Climate Change and Indian Agriculture: Challenges and Adaptation Strategies

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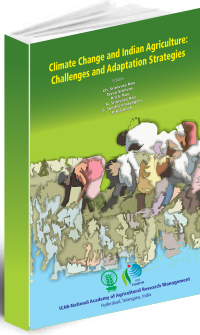
Hyderabad, Telangana, India

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Impact of Climate Change on Host-Pathogen Interactions and its Implications on Crop Disease Management

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Abstract

Natural and human activities have increased the greenhouse emissions and it will continue to boost global temperature in the 21st century. In this paper, we discuss the profound impact of climate on plant diseases — if the climatic conditions are not favourable to disease, a vulnerable host will not be infected by a virulent pathogen. Variable concentrations of CO_2, temperature, and availability of water may induce positive, neutral, or negative effects on disease development. Nevertheless, the basic concept of interactions of host-pathogen-environment may theoretically be applied to all pathosystems. Environmental factors also influence different pathways of plant resistance *viz.*, pathogen pattern-triggered immunity, effector-triggered immunity, RNA interference, and other networks of defence-related hormones. On the pathogen hand, temperature and humidity affect the processes of virulence, such as the development of toxins and virulence proteins, as well as reproduction and survival of pathogenic substances. Most of the laboratory works so far conducted on molecular-level plant-pathogen interactions focused on a few well-established pathosystems and static environmental conditions that represent just a fraction of the whole gamut of complex plant-pathogen-environmental interactions that occur in nature. To address the impacts of climate change on host plant resistance, the future work is urgently required to understand the complex plant-pathogen interactions under variable environmental conditions to understand the multidimensional nature of the interactions and develop climate-ready disease-resistant crop plants.

Keywords: Climate Change, Host-Pathogen Interaction, Climate Resilient Strategies.

I. Introduction

Plant diseases are among the most damaging forces impacting agricultural production worldwide. Owing to the impact of pests and pathogens, the crop production losses are in the range of 20–40 per cent (Kashyap *et al.,* 2017). Chemical and other methods of management have played a significant role in pest and disease control, but pathogens often report 10–16 per cent of the worldwide crop losses (Chakraborty and Newton, 2011). Induced by anthrogenic climate change and climate instability, new pathogens / pathotypes have arisen, crop cultivation methods have changed, and abiotic stresses have created havoc worldwide (War *et al.,* 2016). Alterations in climatic conditions are quite likely to arise in widespread occurrence of these diseases, rapid multiplication of pathogens per season, and increased ability to adapt for off-season survival, thereby increasing their health, volume and size.

The ancient Greeks (370–286 BC) stated that low-altitude crops had a high incidence of disease than crops grown at high altitudes (Ghini *et al.,* 2008). An evaluation of the effect of climate change on plant diseases is of considerable value due to nonlinear dynamic interactions between a plant, pathogen and its atmosphere (Semenov, 2009).

The main climate-change variables expected to affect the intensity and distribution of plant disease involve: temperature rises, enhanced atmospheric CO_2, inadequate rainfall distribution, drought, cyclones and hurricanes (Anderson *et al.,* 2004).

Alterations in one or more of those atmospheric factors may affect the spread and dynamics of plant pathogens 'positive, negative or neutral effects (Fuhrer, 2003). Increasing CO_2 environment increases leaf wax and epidermal thickness and contributes to physical resistance to such pathogenic agents (Fuhrer, 2003). Elevated atmospheric CO_2 leads to higher humidity within the crop vegetation and produces further favorable conditions for pathogen survival (Pangga *et al.,* 2011). Enhanced photosynthetic activity under enhanced CO_2 levels (Fuhrer, 2003) can result in more available plant biomass for colonization and pathogen multiplication.

According to Milus *et al.* (2006) *Puccinia striiiformis* f. sp. *tritici* due to the adjustment to elevated temperatures, the pathotypes emerging in the USA since the year 2000 were violent than older isolates. The global mean temperature rise of 2°C could result mild risk of late blight of potato in tropical areas with >22°C whereas increased risk in temperate areas with > 13°C (Singh *et al.,* 2013). Steplowska *et al.* (2015) analyzed the impact of temperature levels (21 ° C or 27 ° C throughout the day) on the rate of aggregation of virus and satellite RNA (satRNA) in peanut stunt virus (PSV) infected plants with and without satRNA in *Nicotiana benthamiana*, four times and observed signs of disease started to occur in plants grown at 21 ° C and were well formed in those grown at 27° C. Elad and Pertot (2014) reported that drought could increase the risk of root rot pathogens, primarily due to its negative impacts on host physiology. Sturrock *et al.* (2011) also

reinforced that an increased incidence of drought is projected to increase the risk of root pathogens, wound colonizers, and latent sapwood colonizers infecting trees. Chakraborty and Newton (2011) studied the function of rainfall in the development of *Fusarium* head blight mycotoxin in wheat, and showed that it normally declines with low and high temperatures whereas increases with increased number of rainy days and days with high RH.

