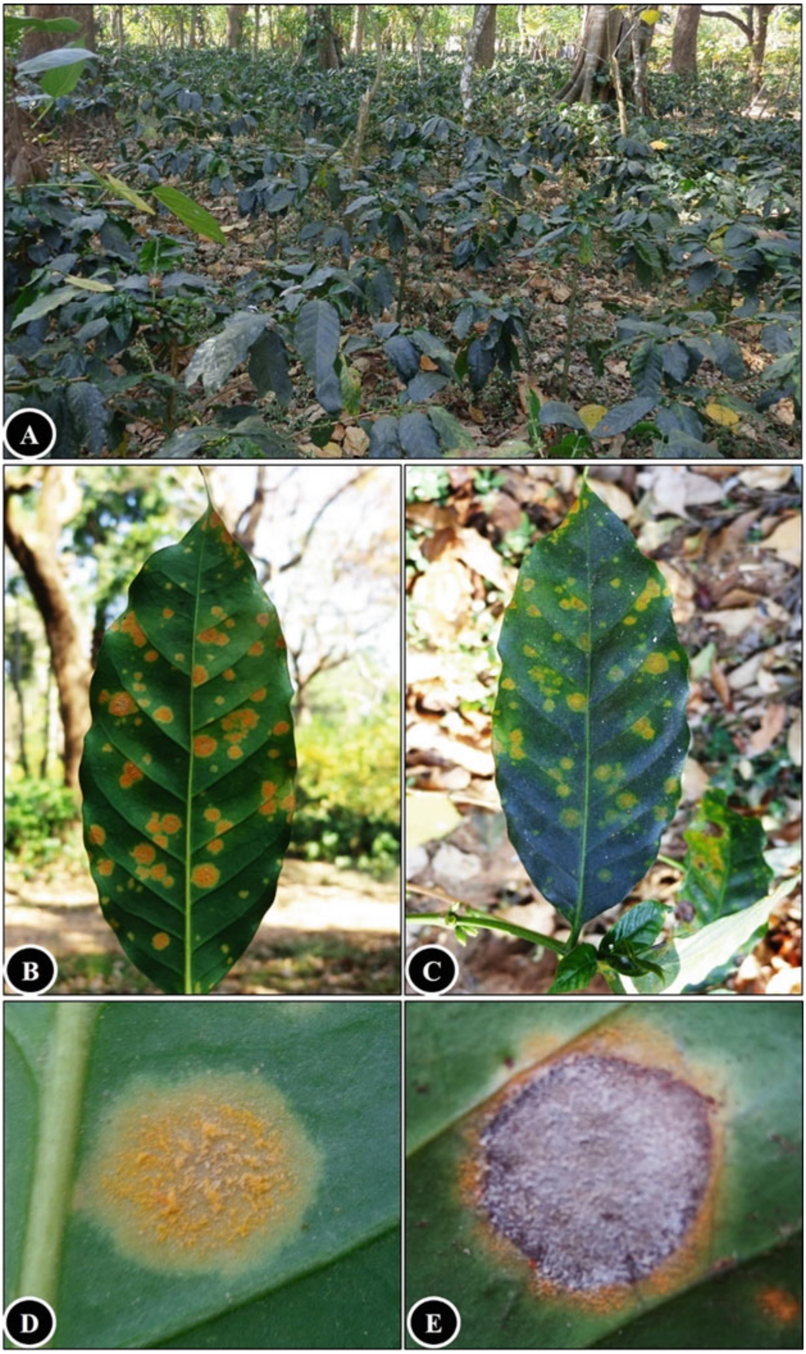

Fig. 6.3 Coffee rust disease caused by *Hemileia vastatrix*: field view of the coffee plantation from Balehonnur region, Karnataka (**a**); individual leaves showing rust pustules in adaxial and abaxial surfaces (**b**, **c**); and immature and mature rust pustules due to colonization of *H. vastatrix* (**d**, **e**)

resistant wheat cultivars developed in the past decades have shown good control; however, an emergence of a new virulent strain was seen in Uganda during 1999 (UG99 or TTKSK) (Singh et al. 2011). The major fungal pathogen associated with maize is corn smut by *Ustilago maydis*, a causative agent of galling and other damages. It is native to the central and southern Americas and spread over to most of the maize-growing areas and caused a 20% loss of crop (Brefort et al. 2009). The soya bean is known for attack by the rust *Phakopsora pachyrhizi*, which causes up to 70% of the loss. It is originated in Asia and spread over to most areas where soya bean is grown. Besides soya bean, the rust also attacks other plants of the family Fabaceae, which can serve as a reservoir of agricultural infections (Hartman et al. 2011).

6.5.1 Diversity of Fungal Diseases of Rice

Rice (*Oryza sativa*) is indeed life for most people in Asia, and scarcity in production and availability could lead to a severe food crisis. Considering the significance of rice globally and also in human life history, the United Nations celebrated the year 2004 as the International Year of Rice. Rice has been recognized as an important crop globally, and it is the main source of energy for the majority of the world's population. It is a staple food for people living in the rural and urban areas of humid and sub-humid Asia responsible for 30–50% of agricultural production (Hossain and Fischer 1995). Rice provides national food security and generates employment and income for the low-income groups. However, its production is influenced by various diseases by fungi, bacteria, viruses, and others. The following sections provide diverse fungal diseases associated with rice in major rice-growing countries.

The Bengal famine in 1942 was in part attributed to brown spot disease in rice (Padmanabhan 1973). The rice blast epidemics in the 1970s in Korea led to a major food crisis (Ou 1985) due to loss of yield up to 10–50 billion US$. Thus, minimizing or managing the disease epidemics and reduction of loss are crucial in sustained rice production. To achieve this goal, it is important to understand the extent of damage brought about by the fungal diseases and to identify shifting disease problems associated with technological advances.

Figure 6.4 presents a comprehensive picture of fungal disease associated with rice in major rice-growing countries. In a nutshell, the major five fungal diseases posed a challenge to world food security. These diseases include (1) rice blast caused by *Magnaporthe oryzae*; (2) sheath blight and sheath rot caused by *Rhizoctonia solani*; and (3) bacterial blight and viral disease tungro. However, the brown spot disease by *Helminthosporium oryzae* is also one of the historically important diseases caused by significant loss of production in the past as well as present. If suitable management practices are not followed, the world has to face a shortage in rice production leading to jeopardy in food security. The post-harvest diseases of rice are also playing a significant role and lead to decline in production due to fungal infestation during storage.

Fungal Diseases Associated with Rice

SEEDLING DISEASE:

Water molds – *Pythium* sp.
Seedling blight – *Fusarium* sp./ *Rhizoctonia* sp.

FOLIAR DISEASE:

Blast – *Magnoporthe oryzae*
Brown Spot – *Bipolaris oryzae*
Leaf Blast – *Pyricularia oryzae*
Stackburn – Trichoconiella padwickii
Leaf Smut – *Entyloma oryzae*
Downy Mildew – *Sclerophthora macrospora*
Collar rot – *Rhizoctonia solani*

SHEATH & CULM DISEASE:

Stem Rot – *Sclerotium oryzae*
Sheath Blight – *Rhizoctonia solani*
Sheath Blotch – *Sarocladium oryzae*
Sheath Rot – *Myrothecium roridum*

ROOT DISEASES:

Root Rot – *Fusarium* sp./*Pythium* sp.
Bakane Disease – *Fusarium moniliformae*

GRAIN DISEASES:

Kernal smut – *Tilletia barclayana*
False Smut – *Ustilaginoidea virens*
Udbatta – *Ephelis oryzae*
Ear Blight – *Helminthosporium oryzae*

Fig. 6.4 Major fungal diseases recorded from principal rice-growing countries

In the process of increasing the rice production, rice seeds appear to be vulnerable to infection by many pathogens. The sheath rot complex and grain discoloration is an important problem faced by the rice growers. This syndrome involves a characteristic browning discoloration or rotting of the flag leaf sheath and discoloration of the grain. The syndrome is widespread in tropical Asia since the introduction of modern semi-dwarf and photoperiod-insensitive rice cultivars. It is more prevalent in the rainy season than in the dry season. In the literature, the causal agent of sheath rot is always associated with *Sarocladium oryzae*. However, many reports projected that sheath rot is a complex problem caused by bacteria as well as fungi. Sheath rot and seed discoloration pathogen includes several fluorescent and non-fluorescent pseudomonads: *Pseudomonas glumae* (syn. *Burkholderia glumae*), *P. fuscovaginae*, and other non-pathogenic bacteria (Cottyn et al. 1996a, b). Similarly, along with *S. oryzae* and others pathogens viz., *Bipolaris oryzae* and Fusarium spp. were also isolated from discolored seeds showed the frequency of *S. oryzae* was lower than 10% (Lee et al. 1986).

The false smut caused by *Ustilaginoidea virens* has long been considered a minor problem in the global rice production. But, reports of severe damage caused by this disease in tropical and temperate regions in Africa, Asia, and America appear to be increasing in recent years. This disease was recently reviewed by Biswas (2001); however, the reduction in yield associated with false smut remains unclear. Similarly, the epidemiology of the disease in association with modern rice production is not well understood. A few reports showed that the high incidence and severity of false smut are correlated with an increase in some parameters involved in modern rice production systems.

6.5.2 Diversity of Fungal Diseases of Maize

Maize is an important cereal crop cultivated globally, and the USA is a major producer fulfilling nearly 35% of the global demand. The USA has the highest productivity (>9.6 tons/ha), and it is twice the global average (4.92 tons/ha). In India, the average maize production is around 2.43 tons/ha. The maize is the third most important food crop in India after rice and wheat. According to an estimate, its production was 22.23 metric tons (2012–2013) mainly during Kharif season, which occupies 80% of the area under cultivation. Maize contributes nearly 9% of the national food production in India. Maize serves as a staple food for humans and livestock and also as a basic raw material for several industrial products (alcoholic beverages, cosmetics, film, food sweeteners, gum, oil, package protein, paper industries, pharmaceuticals, starch, and textile).

Maize is affected by various diseases caused by bacteria, fungi, rusts, smuts, root rots, and ear rots leading to a severe reduction in the yield as well as quality. There are more than 25 fungal diseases that cause significant economic loss in the production of maize. The stalk rot of maize is a major threat in terms of crop loss and seed quality. Important fungal diseases of maize include root disease, foliar diseases, stalk rots, kernel rots, and ear rots. Along with the pathogenic fungi in maize, the secondary metabolites (mainly toxins) produced by these fungi cause major threat to human and livestock health. The major fungal diseases associated with maize at various stages of its growth and development are presented in Fig. 6.5.

Fungal Diseases Associated with Maize

SEEDLING & ROOT DISEASE:

Seed Rots – Pythium species
Seedling blights – *Fusarium* sp./*Rhizoctonia* sp.
Crown Rot – *Rhizoctonia* species
Root Rot – *Fusarium* species
Red Root Rot – *Phoma* /*Pythium* /*Fusarium* sp.

FOLIAR DISEASES:

Southern Corn Leaf Blight – *Bipolaris maydis*
Northern Corn Leaf Blight – *Exserohilum turcicum*
Northern Corn Leaf Spot – *Bipolaris zeicola*
Anthracnose /leaf blight – *Colletotrichum* sp.
Banded Sheath Blight – *Rhizoctonia solani*
Leaf Streak Disease – *Diplodia maydis*
Downey mildew (DM) – *Perenosclerospora graminicola*
Sorghum DM – *Perenosclerospora sorghi*
Crazy top – *Sclerophthora macrospora*
Brown Stripe DM – *Sclerophthora rayssiae*

STALK ROTS:

Gibberella stalk rot – *Gibberella zeae*
Diplodia stalk rot – *Diplodia maydis*
Anthracnose stalk rot – *Colletotrichum graminicola*
Charcoal Rot – *Macrophomina phaseolina*
Fusarium stalk rot – *Fusarium moniliforme*
Pythium stalk rot – *Pythium aphanidermatum*
Lasiodiplodia stalk rot – *Lasiodiplodia theobromae*

EAR and KERNEL ROTS:

Aspergillus Ear rot – *Aspergillus niger* /*A. flavus*
Diplodia Ear Rot – *Stenocarpella maydis*
Fusarium Ear Rot – *Fusarium moniliforme*
Nigrospora ear rot – *Nigrospora spaerica*
Penicillium ear rot – *Penicillium* species

Fig. 6.5 Major fungal diseases associated with maize in principal maize-growing countries

The earliest report of maize disease is that of head smut caused by *Sphacelotheca reiliana* recorded by Cooke (1876). Butler (1918) wrote that this disease was severe in the Kashmir, Himalayas, and other regions of India. In southwest Rajasthan, this disease appears sporadically, and the incidence became as high as 50% in certain fields cultivated by the tribals. In 1893, Watt in his classic book *Dictionary of the Economic Products of India* stated that “It is well known that smut and rust which do so much damage in other parts of the world, also occur in India," which signifies that smut and rust diseases have appeared on corn long back. Later, Butler (1918) recorded maize diseases:

1. Downy mildew caused by *Peronosclerospora philippinensis*
2. Common smut caused by *Ustilago maydis*
3. Head smut caused by *Sphacelotheca reiliana*
4. Common rust caused by *Puccinia sorghi*
5. *Turcicum* leaf blight caused by *Exserohilum turcicum* (Dharanendraswamy 2020)

The stalk rot caused by *Fusarium* spp. is a devastating infection affecting global maize-growing regions. It is a complex disease caused by several fungal pathogens, and it varies from region to region and comprehensively reduces the crop yield by interfering absorption and translocation of water and nutrients leading to premature death (Shan et al. 2017). This serious disease (root and stalk) was first reported from the USA by Pammel (1914) and in India by Arya and Jain (1964) for the first time from Rajasthan. The stalk rot of maize causes premature wilting or drying of plant and finally lodging. The typical symptoms observed during the early phase are premature drying of bottom leaves, eventually leading to death. The diseased stalks lose firmness, and the interior cells of the stalk dissolve (Fig. 6.6). The microscopic observations of stalks suggested softening and reddish coloration, and the pith appeared to be soft, disintegrating, and becoming light-brown to reddish. The infection of stalk was seen up to three inter-nodal regions from the stem-soil interface as reported by Dharanendraswamy et al. (2019a, b, 2020a, b).

