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Wheat blast disease: Bangladesh and global perspectives of blast resistance

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Abstract

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Fearsome wheat blast disease expanded its radius from Latin America to Bangladesh in 2016 with higher degrees of destruction efficiency. In 1985, Brazil was the first hotspot and consecutively Paraguay, Argentina, Bolivia were affected by the wheat blast fungus. Blast fungus *Magnaporthe oryzae* is under pyriculariaceae family with three-celled, pyriform, hyaline conidia. Not only wheat and rice are affected by the blast pathogen but also around 50 grass species can be affected and act as host, but the fungus pathotype is specific and distinct for each plant species. Morpho-biometrical analysis revealed similarity between the *Magnaporthe oryzae* pathotype *Tritici (MoT)* strain of Bangladeshi and Brazil. Through extensive molecular genetics and genomics study unfolded five resistant genes, among those *Rmg2*, *Rmg3*, and *Rmg7* lost viability but *Rmg8* and *RmgGR119* still have resistance. In addition, 2NS translocation from *Aegilops ventricosa* in wheat reports resistance against *MoT*. CIMMYT based Milan variety is regarded as a resistant variety and plant breeders are trying to develop new resistant varieties. But the main problem regarding blast pathogen is breakdown of resistance and evolving virulent races consecutively which is fueled by global warming. A wide range of molecular markers can potentially be used for blast resistance study. Utilization of medium to high-throughput markers like SSR, InDel and SNP gave pace in blast resistance study. Along with that, allele mining has potentiality for finding out source of resistance. In addition, gene pyramiding will play a vital role in introgression of multiple resistant genes into a superior wheat lineage. In future, high-throughput marker technology along with cutting-edge gene editing technology will play a pivotal role. Furthermore, the collaborative research in Bangladesh indicates that international scientific community has taken wheat blast as a serious issue.

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Introduction

From the beginning of agricultural revolution, some terrifying crop diseases appeared in our planet as epidemic that resulted in catastrophe like famine. As for example, the great Irish famine in 1845 late blight disease outbreak in potato where about one million Irish folks died of starvation that estimated approximately 12% of the total population and eventually 1.9 million European people migrated to America as refugee for their survival (Encyclopedia Britannica, 1999). Then Bengal famine in 1943 due to Brown spot disease outbreak in rice caused 40-90% yield reduction and that resulted in death of about two million people by starvation (Gunnell, 1992; Padmanabhan *et al.*, 1973).

In last few decades the intensity of fungal diseases has increased gradually (Fisher *et al.*, 2012). Blast disease is a fungal disease, for which scientists have become concerned and dwelling on to confront it for the sake of mankind. In Latin, blast is called as “Brusone”. Fungus named *Magnaporthe oryzae* (syn. *Pyricularia oryzae*) under pyriculariaceae family is the causal organism of blast disease (Couch and Kohn, 2002). Blast disease has a devastating influence on the yield and production of rice (Skamnioti and Gurr, 2009). Likewise, in wheat the

destruction efficiency of this fungus is beyond word because the crop loss was between 40 and 100% in Latin America (Kohli *et al.*, 2011; Goulart and Paiva, 1990).

Blast is a disease of major cereal belonging to poaceae family members. Rice is the staple food for more than half of the population of the world (Skamnioti and Gurr, 2009). In contrast, wheat is providing 20% calories and protein worldwide and especially 50% in developing countries (CSISA, 2014). Around 531 calories person⁻¹ day⁻¹ was supplied by wheat in the year of 2005 (FAOSTAT, 2010). As it is a disease of principal cereal crops such as rice and wheat, therefore it can demolish the food security of millions of inhabitants of this globe (Fisher *et al.*, 2012; Pennisi, 2010; Liu *et al.*, 2014). In addition to rice and wheat 50 grass species may be affected by this pathogen (Ou, 1985). High degree of host selectivity is present in *M. oryzae* species. (Klaubauf *et al.*, 2014; Kato *et al.*, 2001). *M. oryzae* from rice is genetically distinct from isolates infecting wheat (Urashima *et al.*, 1993; Prabhu *et al.*, 1992; Urashima *et al.*, 1999; Farman, 2002; Faivre-Rampant *et al.*, 2008; Tufan *et al.*, 2009; Maciel *et al.*, 2014; Chiapello *et al.*, 2015; Yoshida *et al.*, 2016). Blast fungus has been classified into some pathotypes according to its crop-specificity, viz., rice (*Oryza*

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pathotype), wheat (*Triticum* pathotype), ryegrass (*Lolium* pathotype), foxtail millet (*Setaria* pathotype) and so on (CIMMYT, 2016).