Host plant resistance is the simplest and most environmentally friendly type of disease management strategies which farming communities welcome. Any adverse effects on the resilience of climate change would have significant effect on crop breeding programs as well as formulating crop systems. Changing environment can alter host – pathogen relationships and host resistance mechanisms (Pedapati *et al.,* 2016). Because of this, there would be shifts in the entire population distribution of hosts and pathogens. Some forage plants, for example, become more resistant to rust diseases with higher temperatures but wheat and oats become more susceptible with higher temperatures (Coakley *et al.,* 1999). Likewise, in both the USA and the Sahel region of Africa, the charcoal root rot caused by *Macrophomina phaseolina* has emerged as a major soybean disease (Groenewald and Crous, 2014; Fones and Gurr, 2017). The decline of oak caused by soil-borne *Phytophthora cinnamomi* has spread from southern Europe towards North along West coast of France due to increase in temperature and

humidity (Fones and Gurr, 2017). The goal of this chapter is to review the impacts of climate change on the resistance of host plants and their effects on programs for disease control. It will also provide an opportunity to target the poor links on host- interactions that can be exploited in developing successful strategies for management.

II. Emergence of New Races or Pathotypes

Current agriculture under changing climate scenario is a source of driving forces for pathogens and host plants and thereby increases peril of epidemics as well as the emergence of new aggressive pathotypes. However, there will be possibility of certain pathotypes as well as the environment is no more favourable for their survival (Webb *et al.,* 2011). Such adaptive evolution along environmental gradients has occurred in mycotoxin forming fungal species*.* Higher temperature regimes in Europe led to the substitution of certain *Fusarium* and *Microdochium* species by *Fusarium pseudograminearum* and thereby increase the risk of mycotoxin contamination (Paterson and Lima, 2010).

Similar has taken place in Canada, extremely toxigenic forms of wheat scab pathogen were evolved in existing *Fusarium graminearum* population (Ward *et al.,* 2008). Yellow rust is typically prevalent in temperate regions. But, the constant evolution of *Pst* strains and their adaptation to higher temperature pose a serious challenge to the

breeders as several major source of wheat resistance to *Pst* was broken down in recent times. For example, virulent high temperature tolerant *Pst* strain has headed up since 2000 in eastern USA (Milus *et al.,* 2009). Mounting temperature for past 11 years has augmented the virulence and aggressiveness of Race 9 of *X. Oryzae* pv. *oryzae* infecting rice having Xa7 resistance gene (Webb *et al.,* 2011). Evolution of increased aggressive strain of *Colletotricum gloeosporioides* having high fecundity was reported after 25 sequential infection cycles at elevated CO_2 (Chakraborty and Datta, 2003). Some of the cases of emergence of climate induced new races resulting in breaking down of host plant resistance are presented below.

II.1 Emergence of Ug99 Races of Wheat Stem Rust Pathogen

As wheat cultivating mega environments switch with oscillating climatic conditions such as temperature variations, abnormal rainfall patterns and rising atmospheric CO_2, there is risk of severe rust infection in varieties suffering from various biotic and abiotic stresses. Climatic vagaries have encouraged faster evolution of new rust pathotypes of novel virulence combinations in wheat stem rust which candevastate the currently resistant wheat varieties. As evident from the breakdown of Sr31 resistance gene in wheat that remained effective for over 30 years until the appearance of 'Ug99' race (Singh *et al.,* 2011). Besides, Ug 99 also harbors broad virulence spectrum against many other effective

resistance genes including Sr 24 and Sr 36 which made scientists to call Ug99 as 'Super race'. Rapid evolution of pathogen resulted in seven races in Ug99 lineage exhibiting identical DNA fingerprint, but differ in virulence patterns. Ug 99 is also called as shifting enemy of wheat due to its fast migration rate. Ug99 was first detected in Uganda in 1998 and spread quickly across different wheat-growing countries in the eastern African highlands, as well as Zimbabwe, South Africa, Sudan, Yemen, and Iran. About 90% of the wheat varieties grown across the globe are susceptible to the Ug99 group of races. It can destroy enough food supply to sustain millions of people as wheat is a major staple crop to ensure global food security.

II.2 Emergence of *Fusarium oxysporum f. sp. cubense* Tropical Race 4

Fusarium oxysporum f. sp. *cubense* is one of the most devastating soil borne fungal pathogens of banana globally. Based on tolerance to temperature, Novel race colloquially known as Tropical Race 4 (Foc TR4) belonging to unique vegetative compatibility group (VCG 01213/16) is considered to be most predominant and destructive, as it can infect not only the popular banana cultivar 'Cavendish' but also all cultivars that are susceptible to the other 3 Focs. Having stronger high temperature tolerance than the others, Foc TR4 pose global threat to banana growing countries under global warming scenario (García-Bastidas *et al.,* 2014). It originated from Indonesia and then spread throughout five Asian "Cavendish"

growing countries and Australia. Recently, its rapid ramification to Africa (Mozambique), Middle East, Indian Sub-continent and Latin America has raised major concerns in international world food security and trade. A great danger of pandemicity is expected in future as 15% of banana production is contributed by clones of Cavendish. The recent detection of TR4 in a block of Grand Naine cultivar in Faizabad district, Uttar Pradesh (26.46379°N, 81.59987°E) could pose a threat as India is one of the largest producers of bananas (Damodaran *et al.,* 2018).

II.3 Emergence and Spread of Wheat Blast

The devastating disease, wheat blast incited by *Pyricularia griseatritici* was first recorded in Brazil in 1985 (Igarashi *et al.,* 1986) and spread to the neighbouring countries and results in crop losses up to 40–100% (Maciel *et al.,* 2011). It was restricted South America until 2016 and led to outbreak in Bangladesh. Currently, wheat blast is treated as major epidemic disease and pose threat to a wheat cultivation in India (Callaway, 2016). The epidemic migration was about 15,000 hectares covering 16% of the cultivated wheat area in Bangladesh causing 100 % yield loss. The main factors promoted the risk of disease outbreak in Bangladesh outbreak in 2016 were the occurrence of ill-timed rainfall and warmer winter before harvest (Islam *et al.,* 2019). Hence, recent climate change and global warming pose escalating risk development and outburst of disease.

III. Emergence of New Pathogen and Disease Scenario Shifts

Climate change induces deep modifications in species geographic ranges worldwide (Albouy *et al.,* 2013). The change in temperature, green house gases and frequency of rainfall, storms and droughts will influence pathogen emergence or introduction in new areas. The climate change has influence on the incidence of plant disease as well as its temporal and spatial distribution. The climate change has impacts from germination and penetration of pathogen to symptoms development in its host; survival and its dispersal to new area. It is having impact in all life stages of pathogen as well as host through which it poses a challenge to many pathosystems (Ahanger *et al.,* 2013). The combined impact of biotic and abiotic stress on plants imposed by climate change would result in host vulnerability to emerging plant pathogens (Atkinson and Urwin, 2012; Gassmann *et al.,* 2016). For example, the emerging pathogen of oak caused by *Biscogniauxia mediterranen* was first reported in Mediterranean oaks and is a serious problem in Mediterranean area; It appeared as a new disease in Slovenia in 2006 of low rainfall area indicates that climate change will lead to outbreak of this disease in north Tuscany (Jurc and Ogris, 2006). Like other organisms, plant pathogens are also influenced by climate change and are expected to alter the distribution and impact on plants. Black Sigatoka or Black leaf streak disease of banana caused by *Pseudocercospora fijiensis* fungus has recently emerged from

Asian countries and is causing major yield losses in Latin America and the Caribbean countries. The study shows that the risk of infection increased by an average of 44.2 per cent across Latin America and the Caribbean banana-growing regions from the 1960s to the 2010s. Climate change favored the temperature conditions and leaf wetting periods for germination of spore and growth of spore (Bebber, 2019).

Based on climate models using projected greenhouse gas and aerosol emission projections predict a rise in global mean temperature by the year 2100 from 1 to 3.5° C (Kudela, 2009). When global warming persists, it should be believed that heat-loving plant pathogenic bacteria to increase. The optimum growth temperature for these bacteria is between 32-36 °C. The bacterial plant pathogens like *Ralstonia solanacearum, Acidovorax avenae* subsp. *avenae* and *Burkholderia glumea* have emerged as a serious threat worldwide; optimum growth temperature for this bacteria is between 32 to 36°C but grows well up to 41°C (Schaad, 2008).The alteration in temperature, wind pattern and rainfall will also alter the evolution rate of virus and its host adaptation; it causes alteration in crop grown areas of introduced species, occurrence and distribution of new weed species, abundance and activity of vectors. Changes in the geographical distribution of crops, geographic expansion of virus and its vector increases the incidence of new encounters between host and virus (Jones, 2009).

IV. Changes in Host Defence Mechanisms

The storehouse of defence compounds in plants are salicylic acid, jasmonic acid, abscisic acid, ethylene, phytoalexins and pathogenesis related proteins. The plant's reaction to salinity, extreme temperature, UV radiation and metal toxicity is controlled by the coalescent signalling of interconnecting pathways and can be of independent or dependent of abscisic acid in plants (Mauch Mani and Mauch, 2005). The interface between disease or resistance depends on the interaction between pathogen derived molecular patterns, plant receptors (surface and intracellular) and pathogen effectors, and effector-recognition factors to induce effector triggered immunity (Andre *et al.,* 2018).

IV.1 Environmental Impacts on Phytohormones

Changes in the environmental conditions confer resistance in hosts mediated through regulation of defence hormones ABA, SA or JA or ET signalling (Huot *et al.,* 2014). For example, *Pseudomonas syringe* infection triggers increase in the both ABA and SA concentrations in plants (de Torres-Zabala *et al.,* 2007). Impaired biosynthesis of ABA and signalling plants are immune to *B. Cinerea* and *P. syringe* (de Torres-Zabala *et al.,* 2007, Audenaert, 2002). Crosstalk between SA and ABA signalling pathway enhances resistance against *P. syringe* but not against *B. cinerea.* In the case of *Pythium irregulare* and *Alternaria brassicicola*, similar patterns were

found (Adie *et al.,* 2007). In *Arabidopsis*, at max temperatures (30°C) plants were susceptible to *P. syringe* due to low level accumulation SA as compared to 23°C (Huot *et al.,* 2017). The pathogen-inducible salicylic acid pathway occurs due to transition of chorismate to isochorismate (Wildermuth *et al.,* 2001) which will be inhibited at high temperature. In contrast, if Arabidopsis exposed at 4°C for more than one week, resistance to *P. syringe* infection is conferred (Kim *et al.,* 2013 & 2017) as the transcription factor, CAMTA (Calmodulin-binding Transcription Activator) triggering expression of SA-responsive gene ICS1 leads SA biosynthesis. High relative humidity controls gene expression needed for biosynthesis and signalisation of jasmonic acid (Cheng *et al.,* 2013).

Elevated CO_2 levels, slow down the photo respiratory rates and induce defense metabolism and PR genes in plants by upregulating ROS (reactive oxygen species) signalling (Graham and Amna, 2017). In C3 plants photorespiration is essential for photosynthesis which maintains high CO2 concentrations in the cells (Long *et al.,* 2006). Photorespiration pathway regulates the production of ROS compounds, plays a key role in pathogenesis. Oxidative stress signalling is activated by CO_2 leads to accumulation of azelaic acid and pipecolic acid metabolites in leaves (Weingart *et al.,* 2004).

IV.2 Impact of Environment on PTI

Pathogen-associated molecular patterns (PAMPs) triggered Immunity (PTI) is a pathway where retained microbial compounds (pathogenic or microbial related molecular patterns) are identified by localized recognition receptors (PRRs) of plant plasma membranes. MAMP microbe-associated molecular pattern triggered immunity genes trigger a signalling cascade that involves the development of protein phosphorylation, ROS, increased production of $Ca2^+$ and gene expression to stop microbial growth (Couto *et al.,* 2016). The protection mechanism known as PTI prevents the multiplication of the various non-pathogenic microbes which plants experience in the environment. The output of PTI can be affected by relative humidity and water availability. Virulent pathogenic bacterial strains also cause leaf apoplasty which causes water-soaked lesions to grow on the leaf due to infection with virulent bacterial pathogens (Schwartz *et al.,* 2017; Xin *et al.,* 2016). By holding water-soaked leaves under high humidity in the apoplast, non-pathogenic *Pseudomonads* induced high levels of PTI in Arabidopsis, bean and tobacco (Ramos, 2010). Daszkowska and Szarejko (2013) reported that as a part of the drought response, absicic acid may interact with jasmonic acid and nitric oxide and stimulated stomatal closure and the regulation of gene expression involved genes that are related to ethylene, cytokinins, and auxin signalling. Contrary to this, stomata open and ABA accumulation in stomatal guard cells decrease under high humidity (Okamoto, 2009). PTI activation results in the closure of stomata after stomatal guard cells have recognized MAMPs (Melotto *et al.,* 2006; Panchal and Melotto, 2017) to protect the apoplastus leaf from penetration of

bacterial pathogens. Panchal *et al.* (2016) indicated that PTI induces stomatal closure in Arabidopsis and bean plants under elevated humidity conditions which is an alternative form of PTI. Similarly, temperature differences or variations can alter PTI signalling. In Arabidopsis temperature of 28°C for a short period of 15 minutes, phosphorylation and expression of the PTI marker gene enhances higher mitogen activated protein kinase (MAPK) after access to PAMP shows enhancement of PTI in high temperature environment.

IV.3 Impact of Environment on ETI

Effector Triggered Immunity (ETI) is an infectivity-promoting pathogen identified by proteins comprising plant resistance (R) and NLR (nucleotide-binding domain and leucine-rich repeat) (Jones *et al.,* 2016). Many R proteins impart resistance to tobacco mosaic virus at extreme temperatures (Witham *et al.,* 1996); *Cladosporium fulvum* in tomato (Jong *et al.,* 2002); *P. syringae* in Arabidopsis; and potato virus X (Wang *et al.,* 2009). However, they do not assemble an efficient ETI at temperatures above 30°C. But Xa7 is more effective against *Xanthomonas oryzae* at elevated temperatures than at lower temperatures (Webb *et al.,* 2011). The destructive effect of high temperature on ETI could be seen in certain plants mutated for autoimmunity, due to constitutive stimulation of ETI and reactive cell death.In Arabidopsis, one popular example is snc1 mutant alleles. SNC1 is an NLR gene of Arabidopsis, in which multiple mutations induce an autoimmune phenotype and enhance immunity to *P. Syringe* but not 28°C at 22°C (Zhu *et al.,* 2010). Transcription

of the SNC1 gene leading to the expression of autoimmune phenotype of snc1 allele were suppressed due to gain-of-function allele of pseudokinase ZED1 at 22°C (Wang *et al.,* 2017). ZED1 is a protein needed for the identification of bacterial effectors i.e. HopZ1a with the ZAR1 R protein (Lewis *et al.,* 2013) andSNC1 and ZED1 proteins formed part of the same high temperature sensitive ETI pathway (Lewis *et al.,* 2013). Temperature regime length impacted ETI leading to loss of *P. syringae* effector AvrRpt2 in Arabidopsis RS2 and eventual suppression of growth of bacteria when plants were grown at 28°C for 3 weeks before infection (Wang *et al.,* 2017). Nevertheless, if plants have been acclimatized at 28°C for just 1 day, there's always development control from ETI, even if the HR cell death linked with ETI is lacking (Menna *et al.,* 2015). It thus seems that habituation at extreme temperatures for brief periods could only be the disarming aspect of the signalling pathways of the ETI. Until now it is not fully known how maximum temperature inhibits ETI. Several studies indicate that one consequence could be at the nuclear localization stage of some R proteins. High humidity can also impact the HR associated with ETI and its effect is synergized at high temperatures blocking complete HR. Both Cf-4/Avr4- and Cf-9/Avr9-dependent HR was not only delayed but also reduced at 95% RH and further Cf-9/Avr9-dependent HR was more sensitive than Cf-4/Avr4-dependent HR (Wang *et al.,* 2005). Similarly, under high humidity levels, the ETI-associated HR is impaired for bacterial effector AvrRpt2 being recognized by RPS2 in Arabidopsis (Xin *et al.,* 2016).

Nevertheless, in some accessions to Arabidopsis, under conditions of high humidity, ETI-associated pathogen population restriction is still evident (Velasquez *et al.,* 2017).

IV.4 Impact of Environment on Quantitative Resistance Traits

Resistance QTL may often be observed only under certain conditions of the environment (soil, atmosphere, pathogen population), or in particular genetic backgrounds or cross forms (Pilet *et al.,* 2017). In wheat, the Yr 36 gene shows partial resistance to many *Puccinia striiiformis* races under high temperature (35°C) conditions due to the presence of kinase enzyme containing START domain (Fu *et al.,* 2009) and also induces resistance to *P. striiiformis* by plants with Sr 13 gene (Zhang *et al.,* 2017). In rice blast pathogen, the highest resistance level was reported at 22°C and also increased Pi54 expression and WRKY45. However, at 32°C some resistance level with low expression levels of Pi54 and WRKY45 which indicated reduced aggressiveness of the pathogen at higher temperatures that resulted in resistance (Madhusudhan *et al.,* 2019).

IV.5 Impact of Environment RNA Interference (RNAi)

Plant virus interactions are most affected by temperature. Many researchers suggested that at low temperature, both virus and transgene triggered RNA silencing mechanisms were inhibited. But in contrast, Roman *et al.* (2013) reported that RNAi remained active at 4°C for grapevine cultivation. In grapevines cultivated between 26°C and 4°C, the

siRNA rates have consistently remained steady, whereas in Arabidopsis grown at 15°C siRNA were highly decreased and nearly undetectable at 4°C. The presence of RNAi suppressors in plant viruses exhibits mechanism of rapid defence in hosts that are affected by temperature change. For example, at 15°C, RNAi mediated defences were expressed in *Nicotiana benthamiana* against Cymbidium ringspot virus infecting orchid but not at 21°C and 27°C (Szittya *et al.,* 2003).

IV.6 Response and Durability of Resistant Genes

Plants are equipped with many complex, highly efficient mechanisms of protection to detect and combat the majority of attacks by various potential pathogens. The host resistance to plant pathogens is the result of a cascade of events caused by resistant genes, major or minor. Large resistant genes found in many types of plants work gene-for-gene. There is a corresponding avirulence gene in the pathogen for each resistance gene at the host (Flor, 1971). Only the corresponding avirulence gene present in the pathogen against the host's resistance gene may initiate the hypersensitive reaction (HR) which leads to incompatibility. Resistance and avirulence, susceptibility and virulence, respectively, are inherited in a dominant and recessive manner. The HR results in complex interactions between the resistance products and the avirulence genes at the cellular level.

Host plant resistance requires the deliberate use, alone or in combination, of resistant crop

varieties to fight plant pathogens. A major plant breeding aim is to establish cultivars resistant to one or more pathogenic agents. The breeders have historically used source of resistance from the resistant varieties or wild crop relatives to introgress to produce disease-resistant cultivars. For many countries, including India, many R genes have been detected and integrated into crop cultivars (Sundaram *et al.,* 2008; Gururani *et al.,* 2012; Lalitha Devi *et al.,* 2013). Climate change, especially high temperatures, results in a breakdown of immunity and R-gene products, rendering plants susceptible to pathogen attack (Coakley *et al.,* 1999; Garrett *et al.,* 2006). The wheat variety transformed with Yr36 at high temperatures (25-35 ° C) confers resistance to stripe rust but is susceptible to pathogen at low temperatures (15 ° C) (Uauy *et al.,* 2005). Reducing the breakdown of resistance resilience in plants, a good understanding of the pathogen population and its distribution before formulating sustainable disease resistance strategies; deployment of varietal mixtures of major R genes rather than single R genes; multiple gene deployment through Marker Assisted Breeding (MAS) programs; single / multiple disease resistance; and gene pyramiding to increase the durability of resistance genes. For example, under high temperature, IRBB4 carrying Xa4 gene and IRBB7 carrying Xa7 showed reduced resistance level and high resistance level, respectively. However, due to the complementary effect of Xa4 (Dossa *et al.,* 2020) when both genes (Xa4+Xa7) were pyramidized in IRBB67 increased resistance level under high temperature could be

relized.In addition, host resistance combined with other management activities, such as crop rotations and judicious fungicide applications, may also increase the resistance's longevity.

V. Climate Resilient Host Plant Resistance

Global climate change will lead, due in part to, to complex, extreme, and location-specific impacts on agricultural production in the immediate future. Changes in pathogen dynamics and invasiveness, caused by climate change. Alterations in climate are commonly expected to result in a rise in average temperatures of about 1–2 ° C by 2100, as well as a rise in the frequency of extreme events like high temperature, storms or drought (Cook *et al.,* 2016; Kirtiman *et al.,* 2013; Coolins *et al.,* 2013; Albouy *et al.,* 2014; Seebens *et al.,* 2015). These developments can affect the appearance of new pathogenic races in new areas. Climate increases host resistance, as well as the virulence of many pathogens (Garrett *et al.,* 2011). It also drives the distribution of species, both grown and wild, to alter patterns of trade (Albouy *et al.,* 2014; Seebens *et al.,* 2015). Some of the lesser pest species have already gained serious status in recent years due to fluctuating climatic conditions. Consequently, more frequency of high temperatures, storms or droughts, a quantum leap in the use of insecticides, a shift in the pattern of virulence, the proliferation of pathogens in new areas was expected (Rakesh *et al.,* 2018).The major factors likely to influence the severity and

spread of plant disease include: elevatedCO2, indiscriminate distribution of rainfall, elevated humidity, drought, cyclones and hurricanes, and warmer winter temperatures (Berry *et al.,* 2002; Anderson *et al.,* 2004). Changes to some (or all) of these factors can influence the spread and biology of different plant pathogens (Coakley *et al.,* 1999; Fuhrer, 2003).

V.1 Interaction Among Biotic and Abiotic Stress Tolerance Genetics

The crops are continuously faced with both biotic and abiotic stresses thus raising their productivity. Plants react differently to multiple stresses than how they do to individual stresses, although the response to simultaneous stresses is a much more complicated scenario, involving various physiological, molecular and cellular adaptations. Plant explicitly reacts when faced with more than one stress at the same time, and the response cannot be predicted based on the reaction of the plant to individual stress. Whether simultaneous stresses are either antagonistic, synergistic or additive, is not well known, causing more or less sensitivity to a specific form of stress. Plants can withstand concurrently both abiotic and biotic stress stimuli as evidenced by the link between the responses to these two stresses (Atkinson and Urwin, 2012). One potential consequence of simultaneous stress exposure is that plants that can cope with one stress could defend themselves against other stresses. This phenomenon was referred to as cross-tolerance, showing a good regulatory

mechanism allowing plants to quickly adapt to a changing environment (Suzuki *et al.,* 2012). This crosstalk can be synergistic or antagonistic and include phytohormones, transcription factors, kinase cascades, and reactive oxygen (ROS) species (Anderson *et al.,* 2004). Achuo *et al.* (2006) reported that increase in the ABA content of tomato leaves under drought stress also simultaneously increased resistance against *Botrytis cinerea*. However, salt stress decreased susceptibility to *Odium neolycopersici* but not to *Botrytis cinerea*. This variation could be due to different patterns of gene expression under these stresses. Production of ROS signalling molecule after the sensation of stress although high levels of ROS lead to cell death; lower levels were responsible for controlling the stress responses of the plant (Choudhury *et al.,* 2013). ROS is primarily involved in signalling in biotic stress. Again, this may reduce the oxidative stress caused by abiotic stress (Kissoudis *et al.,* 2013). Mitogen-activated protein kinases (MAPK) signal molecules which are activated by the stimuli of stress. MAPKs are involved in multiple stress responses with possible functions in combination of biotic and abiotic stresses. Molecular patterns associated with pathogen (PAMPs) such as flagellin activated MAPK cascade to create pathogen response signals. Additionally, MAPKs viz. MPK3, MPK4, and MPK6 were expressed against different abiotic stresses (Chinchilla *et al.,* 2007).PR genes were expressed when a plant was subjected to abiotic stress that ensured resistance to disease.PR proteins are essential for plant protection to pathogens, and when

plants are attacked their expression is strongly up-regulated. Abiotic stress can result in the expression of different transcription factors (TFs) in plants such as No Apical Meristem ATAF and Cup-Shaped Cotyledon (NAC), C-repeat Binding Factors (CBF), and abscisic acid (ABA) mediated MYB. Even though the specific role of ABA in the regulation of biotic stress tolerance in abiotic stress is still a matter of debate, though resistance was enhanced to biotic stress following abiotic stress in some specific cases. This is due to the over-expression of TFs which induce PR gene up-regulation (Seo *et al.,* 2010). Plants understand the signals of biotic and abiotic stresses, and activate different molecules and those signals that are specific to both stresses will contribute to the protection against a specific stress combination and thus improve plant's resistance.

V.2 Breeding Technologies for Climate Smart Crop Cultivars

Farmers are introducing new varieties based on yield, efficiency and agronomic properties. Accordingly, crop adaptation to climate change will result primarily from breeding programs integrating abiotic and biotic tolerance and resistance features that promote plant resistance and pathogen susceptibility. Core elements of climate change adaptation are (i) exposure to other field germplasm currently experiencing climate change consequences; (ii) rapid breeding cycles for the generation of new environment-friendly cultivars; (iii) assessment of new cultivars under the full spectrum of environmental conditions and (iv) seed systems.

a. Access to Elite Germplasm

Access to genetic diversity is supported by ex situ plant germplasm collections of National Agricultural Research Systems (NARS) and international gene banks. Such collections mainly consist of landraces, which are essential sources of stress tolerance. Introduction of different traits into cultivated crop varieties by marker-assisted selection, gene pyramidization, QTL breeding, whole genome-wide mapping study of associations and other approaches. There have been several attempts to integrate both abiotic and biotic resistance from wild germplasm into cultivated plants. King *et al.* (2013) introgressed entire genome of wild grass species into forage grasses. An advanced rice breeding line evolved with two insect resistance genes, 6disease resistance genes and two main QTLs imparting tolerance to salt and flood (Das and Rao, 2015). Many breeding approaches are unable to explicitly use accessions as donor parents because of the yield penalty typically associated with it. Elite varieties from various climates in their own target regions are important building materials for the future climate. Some public collections of germplasm acquire and retain older elite enhanced varieties under different climatic conditions. Small national programs and regional seed companies, on the other hand, typically lack the international connections to share germplasm among nations. The new elite materials that are constantly being produced by breeding programs are strongly focused on developing commercial varieties with improved abiotic and biotic tolerance available for use by national programmes.

b. Non Molecular Breeding Methods

One of the most successful ways to grow new varieties to mitigate the impact of climate change is to establish shorter and faster breeding cycles. Such methods may help to resolve biotic and abiotic stresses in developing cultivars.

Single seed descent method, this is an alternative approach to the pedigree process used by cereal breeders for decades. This approach accomplished in the field faster than under normal conditions mainly by controlling plant growth conditions so that flowering and seed set. The advantages of this approach are technological simplicity, speed, less resource requirement and low cost (Fahim *et al.,* 1998).

Doubled haploids formed when haploid cells of pollen grains undergo doubling of the chromosome. This approach instantly forms entirely homozygous lines within a short time span (Mishra and Rao, 2016). This is achieved in organisms adapted to tissue culture. This approach has been used for years in rice breeding (Pauk *et al.,* 2009) for the development of many varieties.

CIMMYT originally introduced the shuttle breeding method in the Wheat breeding system. Every year, this device permitted an extra generation by using a specific field position. The advantage of this method was improved diversity, as the field sites conflated with a broad variety of different diseases and atmospheric conditions (Ortiz *et al.,* 2007). Subsequently, due to the enforcement of intellectual property rights and the security of the national germplasm, there were many logistical issues, primarily about the flow of seed across international borders. Under NARS, however, this practice of developing initial generations through crossing is conducted centrally and then shared among partners across agro-ecologies for further selection so that region specific selections are made. This method can lead to the release from a few crosses of more number of region- varieties.

Backcross breeding is a method widely used to insert a desired gene into a famous cultivar. The parent used for backcrossing has many desirable traits but is deficient in only a few characters. MAB effectively identifies the target gene and allows for the preservation of the original traits with the same variety (Collard and Mackill, 2008). This approach is often used to combine several genes into a single recipient that is generally referred to as pyramiding genes. Improving stress tolerance in rice has been promoted as a target for rice breeding and this strategy has been made an application to improve abiotic stress tolerance in rice (Gregorio *et al.,* 2013). It is worth noting that an evaluated gene(s)/QTL(s) is a basic requirement for the system's implementation.

Genomics-based approaches extend the pool of genetic diversity open to breeders by providing incomparable incentives to tap into wild crop relatives (Tuberosa *et al.,* 2011). Especially under abiotic stress condition, genomic selection may offer the most appropriate solution to the required level of yield potential. Marker assisted selection is

a viable choice for QTL, while QTL cloning would be encouraged by increased use of reliable phenotyping (Araus and Cairns, 2014), sequencing (Imelfort *et al.,* 2009), and recognition of candidate genes by the principle of omics (Gupta *et al.,* 2013). Cloned QTL would provide better conditions in wild germplasm for novel alleles that lead to abiotic and biotic stress tolerance (Salvi *et al.,* 2007). Taking innovative genomics technologies to counter the adverse impacts of climate change would remain a challenging undertaking. This includes a multidisciplinary approach to the production of crops that are more climate sensitive.

Big data analytics is the method of exploring multiomics datasets and developing smart apps in the creativity of plant breeding. The method involves three main elements - data collection, processing, and inference leading titbits into the core genetics and streamlined breeding methods. Eight essential omics big data attributes are Duration – duration of picture, detector and genome content; acceleration – pace at which information is absorbed and extracted; diversity – diversity of information, including organized, semi-organized and unorganized data; variability – information with rapidly changing structure and meaning; accessibility – visible viewing of data; Reality – data quality, precision and reliability; utility – obtaining keen insight or valuable knowledge from records avoiding loss of information; and perplexing – modelling effectiveness. Vexing is closely linked to the Next-Gen AI architecture, which incorporates human intelligence and

profound learning for comprehensive and dogmatic analytics.

VI. Conclusion and Future Prospects

Recent changes in climatic conditions have posed potential threat to global food and nutritional security, including impacts on plant diseases and emergence of new diseases/pathotypes/races. These situations call for global research efforts in a cohesive manner to evolve agro-ecology based solutions to different crop production systems. Some of the efforts are shown below.

- The difference in the influence of environmental factors such as temperature, relative humidity, CO_2 etc. on the production of diseases is most evident based on plant and pathogen species. But it is very difficult to estimate a general outcome for all illnesses.

- To study plant immunity and pathogenic virulence systems, optimum and extreme environmental conditions are to be established to establish the deviations in plant immunity or pathogenic virulence as altered by deviant environmental conditions. The statistical relationships as used in the metabolic theory of ecology (MTE) may be extended to these systems also to determine the impact of environmental factors on human diseases (Altizer *et al.,* 2013).

- MTE works by integrating the metabolic rate, mass and temperature of organisms (Brown *et al.,* 2004). This

information will be used to effectively predict the response of host plants and plant pathogens to the ever changing climatic conditions.

- There are important differences between the lack of field-scale, cellular and genomic data on animals. Thus, through assessing the impact of pathogen through climate change at a cellular or genetic stage, it can provide insight into the prevalence of particular plant disease in future environment, thus helping to introduce potential management opportunities.

- Study of long-term datasets would help improve the ability to mitigate new threats presented by climate change for emerging pathogens and help to prevent any potential emergence of pathogens that could be motivated by climate change scenarios.

- Basic work on plant immune signal reduction under abiotic stress conditions will provide a brief overview of environmental vulnerabilities that will provide the basis for the creation of a new generation of plant varieties that will be more resilient to environmental variability. Recent attempts have been successful in reducing the harmful effects of the immunity-related gene expression (Xu *et al.,* 2017).

- Future breeding programs will aim to integrate abiotic and stress tolerance for new enhanced varieties that encourage plant resistance and disadvantage pathogen

virulence. These characters can mostly be found in near wild relatives of crops grown in the hotspot areas. Traits may be implemented by gene pyramiding, marker-assisted selection, a study of the whole genome-wide association mapping (GWAS) and other biotechnological approaches. Other approaches include the use of crop variety mixtures which cover a range of climatic and pathogenic conditions and thereby reducing the blast incidence and also almost doubled yields in rice (Zhu *et al.,* 2000).

- The public's refusal to consider genetically modified crops is a major concern about the genetic modification of plant traits. But advent of CRISPR (Clustered regularly interspersed short palindromic repeats) technology helps to minimize these concerns. New technologies will also allow us to predict potential epidemics accurately by using nanosensors to detect field-based pathogen populations (Kwak *et al.,* 2017) well before it reaches the epidemic process.

- High-throughput phenotyping technology is a promising method for identifying disease-resistant and environmental stress tolerant plants (Fahlgren *et al.,* 2015). Microbe-mediated host plant resistance modulation has been reported against abiotic stresses (Rolli *et al.,* 2015). Unleashing the potential of understanding the plant microbiomes could help in both disease suppression and possible

enhancement of environmental tolerance.

- The limited research efforts with a few plant species and biotrophic pathogens to understand impact of climate change should be expanded to more host-pathogen systems to arrive at meaningful conclusions.

- Worldwide, only comprehensive studies have been carried out to date on the environmental impacts of major diseases. A few scientific research works are conducted on plant diseases under practical field conditions that imitate climate change and this seriously limits the creation of options for enhancing crop tolerance or improving climate-change disease management practices.

- Future research aimed at tackling the impact of environmental factors on plant disease would rely on the complex existence of the prevailing conditions. Controlled growth chambers that are similar to the complex situations to which plants and pathogens are exposed in nature are required to replicate and validate field trials and laboratory results. Future studies of plant-pathogen interactions will therefore be focused on multi-faceted interactions of host-pathogen-environment systems to represent natural ecosystems and farm fields.

- Risk analyzes of disease should be conducted properly on the basis of host-pathogen interactions and more focus should be put on host reaction

and adaptation research to understand how the imminent climate change could impact the etiology of plant disease.

VII. References

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