Although *Fusarium verticillioides* is the major causative agent of stalk rot, there are several fusaria that cause stalk rots: *F. acuminatum*, *F. avenaceum*, *F. merismoides*, *F. nivale*, *F. subglutinans* (*F. semitectum*), *F. roseum*, *F. solani*, and *F. sulphurcum* (Rintelen 1965; Kommedahal et al. 1972; Dorn et al. 2009; Nur-Ain-Izzati et al. 2011). However, in India, only *F. moniliforme* and *F. semitectum* are the causative agents of stalk rot of maize (Lal and Dwivedi 1983; Khokhar et al. 2013, 2014). Recently, association of *F. equiseti* and *Lasiodiplodia pseudotheobromae* with post-flowering stalk rot of maize was also reported by Dharanendraswamy et al. (2020a, b).

6.5.3 Diversity of Fungal Diseases of Vegetables

Vegetables are an important source of regular diet, and India produces a significant quantity of vegetables annually. The fungal diseases associated with the vegetables are also causing significant loss of food leading to severe economic loss. A list of common fungal diseases associated with vegetables is provided in Table 6.3. Fungi damage the hosts by killing cells and causing plant stress. The fungal infection can be through infected seeds, soil, crop debris, nearby crops, and weeds. Some of the fungal diseases that occur on different vegetables include anthracnose and rots caused by various species of *Colletotrichum*, *Botrytis*, downy mildews, *Fusarium*,

Fig. 6.6 (**a**–**j**) Stalk rot of maize: It is one of the complex diseases caused by several fungal species

powdery mildews, rusts, *Rhizoctonia*, *Sclerotinia*, *Sclerotium*, *Phytophthora*, and others. Some of the other diseases which are specific to a particular crop include clubroot (*Plasmodiophora brassicae*) in brassicas, leaf blight (*Alternaria* sp.) in carrots, and red root complex in beans (*Gibberella* sp.). Some fungi that cause highly prevalent foliar diseases include downy mildews, powdery mildews, and white blister. Similarly, soil-borne diseases like clubroot and other diseases are caused by the species of *Fusarium*, *Pythium*, *Rhizoctonia*, *Sclerotinia*, and *Sclerotium*.

The following sections deal with the diversity of fungal diseases associated with a few vegetable crops (cowpea, common bean, brinjal, and tomato) cultivated in Karnataka state, southern India. Cowpea is an important pulses crop and is the livelihood of millions of people in the tropics (Quin 1997). The crop provides food and animal feed and strengthens the economy of the rural population. There are new emerging diseases due to fungi and fungi-like organisms being increasingly reported in many regions (Farr and Rossman 2018). The new fungal diseases on cowpea caused by various fungal pathogens are becoming the major constraints to the cowpea production. Recently, various workers have reported the occurrence of root rot and dry root rot disease caused by *F. equiseti* (Li et al. 2018), *F. oxysporum* (Shrestha et al. 2016a), and *F. proliferatum* (Shrestha et al. 2016b) from the USA; target leaf spot disease caused by *Corynespora cassiicola* from China (Li et al. 2014); and leaf spot disease caused by *Pestalotiopsis* sp. (Mahadevakumar and Janardhana 2014) and *Dactuliophora* sp. (Mahadevakumar and Janardhana 2012) and collar rot caused by *Aplosporella hesperidica* (Deepika et al. 2020) from India.

In recent past, common bean (*Phaseolus vulgaris*) production is limited due to various plant diseases caused by bacteria, fungi, viruses, phytoplasma, and other biotic factors. Studies have been carried out throughout the world on the fungal diseases of common bean and other leguminous plants. Stem rot (*Sclerotium rolfsii*), root rot (*Pythium* and *Rhizoctonia solani*), charcoal rot (*Macrophomina phaseolina*), wilt (*Fusarium oxysporum*), southern blight and leaf spot (*S. rolfsii*, *Alternaria*), powdery mildew (*Erysiphe polygoni*), ashy stem blight (*M. phaseolina*), rust (*Uromyces phaseoli*), anthracnose (*Colletotrichum lindemuthianum*), and many more fungal diseases have been recorded on bean (Hagedorn and Inglis 1986; Abawi and Pastor Corrales 1990; Allen et al. 1996; Mahadevakumar et al. 2015a, b, c). *Fusarium* also causes different diseases in beans like root rot, wilt, decline and damping-off, and so on. Cramer et al. (1996) characterized the *Fusarium* isolates causing wilt disease in and around the central plains of the USA, while Roman-Aviles et al. (2003) described the root rot of common beans caused by the *Fusarium solani* in Michigan. The common bean decline is also reported to be caused by *F. solani*, *F. oxysporum*, *F. sambucinum*, *R. solani*, and *Pythium debaryanum* (Saremi et al. 2011). The fungal diseases of common bean in subterranean regions are *Aphanomyces* root rot, black root rot, *Fusarium* root rot, *Fusarium* yellows (wilt), *Phymatotrichum* root rot, *Pythium* root rot, *Rhizoctonia* root rot, and southern blight and stem rot. Similarly, the fungal diseases of aerial parts include *Alternaria* leaf and pod spot, angular leaf spot, anthracnose, *Ascochyta* leaf spot, ashy stem blight, *Cercospora* leaf spot, *Chaetoseptoria* leaf spot, *Diaporthe* pod

Table 6.3 Some of the common fungal diseases associated with vegetable crops

Disease	Causal organism	Crops affected	Symptoms
Anthracnose	*Colletotrichum* spp.	Wide range of crops: cereals, fruits, oil-yielding crops, pulses, and vegetables	Typical symptoms begin with sunken and water-soaked spots appearing on leaves, stems, and/or fruit
Black root rot		Beans, cucurbits, lettuce, and other vegetable crops	Blackening of roots; stunted plants
Botrytis rots—for example, gray mold	*Botrytis cinerea*	Beans, brassicas, capsicum, celery, cucumber, lettuce, and tomato	Softening of plant tissues in the presence of gray fungal growth
Charcoal rot	*Macrophomina phaseolina*	>500 host range reports	–
Club root	*Plasmodiophora brassicae*	Members of Brassicaceae (cabbage, cauliflower, radish, and others)	Plants are yellow and stunted and may wilt in hotter parts of the day; large malformed club roots
Damping-off	*Aphanomyces*, *Fusarium*, *Pythium*, *Phytophthora*, and *Rhizoctonia*	Many vegetable crops: beans, beetroot, brassicas, carrots, coriander, cucurbits, eggplant, leafy vegetables, spring onions, and tomato	Young seedlings have necrotic stems or roots; seedlings die or show a reduction in growth
Downy mildews	Obligate parasites are host-specific except for a few species having a wide host range	Cucurbits, grapes, horticultural crops, maize, onions, pearl millet, rose, sorghum, and vegetables	Yellowish leaf spots and streaks then turn into brown
Fusarium wilts and rots	Various species of *Fusarium* (*F. oxysporum* and *F. solani* are frequent)	Wide host range: Beans, brassicas, carrots, cucurbits, herbs, onions, peas, potato, spring onions, and tomato	Causes severe root and crown rots or wilt diseases by attacking roots and basal stems
Powdery mildews (some species are restricted to particular crops or crop families)	Obligate parasites are host-specific except for a few species having a wide host range	Wide host range and very common especially in greenhouse crops: cucurbits and vegetable crops	Small, white, powdery patches on most aboveground surfaces; usually observed first on undersides of leaves but eventually cover both surfaces
Pythium rots	*Pythium aphanidermatum* and other species	A wide range of vegetable crops and horticultural crops	Usually infects at the early seedling stages and kills the seedlings or may infect at any

(continued)

Table 6.3 (continued)

Disease	Causal organism	Crops affected	Symptoms
			stage of its growth and development
Rhizoctonia rots	*Rhizoctonia solani*	Wide host range: Beans, beets, brassicas, capsicum, carrots, cucurbits, lettuce, peas, potato, and tomato	Range of symptoms depending on the crop being grown, but can affect fruits, roots, leaves, stems, and tubers; plants wilt and may collapse and die
Rust diseases	Obligate biotrophic organism in some cases exhibits host specificity	Coffee, cowpea, groundnut, maize, sorghum, soybean, wheat, yard long bean, and others	Small, red, or reddish-brown pustules that form on the underside of the leaves and sometimes on the pods as well
Sclerotinia rots	*Sclerotinia sclerotiorum* and *Sclerotinia minor*	Most vegetable crops, pulses, and cereals	Water-soaked rotting of stems, leaves, and sometimes fruit; followed by a fluffy, white, and cottony fungal growth, which contain hard black pebble-like sclerotia
Sclerotium rots	*Sclerotium rolfsii* and *S. cepivorum*	*S. rolfsii* has a wide host range (>500 hosts are reported); *S. cepivorum* affects only onions, garlic, and related *Allium* (leeks, shallots, and spring onions)	*S. rolfsii* affects lower stem and root causing rots; coarse threads of white fungal growth surround the diseased areas; *S. cepivorum* produce yellowing and wilting and fluffy fungal growth containing black sclerotia forms at the bases of bulbs
White blister/white rust	*Albugo candida*	Members of Brassicaceae (cabbage, cauliflower, radish, and others)	Produces white blisters and swellings on leaves of affected plants

blight, downy mildew, *Entyloma* leaf smut, gray leaf spot, scab, rust, web blight, powdery mildew, and others (Schwartz et al. 2005).

Brinjal (*Solanum melongena*) is another essential vegetable crop cultivated in tropics and subtropics and grown extensively in China, India, Bangladesh, Pakistan, and the Philippines. It is also cultivated in America, Europe, and other parts of Asia. In India, brinjal is one of the most important vegetable crops (Zeven and Zhukovsky 1975; Rashid 1976; Sekara et al. 2007). It is susceptible to various biotic and abiotic stresses during its growth and development. Along with biotic stress, fungal pathogen infections such as leaf blight and fruit rot (*Phomopsis vexans*), damping-off (*Pythium aphanidermatum*), wilt (*Verticillium dahliae*), leaf spots (*Alternaria melongenae* and *Cercospora melongenae*), and root rot (*Sclerotinia sclerotiorum*) are associated with brinjal (Shivaprakasam and Soumini 1974; Iqbal et al. 2003). Fruit rot and leaf blight caused by *Phomopsis vexans* are major threats decreasing yield as well as market value (20–30%) (Beura et al. 2008; Pandey 2010). Diseases caused by *Phomopsis vexans* have been reported from Assam, Jammu, Karnataka, and Pantnagar (Srinivasa et al. 2005; Thippeswamy et al. 2005; Akhtar and Chaube 2006; Muneeshwar et al. 2011; Das and Sarma 2012; Jayaramaiah and Janardhana 2011; Mahadevakumar 2016; Mahadevakumar and Janardhana 2016c; Mahadevakumar et al. 2017).

6.6 Top Ten Fungal Diseases

Emerging infectious diseases caused by plant pathogens could lead to unexpected and serious epidemics. Farmers spend billions of dollars on disease management without adequate technical support; thus, the disease devastates natural ecosystems and causes habitat loss (Bellard et al. 2012). Yield loss causes hunger and starvation especially in underdeveloped countries, due to limited access to disease control, which causes annual losses of common major crops up to 30–50%. In some years, the losses are much severe, and the results were catastrophic for those who extensively depend only on the food crop (Flood 2010). The major food disease outbreaks have caused devastating famines and mass migrations of population throughout the history.

In 2012, a team of scientists surveyed to gather information on the most influential fungal pathogen or top ten fungal pathogens (Dean et al. 2012). These fungal pathogens were considered very important from the scientific and economic point of view. Accordingly, among the top ten most important fungal pathogens, *M. oryzae* stands as the topmost fungal pathogen causing blast disease in *Oryza sativa*. Table 6.4 lists rice blast pathogen, and most of the serious plant pathogens come across in many crop plants including vegetables, cereals, millets, horticultural crops, forest trees, and other economically important plant species. The genus *Botrytis* having more than 200 hosts causing significant economic damage is considered in the second position; *Puccinia* sp. causing wheat rust, a serious disease in major wheat-growing regions, is in the third position; and *Fusarium* spp. associated with more than 500 plant species causing diseases (in the field and post-harvest conditions) occupied the fourth and fifth positions in the list of pathogens. *Fusarium oxysporum* and *Blumeria graminis* occupied the sixth and seventh positions as the most important fungal pathogens in the world, respectively. Members of basidiomycetes including smut (*U. maydis* causing corn smut disease) and rust (*M. lini*) associated with flax rust were placed in the ninth and tenth positions, respectively. The genus *Colletotrichum* has occupied the eighth position and was well known to cause many diseases (anthracnose, blights, dieback, and others) in various crop

Table 6.4 Major fungal diseases in the world (top ten fungal pathogens)

Top ten	Fungal pathogen	Disease	Host
1	*Magnaporthe oryzae*	Blast disease	*Oryza sativa*
2	*Botrytis cinerea*	Fruit rot and gray mold	>200 host species
3	*Puccinia* spp.	Rust on wheat	*Triticum aestivum*
4	*Fusarium graminearum*	Head blight	*Zea mays*
5	*Fusarium oxysporum*	Vascular wilt	Wide host range
6	*Blumeria graminis*	Powdery mildew	*Hordeum vulgare*
7	*Mycosphaerella graminicola*	Septoria leaf blotch	*Triticum aestivum*
8	*Colletotrichum* species	Anthracnose, fruit rots, and dieback	>500 host species
9	*Ustilago maydis*	Corn smut	*Zea mays*
10	*Melampsora lini*	Flax rust	*Linum usitatissimum*

plants. However, among *Colletotrichum*, there are over 1000 species; most of them are regarded as pathogenic, and some of them are also endophytes. It has been widely considered as a model fungus to study the lifestyle behavior of hemibiotrophs. Although the list provides the most significant fungal pathogens, there are several serious plant pathogens, which play a pivotal role in agricultural production, and those that are not included in the list are *Phytophthora* spp. (late blight and damping-off), *Sclerotium rolfsii* (southern blight and foot rot), *Puccinia arachidis* (groundnut rust), downy mildew diseases, *Rhizoctonia solani* (damping-off), *Phakopsora pachyrhizi* (Asian soybean rust), and *Diaporthe* spp. (associated with many economically important crop plants causing a wide range of disease). Further, it necessitates that this top ten list of fungal pathogens needs revision periodically to focus on control measures of diseases.

6.7 Diversity of Major Disease-Causing Fungal Genera

6.7.1 Colletotrichum

The genus *Colletotrichum* has a wide number of species affecting economically important crops. This genus primarily occurs abundantly in tropical and subtropical regions, but there are some important/novel species causing diseases in crops grown in temperate regions too. Diseases caused by *Colletotrichum* species lead to severe loss of production of various agricultural commodities in the field as well as post-harvest stages (Dean et al. 2012).

In temperate regions, fruit productions of high-value crops like strawberry, mango, citrus, avocado, banana, and others are severely affected. In Africa, species of *Colletotrichum* are known to cause devastating disease of coffee berries, which also causes significant economic loss to cereal growers, and also affect the important crops like maize, sugarcane, and sorghum. In the top ten fungal pathogens of the world, the genus *Colletotrichum* is voted to the eighth rank based on the perceived scientific and economic importance (Canon et al. 2012; Dean et al. 2012). *Colletotrichum* often cause anthracnose and other diseases which include red rot disease sugarcane, coffee berry disease, crown rot of strawberry, and banana and brown blotch of cowpea (Lenné 2002; Canon et al. 2012). Further, many *Colletotrichum* spp. are latent plant pathogens, and some of them are recorded as endophytes and saprobes, and they can switch to a pathogenic lifestyle when host plants are subjected to stress conditions or during post-harvest storage (Crous et al. 2016). The germinating conidia develop the appressorium through which the infection initiates by penetrating the cuticle of fresh tissues or occasionally through the epidermal cells via hyphal structures (Bailey and Jeger 1992; Deising et al. 2000).

The typical symptoms of anthracnose by *Colletotrichum* include the development of necrotic lesions on leaves, stems, flowers and fruits, and crown, and it also causes stem rots, seedling blight, and so on (Waller et al. 2002; Agrios 2005). The disease symptoms associated with *Colletotrichum* recorded from Karnataka have been represented in Fig. 6.7. Many species are seed-borne, dwell in soil saprobically on dead plant debris, and may spread disease through conidial dispersal by water splash as well as air transmission of ascospores from the sexual morph (Nicholson and Moraes 1980).

The genus *Colletotrichum* is a major threat among pathogenic fungi as it can thrive on a wide host range in warmer and humid environments and present globally (Ford et al. 2004; Shenoy et al. 2007; Damm et al. 2009; Diao et al. 2014; He et al. 2016; De-Silva et al. 2017). The anthracnose in several vegetables, fruits, and other crops is associated with *Colletotrichum* infections (Hyde et al. 2009). In pepper, tomato, potato, cabbage, and papaya, anthracnose is a destructive disease responsible for significant yield loss (Than et al. 2008; Hyde et al. 2009; Liu et al. 2016; He et al. 2016; Torres-Calzada et al. 2018). In India, this pathogen has been reported in chili, tomato, and garlic (Saxena et al. 2014; Saini et al. 2017; Salunkhe et al. 2018). Identification of *Colletotrichum* spp. is solely relied on morphological characteristics (Sutton 1992). Some of the species of *Colletotrichum* exhibit conidial overlapping; thus, molecular identification tools are being employed recently (Sherriff et al. 1995; Hyde et al. 2009; Canon et al. 2012; He et al. 2016). The important crop plants affected by *Colletotrichum* anthracnose are presented in Table 6.5 and Fig. 6.7.

6.7.2 Diaporthe

The genus *Diaporthe* belongs to *Diaporthaceae* under *Sphaeropsidales* of mitosporic fungi. It is typified by *Diaporthe eres*, an asexual form referred to as *Phomopsis* (Dissanayake et al. 2017a, b; Senanayake et al. 2017). The nomenclature is considered for genus name *Diaporthe* over *Phomopsis* based on the priority of publication (Rossman et al. 2014). Earlier, the identification of various *Diaporthe*

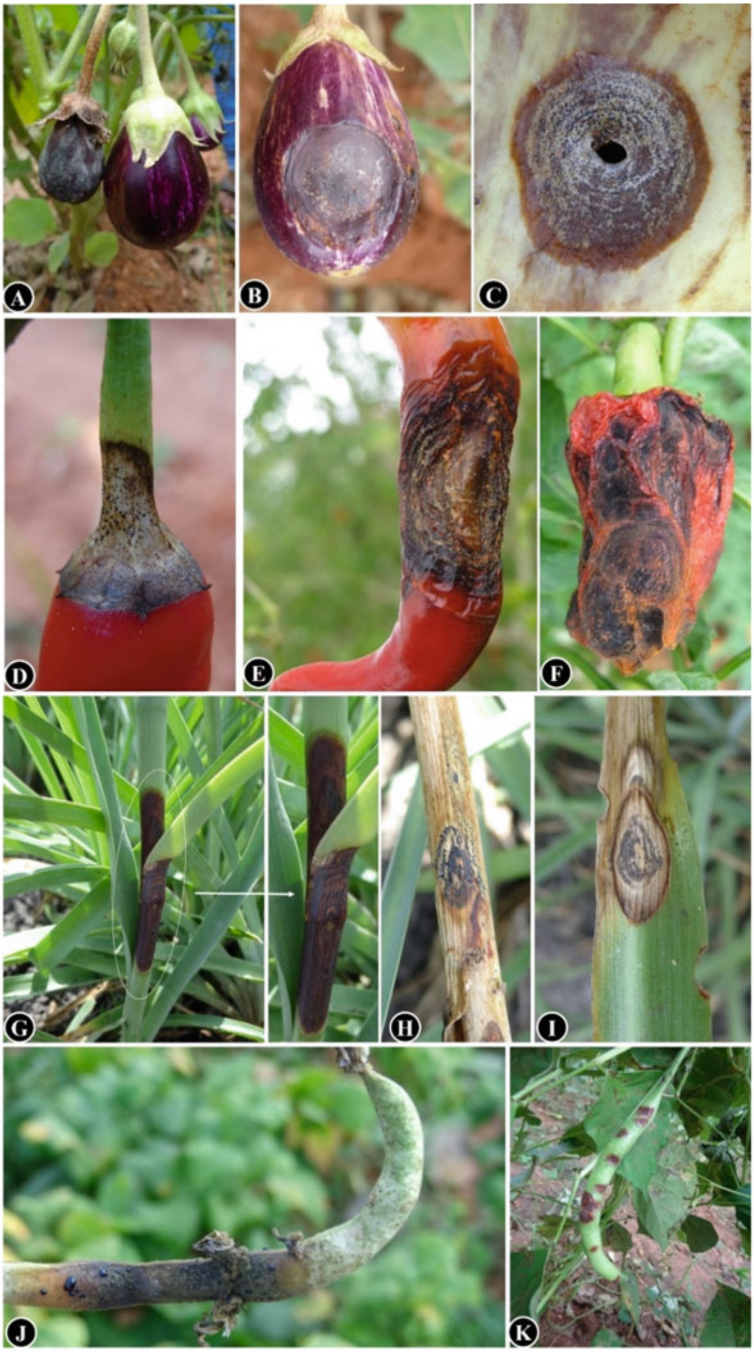

Fig. 6.7 Anthracnose disease caused by various species of *Colletotrichum*: eggplant fruit rot (**a**); caused by *C. parasitica* on eggplant fruits (**b**, **c**); on *C. capsici* (**d**, **e**); on bell pepper caused by *C. capsici* (**f**); on *Polianthes tuberosa* caused by *C. truncatum* (**g**–**i**); and on beans caused by *C. lindemuthianum* (**j**, **k**)

Table 6.5 Diversity of *Colletotrichum* spp. associated with agriculturally important crops

Host	Disease	Causal organism	Reference
Apple	Fruit rot	*C. acutatum*, *C. fioriniae*, *C. fructicola*, *C. gloeosporioides*, *C. karstii*, *C. nymphaeae*, *C. siamense*, and *C. theobromicola*	Velho et al. (2015), Munir et al. (2016), Park et al. (2018)
Banana	Anthracnose	*C. gloeosporioides*, *C. karstii*, *C. musae*, *C. paxtonii*, *C. scovillei*, *C. siamense*, *C. tropicale*, and *C. theobromicola*	Vieira et al. (2017), Zhou et al. (2017)
Bell pepper	Anthracnose and fruit rot	*C. brevisporum*, *C. fructicola*, *C. scovillei*, *C. siamense*, *C. sichuanensis*, and *C. truncatum*	Ramdial and Rampersad (2015)
Brinjal		*C. fioriniae*	Xu et al. (2018)
Butter fruit/avocado (*Persea americana*)	Anthracnose	*C. alienum*, *C. boninense*, *C. fructicola*, *C. gloeosporioides*, and *C. karstii*	Giblin et al. (2018), Kimaru et al. (2018)
Chickpea (*Cicer arietinum*)		*C. dematium* and *C. truncatum*	Nene et al. (2012), Mahmodi et al. (2013)
Chili (*Capsicum annum*)	Anthracnose, fruit rot, and stem blight	*C. cairnsense*, *C. cliviae*, *C. gloeosporioides*, *C. queenslandicum*, *C. siamense*, *C. simmondsii*, and *C. truncatum* (*capsici*)	Than et al. (2008), Saxena et al. (2014), De-Silva et al. (2017), Saini et al. (2017)
Citrus	Anthracnose, post-bloom fruit drop, and stem-end rot on fruit	*C. boninense*, *C. catinaense*, *C. gloeosporioides*, *C. helleniense*, *C. hystricis*, *C. karstii*, *C. limonicola*, and *C. novae-zelandiae*	Guarnaccia et al. (2017)
Coffee (*Coffea arabica* and *C. robusta*)		*C. acutatum*, *C. asianum*, *C. boninense*, *C. capsici*, *C. fragariae*, *C. fructicola*, *C. gloeosporioides*, *C. kahawae* subsp. *kahawae*, and *C. siamense*	Prihastuti et al. (2009), Nguyen et al. (2010), Canon et al. (2012), Silva et al. (2012)
Cotton (*Gossypium hirsutum*)	Anthracnose	*C. gossypii* var. *cephalosporioides*	Moreno-Moran and Burbano-Figueroa (2016)
Cowpea	–	*C. gloeosporioides* and *C. lindemuthianum*	
Mango	Anthracnose	*C. asianum*, *C. cliviicola*, *C. cordylinicola*, *C. endophytica*, *C. fructicola*, *C. gigasporum*, *C. gloeosporioides*, *C. karstii*,	Mo et al. (2018), Li et al. (2019)

(continued)

Table 6.5 (continued)

Host	Disease	Causal organism	Reference
		C. liaoningense, *C. musae*, *C. scovillei*, *C. siamense*, and *C. tropicale*	
Mung bean	–	*C. acutatum*, *C. lindemuthianum*, and *C. truncatum*	Shen et al. (2010), Roopadevi and Jamadar (2015)
Murraya koenigii	Anthracnose and leaf spot	*C. gloeosporioides*, *C. karstii*, *C. siamense*, and *C. simmondsii*	Padman and Janardhana (2012), Guarnaccia et al. (2017)
Papaya	Anthracnose	*C. acutatum*, *C. capsici*, *C. gloeosporioides*, and *C. truncatum*	Torres-Calzada et al. (2013)
Pigeon pea (*Cajanus cajan*)	–	*C. truncatum*	Khan and Singh (1975)
Pomegranate	–	*C. acutatum*, *C. fioriniae*, *C. gloeosporioides*, *C. nymphaeae*, *C. simmondsii*, *C. theobromicola*, and *C. siamense*	Jayalakshmi et al. (2015), Xavier et al. (2019)
Pyrus species	Anthracnose and leaf blight	*C. aenigma*, *C. citricola*, *C. conoides*, *C. fioriniae*, *C. fructicola*, *C. gloeosporioides*, *C. jinshuiense*, *C. karstii*, *C. plurivorum*, *C. pyrifolia*, *C. siamense*, and *C. wuxiense*	Fu et al. (2019)
Tomato	Anthracnose	*C. acutatum*, *C. coccodes*, *C. dematium*, and *C. gloeosporioides*	Dillard (1989), Byrne et al. (1997), Sanogo et al. (1997), LeBoeuf (2007)
Tuberose (*Polianthes tuberosa*)	Anthracnose	*C. truncatum*	Mahadevakumar et al. (2019)

species was based on morphological characteristics and also on host details (Brayford 1990; Rehner and Uecker 1994). With the advancement in sequencing platforms, the species diversity associated with a particular crop plant was discarded, and identity and assignment of species were considered over by multi-locus barcoding including internal transcribed spacer ribosomal DNA (ITS-rDNA), elongation factor-1a (EF-1α), β-tubulin, partial histone H3 (HIS), and calmodulin (CAL) of DNA sequences along with morphological characteristics (Udayanga et al. 2011; Gomes et al. 2013; Gao et al. 2017; Guarnaccia et al. 2018; Yang et al. 2018). In the recent studies on systematics, pathology, and environmental microbiology/ecology (endophytes), *Diaporthe* is primarily based on the usage of multi-locus approach, and it helped to resolve the species boundaries of *Diaporthe*/*Phomopsis* genus

(Udayanga et al. 2011, 2014a, b; Gao et al. 2017; Marin-Felix et al. 2019). Various species under the genus *Diaporthe* have been reported as endophytes (e.g., in a large number of medicinal plants), many of them are pathogenic causing severe damage to crops (leaf blight and fruit rot of eggplant; dieback of citrus), and some of the species are also regarded as saprobic on a wide range of hosts worldwide (Mahadevakumar et al. 2014, 2017; Liu et al. 2015; Hyde et al. 2016; Marin-Felix et al. 2019). Common diseases are dieback in forest trees (Yang et al. 2018); leaf and pod blights and seed decay in soybean (Udayanga et al. 2015); leaf spots in tea (Guarnaccia and Crous 2017); melanose, stem-end rot, and gummosis in *Citrus* spp. (Mondal et al. 2007; Udayanga et al. 2014a; Mahadevakumar et al. 2014; Guarnaccia and Crous 2017, 2018); and stem canker in sunflower (Muntañola-Cvetković et al. 1981; Thompson et al. 2011).

Phomopsis cane and leaf spot caused by *Diaporthe* species on the grapevine is one of the most complex grapevine trunk diseases worldwide (Úrbez-Torres et al. 2013; Dissanayake et al. 2015; Guarnaccia et al. 2018). The symptoms include breakage of shoots, stunting, dieback, loss of vigor, reduced bunch set, and fruit rot (Pine 1958, 1959; Pscheidt and Pearson 1989; Pearson and Goheen 1994; Wilcox et al. 2015). On the infected stem, brown to black necrotic irregular lesions could be seen. Once the clusters are infected, rachis necrosis and brown and shriveled berries during harvest time could be seen (Pearson and Goheen 1994). More than one *Diaporthe* species is frequently reported as causative agents from one geographical region (Dissanayake et al. 2015; Guarnaccia et al. 2018). Earlier, grapevine trunk disease was known to be caused by *Phomopsis viticola*, but the current knowledge on trunk diseases gives a different picture. Advancement in the field of molecular biology and techniques (sequencing platforms) revealed the occurrence of high diversity of pathogenic *Diaporthe* species associated with grapevine.

There are about 33 *Diaporthe* spp. known to cause dieback in grape-producing countries (Table 6.6) (Mostert et al. 2001; Van Niekerk et al. 2005; Udayanga et al. 2011, 2014a, b; White et al. 2011; Baumgartner et al. 2013; Úrbez-Torres et al. 2013; Hyde et al. 2014; Dissanayake et al. 2015; Guarnaccia et al. 2018; Lesuthu et al. 2019). All these species are associated with one disease; they differ in their symptoms, aggressiveness, and virulence, which differs from region to region and the variety of grape. In general, *D. ampelina* has a long history as the most common and severe pathogenic species together with *D. amygdali* (Mostert et al. 2001; Van Niekerk et al. 2005). *Diaporthe perjuncta* and *D. ampelina* cause cane bleaching (Kajitani and Kanematsu 2000; Mostert et al. 2001; Van Niekerk et al. 2005; Rawnsley et al. 2006). In South Africa, *D. ampelina*, *D. nebulae*, and *D. novem* have been reported to be most virulent species associated with grapevines. Further, *D. eres* was reported as a weak to moderate pathogen in many regions (Kaliterna et al. 2012; Baumgartner et al. 2013). In China, so far, four *Diaporthe* spp. are reported to cause grapevine dieback disease (*D. eres*, *D. hongkongensis*, *D. phaseolorum*, and *D. sojae*) (Dissanayake et al. 2015). These results specify the intricacy and high species richness of *Diaporthe* associated with the grapevines (Lesuthu et al. 2019).

Table 6.6 Diversity of *Diaporthe* spp. associated with grapevine trunk disease

Host	*Diaporthe* species	Reference
Grapes (*Vitis vinifera*): Associated with grapevine dieback	*D. eres*	Manawasinghe et al. (2019)
	D. gulyae	
	D. hubeiensis	
	D. pescicola	
	D. sojae	
	D. unshiuensis	
	D. vinifera	
Grapes: Grapevine swelling arm	*D. ambigua*	Dissanayake et al. (2017a, b)
	D. ampelina	Úrbez-Torres et al. (2013), Lawrence et al. (2015)
	D. amygdali	Gomes et al. (2013), Guarnaccia et al. (2018)
	D. australafricana	Gomes et al. (2013)
	D. baccae	Guarnaccia et al. (2018)
	D. bohemiae	
	D. celeris	
	D. chamaeropis	Lawrence et al. (2015)
	D. cytosporella	Lawrence et al. (2015), Dissanayake et al. (2017a, b), Guarnaccia et al. (2018), Farr and Rossman (2019)
	D. eres	
	D. foeniculina	
	D. helianthi	
	D. hispaniae	Dissanayake et al. (2017a, b)
	D. hongkongensis	
	D. hungariae	Guarnaccia et al. (2018)
	D. kyushuensis	Kajitani and Kanematsu (2000)
	D. nebulae	Lesuthu et al. (2019)
	D. neotheicola	Úrbez-Torres et al. (2013)
	D. nobilis	Lawrence et al. (2015), Dissanayake et al. (2017a, b)
	D. novem	Lawrence et al. (2015)
	D. perjuncta	Mostert et al. (2001)
	D. perniciosa	Stoykow and Denchev (2006)
	D. phaseolorum	Dissanayake et al. (2017a, b)
	D. rudis	Guarnaccia et al. (2018)
	D. serafiniae	Lesuthu et al. (2019)
	D. sojae	Dissanayake et al. (2017a, b)
Cane and leaf spot	*Phomopsis viticola*	Pscheidt and Pearson (1989)

6.7.3 Sclerotium rolfsii

Sclerotium rolfsii (or *Athelia rolfsii*) is a potent fungal pathogen causing diseases on a wide variety of plants including cereals, vegetables, fruits, ornamentals, and turfs at various stages of growth (Aycock 1966; Punja 1985; Smith et al. 1989; Mullen 2001). This pathogen is known to persist in the soil for 2–3 years and capable to cause infection when the new crop comes up (Smith et al. 1989). The disease has been named as southern blight or southern stem blight. The pathogen is known to cause infection in all stages of plant tissues although it is known to generally infect the lower part of the stem at the soil-air interface (Mullen 2001). This pathogen is also known to attack seedlings, herbaceous plants, woody plants, fleshy roots, bulbs, and fruits (Mullen 2001). The most important crop plants associated with southern blight and leaf spot diseases include southern blight of common bean (*Phaseolus vulgaris*), leaf spot of Indian jasmine (*Jasminum multiflorum*), boll rot of cotton (*Gossypium hirsutum*), fruit rot of pumpkin (*Cucurbita maxima*), and southern blight of wild coffee (*Psychotria nervosa*) (Mahadevakumar et al. 2015a, b, c; Mahadevakumar and Janardhana 2014, 2016a, b; Mahadevakumar et al. 2018).

6.8 Diversity of Emerging Fungal Pathogens in Agro-Ecosystem

The global increase in virulent infectious diseases of natural populations and managed landscapes are mainly due to unprecedented fungal diseases leading to severe economic loss and threat to food security (Fisher et al. 2012). The plant pathogens could enter agricultural ecosystems by several mechanisms like host tracking, host jumps, hybridization, and horizontal gene transfer. Agro-ecosystem is defined as "the ecosystem that develops on farmed land, which includes both the crop species and its associated micro- and macro-organisms" (Stukenbrock and McDonald 2008). A long timescale is necessary for the development of complex biochemical machinery of pathogen attack and plant defense in pathogen-plant interactions, but the agriculture is fairly recent, and domestication faces the severity of acclimatized pathogens (Balter 2007; Stukenbrock and McDonald 2008). The development of new crop cultivars and agricultural practices has resulted in the emergence of new pathogens causing significant variation population of pathogens preexisting on the wild ancestors of the cultivated crops. The new agro-ecosystem provided a denser and genetically more uniform host population that enabled the pathogen transmission compared to the natural habitats (Stukenbrock and McDonald 2008).

The introduction of plants or pathogens into new environments could result in novel host-pathogen interactions, where pathogens cause severe damage in native host populations. For example, the introduction of the potato late blight pathogen *Phytophthora infestans* into Ireland in the mid-nineteenth century caused the Irish potato famine (Goodwin et al. 1994), and the movement of the wheat stripe rust pathogen *Puccinia striiformis* f. sp. graminis into the USA long ago caused severe economic losses (Carleton 1915). The host and the pathogen coevolved during the process of host domestication and the development of the agro-ecosystem specific to the host crop. During domestication, the selection and cultivation of desired host genotypes simultaneously select pathogen genotypes that are adapted to the selected individuals in a specific agro-ecosystem (Stukenbrock and McDonald 2008). However, nowadays, a greater number of new disease reports indicate either new or crossing the host barrier or crossing the geographic location and becoming more serious constraints to modern agriculture. Even though the western countries have adopted different strategies to oversee the emergence of new diseases (along with fungi, viruses, bacterial diseases, and others), new diseases are emerging. India is yet to adopt modern diagnostic techniques for disease diagnosis and to suggest solutions or management strategies. As a result, a wide range of new outbreaks are unnoticed or not recorded so far, or the existing host-pathogen system needs to be explored at the genetic level. This strategy supports breeding programs to develop new cultivars, hybrids, or varieties for improved and sustained agricultural production.

The most neglected part of understanding the fungal diseases and their impact on human life is storage diseases. Every agricultural product consumed directly or after harvest will be subjected for storage depending on the type of produce. The storage fungi produce diverse secondary metabolites, which are toxic to the human being as well as livestock. Once the stored agricultural produce is affected by storage fungi, they will be unfit for consumption. In vegetables, the moisture content favors the development of various molds that cause damage. In Fig. 6.8, some of the common storage fungi are presented which include association of *Aspergillus* on cucumber; *Rhizopus* on jackfruit; *Alternaria* on apple; and *Colletotrichum* on watermelons, mango, and others.

6.9 Perspectives and Future Outlook

Production of sufficient food with assured quality and quantity remains of paramount importance for the sustenance of quality life. Inadvertent introduction of pathogenic fungi has adverse consequences on the cultivated crops throughout the world. The economic concussions by such introductions result in loss of yield, increased cost of cultivation, and disease control. Fungi being a unique group of organisms that have the potential of earning billion-dollar profit as the source of a wonder drug have also incurred a billion-dollar loss to a nation by their virulence. Diverse pathogenic fungi are the sole reason for more than 80% of crop loss in the Indian subcontinent. The plant pathogens also play a crucial role in regulating host populations in the geographic and ecological setup of a natural ecosystem. As a result, they can distress the availability of food sources to other living systems (Lindahl and Grace 2015). The majority of diverse microbial pathogens exhibit a high genetic variability due to narrow generation time, maximum population size, and rapid adaptability to various environmental conditions (Alberts et al. 2002; Lindahl and Grace 2015). Therefore, it is necessary to understand the plant pathogens at the genetic and population level to develop sustainable management practices in agriculture.

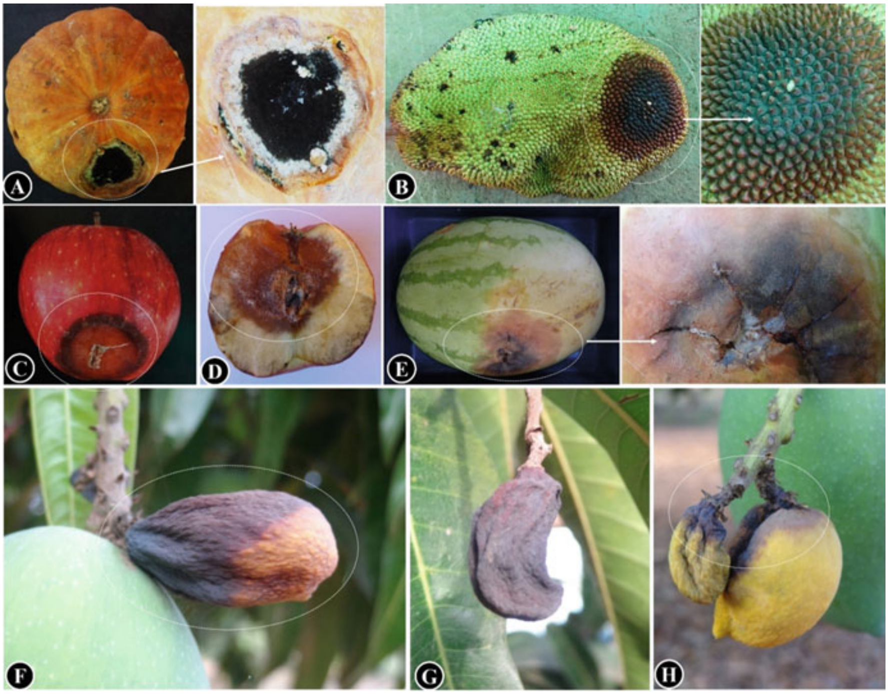

Fig. 6.8 Fungal diseases associated with fruits and vegetables (storage/post-harvest): *Aspergillus* rot of cucurbits (storage fungal disease) (**a**); soft rot of jackfruit (*Rhizopus* sp.) (**b**); apple fruit rot (storage/post-harvest disease) (**c**, **d**); fruit rot of watermelon (*Colletotrichum* sp.) (**e**, **f**); and on mango fruits (*Colletotrichum* sp.) (**f**–**h**)

To combat the diseases caused by fungal plant pathogens globally, it is crucial to confirm whether the same species/genotypes are present in other countries, as each species/genotype can possess varied attack patterns and responses to fungicides as well as climatological conditions. It is also necessary to follow what are their host ranges and mating strategies to relate to different disease control mechanisms. The movement of agricultural and forestry produce is inextricably cross-linked between geographic regions, and in turn, it becomes a global concern. Knowledge on which pathogen occurs and its attack on crop facilitates to enhance the yield and reduce the economic loss. Systematic and extensive research on emerging diseases has not been attempted especially in India on various crop plants. In terms of intensive plant material exchange and climate change, result in new pathogens needs stringent quarantine measures. Future plant disease management should aim at improving the food safety for a growing population with scope for simultaneous attempts to conserve the ecosystem integrity. Insights into the alternate food crops, traditionally important plant resources, and collateral hosts are vital to control the impact of pathogens. The diversity of fungal pathogens associated with a crop provides necessary strategies to adapt for biological control methods to manage diseases.

Caution should be exercised to follow up on the diversity of new and emerging fungi detrimental to crop production and food preservation to fulfill the needs of the teeming population.

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