

Progress in Biological Control

Jean Michel Mérillon
Kishan Gopal Ramawat *Editors*

Plant Defence: Biological Control

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Progress in Biological Control

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Preface

Approximately 6.6 billion humans now inhabit the Earth. Notably, the human population has grown nearly ten-fold over the past three centuries and has increased by a factor of four in the last century. Therefore, demand for food, feed and fodder is ever increasing.

Plant diseases worldwide are responsible for billions of dollars worth of crop losses every year. Productivity of crops is at risk due to the incidence of pests, pathogens and animal pests. Crop losses to pests can be substantial and may be reduced by various control activities. Estimates on the crop loss are available for major food and cash crops on the world level. Among crops the total loss potential of pests world-wide varies from 25 to 40%. Globally, enormous losses of the crops are caused by the plant diseases, which can occur from the time of seed sowing in the field to harvesting and storage. Important historical evidences of plant disease epidemics are Irish Famine due to late blight of potato (Ireland, 1845), Bengal famine due to brown spot of rice (India, 1942) and Coffee rust (Sri Lanka, 1967). Such epidemics had left their effect on the economy of the affected countries and deep scar on the memories of human civilization.

Plant diseases, caused primarily by fungal and bacterial pathogens, cause losses of agricultural and horticultural crops every year. These losses can result in reduced food supplies, poorer quality of agricultural products, economic hardship for growers and processor and results ultimately in higher prices for the consumers. For many diseases, traditional chemical control methods are not always economical nor are they effective, and fumigation as well as other chemical control methods may have unwanted health, safety and environmental risks.

Biological control involves use of beneficial micro-organism, such as specialised fungi and bacteria to attack and control plant pathogens and diseases they cause. Biological control offers an environmental friendly approach to the management of plant diseases and can be incorporated in to cultural and physical controls and limited chemical uses for an effective integrated pest management system. Due to the high cost of synthetic pesticides and concerns over environmental pollution associated with the continuous use of these chemicals, there is a renewed interest in the use of botanicals and biological control agents for crop protection. Benefits and

risks are always associated with new technologies and their utilization. These types of considerations have encouraged microbiologists and plant pathologists to gain a better knowledge of biocontrol agents, to understand their mechanism of control and to explore new biotechnological approaches to induce natural resistance. This book provides a comprehensive account of interaction of host and its abiotic stress factors and biotic pathogens, and development of biological control agents for practical applications in crops and tree species, from temperate to subtropical regions. The contents are divided into the following sections:

- General biology of parasitism
- Applications of biological and natural agents for disease resistance
- Host parasite interaction
- Mechanism of defence

The chapters have been written by well known workers in their research field.

The book is primarily designed for use by upper undergraduates and post graduates studying crop protection, agricultural sciences, applied entomology, plant pathology, and plant sciences. Biological and agricultural research scientists in biotechnology, forestry, plant pathology and post harvest technology, crop management and environmental sciences, agrochemical and crop protection industries, and in academia, will find much of great use in this book. Libraries in all universities and research establishments where agricultural and biological sciences are studied and taught should have multiple copies of this very valuable book on their shelves. The editors wish to thank all the contributors and staff of the Springer for their cooperation in completion of this book.

Prof. J.M. Mérillon and Prof. K.G. Ramawat

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Part I
General Biology of Parasitism

Chapter 1

Co-evolution of Pathogens, Mechanism Involved in Pathogenesis and Biocontrol of Plant Diseases: An Overview

Jaya Arora, Shaily Goyal, and Kishan G. Ramawat

Abstract Plant pathogens pose a serious problem for global food security. More sustainable and reliable food production will be needed to support the human population for the upcoming years. To develop efficient, economic and environment friendly biocontrol measures, a deep understanding of diseases is required. The Phytopathology has four main objectives (i) etiology, (ii) pathogenesis, (iii) epidemiology and, (iv) control, which should be considered for an overall knowledge about a plant disease. Understanding of the plant response to the pathogen attack has advanced rapidly in recent years; still many plant diseases are unpredictable either due to emergence of new pathogenic strains or due to mutagenic changes in present strains, which cause a failure in all preventive measures. In this review, lacuna in present control measures and future requirements in disease management are discussed in the light of recent advances made in molecular mechanisms and components involved in pathogen defense in plants as well as how pathogens are continuously co-evolving. The complex picture of pathogen defense in plants is beginning to be unraveled but a lot more still remains unclear.

1.1 Introduction

Plant diseases cause economic threats to conventional and organic farming systems. Most of the infectious plant diseases have their characteristics mode of spread and symptoms. The understanding of these characteristics helps in possible control strategies; assess economic impact and the socio-economic consequences

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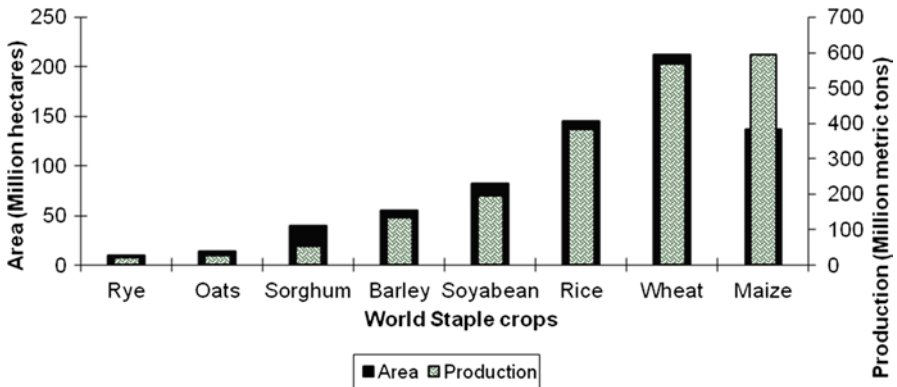