Wheat blast primarily attack on spikes; the affected spikes become bleached and that results either deformed seed or no seed development. This disease may attack the highly susceptible line at the seedling stage under inoculated condition (USDA, 2013). The highly affected wheat head can be dead and as a result, drastic yield reduction may happen. So the most common identifiable symptom is bleaching of spikelets and entire head at the premature stage (Igarashi, 1990; Urashima et al., 2010; Malaker et al., 2016).

Blast fungus is an ascomycete fungus which has pyriform macro-conidia with an approximate size of $20 \times 10 \mu\text{m}$. Macro-conidia are generated on conidiophore. In a favorable environment, macro-conidia germinate and appressorium is produced which remains at the apex of the germ tube. Further, an infection peg initiates and enter into the plant tissues. The appressorium is bowl-shaped and melanin is present in the wall of appressorium (Kato, 2001). The three-celled pyriform conidia get attached tightly to plant surface using spore beak mucilage which is produced by conidium hydration (Howard and Valent, 1996). Ascospores and micro-conidia are also formed in case of sexual reproduction. Although sexual reproduction has not been observed in nature but some strains follow sexual reproduction in controlled condition (Yaegashi and Udagawa, 1978). The sexually fertile blast isolates of wheat are capable of producing functional ascospores in suitable condition. Ascospores are generated in unordered asci and 'perithecia' named fruiting body bears the asci (Urashima et al., 1993). The fertile isolate also produces sickle-shaped, minute micro-conidia having the length of 6.0 micrometers and the breadth of 0.7 micrometers. From phialides, the micro-conidia are produced and under favorable conditions conidia germinate (Chuma et al., 2009). Due to polycyclic in nature, blast fungus is capable of producing spore repeatedly within seven days under wet and hot weather (Boddy, 2016). The whole genome sequence revealed that this filamentous fungus has 7 chromosomes with 40.3 Mb genome size bearing 11,109 protein encoding genes (Dean et al., 2005).

For the outbreak of blast disease the environmental condition is one of the key factors. Accurate weather condition which triggers the epidemic is not clear, but most of the blast epidemic happened in wet weather. It is observed that continuous rainy days with a mean temperature between 18- 25°C during the flowering stage, accompanied by hot, humid, sunny weather is responsible for blast epidemic (Kohli et al., 2011). In controlled condition, at 30°C the potency of blast disease rises and that is enhanced by a prolonged wetting period. A 25°C with lower wetting period lesser than 10 hours dwindled the intensity of blast disease. By contrast, 25°C temperature accompanied by 40 hours of

wetting increased the disease potency which exceeded 85% (Cardoso et al., 2008). Global warming is one of the significant reasons for dissemination and development of blast disease (Kholi et al., 2011).

Dispersal of blast fungus may be occurred by seed (Goulart and Paiva, 1990). But the role of seed in epidemic development is very trivial because airborne conidia from various alternative host infect the spike of wheat (Prabhu et al.1992; Urashima et al., 1993). Certain grass weeds (*Eleusine indica*, *Echinochloa crusgalli*, *Brachiaria plantaginea*, *Cenchrus echinatus*, *Pennisetum setosum*, *Rhynchelytrum roseum*, *Hyparrhenia rufa*, *Digitaria sanguinalis*) are alternative host of *Pyricularia* but their role in epidemiology are not presumed properly (Prabhu et al., 1992). Considering these facts the present review was attempted to overview the perspectives of wheat blast resistance status globally and future prospects of utilizing molecular marker technology and genomics to combat this disease.

Reports of blast disease

In 1985 blast of wheat was first identified in Brazil, Parana province was the hotspot (Igarashi et al., 1986). In 1996, first epidemic occurred in Bolivia (Barea and Toledo, 1996). Consecutively, Paraguay and Argentina were attacked by wheat blast disease and resulted in 70-80% loss of total production (Alberione et al., 2008; Viedma and Morel, 2002). Due to the potency of *Magnaporthe oryzae* pathotype *Triticum* (*MoT*), some part of Latin America abstained themselves from cultivating wheat (Callaway, 2016). In 2011, a blast affected spikelet was found in an experimental field of USA possibly due to host jump in the wheat spikelet (Callaway, 2016).

In February 2016, wheat blast disease was reported in Asia for the very first time. Local authorities and the media reported about massive outbreak of wheat blast in Bangladesh (Callaway, 2016). The disease symptom of wheat blast was first noticed in Chuadanga and Meherpur district in mid-February in Bangladesh. This terrifying disease spread to the adjoining four districts within two weeks and in addition a coastal district named Bhola, far apart of those four districts, was reported to be affected by wheat blast (The Prothom Alo, 2016; Islam et al., 2016). Due to wheat blast epidemic, around 15000 ha land was affected which is almost 3.5% of total wheat coverage in Bangladesh and that incidence dwindled total wheat production by 15% in 9 districts (Islam et al., 2016; Malaker et al., 2016; The Daily Star, 2016a). Plant pathologists of Wheat Research Centre (WRC) of Bangladesh Agriculture Research Institute (BARI) have predicted that there is a risk of spreading this disease in China, India, and Pakistan whilst those countries occupied the position of second, third and seventh position, respectively in wheat production (Islam et al., 2016; Index Mundi, 2016).

The current wheat production trend can cope with the demand up to 2020 and in 2050 the yield gap will be

around one ton ha⁻¹. Along with the yield gap, evolving new pathogen race, pest, and climatic instability will increase the risk of reduced food production and tends to food insecurity. Various studies are supporting this phenomenon and evolving new virulent strains of *Phytophthora infestans*, *Puccinia striiformis* and *P. graminis* are the evident examples (Fig. 1, Mondal *et al.*, 2016; Garrett *et al.*, 2006; Hovmoller *et al.*, 2008; Singh *et al.*, 2011; Cooke *et al.*, 2012; Bebbler *et al.*, 2013). So, it is urgent to develop new wheat varieties with durable blast resistance.

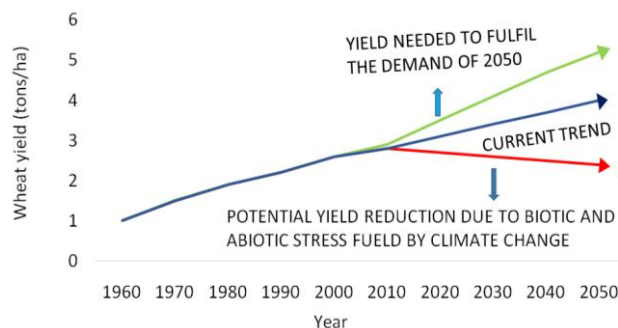


Fig. 1. Overall scenario of global wheat production trend (Redrawn from Global Rust, 2016)

Resistance research for blast disease

After first blast outbreak in 1985 in Brazil, scientists started searching for sources of resistance for confronting this terrifying disease but the way was much harder than the scientists thought (Urashima *et al.*, 2004; Prestes, 2007; Cruz *et al.*, 2010, 2016). Previous studies concluded that, the genetic basis of resistance is not well defined for large-scale variation in virulence within blast fungus (Urashima *et al.*, 2004). Some Brazilian cultivar like IPR 85 and CD 113 and BR 18 showed the moderate level of resistance against blast, while Bolivian cultivar named Paragua CIAT and Parapeti CIAT showed a comparatively higher level of resistance. But cultivar named Milan derived from CIMMYT (International Maize and Wheat Improvement Center) line showed the highest level of resistance (Kholi *et al.*, 2011).

The resistance against blast pathogen so far made is based upon R gene. The main problem based on R gene resistance is “breakdown of resistance” due to the high level of pathogenic variance within blast pathogen (Kiyosawa, 1982; Leach *et al.*, 2001). Genetic studies showed that wheat blast pathogen (*Magnaporthe oryzae Tritici*) postdate a gene-for-gene relationship alike rice blast patho-system (Silué *et al.*, 1992; Anh *et al.*, 2015). Though dozens of R genes have been identified for rice blast but in wheat, the range of identified R genes is very narrow (Liu *et al.*, 2014; Cruz *et al.*, 2016). But few R genes have been identified by scientists. “*Rmg1*” (Rwt 4) is responsive against *Avena* isolate but not for *Triticum* isolates (Takabayashi *et al.*, 2002). Then “*Rmg4*”, “*Rmg5*” showed resistance to *Digitaria* isolate but not against *Triticum* isolate (Nga *et al.*, 2009). “*Rmg6*” was ineffective against *Triticum* isolate but responsive

against *Lolium* isolate (Vy *et al.*, 2014). Thus, it is evident that these four genes are inappropriate for resistance against wheat blast disease. But in opposite direction four R genes have been identified which are responsive against *Triticum* isolate. “*Rmg2*”, “*Rmg3*” were identified from a common wheat variety named Thatcher (Zhan *et al.*, 2007) and previously these two R genes showed resistance in seedling stage but a later study revealed, these two resistance genes lost the resistance status (Anh *et al.*, 2015). Afterwards, *Rmg7* was identified from tetraploid *Triticum dicoccum* but the astute *MoT* strain has overcome the R gene (Cruz and Valent, 2017). Another R gene has been identified named as “*Rmg8*”, derived from hexaploid wheat. This “*Rmg8*” gene is a dominant gene showing high resistance against *Triticum* isolate *Br48* and occupying the long arm of 2B chromosome (Anh *et al.*, 2015). Along with *Rmg8*, Wang *et al.* (2018) found another wheat blast resistance gene in a local landrace *GR119* that gene was designated as *RmgGR119*. In *GR119* the cumulative effect of *Rmg8* and *RmgGR119* gave a strong blast resistance status (Wang *et al.*, 2018).

During studying wheat head resistance trait Cruz *et al.* (2016) have found a wild chromosome segment (2NS translocated from *Aegilops ventricosa*). In 2014 and 2015, it was tested in Bolivia and scientists concluded that this 2NS chromosome segment is resistant against wheat head blast (Cruz *et al.*, 2016). CIMMYT based variety Milan containing 2NS segment showed resistance against wheat blast (Cruz *et al.*, 2016). Thus, the contemporary resistance research in wheat blast is *Rmg8*, *RmgGR119* gene and 2NS translocation based. From the previous study, it is distinct that “breakdown of resistance” may occur of this resistance genes or segment and new virulent pathogen may evolve. In 2016, epidemic happened in Bangladesh and this *MoT* strain was more virulent than before (CIMMYT, 2016). So, searching for new resistance gene in unexamined genotypes, landraces, weediforms and close related species is an urgent need. Plant scientists have to do this before the evolution of this deadly fungus, otherwise, the world will face a catastrophe.

Molecular genomics and genetics for blast disease resistance

Studying molecular genomics and genetics explicitly in wheat is the prerequisite for developing blast disease-resistant durable cultivar. QTL identification, QTL mapping, gene pyramiding, Allele mining for Marker assisted selection (MAS), Marker-assisted backcrossing (MABC) using molecular markers and relevant biotechnological approaches are the probable approaches for confronting wheat blast.

Considering the interaction between resistance gene(s) and pathogen reproduction, blast resistance can be stratified into two categories, one is complete resistance and another is partial resistance. Though complete resistance is monogenic (not durable in general), single

R gene is responsible for resistance and complete resistance is coined as qualitative resistance. Complete resistance occurs due to the incompatibility between fungus strain and host, as a result, reproduction of fungus restricted (Wang *et al.*, 1994). In rice, Ashkani *et al.* (2015a) successfully characterized and cloned 22 rice R genes which refer to complete resistance. But the lower durability is the main shortcoming of the monogenic R gene based resistance (Cruz and Valent, 2017). In another direction, partial resistance is a quantitative attribute and non-race specific controlled by many minor genes and every minor genes cumulative effect results in resistance. Quantitative Resistance Loci (QRL) controlled the partial resistance and in partial resistance, the pathogen reproduction is dwindled due to a limited interaction between host and pathogen (Wang *et al.*, 1994; Young, 1996). In rice, the breakdown of resistance occurs after a few years due to *M. oryzae* overcome the virulence and quantitative resistant loci can be a possible source for durable resistance against the blast pathogen and previously QRL detection was used for identifying resistant genes against blast (Song and Goodman, 2001; Wang *et al.*, 1994; Fukuoka and Okuno, 2001; Miyamoto *et al.*, 2001; Tabien *et al.*, 2002; Zenbayashi *et al.*, 2002; Chen *et al.*, 2003; Sallaud *et al.*, 2003; Talukder *et al.*, 2004; Wu *et al.*, 2005; Ashkani *et al.*, 2013a,b). So, for tackling blast epidemic for a short period, monogenic R gene is one of the probable options which can confront blast disease. In contrary, for durable resistance introgression of Quantitative Resistance Loci (QRL) will play a vital role in the blast resistance breeding program. Moreover, if a cultivar contains both monogenic and polygenic resistance the durability, stability will be far better compared to any resistant cultivar but in practice that would be challenging.

Allele mining is one of the potential ways of identifying blast resistant genes. Allele mining used for identifying a target allele of gene using the broad information related that specific gene from a broad spectrum germplasm and this technique has the higher potentiality for crop improvement (Ashkani *et al.*, 2015a). Generally, local landraces and wild relatives are the sources of useful alleles (Tanksley and Nelson, 1996). Commonly two approaches are being used for extensive allele mining one is EcoTilling and another is sequence based allele mining. EcoTilling is comparatively easier and cost-effective than sequence-based allele mining (Kumar *et al.*, 2010; Ashkani *et al.*, 2015b). Allele mining consists of identification of allele, allelic variation identification, characterization of allelic variation, and identification of haplotype, studying haplotype diversity, evolutionary relationship study, and analysis of similarity and development of molecular markers for identifying and differentiate a specific allele from one another (Ashkani *et al.*, 2015b). So identifying resistant allele by using allele mining is a distinct way of getting resistance from unexamined varieties, landraces, and wild cultivar.

Furthermore, gene pyramiding is another distinct way of getting sustainable resistance against blast. Gene pyramiding is cumulating genes in a single line. Various genes are identified in different parents then accumulated into a single genotype. Gene pyramiding technique is broadly used in developing disease and pest resistance durable cultivar (Ashkani *et al.*, 2015a). For instance, many R genes refer resistance against blast pathogen but could not withstand due to break down of resistance. If all the R genes are introduced in the same genotype, the resistance will be far better than a single R gene controlled genotype and it will give a sustainable solution. In rice blast disease, gene pyramiding considered as one of the best ways for getting long-lasting resistant cultivar (Koide *et al.*, 2010). This gene pyramiding can be accelerated by using marker-assisted selection where the molecular markers are commonly used for identifying the desired alleles and recombining all genes properly into a single genotype (Joshi and Nayak, 2010). Finally, it can be stated that identification of QTLs, allele mining and gene pyramiding are the sequential activities to develop genotypes with blast resistance. Developing and utilization of molecular markers is the useful way of screening, identification, and characterization of blast resistant gene.

Potential application of molecular and biotechnological tools for blast disease resistance variety

For improving disease resistance in crop, current agricultural system follows three fundamental principles. The first approach is improving cultural practice for crop production. The second approach is using conventional breeding or marker-assisted breeding for developing disease resistance cultivar and the third approach is the direct insertion of resistance gene into a superior cultivar, it can be also coined as 'genetic modification' of a crop (Baulcombe, 2004). Marker assisted selection has a potentiality for screening and developing resistant cultivar. Some other biotechnological tools utilize specialized promoters where modification of target protein structure is the key for transgenes' performance (Helliwell *et al.*, 2013). Agrobacterium-mediated gene transfer makes transferring a target transgene possible in wide range of species and use of different promoters can regulate the expression of a genes related to resistance (Baulcombe, 2004).

To date, molecular markers have opened a new era in case of molecular plant breeding. In rice breeding, molecular markers played an immense role in identifying, improvement, selection and germplasm collections (Wang *et al.*, 2007). Additionally, many researchers reviewed the usefulness of molecular markers in rice breeding (Temnykh *et al.*, 2001; Semagn *et al.*, 2006; Lang *et al.*, 2008; Kumar *et al.*, 2009). So, it can be inferred that molecular markers can be utilized in wheat breeding and specifically for blast resistance. New biotechnological tools have been given a new pace in molecular biology including resistance study. In the 21st

century, new techniques have been discovered which giving scientists' new hope. The technology termed as genome editing (GE) technology can distinctly modify or repair even a single nucleotide. The CRISPR/Cas9 is the most promising GE technique, released in 2012 that is based on defense mechanism of bacteria against the virus (Gasiunas *et al.*, 2012; Jinek *et al.*, 2012; Cong *et al.*, 2013). Recently a rice blast resistant line has been released using CRISPR/Cas9 and this is the new hope for the plant breeders (Wang *et al.*, 2016). Notably, the success of CRISPR/Cas9 in rice is higher compared to wheat, because of genome flexibility of rice compared to genome complexity in wheat. In wheat, till now regeneration from genome edited protoplast was not possible. The scientists of Chinese Academy of Sciences obtained the first CRISPR/Cas9 edited wheat plant that has emerged as a new hope (Wang *et al.*, 2014).

In contrast to CRISPR/Cas9, Target Induced Localized Lesion in Genome (TILLING) is also a good alternative not only because the mutagenized plant can be grown in field condition but also the wheat hexaploid genome has high sustainability against mutation (Chen *et al.*, 2012). TILLING is a reverse genetic approach discovered in 2000 which is based on point mutation (Greene *et al.*, 2003). Like other genome-editing techniques transcription activator-like effector nuclease (TALEN) is one of the potential approaches. TALEN has been successfully deployed to develop blast resistant rice plant (Malzahn *et al.*, 2017; Li *et al.*, 2012). So, it can be expected that the modern GE technique will play a crucial role in blast resistance study as well as in the sphere of molecular biology with a new dimension.

Molecular markers and blast resistance study

After discovery, the marker technology is assisting plant breeders to identify the changes in DNA level. In major crop species, a large number of a disease-resistant trait is directly linked with various molecular markers, markers are being used extensively to find out loci and targeted genomic region in breeding programs (Phillips and Vasil 2001; Jain *et al.*, 2002; Gupta, 2004). Molecular markers are also being used for gene introgression using phylogenetic analysis, characterization of germplasm and backcrossing (Jain *et al.*, 2002).

Simple Sequence Repeat (SSR) or micro-satellite markers have largely been used compared to other marker system until date. From wheat isolates, thirty-eight genomic SSR loci of *MoT* has been characterized and new SSR markers have been developed (Pereira *et al.*, 2014). SSR marker used to confirming a gene named *RmgTd(t)* provides mild resistance to tetraploid wheat against *MoT* and mapping of *Rmg8* gene of hexaploid bread wheat (Anh *et al.*, 2015; Cumagun *et al.*, 2014). Using SSR markers many resistant genes have been unleashed in rice, like *Pi-ta2*, *Pi-kh*, *Pi-b*, *Pi-z*, *Pi-9*, *Pi-2* and so on. Huge online database information is available in "[http:// www.gramene.org](http://www.gramene.org)" regarding SSR marker which has been developed and validated for rice

blast research. SSR markers have been used successfully for gene identification, QTL mapping, pyramiding and backcrossing (Sallaud *et al.*, 2003; Ashkani *et al.*, 2013a,b; Singh *et al.*, 2012; McCouch *et al.*, 1994; Ashkani *et al.*, 2011; Correa Victoria *et al.*, 2001).

The discovery of InDel and SNP marker has begun a "renaissance" in the field of molecular marker technology. In rice blast resistance study, InDel marker has been developed and utilized for resistant genes like *Piz*, *Piz-t*, *Pik*, *Pik-m*, *Pik*, *Pik-m*, *Pik*, *Pi39*, *Pi50(t)*, *Pi-jnw1*. In a rice restorer line named *Hanghui 1179*, resistant genes has been analyzed using InDel marker (Hayashi *et al.*, 2006; Zhou *et al.*, 2017).

Single Nucleotide Polymorphism (SNP) has taken the supremacy over SSR as they are unique and plentiful in high and ultra-high-throughput automation. Haplotyping is capable of finding out polymorphism within a single base pair (Mammadov *et al.*, 2012). SNP markers have been developed for blast resistant genes named *Piz*, *Piz-t*, *Pit*, *Pik*, *Pik-m*, *Pikp*, *Pita*, *Pita-2*, and *Pib* respectively in Japan for blast resistance rice breeding program (Hayashi *et al.*, 2004; Hayashi *et al.*, 2006). Then, transcriptomic SNPs identified for studying *MoT* and this study revealed that wheat blast causing strain of Bangladesh has close similarity with Brazilian isolates. From revealed transcriptomic SNPs new SNP marker will be developed and characterization of newly evolved *MoT* strain will be easier (Islam *et al.*, 2016; Fig. 2).

From the above discussion, it is noticeable that utilization of marker technology has given a pace in blast resistance research and with the elapse of time the accuracy of marker technology is increasing. So it is expected that in marker assisted selection for blast resistant wheat variety modern cutting edge markers like SNP and InDel will play a pivotal role.

Bangladesh and wheat blast

The scientists of Bangladesh Agriculture Research Institute (BARI) reported the first occurrence of the wheat blast to Government of Bangladesh (GoB) in February 2016. Then GoB alerted national, regional and international levels that wheat blast could be epidemic in South-Asia (ACIAR, 2017). Instantly the pathologists of Government organization (Go) and Non-government organizations (NGo) visited 39 spots of 8 districts and collected disease samples along with necessary information by a team consisted with members from UN Food and Agriculture Organization (FAO), Bangladesh Agricultural University, Department of Agriculture and Food, Western Australia (DAFWA) and Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU). In late March 2016, GoB formed a core committee and that core committee gave future action plan to the Ministry of Agriculture (MoA) to confront the wheat blast. As an immediate action, they forbade to store any infected seeds and all infected grain must be slashed and burned. Then the core committee suggested

for seed treatment, test for *MoT*, and assess the host specificity as a short-term action. As a long-term work plan, the core committee recommended identifying sources of resistance using conventional and molecular breeding approaches, finding out alternative host of *MoT*, generating a forecasting model for blast outbreak, assessing seed health before variety release, maintaining strict quarantine system and finally providing training

and workshop to extension personnel so that as they can increase their diagnosis skill (The Daily Star, 2016b; Personal communication, Professor Dr M Bahadur Meah, Chairman of Core committee formed by Government of Bangladesh for immediate suggestions during wheat blast epidemic).

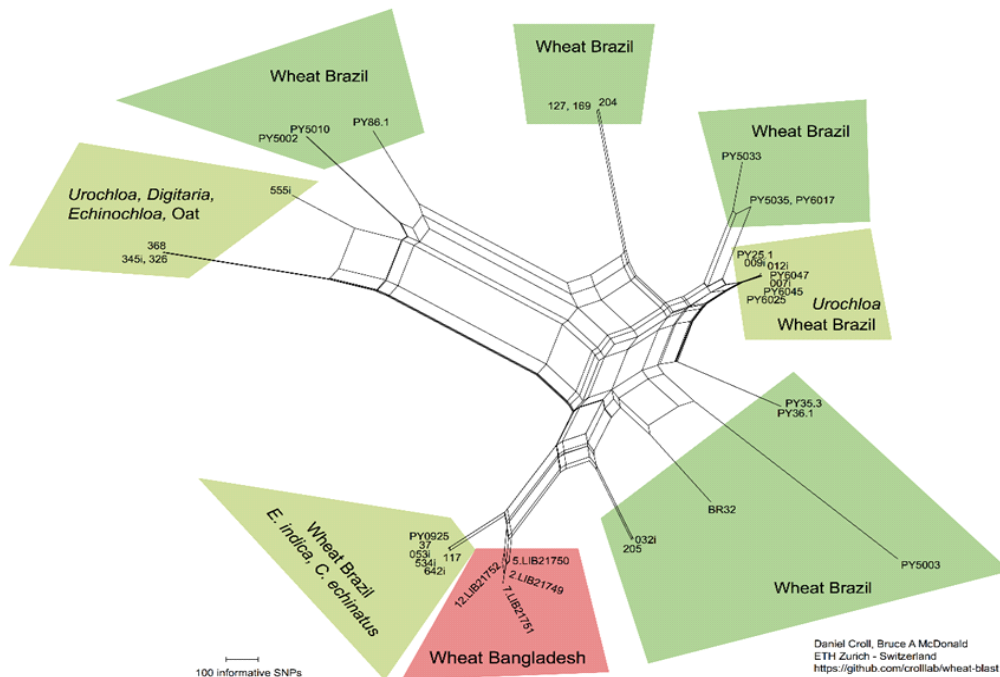


Fig. 2. Closeness of *MoT* from Brazilian and Bangladeshi isolates (Pathogen-genomics, 2016)

At this juncture of epidemic in 2016, BSMRAU conglomerated with The Sainsbury Laboratory and The Genome Analysis Centre (TGAC) respectively to initiate an “OpenWheatBlast” (<http://s620715531.websitehome.co.uk/owb/>) database where relevant information about wheat blast would be available and till date they are working on wheat blast resistance (Islam et al., 2016; The daily star, 2016a).

Now, many national and international organizations are working independently or collaboratively in Bangladesh. After the epidemic in Bangladesh in 2016, Australian Center for International Agriculture Research (ACIAR) has taken an initiative along with CIMMYT to develop durable blast resistant wheat variety (CIMMYT, 2017a). Indian Council of Agricultural Research (ICAR) granted a budget to carry out research in south Asia that will be led by CIMMYT (CIMMYT, 2017b). Additionally, United States Agency for International Development (USAID) is running projects named the Climate Services for Resilient Development (CSR) and the Cereal Systems Initiative for South Asia (CSISA), the CGIAR Research Program on Wheat by CGIAR and the Durable Genetic Gains in Wheat (DGGW) funded by Bill & Melinda Gates Foundation. After the wheat blast epidemic, they also paid heed to this issue (ACIAR, 2017).

For developing skilled manpower, training and workshops are being arranged in Bangladesh. In April 2017, CSISA led by CIMMYT carried out a 12 days long training aimed at surveillance and monitoring on blast. Experts from Cornell University, Kansas State University, CIMMYT, and CGIAR research program on wheat facilitated the training (CSISA, 2017). Then in February 2018, CIMMYT organized a training for young wheat researchers to provide exposure on using modern tools like artificial intelligence based disease identification using the smartphone and so on (CIMMYT, 2018).

In 2017, Wheat Research Centre (WRC) of BARI released a wheat variety named BARI Gom33 (parentage of BARI Gom33 is Kachu/Solala) is blast resistant as well as Zinc enriched (CIMMYT, 2017b; Personal communication, Dr Naresh Chandra Deb Barma, Director General, Bangladesh Wheat and Maize Research Institute). Moreover, GoB has taken the policy to discourage the farmers from wheat cultivation for a few years in the vulnerable districts and to replace wheat with alternate crops like boro rice, chickpeas, potatoes etc. (CIMMYT, 2019). So it is evident that, the international research community especially CIMMYT, ACIAR and Kansas State University (KSU) along with GoB have taken this issue seriously and their quick

response towards the wheat blast have given a leap of hope in Bangladesh. Additionally, the collaborative research programs amongst Go and NGo have added a new dimension.

Future outlook of blast resistance research

The discussed information indicates that, in future the control of wheat blast will be one of the greatest challenges for scientists because of adverse effect due to climate change. Plant breeders will search for novel resistant genes in unexamined variety, landraces, weediforms, and closely related species and will try to identify and introgress into high yielding sustainable wheat varieties. Additionally, more 2NS translocation based wheat variety will be introduced as blast resistant variety. Mutation breeding will play a vital role in developing wheat blast resistant cultivar where seed irradiation may create variation with blast resistance. Then scientists will try to explore more protein domains like nucleotide-binding site (NBS), leucine-rich repeat (LRR), coiled coil(CC) and nucleotide-binding site leucine-rich repeat (NBS-LRR) from unexamined sources in quest of resistance. For shortening the breeding cycle quick breeding methods i.e. Rapid Growth Analysis (RGA) will be utilized. The host-pathogen interaction study will be carried out to reveal the pattern of “breakdown of resistance” and pathologists will try to dissect the ecology of *Magnaporthe oryzae* along with host specificity and cross infection pattern.

More high-throughput and allele specific marker like SNPs and InDels will be developed and utilized with cost-effective, quick genome studying platform, especially the next generation sequencing platforms will be replaced by modern sequencing platform and may be used in the unexamined wheat genome and as a result the marker-assisted breeding will be more dynamic. Allele mining and other *in silico* analysis will be accelerated due to new cutting-edge bioinformatics tools. Previous studies showed that, in eukaryotes MicroRNAs (miRNAs) have role in the defense mechanism, so identifying and utilizing miRNAs of wheat will give a pace (Katiyar-Agarwal and Jin, 2010). In addition, newly developed modern forecasting model may be a key factor in preventing blast epidemic.

Additionally, gene transfer technique will play a big role but will bring out controversy because of biosafety issue. Finally, the newly developed cutting-edge technology like TALEN, TILLING, CRISPR/Cas9 may play a vital role in developing Genetically Edited wheat resistant against wheat blast. In addition, nanotechnology will be deployed, like NANO GREEN named Nano-molecules has been used against rice blast (Srivastava *et al.*, 2017).

Indeed these new biotechnological and bioinformatics tools are giving aspiration for confronting wheat blast as like as any other biotic stress. In future, collaborative research horizon will be more intensified and knowledge

exchange and sharing will generate a big data platform for scientists.

Conclusion

The identification of blast disease and epidemic occurrence in Bangladesh has given a push to the scientific world. Additionally, the devastating effect of *Magnaporthe oryzae* in Brazil, Bolivia, Uruguay, and Argentina is giving urges to the plant breeders. