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Phytophthora: A Member

of the Sixth Kingdom Revisited **TP as a Threat to Food Security in the Twenty-First Century**

S. Guha Roy

Abstract

 This genus *Phytophthora* has a long history in modern science. The reemergence of *Phytophthora* spp. causing damages in almost all ecological niches along with advancement in molecular technologies and discovery of new species has led to a renewed interest in *Phytophthora* spp. All of which has led to significant changes in the way the taxonomy of *Phytophthora* is now being studied. The genus *Phytophthora* infects an array of spices and plantation crops, and this scenario vis-à-vis *Phytophthora* spp. has been discussed here with special reference to black pepper, onion, garlic, leek, chilli, cocoa, coconut and rubber. Possible approaches for management of these diseases using databases derived from population characterisation through a correlation of their phenotypic and genotypic diversity have been discussed. Molecular tools that can be used for the production of such databases have also been discussed.

19.1 Introduction

 The existence of man on Earth is mostly dependent on the ability of plants to harness light and produce oxygen and organic matter. Domestication of plants for agriculture resulted in many great civilizations of the past: Asian civilizations based on rice, Middle Eastern on wheat and barley and American on maize and potato. Like in the past centuries, the staple food of the world population today also depends on only a few major crops: wheat, rice, maize and potato (FAO 2002). However, mankind alone is not in the need to live off plants; a large number and different types of pathogens attack plants and, having 'fine-tuned' their ability to parasitize the living plants throughout evolutionary history, are at considerable advantage in competing to obtain nutrients from this primary food source and therefore are our competitors and enemies too (Strange and Scott 2005)! Worldwide crop loss due to pathogenic diseases, insects and weeds accounts for 31–42 % of the potential crop production capacity; without protective measures, this loss would be greater than 50 % (Agrios 2005).

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 Approximately 10,000 fungal species are considered to be plant pathogenic (Farr et al. 1989; Agrios 2005) out of the 72,000-100,000 fungal species identified till date, but, considering that this represents only a small fraction of the fungal kingdom, estimated to include \sim 1.5 million species (Hawksworth 1991, 2001; Hawksworth and Rossman 1997), the actual number of plant pathogenic fungi is likely to be much greater than 10,000!

 Diseases caused by fungi are well established as major constraints of food, fibre and crop production. Equally devastating, if not more, among the fungi is a group of organisms which differ from the 'true fungi' in many characteristics (chitin- less cell wall (Bartnicky-Garcia and Wang 1983), sterol metabolism (Warner and Domas 1987; Wete 1989; Köler 1992; Griffith et al. 1992), other metabolic pathways (Hendrix 1970; Wang and Bartnicky-Garcia 1973; Elliot 1983), storage compounds (Wang and Bartnicky-Garcia 1974; Coulter and Aronson 1977; Bartnicky-Garcia and Wang 1983; Rast and Pfyffer 1989; Pfyffer et al. 1990; Griffith et al. 1992), tubular cristae in mitochondria (Alexopoulos et al. 1996), differential sensitivity to monomeric aluminium (Fichtner et al. 2006) and motile heterokont zoospores (Desjardins et al. 1969)) referred to as 'pseudofungi' by most mycologists and is placed into a new domain of life called Stramenopila (Cavalier-Smith 1987; Leipe et al. 1994; Beakes 1998).

 The Stramenopila includes *Oomycetes* such as 'phytophthoras', 'downy mildews' and 'Pythia', which form a unique branch of eukaryotic plant pathogens with an independent evolutionary history (Kamoun et al. 1999) showing a distant evolutionary relationship with true fungi (Gunderson et al. 1987 ; Förster et al. 1990 ; Baldauf et al. 2000). The fact that oomycetes are not related to fungi is particularly relevant for heterologous expression of genes and comparative genomics and genetics in general. Still, despite their different evolutionary origins, the morphology of the hyphae, their mycelium-like growth and the airborne spores show remarkable resemblance to fungi. Oömycetes and fungi are probably one of the best examples of convergent evolution.

 The *Oomycetes* contain some of the most destructive of plant pathogens; among them, some species of the genera *Phytophthora*, *Pythium* (rots, blights and damping off) and *Peronospora* and *Plasmopara* (downy mildews) stand out; in fact, the name *Phytophthora* means 'plant destroyer'. The genus *Phytophthora* with more than 108 members is presently placed in the kingdom Stramenopila (Belbahri et al. 2006), under the phylum Heterokonta, subphylum Pernosporomycotina, class Pernosporomycetes (Oömycetes), subclass Pernosporomycetidae, order Pythiales and family Pythiaceae. The taxonomy of *Phytophthora* has undergone an evolution in the way it has been studied, from the era of six morphospecies groups (Waterhouse 1963; Newhook et al. 1978; Stamps et al. 1990) to the era of phylogenetic clades (Cooke et al. 2000) and ITS fingerprinting-based keys (Gallegly and Hong 2008) and now to a new era of an integrated morphological and phylogenetic key (Ristaino 2011), and has been reviewed by Guha Roy and Grünwald 2014.

 This genus *Phytophthora* has a long history in modern science. The scientific discipline of plant pathology was born in the early 1860s when Anton de Bary recognised *Phytophthora infestans* as the pathogen causing potato late blight responsible for the Irish potato famine in the 1840s (Abad and Abad 2003 ; Aragaki and Uchida 2001). It also brought about the first formulated use of a fungicide. In addition to this substantial social and historical impact, even considering merely a handful of *Phytophthora* spp. (e.g. *P. sojae*, *P. infestans*) documented to cause significant economic impacts, costs amount to anywhere between two and seven billions of dollars per crop per year worldwide in combined crop losses and management costs not even considering the less quantifiable but equally large impacts to natural ecosystems severely affected by some species (e.g. *P. cinnamomi* , *P. ramorum*).

Phytophthora pathogens also have a large impact on native ecosystems, forests and agricultural crops. The past decade has seen the discovery of a large number of phytophthoras especially from aquatic and forest ecosystems, and a wealth of information is now available on some of the phytophthoras attacking crops and plantations. Only the advances and their possibilities in horticultural and spice crops will be discussed here as exhaustive reviews are already available on the other ecosystem niches (Lamour and Kamoun 2009; Guha Roy 2008; Guha Roy and Grünwald 2014).

Phytophthora is now considered as one of the most important and destructive genera of plant pathogens in temperate and tropical regions, causing annual damages of billions of dollars (Drenth and Guest 2004) due to its high virulence and epidemiological ability to spread rapidly throughout the world.

19.2 The Spice Scenario vis-à-vis Phytophthora

 The genus *Phytophthora* infects an array of spices and plantation crops. Some of the important diseases caused by *Phytophthora* are azhukal disease of cardamom, foot rot of black pepper, white tip of leek, leaf blight of onion and garlic, root rot of chilli, bud rot of coconut, abnormal leaf fall of rubber, wilt of *Piper betle* , koleroga of arecanut and some diseases of cocoa. Some of them have been discussed in the following paragraphs:

19.2.1 Phytophthora in Black Pepper

Phytophthora foot rot and leaf rot of black pepper are a serious problem in all black peppergrowing countries like India, Indonesia, Vietnam, Malaysia, Brazil, Thailand, Madagascar, etc. India and Indonesia are the main producers of pepper and account for more than 50 % of the world production. On a global scale, losses due to this disease have been estimated to be US\$ 4.5– 7.5 million per annum (de Waard 1979). The disease was first reported in 1885 in Lampung, Indonesia and has been called foot rot disease since 1928 (Muller 1936). The disease starts as

dark brown spots on tender leaves at the lower region of the bush which enlarge rapidly covering the major area of leaf. These leaf spots have characteristic 'fimbriate margins' and infected leaves drop off prematurely. The fungus also infects green stems and branches causing rotting. In the case of root rot, infection that starts on the fibrous root system reaches the main root and ultimately the collar region or foot region of the bush (http:// iisr.agropedia.in/content/phytophthora-diseaseblack-pepper).

 In India, Kerala accounts for over 97 % of the area under pepper cultivation where it is a serious and dreaded disease even affecting coconut, arecanut and rubber plantations in the vicinity (Pruthi 1993; Chowdappa et al. 2003a). Different *Phytophthora* spp. are found to be associated with *Phytophthora* foot rot and leaf rot of black pepper in different geographical regions. In India, the disease was first reported way back in 1902 (Barber 1902 ; Butler 1906), and currently, *P. capsici* and *P. tropicalis* and isolates having similarity to both have been molecularly identified as being associated with the disease (Chowdappa et al. $2003b$; Annual Report IISR $2012-2013$); in Indonesia, where it has a long history of cultivation as Hindu migrants probably took pepper to Java between 100 BC and AD 600 (Purseglove et al. 1981), it is affected by *P. capsici* where it causes 52 % yield reduction (Purwantara et al. 2004). In Vietnam, which is now the world's second largest pepper exporter, though the disease was first reported in 1952, the identity of the causal agent was only recently conclusively determined as *P. capsici* (Truong et al. 2008) with low genetic diversity (Truong et al. 2010) but more adapted to black pepper hosts (Truong et al. 2012). Disease losses in Vietnam account to 15–20 % (Drenth and Sendall 2004). In Malaysia, pepper cultivation started with the British organised plantings of pepper in the early nineteenth century (Purseglove et al. 1981). Malaysia is now the fourth largest producer of black pepper in the world (PMB 2001), and currently, 95 $%$ of the pepper produced in Malaysia is grown in Sarawak (PMB 2001) where *P. capsici* is the causal agent and the rest in Johor from where *P. nicotianae* has also been isolated (Lee and Lum 2004). On the other hand, the causal agents reported from Thailand are *P. palmivora* , *P. nicotianae* and *P. capsici* (Sangchote et al. 2004), while only *P*. *capsici* has been reported from Turkey on black pepper where it is very destructive and has the greatest economic importance. *P. capsici* is very dangerous for pepper spice and pepper paste production because it causes up to 100 % drying and killing of pepper plants under conditions of poor drainage and incorrect irrigation practices (Biçici and Cinar 1990).

- For the management of *Phytophthora* foot rot in black pepper, crop should be sprayed with 0.25 % Ridomil Gold 68 (WP) or 0.3 % potassium phosphonate during June and August and also drenching the soil with 3 l per vine and 1 kg of neem cake with 50 g of *Trichoderma harzianum* to the root zone of vines twice in a year.
- Biocontrol agent 1 % *Pseudomonas fluorescens* application to the vine as spraying (@ 2 l/vine) and drenching (@ 3 l/vine) during June and the second week of August for management of *Phytophthora* root rot was helpful [http://uhsbagalkot.edu.in/AICRP_sirsi.aspx].

19.2.2 Phytophthora in Onion, Garlic and Leek

- (a) *Phytophthora porri* affects different alliums like leek, onion and garlic. White tip is one of the important foliar diseases of leek in Western Europe. The disease has been mainly reported from Europe, Canada and Japan. In Japan, a loss of 70 % or more is found in onion. The disease spreads rapidly on cool, wet weather. On onion and garlic, this pathogen causes water-soaked leaf blight and root rot symptoms. Early symptoms of leek leaves consist of irregularly shaped water-soaked lesions. Older lesions develop a bleached white centre with water-soaked margin which disappears in dry condition.
- (b) *Phytophthora nicotianae* causes damping off of green onion seedlings and leaf blight and rot of green onion. On onion leaves, spots begin as small, irregularly shaped, water-

soaked lesions on the young and mature leaves. In a few days, these spots expand, girdling the leaf and causing the tissue above the infection point to wither. As the infection progresses, healthy tissue is invaded, eventually killing the entire leaf. Infected plants have a mix of healthy and withered leaves with some leaves showing a characteristic of half-infected, half-healthy symptom. Splashing water from raindrops or irrigation helps to move spores from infected plants to nearby healthy plants. Effective disease control begins with prevention and proper water management to minimise excess moisture on the plants. Ridomil 81 W can be applied to green onion up to 14 days prior to harvest. Also, label directions are to be read carefully and chemicals applied responsibly [http:// www.extento.hawaii.edu/kbase/crop/type/p_ nicoti.htm].

19.2.3 Phytophthora in Chilli

 Phytophthora blight, caused by *Phytophthora capsici* , is a devastating disease on both bell and non-bell peppers. The major symptom is root rot and wilt. However, more precisely, *Phytophthora capsici* infects roots, crowns, stems, leaves and fruit, causing seedling damping off, stem lesion, stem blight, leaf spot and fruit rot. It is a soilborne pathogen which can produce several types of spores, enable it to spread throughout the field and to persist in the field between crops. *P. nicotianae* has also been found to be pathogenic on chilli pepper in Tunisia, NW and Western Spain, but the symptoms described are that of collar and root rot in contrast to fruit rot reported from the Indian subcontinent and those of seedling blight as the isolates were suggested to be different and this *P. nicotianae* is more adapted to their hosts (Andrés et al. 2003; Darinea et al. 2007; Saadoun and Allagui 2008; Rodríguez-Molina et al. 2010).

 No single strategy should be used to control Phytophthora blight of pepper. A combination of methods is needed to effectively control this disease. The following practices can help to manage Phytophthora blight in pepper fields:

- 1. Fields to be selected with no history of Phytophthora blight, if possible.
- 2. Select fields that did not have peppers, cucurbits, eggplants or tomatoes for at least 3 years.
- 3. Selected fields are to be well isolated from infested fields with *P. capsici*.
- 4. Well-drained fields are to be chosen. Low areas or the areas which do not drain well are to be avoided.
- 5. Excessive irrigation is to be avoided.
- 6. Seeds should not be saved from a field where Phytophthora blight occurred.
- 7. Resistant varieties are to be planted, whenever it is possible.
- 8. Fungicides may be used to reduce Phytophthora infection in pepper fields.

19.2.4 Phytophthora in Cocoa

Phytophthora pathogens are responsible for some of the most serious diseases of cocoa including *Phytophthora* pod rot (PPR) or black pod, stem canker, leaf and seedling blight, chupon wilt and flower cushion infections. PPR causes $10-30\%$ annual losses in the production of cocoa beans globally and much higher losses locally in particularly wet and humid conditions. The estimated losses in the production in Asia, Africa and Brazil are 450,000 t annually, worth an estimated value of US\$ 423 million (Drenth and Sendall 2004). Stem canker causes further losses and also tree deaths. Eight species of *Phytophthora* have been isolated from diseased cocoa, but most losses in the production are caused by *Phytophthora palmivora* , *P. megakarya* , *P. capsici* and *P. citrophthora* , and these vary in both their aggressiveness and the level of crop loss caused (Appiah et al. 2004). *Phytophthora megakarya* is the most aggressive and can cause between 60 and 100 % crop loss (Djiekpor et al. 1981; Dakwa 1988). In contrast, *P. palmivora* is less aggressive and can cause crop losses of 4·9– 19 % (Blencowe and Wharton 1961; Dakwa 1984); this species is more aggressive than *P. capsici* (Lawrence et al. 1982). *Phytophthora* *citrophthora* is more aggressive than *P. palmivora* or *P. capsici* and requires less time for zoospore germination and penetration on unwounded, detached pods (Campêlo et al. 1982). Sequence analysis showed that the four main cocoaassociated species formed two distinct groups, one comprising *P. capsici* and *P. citrophthora* and the other *P. palmivora* and *P. megakarya* (Appiah et al. 2004). Single reports of other *Phytophthora* species causing black pod include *P. botryose* (Chee and Wastie 1970), *P. heveae* (Lozano and Romero 1984) and *P. katsurae* (Liyanage and Wheeler 1989a) and *P. megasperma* (Zentmyer 1988), although these are not considered major problems for cocoa production.

 The relative impact of each of these species of *Phytophthora* varies from region to region. In India, both *P. palmivora* and *P. capsici* cause black pod disease, but the *P. palmivora* isolates are of a single clonal lineage also infecting the coconut plantations below which it is cultivated as an understory crop, while on the other hand, the *P. capsici* isolates from cocoa belong to two genetic subgroups (Chowdappa et al. 2003b). A detailed sequence analysis of worldwide collection of *P. capsici* isolates from cocoa as well other hosts and comparison with published literature suggested that *P. capsici* isolates from cocoa may be closely related to *P. tropicalis* (Appiah et al. 2004). In Southeast Asia, *P. palmivora* seems to be the principal pathogen, while *P. megakarya* has only been found in West Africa (Brasier et al. 1981). In Africa, *P. megakarya* tends to be the principal pathogen, while in the Americas, *P. capsici* and *P. citrophthora* are the main causal agents of pod rot (Erwin and Riberio 1996) worldwide. *P. palmivora* is one of the most serious pathogens on cocoa, and in Southeast Asia, this species accounts for almost all of the Phytophthora diseases of cocoa. The most effective control measures are the introduction of resistant cocoa genotypes and farm management practices such as the removal of infected pod husks, proper pruning of the canopy and judicious selection of shade species and associated crops (McMahon and Purwantara 2004).

19.2.5 Phytophthora Diseases of Coconut

Coconut (*Cocos nucifera*) is one of the most valuable plant species in the tropics, providing oil, coconut milk, fibre from the husk, palm wine and timber for furniture and construction with its primary centre of origin in Asia and some secondary centres of origin in Central and South America. Rots caused by *Phytophthora* spp. lead to palm death (by bud rot) and/or yield reduction (by premature nut fall) (Waller and Holderness 1997) and are prevalent in all coconut-growing regions of the world. The disease though sporadic in nature causes severe losses. The earliest visible symptoms are the paling of leaves in the inner whorl followed by collapse of the spear leaf. Bud rot causes a total loss of the palm, since the apical portions are destroyed and will not regenerate further. The principal causal agent in India, Philippines, Indonesia and Malaysia is *P. palmivora* ; In Indonesia, *P. arecae* and *P. nicotianae* have also been found in association with these diseases (Thevenin 1994). *Phytophthora nicotianae* is rarely encountered, and it is usually associated with cocoa and infested soil (Waroka and Thevenin 1992).

 The economic impact of the disease on a country's economy can be exemplified by what has happened in the Philippines in the recent past. The Philippines was the number one coconut producer in the world during 1976–1986, but the average productivity has declined in the past decade (1991–2000) with an average production of 669 kg/ha. Although *Phytophthora palmivora* was known to cause bud rot and fruit and immature nut fall in the Philippines, the disease losses were relatively low. This changed dramatically after the introduction of highly susceptible MAWA hybrids, which are a cross between Malayan yellow dwarf and West African tall, both of which are known to be susceptible to Phytophthora. The Philippines now lags behind India, which produces, on average, 732 kg/ha, and Indonesia with an average production of 1,041 kg/ha. This lower productivity can be attributed to a number of factors, but all of which are related to disease outbreaks. Bud rot and fruit rot were major causes of the large loss of coconut trees and the significant decrease in the production (Concibido-Manohar 2004).

19.2.6 Phytophthora Diseases of Rubber

 The major rubber-grower countries are Indonesia, Thailand, Malaysia, China and India, each with more than a million hectares. There are several different types of symptoms caused by *Phytophthora* spp. on rubber trees: (1) abnormal leaf fall, (2) black stripe of the tapping panel, (3) stem or patch canker and (4) pod rot (Sdoodee 2004). Abnormal leaf fall was recorded from Kerala in India as early as 1910 (McRae 1918) and can reduce 30–50 % of the production (Pillai 1982). Black stripe disease was first noted in Sri Lanka and is widespread in Southeast Asia as well as Africa and America. Other Phytophthora diseases are also common throughout most rubber- growing areas. Black stripe and leaf fall cause serious damage, but economically important outbreaks are confined to areas with long periods of high rainfall. Although patch or stem canker is widespread, recent records of high economic impact are few. At least six species of *Phytophthora* have been reported to be associated with diseases of rubber including *P. botryosa* , *P. heveae* , *P. meadii* , *P. palmivora* , *P. capsici* and *P. nicotianae* . However, *P. palmivora* and *P. meadii* are isolated most frequently as the causal agents (Sdoodee 2004). The identity of the species varies with geographical regions; in India, Myanmar and Sri Lanka, it is predominantly *P. meadii* (Liyanage 1982; Kochuthresiamma et al. 1988; Johnston 1989; Chowdappa et al. 2003a), whereas in Malaysia, Thailand and Vietnam, *P. palmivora* and *P. botryosa* are implicated (Chee 1969; Tsao et al. 1975; Duong et al. 1998). In China, although the main species involved appears to be *P. citrophthora*, other species including *P. palmivora*, *P. meadii* , *P. nicotianae* and *P. capsici* were also found to infect rubber (Zeng and Ward 1998). There are also reports of *P. citrophthora* infecting rubber in Indonesia (Liyanage and Wheeler 1989a, b). In Brazil, *P. capsici* was reported to be the main species associated with black stripe and stem canker, but *P. palmivora* and *P. citrophthora* were also isolated from diseased rubber (Dos Santos et al. 1995).

19.3 What Needs to Be Done?

 Quality enhancement in spice crops/horticultural crops must necessarily include incorporation of improved control strategies along with those of quality control and agronomical practices. There has been an evolution in the way control strategies were thought of – from the days of chemical to biological to IPM strategies to that of decision support systems (DSS) and databases for specific crops and/or pathogens. Recently, such databases are being increasingly advocated and recommended by extension workers worldwide for timely diagnostic and mitigatory advice to achieve higher productivity (http://iapps2010. wordpress.com/2013/11/07/ plant-protection-clinics-in-asia-3/).

For the latter to work, the first prerequisite is an accurate identification and sensitive detection of the pathogen. This is critical for regulatory action and disease management; especially faced with agricultural security concerns, the importance of diagnostic capacity cannot be overemphasised. Traditional culture-based detection and diagnostic methods for *Phytophthora* are inadequate as classical taxonomy of the genus is still based on often inconsistent morphological markers (Duncan and Cooke 2002). Combined with this is the fact that there is display of considerable morphological plasticity within some taxa limits (Brasier and Griffin 1979; Erwin and Riberio 1996; Appiah et al. 2003), and also the need for specialised expertise and time makes species identification based on morphological criteria difficult (Brasier et al. 1981; Erwin and Riberio 1996). This often leads to misidentification (Hall 1998), which, in turn, is detrimental to both practical control and clear scientific communication. Moreover, various reports on molecular identification of the *Phytophthora* pathogen have proved that in the past, new species have been wrongly assigned to current taxa and conversely, morphological variants of the existing taxa incorrectly assigned as new disease threats when the identifications were solely based on morphological criteria (Chowdappa et al. 2003a, b; Mirabolfathy et al. 2001; Guha Roy et al. 2006). Also, several species 'complexes' can be observed in phylogenetic trees showing the presence of potential cryptic species. Presently, powerful molecular techniques combined with morphological characterisation and a renewed interest in probing of the environments have led to discovery of new species, novel variants within species and hybrids and provided a better resolution of species 'complexes' with differentiation of the species therein (Grünwald and Goss 2011).

 In the last decade, traditional detection methods have been complemented by various molecular methods for *Phytophthora* (Martin and Tooley 2003, 2004; Schaad et al. 2003; Kong et al. 2003a, c), especially involving PCR amplification of pathogen-specific nucleic acid targets and serological detection of specific pathogen proteins (Benson 1991; Hardham and Cahill 1993). These available diagnostic techniques are effective but can detect only single target pathogen per assay. For parallel detection of multiple phylogenetically diverse organisms simultaneously, as is present in nature, microarray-based diagnostics have been developed (Fessehaie et al. 2003; Bodrossy and Sessitsch 2004; Lievens et al. $2005a$, b, 2006). A specific microassay-based diagnostic method using padlock probes (PLP) (Szemes et al. 2005) detects the presence of *Phytophthora* from leaves, roots, soil and stream water and even from air in the multi-institutional Global Phytophthora Network (GPN) project.

 While assessment of the diversity, distribution and dynamics of *Phytophthora* in nature requires the deployment of accurate diagnostic methods, implementation of effective control strategies also requires more knowledge about the genetic structure of population of plant pathogens (Wolfe and Caten 1987), as control strategies must target a population instead of an individual if they are to be effective. Defining the genetic structure of a population is a logical first step in studies of fungal population genetics because the genetic structure of a population reflects its evolutionary history and its potential to evolve: aspects important for formulating disease management strategies. 'Genetic structure' refers to the amount and distribution of genetic variation within and among populations (McDonald 1997).

 In fungi that undergo both asexual and sexual reproduction, it is necessary to differentiate between diversity at individual locus, 'gene diversity', and diversity based on the number of genetically distinct individuals in a population, 'genotype diversity'. Taken together, gene and genotype diversity constitute genetic diversity (McDonald 1997). It is, however, important to distinguish between studies of population diversity and population genetics; the former yield the raw data, to which the latter can be applied to answer questions on the fundamental mechanisms and process of genetic change in populations (Cooke and Lees 2004).

 Detection of diversity is usually done through the use of phenotypic and genotypic markers that are selectively neutral, highly informative, reproducible and relatively easy and inexpensive to assay. It is clear, however, that no single marker system would be adequate for all aspects of research on the diversity of *Phytophthora* species (Milbourne et al. 1997). The choice of genetic marker can have a substantial impact on the analysis and interpretation of data. As *Phytophthora* reproduce mainly asexually, producing a population structure that is largely composed of clonal lineages, a neutral marker such as a DNA fingerprint, may be used to address both questions relating to roles played by population size, mating systems and gene flow and also for questions relating to effects of selections, for which usually selective markers are used, assuming there is complete correspondence between genotype (DNA fingerprint) and phenotype (e.g. pathotype) (McDonald 1997). However, such assumption may not be valid as variable pathotypes can arise within the same clonal lineages (Drenth et al. 1996; Goodwin et al. 1995; Abu-El Samen et al. 2003).

 Though it is best to use a widest practical array of genetic markers, combining a mixture of selected and neutral unlinked markers encompassing the nuclear (and mitochondrial) genome(s) distributed across many chromosomes, the number of marker loci assayed varies with the objective and resources available to the

investigator. However, choicest markers are multilocus and have deeper resolving power like those of simple sequence repeats (SSRs) or single nucleotide polymorphisms (SNP). High throughput and massive parallel computing power have allowed multiplexing of these primers in recent times allowing assessment of field level diversity possible in shorter periods of time. Very recently, next-generation sequencing (NGS) has opened up the possibilities of looking at transcriptional polymorphisms of the pathogen population in the field allowing us to detect whether the isolates are under selection pressure and rapidly evolving and also the variability of the pathogen transcribed effectors that are the key in inducing the disease. These information would allow us to make informed choices by predicting about whether a particular fungicide or new host lines/varieties would be effective against the pathogen population.

 In the coming decade, these next-generation technologies of sequencing, proteomics and metabolomics will have increased throughput and decreased costs. The upcoming fourthgeneration technologies like single molecule real-time sequencing technology (SMRT) which is already available commercially are supposed to bring down the costs to about approx. Rs. 1.50 (3 cents) per Mb, and sequencing of a whole field population of *Phytophthora* spp. will come down to about Rs. 30, 000/- (\$500)! Community and population cellular components can then be measured dynamically over space and time.

 However, in the Indian scenario while that will be sometime in coming, we can as of now create databases from pathogen population data collected from neutral markers (like SSRs) and associate them with field data like germination temperature, mating type, fungicide sensitivity, morphological phenotypes and others like effector diversity and geographical location. Each cluster formed as a result of use of genetic markers can then be completely characterised. Once such a database is formed, it can be useful as a diagnostic aid to predict the characteristic of the pathogen population and prescribe control measures against that pathogen population. Since Phytophthora populations vary geographically

and devastation times are typically 48–72 h, there is very little time to run series of traditional tests and then prescribe measures. In a typical scenario, once an infected sample is brought to the diagnostic centre/plant health clinic, a single quick molecular marker assay (in a few hours time) would assign the pathogen to a previously characterised pathogen population cluster. Once the match is done, it would become very easy to accurately prescribe control measures. The same information will be very helpful to create DSS specific for crops and their pathosystems.

19.4 Conclusion

The twenty-first century has already seen a major paradigm shift in our understanding of the biology, evolution and genetics of the genus *Phytophthora* as well as the tools and approaches used to develop novel approaches for disease management. The combination of novel tools and approaches provided by the convergence of genome sequencing, computing power and novel genomic/biotechnological tools paints a promising picture of the future of Phytophthora disease management. At the same time, *Phytophthora* pathogens continue to emerge at an accelerated rate due to increased global travel and trade (Guha Roy and Grünwald 2014). Also, selection pressures of random fungicide usage, changing climatic conditions and misdirected (due to little or no knowledge about pathogen populations) control measures have increased coevolutionary rates as evidenced from transcriptional profiling of effectors. The only way we can tackle this menace is if we also 'coevolve' in our approach and adopt novel tools and approaches facilitated by newer technologies to combat it.

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