Fig. 1.1 World production and area under cultivation of staple crops

of their dissemination. Their effects range from mild symptoms to catastrophes in which large areas of food crops are destroyed. Fourteen crop plants provide the bulk of food for human consumption, which are likely to be infested from any of the major plant pathogens including viruses, bacteria, oomycetes, fungi, nematodes, and parasitic plants [1].

Human population is projected to grow at approximately 80 million per annum, increasing by 35% to 7.7 billion by 2020 [2]. With the ever-increasing population there is an increasing demand for food and fodder. According to the Production Estimates and Crop Assessment Division, Foreign Agriculture Service (FAS), United States Department of Agriculture (USDA, 2002/2003) a comparative data of major staple crops production and total cultivated area over the world is presented in the Fig. 1.1 [3].

At least 10% of global food production is lost by plant diseases; either as yield loss or as quality loss, both are included in the concept of crop loss. Food shortage and the damage to the food production, caused by plant pathogens, results in undernourishment of roughly 826 million people in the world, of which 792 million people are in the developing world and 34 million in the developed world [4]. Although the ability to diagnose diseases and the technologies available for their control are far greater than in the past, it is necessary to accumulate loss data, including the importance of pests, key pests and their control for evaluating the efficacy of present crop protection practices [5]. A major portion of crop is also lost due to non-native crop species. Crop loss due to non-native species invasions in the six nations viz., United States, United Kingdom, Australia, South Africa, India, and Brazil, is more than US\$ 314 billion per year [6].

Although there is an extensive bibliography available regarding the biology, symptoms, distribution and crop losses by some pathogens, concise data on the mechanism of pathogenesis and their possible control measures are essential to interpret with present scenario of plant diseases. The present article is intended to overview plant pathogenesis and its control.

1.2 Epidemiology

The socio-economic effects of disease epidemics and the consequent crop losses have been well documented. There are some iconic invasive diseases, often exemplified due to their large demographic impacts on communities that are dependent on a single staple crop, resulting into epidemics. Some emerging infectious diseases cause famine and favour human diseases, and technical crises for the management of whole agricultural communities. Frequently cited examples include the Irish potato famine caused by *Phytophthora infestans*, the oomycete plant pathogen, with one million deaths and two million emigrations from 1845 to 1847 in Europe [7]. The high dependence of large Irish population on potato for sustenance, the lack of resistance in the plant to the pathogen, and wetness of the environment caused *Phytophthora* to take an epidemic form. Its most notorious species, costing annually on a global basis in excess of \$5 billion in terms of losses of the potato crop and control measures [8].

Great Bengal Famine (Rice brown spot) of 1943 and the southern corn leaf blight epidemic of 1970–1971 in the USA were the two another big disasters caused by fungal pathogens of the genus *Cochliobolus*. The former one was caused by *C. miyabeanus*, an estimated two million people died owing to the high dependence of most of the population on a single crop, rice. Pathogen's spread was favoured by the environmental conditions pertaining at that time [9]. In the USA, the corn (maize) crop was completely destroyed by *C. heterostrophus*, named race T, which was specifically virulent for maize containing a cytoplasmically inherited gene for male sterility (Tcms). It had been incorporated into about 85% of the American crop by 1970 due to self-fertilization and favourable climatic conditions. Alternative sources of nutrition were plentiful, so no one died and the endemic brought to an end by the withdrawal of susceptible varieties and the establishment of new hybrids [10]. Corn Leaf Blight is renowned for having set a record in terms of economic losses produced on a single agricultural crop in a single season with estimated historic losses of \$1 billion [11].

During the first 50 years of the nineteenth century, in Ceylon (now Sri Lanka), there was a massive increase of coffee cultivation by British planters. In 1868, there was total elimination of coffee trees by a rust fungus *Hemileia vastatrix*, which was likely to have spread from Ethiopia, the center of origin of both the plant and its rust [12]. By 1905, the coffee cultivation area in Ceylon had shrunk from 275,000 acres in 1878 to around 3,500 acres in 1905 [13]. Because of the epidemic, coffee had to be replaced, fortunately with success, by tea.

The threat of epidemics occurring with catastrophic consequences has been sharply reduced in developed countries compared to developing countries, due to technological advances such as, diagnostics, agronomic practices and the use of specific disease management strategies [14]. Re-emergence of a disease is the coincidence of a number of unfortunate events, including many anthropogenic activities such as introduction of plant species into new area. But many such introduced species, like corn, wheat, rice, domestic chicken, cattle, and others are beneficial

and now provide more than 98% of the world food supply with a value of more than US\$ 5 trillion per year [15]. However, alien plant species (introduced plant species) are also known to cause major economic losses in agriculture, forestry, and several other segments of the world economy [16, 17]. Some pathogen communities are introduced together with a newly introduced plant species and resulted in an emerging disease to that new area. Besides trading of whole living plants, alien pathogens can be introduced through vegetables, germplasm, and grafts or via international seed trading. For example, it has been estimated that at least 2,400 different plant pathogens were contained in the seeds of 380 plant genera [18], and that up to one third of the plant pathogenic viruses are transmissible through seeds to at least one of their hosts [19]. Many factors affect the dissemination and infection by an introduced pathogen like in Pierce's Disease of grapevine, caused by the bacterium *Xylella fastidiosa*. It was first reported in California as not being serious for more than a century, but in 1997 a new vector, *Graphocephala atropunctata*, was introduced in California. This allowed the rapid development of the disease in the vineyards, with estimated damage of 6 million dollars in 1999 [20]. Lacking the elements favoring their further dissemination, some pathogens may remain restricted to their area of introduction, making very limited impact. Another example of epidemic occurred due to some introduced variety is vine downy mildew disease caused by *Plasmopara viticola* in France from 1868 to 1882. This disease was first observed in America in 1834, and then the pathogen was carried to Europe on American stock, where it was first recorded in France. From France, the mildew-pathogen spread throughout Europe, where it is now a very notorious pathogen. Losses in Europe have been enormous due to this disease. The greatest losses to American viticulturists from this disease are incurred in Northern United States; where in some localities it is estimated that 25–75% of the crop is destroyed [21].

There are some more emerging infectious diseases of crops that are challenging the current preventive measures of farmers, such as Cassava Mosaic Virus (CMV), Banana *Xanthomonas* Wilt (BXW), stem rust of wheat, Citrus Huanglongbing etc. Among them the effects of CMV disease on the farming communities in Uganda became apparent in the early 1990s. The initial impact was greatest in the north-eastern areas of the country, because the particular cultivars were susceptible to the virus. Here, cassava production between 1990 and 1993 was reduced by 80–90% and many farmers stopped its cultivation [22]. The cultivation of other crops, mainly sweet potatoes were preferred at that time to overcome the situation. Several attempts have been made to quantify the losses due to the virus, the most reliable estimate being around 600 thousand tonnes per year valued at 60 million dollars [23]. CMV is the most important disease of cassava in Africa, Sri Lanka and Southern India [24].

The disease caused by the bacterium *Xanthomonas campestris* pv. *musacearum* to banana plantations, known as BXW is one of the most important emerging risks. This disease was initially reported in Ethiopia about 40 years ago on *Ensete ventricosum*, a genus closely related to *Musa* [25]. It was reported in Uganda in 2001 on banana and from there it has spread rapidly to all regions of Africa where the crop is grown. No varieties of banana have complete genetic resistance, but they differ in degree of susceptibility [26]. It has been estimated that, if not controlled,

the pathogen can increase the area infected at a rate of 8% per year [27]. The damage caused by the disease each year is estimated at \$2 billion. A recent study estimated 53% loss in yield of banana production in Uganda in last 10 years. Production losses caused by the disease threaten the food security of about 100 million people and the income of millions of farmers in the Great Lakes region of Central and Eastern Africa [28].

One of major epidemics occurred in the 1940s and 1950s in Australia and the United States is stem rust or black rust of wheat caused by microscopic fungus, *Puccinia graminis* f. sp. *Tritici* [29]. It took more than a decade to find out cause of re-emergence of stem rust due to its complex life cycle that requires barberry (*Berberis vulgaris*) as well as a cereal species. Another recently worldwide occurring most destructive disease of all citrus pathosystems is Huanglongbing, the yellow shoot disease. The disease is associated with three bacteria: *Candidatus liberibacter asiaticus* (Las), *C.L. africanus* (Laf), and *C.L. americanus* (Lam). To date, there has been a decline in all commercial citrus industries that have faced the disease [30].

Nowadays epidemiological models are constructed to increase understanding of the complex interactions between vectors, pathogen, host plants, and the environment. If these are accurate and validation with field data is demonstrable for a range of epidemiological scenarios, it can be used for decision support over targeted control of epidemics [31, 32].

Food crisis in developed countries due to failure of a crop can be overcome as the impact of plant disease is mostly an economic issue but in developing countries it can be a primary cause of starvation and today developing countries are more integrated into the global economy than in past decades. Stepping up investment in the agriculture sector can be one of the solutions to combat the situations. Such initiatives can achieve success when new diseases are recognized early in their emergence and before they have spread beyond a reasonable containment zone that can only be managed by quarantines or eradication efforts.

1.3 Co-evolution of Plants and Their Pathogens

Darwinian paradigm of ‘variation and selection results in evolution’ plays an important role in predicting evolution of pathogens in nature. Nowadays, alarming disclosure is that the vaccines and chemical therapies used by medicinal and agricultural industries are perhaps the main forces driving the evolution of viral and microbial pathogens [33]. These evolutionary causes can further be used in the development of effective and sustainable treatments of micro parasitic diseases.

“Co-evolution” includes population-level processes of reciprocal adaptation of interacting species. Reciprocal traits involved in co-evolution include pathogen infectivity and host resistance. As host defences may reduce the fitness of parasite, host and parasites may co-evolve, defining co-evolution as the process of reciprocally adaptive genetic change in two or more species. Accordingly three conditions

that should meet for host pathogen co-evolution are (1) genetic variation in the relevant host and pathogen traits; (2) reciprocal effects of the relevant traits of the interaction on the fitness of host and pathogen; (3) dependence of the outcome of the host-pathogen interaction on the combination of host and pathogen genotypes involved [34]. For plant-virus co-evolution taking *Arabidopsis thaliana* as model system, there are only partial evidences regarding the detrimental effects of highly virulent viruses in crop production. In such cases, the infection is not necessarily linked to a fitness decrease and the changes in the genetic structure of virus population or a resistance factors introduced by breeder through genetic manipulation of the host plant [35]. Understanding the forces driving co-evolutionary trajectories requires accounting for both within and among-population processes in space and time [36].

Theoretical studies of co-evolution date back over 40 years. Many host pathogen interaction models have been studied. In which primarily animal-virus system of European rabbit-myxoma virus system is a classical example. When the virus was introduced into a local virus population, phenotypic changes were observed in both pathogen and host components of virulence [37]. Plant defence systems have similarity to mammalian innate cellular immunity at a molecular level, and utilize analogous components to recognize pathogen-derived signals and induce defence responses. In both systems pathogens deliver effector proteins into their respective host cells to mimic, suppress, or modulate host defence signaling pathways and to enhance pathogen fitness. On the host side, plants and animals have evolved refined surveillance mechanisms to recognize various pathogens [38, 39]. These evolutionary commonalities combined with ethical issues that limit experimental manipulations in animal populations, make plant-based systems powerful models for studying the impacts of genetic variation in host disease resistance [40].

Co-evolution is a dynamic process, which occurs in cycles. In first phase of a cycle, plant develops some resistant character against its attacking pathogens; these resistance characters reduce the survival or virulence of attacking pathogens. This initiates second phase of a co-evolutionary cycle: the evolution of counter-resistance by attacking pathogens, to evade plant resistance mechanisms; each partner continually evolving just to keep pace with the other, like an evolutionary game of “ping-pong” [41–43]. This process is vibrantly termed as ‘Red Queen’ dynamics [34]. There are several examples in which natural enemies exhibit such characters that can be interpreted only as having evolved to confer counter resistance. For example, seeds of the tropical legume *Dioclea megacarpa*, which contain the non-protein amino acid L-canavanine, are toxic to most insects because their arginyl-t-RNA synthetases also incorporate L-canavanine into proteins. However, the bruchid beetle *Caryedes brasiliensis*, whose larvae feed solely on *D. megacarpa*, has evolved a modified t-RNA synthetase that distinguishes between L-canavanine and arginine [41, 44]. So the beetle has co-evolved according to its host resistance. Similarly, chitinase evolution in *Arabidopsis* and related species in the genus *Arabis* exhibits remarkable similarities to receptor evolution. Plant chitinases are co-evolving with pathogen chitinase inhibitors [45]. However, in some cases counter resistance of a plant against its natural enemy may have additional physiological or ecological functions. Thus, it is a matter of debate whether the resistant characters

are a part of natural selection imposed by natural enemies or only have routinely defensive role in plant physiology [41].

In a phylogenetic analysis done by Richards et al. [46], phytopathogens are extremely important because of their economic impact in the field of agriculture. Most of the evolutionary relationships are studied between oomycetes and the fungi, as most of the economically important plant pathogens are found among these groups. Lateral gene transfer is considered as one of the contributing factor for emergence of new phytopathogen. There are several reports on acquisition of prokaryotic genes by microbial eukaryote while there have been few reports on eukaryote-to-eukaryote gene transfers, as a dense taxon sampling is needed to identify donor and recipient lineages for transfer events [47–49]. The gene exchange in unrelated organisms of prokaryotic origin could be both the cause and consequences of adaptation to similar environments, and result in extensive convergent evolution [50]. New disease can also results by acquisition of a new gene function such as Tan spot of wheat is believed to have emerged as a result of lateral gene transfer of the gene for Tox A from the related wheat pathogen *Stagonospora nodorum* in *Pyrenophora tritici-repentis*. The most common evidence for lateral transfer is that genes isolated from the proposed recipient are absent in closely related species but present in more distantly related species [51, 52].

There is a growing appreciation among ecologists that long-term evolutionary history has a major role in explaining the composition and structure of ecological communities and phylogenetic approaches are essential in achieving explanation [53]. Sirtuin genes are found in all eukaryotes examined so far, including plants, fungi, and animals. It is therefore safe to assume that sirtuins are very ancient enzymes that existed in the common ancestor of today's eukaryotes, possibly more than a billion years ago. Sirtuin enzymes evolved early in life's history to increase somatic maintenance and survival during times of adversity. The xenohormesis hypothesis of Howitz and Sinclair proposes that primordial species synthesized polyphenolic molecules to stimulate sirtuins during times of stress. Plants have retained this ability. Survival pathways in fungi and animals have retained the ability to respond to plant stress signalling molecules because they provide useful information about the state of the environment and/or food supply. This ability would allow organisms to prepare for and survive adversity when they might otherwise perish [54].

Many plant pathogens are limiting factors in food production throughout the world. Agro-ecosystems will need to be re-engineered to prevent the continuous emergence of new pathogens. A combination of environmental, species, and genetic heterogeneity should be reintroduced into the agro-ecosystem to make it less conducive to pathogen emergence. For example, environmental heterogeneity can be increased by combining agriculture and forestry or with other mixed cropping systems. Crop species diversity can be increased through faster and more complex crop rotations, planting of species mixtures, and by decreasing average field size. Genetic diversity within monocultures can be increased by growing several different cultivars of the same host in patches within the same farm. The result of re-engineering the agro-ecosystem will be to develop more sustainable and reliable food production that will be needed to support the human population for the upcoming years.

1.4 Mechanisms of Plant Disease Resistance

The emergence of a new disease is an output of a number of conditions and steps, including the enhanced fertility of the new pathogen, enhanced survival from season to season, and spread around the world. It also depends on plant's resistance abilities to defend pathogen attack. Plant populations are often genetically polymorphic for resistance to pathogens. Pathogens are, in turn, polymorphic for virulence genes that can evade plant resistance. Plants exhibit two types of resistance: horizontal and vertical resistance. Horizontal resistance is polygenic, and acts against all races of a particular pathogen. Vertical resistance, conferred by the R-genes, is oligogenic, and can be overcome by a change of race. Horizontal resistance slows down the rate at which disease increases in the field. Vertical resistance reduces the initial amount of inoculum from which the epidemic begins. A slow rate of disease increase in the field greatly enhances the benefit from reducing the initial inoculum. Therefore, horizontal resistance greatly enhances vertical resistance: horizontal resistance activates the R-genes [55, 56]. The definitive character of vertical resistance is gene-for-gene relationship as in vertical resistance there are single genes for resistance in the host plant, and there are also single genes for parasitic ability in the parasite [57].

Advances in understanding host-pathogen co-evolutionary interactions requires knowledge of the molecular basis of host resistance and pathogen virulence; so in 1991, researchers began assaying different inbred accessions of *Arabidopsis*, and found considerable variation in disease resistance and susceptibility among them, following inoculation with strains of the bacterial pathogen *Pseudomonas syringae* [58, 59]. Studies revealed that some of this variation resulted from the recognition of specific bacterial avirulence genes, *avrRpt2* and *avrRpm1*, which were capable of restricting the growth of an otherwise virulent *P. syringae* isolate. This was the first step in identifying *avr-R* gene pairs in *Arabidopsis*, and opened the door to using the strengths of *Arabidopsis* to analyze the key genetic idea in plant pathology: the gene-for-gene hypothesis [60, 61] and till date *Arabidopsis* has been an excellent model for answering fundamental question in molecular plant-microbe interactions [62]. The concept of mutation of avirulence genes leading to the defeat of resistant cultivars is also a step convincing for gene-for-gene hypothesis. Point mutations have been implicated in the mutation of avirulence genes in fungal pathogen races [63]. For example, cloning and sequencing of specific avirulence (*Avr*) genes in *Melampsora lini* found evidence for functional changes in the coding regions of targeted *Avr* genes that occurred almost exclusively via non-synonymous mutations [64]. These observations provide strong independent evidence for the operation of selection on these genes.

1.4.1 Host-Parasite Interaction

The initial interactions of pathogen and plant are the determining factors for disease development. In a bacterial infection, it first colonize the leaf surface then enter leaf mesophyll tissue through natural stomatal openings, hydathodes, or wounds, thus

making their first contact with internal host cells and remain in apoplast of plant cells; whereas fungi extend their hyphae, which either directly penetrate the epidermis or differentiate to form specialized nutrient exchange structures such as haustoria. After initial contact the potentially infectious agents produce microbe-associated molecules, such as bacterial flagellin, lipopolysaccharide (LPS) and fungal chitin, termed as MAMPs (microbe-associated molecular patterns) [65–67]. The recognition of different MAMPs presumably by specific plant pattern-recognition receptors (PRR) activates the common signaling pathways including MAP kinase (MAPK) cascade, defence gene transcription, rapid microbursts of reactive oxygen species (ROS) and callose deposition to strengthen the cell wall at sites of infection as a result of complex cellular remodelling [68, 69]. Plants have evolved a variety of PRRs to perceive diverse microbial patterns [70]. Many MAMP receptors have been isolated and characterized by using biochemical and genetic approaches. Initially a 75-kDa soybean plasma membrane protein was purified as the binding protein for hepta- β -glucan, the cell wall component of oomycetes [71]. The understanding of MAMP perception was greatly advanced with the isolation of the putative bacterial flagellin receptor FLS2 in *Arabidopsis*. FLS2 is a transmembrane receptor-like kinase (RLK) with extracellular leucine rich repeats (LRR) domain [72]. There is large number of RLKs in plants, with more than 600 in *Arabidopsis* [73].

One of the earliest responses at the time of pathogen attack is the generation of ROS including superoxide anion (O_2^{-2}), hydrogen peroxide (H_2O_2), and hydroxyl radical (OH^-) [74]. On interaction with MAMPs there is a rapid influx of calcium ions (Ca^{2+}) in cytosolic compartment which is often correlated with the production of ROS. Similar response was observed in *Arabidopsis* leaf cells [75]. Beside this early Ca^{2+} influx into the cytosolic compartment, a rapid efflux of potassium (K^+), chloride (Cl^-) ions and extracellular alkalinisation of elicited cell cultures has also been observed [76]. The plant ROS is toxic to pathogens directly and cause strengthening of host cell walls via cross linking of glycoproteins [77]. ROS generation lead to a hypersensitive response (HR) that results in a zone of host cell death, which prevents further spread of biotrophic pathogens [78, 79]. In addition to the described direct effects, ROS can also serve as signals that lead to the activation of other defence mechanisms in conjugation with salicylic acid (SA) and nitric oxide (NO) [80]. It acts as intercellular or intracellular second messenger during signal transduction of defence response [81]. Several mechanisms have been proposed for ROS generation in plants such as NADPH-oxidase and superoxide, peroxidase and hydrogen peroxide, nitric oxide, oxalate oxidase, lipid peroxides and oxylipin production [82]. Of these mechanisms, the plasma membrane NADPH-dependent oxidase system has received the most attention because of its similarity to the mammalian oxidase system that initiates ROS production in phagocytes and B lymphocytes as a response to pathogen attack [83, 84]. A rapid elevation of ROS specifically in resistant wheat and non host rice plants attacked by Hessian fly larvae was observed. Global analyses of gene transcripts known to be or potentially involved in ROS homeostasis indicated that class III peroxidases and oxalate oxidases, instead of NADPH-dependent oxidases, were likely the source of ROS generation in wheat plants during incompatible

interactions [85]. In barley (*Hordeum vulgare*) ROS production has been associated with the formation of defensive barriers against powdery mildew and there is a polarized delivery of ROS, in vesicles inside the cell, which might contribute to inhibition of pathogen growth [86, 87].

1.4.2 Pathogenesis Related (PR) Proteins

PR proteins, initially defined as b-protein, are encoded by the host plant in response to stress generated by various types of pathogens and also by the application of chemicals that induce similar stresses [88]. PR genes get expressed in response to salicylic acid (SA), jasmonic acid (JA) and ethylene (ET) as a part of systemic acquired resistance (SAR) in plants [89]. PR proteins originally were divided into five groups (PR1–PR5) on the basis of findings of serological and sequence analysis, afterwards another six groups of proteins induced by pathogens were recommended for inclusion in PR proteins [90]. The five classic PR protein groups have been divided into acidic and basic subclasses on the basis of chemical properties, cellular localization and the mechanisms by which they are induced [91]. Acidic PR proteins, including PR1 α, β -1,3-glucanases and acidic chitinases, are induced by tobacco mosaic virus (TMV) infection or SA [92] while basic PR proteins, like PR1b and basic chitinases, are efficiently induced by wounding or ET and JA treatment [93]. The other six groups include proteinase inhibitors, lysozymes and peroxidases, and can also be elicited [94].

1.4.3 R (Resistance) Gene

Plant–pathogen interactions are governed by specific interactions between pathogen Avr (avirulence) gene loci and alleles of the corresponding plant disease resistance (*R*) locus in a variety of host plants, directing responses toward a broad diversity of pathogens including bacteria, fungi, oomycetes, nematodes, and viruses, and even insects. Pathogen's Avr genes encode specific elicitors of host defence responses. When corresponding *R* and Avr genes are present in both host and pathogen, the result is disease resistance, if either is inactive or absent, this results in disease establishment [95]. A set of structurally similar R proteins determines the recognition of a diversity of Avr proteins (type III effector proteins). These type III effectors effectively suppress MAMP mediated immune responses. However, plants have coevolved R proteins to recognize effector proteins and induce potent gene-for-gene resistance [66, 67]. The vast majority of R genes encode proteins containing a nucleotide-binding site (NBS) and leucine-rich repeats (LRRs) [96]. However, the biochemical functions of the majority of the type III effectors remain elusive. Recent structural studies of type III effectors from both mammalian and plant pathogens have revealed important functional information. By these studies, the strategies

employed by plant pathogens to promote virulence can be revealed and their prevention can be determined [97].

1.4.4 Plant Hormones and Defence

The interaction between plant hormone signaling and plant pathology is complex and intertwined. Genetic screens in *Arabidopsis* have defined many of the pathways involved in the synthesis, perception and effect of plant hormones [98]. These phytohormones are capable of transducing normal development signals such as seed germination, seedling establishment, cell growth, respiration, stomatal closure, senescence-associated gene expression, responses to abiotic stresses, basal thermo tolerance, nodulation in legumes, and fruit yield or adverse environmental stimuli to plant cells for initiating protective responses. Thus plant hormone signaling plays a major role in determining the outcome of plant–pathogen interactions [99, 100]. The best-characterized defence hormones include SA, JA and ET. Critical components of the SA pathway were revealed via genetic screens in *Arabidopsis*. Transduction of the SA signal leads to activation of genes encoding PR proteins, some of which have antimicrobial activity. The regulatory protein NONEXPRESSOR OF PR GENES1 (NPR1) is required for transduction of the SA signal because mutations in the NPR1 gene render the plant largely unresponsive to pathogen-induced SA production [101]. In *Arabidopsis*, JA biosynthesis is initiated by a wound-mediated release of α -linolenic acid from chloroplastic membranes, followed by the activity of several chloroplast-located enzymes, including 13-lipoxygenase (LOX). Silencing of LOX3, in *Nicotiana attenuata* plants, has been shown to reduce JA levels and impair both direct and indirect defences in LOX3-silenced plants [102]. The JA receptor was recently identified to be CORONATINE INSENSITIVE1 (COI1), an F-box protein required for response to both coronatine (pathogen-derived phytohormone, responsible for stomatal opening to allow entry into the mesophyll) and JA [103]. ET is known to be involved in mediating plant defence responses against herbivores [104]. In *Arabidopsis*, ET signal transduction is initiated by ET perception through multiple membrane-bound receptors: ETHYLENE RESPONSE1 (ETR1), ETR2, ETHYLENE RESPONSE SENSOR1 (ERS1), ERS2, and ETHYLENE INSENSITIVE4 (ETI4) [105]. All the signaling pathways involved in defence mechanism interact in a complex manner demonstrated by the antagonism of SA and JA, as well as the synergism between JA and ET [106, 107].

Though plants have developed various mechanisms to evade the pathogens yet occurrence of disease is very frequent. In the future, we are likely to see a rapid expansion in our knowledge of alternative mechanisms of resistance, such as efflux systems of the kind associated with multidrug resistance, innate resistance due to insensitivity of the target site of phytopathogens, and other novel mechanisms. The manipulation of plant biosynthetic pathways to alter antibiotic profiles will also tell us more about the significance of secondary metabolites for plant defence. Exploiting the knowledge of the Biochemistry and Molecular Biology of disease in order to increase resistance will also be helpful in disease prevention.

1.5 Control Measures

One of the major aspects of plant pathology is to enhance crop production by introducing genetically improved (high-yielding, less susceptible to pathogens) cultivars, enhanced soil fertility via chemical fertilisation, pest control via synthetic pesticides, and irrigation. Besides physical control methods e.g. mowing, slashing, burning, flooding, hand removal, physical barriers (i.e. netting, fences), use of pesticides is very common method for controlling various phytopathogens. The use of synthetic pesticides in the US began in the 1930s and became widespread after World War II. By 1950, pesticide was found to increase farm yield far beyond pre-World War II levels. Farmers depend heavily on synthetic pesticides to control insects in their crops. There are many classes of synthetic pesticides. The main classes consist of organochlorines (e.g., Dichlorodiphenyltrichloroethane: DDT, toxaphene, dieldrin, aldrin), organophosphates (e.g., diazinon, glyphosate, malathion), carbamates (e.g., carbofuran, aldicarb, carbaryl), and pyrethroids (e.g., fenpropanthrin, deltamethrin, cypermethrin). The use of synthetic pesticides in agriculture comes with a cost for the environment, and the health of animals and humans. Exposure to pesticides can cause acute or chronic effects on animals and humans, especially in the reproductive, endocrine, and central nervous systems. So in 1996, US Environment protection agency (EPA) applied Food Quality Protection Act [108] which regularizes the pesticide registration procedures. Therefore, the need for discovery and development of some natural product-based pesticides gain momentum. Organic pesticides like rotenone obtained from *Derris* root and pyrethrum obtained from *Chrysanthemum* flower heads were discovered in nineteenth century at the time of European Agriculture revolution. Such organic pesticides are the chemicals that plants use to protect themselves from parasites and pathogens. Essential oils such as pine oil, clove oil, citronella oil are commercialized in various compositions and have herbicidal activity [109]. Inorganic pesticides like borates, silicates and sulphur, work as poisons by physically interfering with the pests. Current inorganic pesticides are relatively low in toxicity and have low environmental impact. Borate insecticides, for example Bora Care and Timbor, in particular, have many uses in structural pest management. Biorational pesticides are those synthetic, organic, or inorganic pesticides that are both, low toxic and exhibit a very low impact on the environment [110]. These are some direct methods of controlling pathogens by applying chemicals, besides this biological and genetic control methods are some of the methods which are being dynamically used since last decades. Both methods are described here in brief.

1.5.1 Biological Control

Biological control, as most commonly construed, is the use of living organisms to control pests. Plant pathogens, insects, nematodes and weeds are controlled by the use of some biologicals. It is the direct inoculation of microbial agents (also called antagonists) into soils or onto host surfaces for immediate benefit [111–113].

Plant growth-promoting bacteria control the plant damage by phytopathogens. This involves different mechanisms including: out competing the phytopathogen, physical displacement of the phytopathogen, secretion of siderophores to prevent pathogens in the immediate vicinity from proliferating, synthesis of antibiotics and synthesis of a variety of small molecules. All these steps can inhibit phytopathogen growth, production of enzymes that inhibit the phytopathogen and stimulation of the systemic resistance of the plant [114]. Intensive screens have yielded numerous candidate organisms for commercial development. Some of the microbial taxa that have been successfully commercialized and are currently marketed as EPA-registered biopesticides in the United States include bacteria belonging to the genera *Agrobacterium*, *Bacillus*, *Pseudomonas*, and *Streptomyces* and fungi belonging to the genera *Ampelomyces*, *Candida*, *Coniothyrium*, and *Trichoderma* [115]. More studies on the practical aspects of mass-production and formulation need to be undertaken to make new biocontrol products stable, effective, safer and more cost-effective. Now-a-days detailed studies have been done on mechanism of these biological agents, how they reduce damage inflicted by pathogen, for example the role of the indigenous plasmids of *Pseudomonas aeruginosa* (D) and *Azospirillum* species isolates in fungal antagonistic property are clarified and more efficient bacterial transformants in controlling the plant pathogen *Fusarium solani* by chitinase gene transfer have been produced [114]. Recently a Gram-negative rhizobacterial isolate (LSW25) antagonistic to *Pseudomonas corrugata* (a vein necrosis pathogen of tomato) and promotes the growth of tomato seedlings by increasing calcium uptake, was isolated from surface sterilized tomato roots [116].

Currently, there has been revival of interest in use of bacteriophages for control of bacterial plant diseases [117]. Phage could play an important role in limiting bacteria in the soil, due to the presence of the lytic cycle. Using the strategy of phage application proposed by L. E. Jackson [118], bacterial spot of tomato was significantly controlled than the standard copper-mancozeb treatment. Additionally, the yield of extra-large fruits was significantly higher on phage-treated plants than on copper-mancozeb treated ones. The phage mixture reduced disease severity of bacterial spot by 17%, whereas copper-mancozeb application caused 11% reduction [119]. The first commercial company to produce phages specifically for control of bacterial plant diseases was AgriPhi, Inc., established by L. E. Jackson [118].

1.5.2 Genetic Control

Each year there is great crop loss caused by pathogenic bacteria, phytoplasmas, viruses and viroids. These microorganisms are difficult to control, as they multiply at an exponential rate and many of them can remain latent in “subclinical infections”, and/or in low numbers, and/or in some special physiological states in propagative plant material and in other reservoirs [120, 121]. In this context, rapid, cheap, sensitive, specific and reliable identification methods of pathogens are required to apply treatments, undertake agronomic measures or proceed with eradication practices,

particularly for quarantine pathogens. Increasingly, modern diagnostic tools are being based on the DNA characteristics of the pathogen as they present adequate diversity to distinguish species, strains, substrains, isolates, and even individuals; and offer convenience of detection using modern bio-techniques such as polymerase chain reaction (PCR) or Reverse Transcription (RT)-PCR [122]. Using RT-PCR technique detection of Cherry green ring mottle virus and Cherry necrotic rusty mottle virus in *Prunus* spp. has been done [123]. Further advancement in detection methods has been done by developing micro-array technology which provides the next generation of DNA diagnostics to measure different pathogens in a massively parallel manner on a single chip and avoid laborious confirmation procedures. A porous capillary solid phase micro-array system is shown for plant-pathogenic *Phytophthora* spp. multiplex detection [124]. Besides diagnostic methodology transformation techniques have been used to develop resistant varieties. Till date there are several examples of transgenic plants development for disease resistance, some of them are given here. A cloned non host gene (Rxo1) from maize with resistance to Bacterial leaf streak (BLS) of rice caused by *Xanthomonas oryzae* pv. *oryzicola* (Xooc), was transferred into four Chinese rice varieties through an *Agrobacterium*-mediated transformation system. Molecular analysis of the transgenic plants showed the integration of the Rxo1 gene into the rice genomes [125]. Likewise transgenic tobacco plants with synthetic gene of antimicrobial peptide Cecropin P1 were obtained, which exhibit enhanced resistance to phytopathogenic bacteria *Pseudomonas syringae*, *P. marginata*, and *Erwinia carotovora* [126].

The transgenic technology is meant to carry genetic uniformity in the crops with disease resistance as the most promising applications of genetically modified crops. However, the growth of transgenic technologies in agricultural practice has been limited by public opinion in some countries. The process of genetic engineering can introduce dangerous new allergens and toxins into foods that were previously naturally safe. At present, only two traits are the subject of the commercialized transgenic biotechnology: herbicide (glyphosate) tolerance and insect resistance conferred by the Bt gene from *Bacillus thuringiensis*. This means that new technologies to fight weeds and insects are in place, and are in itself a noteworthy and positive step. In future new findings will give us many genes for insect and disease resistance, and then we may feel more secure from the genetic vulnerability that may be presented at the current stage of development of the technology.

1.6 Conclusion

Plants are immobile and as such are incapable of escaping attack by insect and microbial pests. Crop losses due to pests can be devastating to the point of creating a famine. Fungal and bacterial pathogens account for the greatest overall losses associated with plant diseases. One of the primary objectives of conventional plant breeding was to develop resistance to plant diseases. Results, however, were limited due to the length of time needed to develop varieties through conventional breeding,

the lack of suitable donor varieties, and the ability of microbes to adapt by neutralizing plant defense mechanisms. Now-a-days plants are genetically modified not only to increase quality of food but also to sustain the environmental threats including pathogens with increased shelf life. Availability of pathogen-free germplasm to different organization in a safe and timely fashion is the need of hour. There is much to be done to expand our knowledge of plant pathogens and our ability to deal with them. The identity of many damaging pathogens that currently exist has not been done and the severity of the symptoms they cause is often subjective and qualitative rather than objective and quantitative. Plant pathogen populations are also genetically variable with time and space. Although there have been many epidemiological studies, it is difficult to predict the origin of the next plant disease catastrophe that will affect one or other of our crops vital to food security in some part of the globe. Pathogens that have evolved new virulence characteristics can also give rise to some famine conditions. There is a need for adoption of novel and potentially valuable opportunities for crop improvement - especially in developing countries, where new developments are most needed to enhance food security.

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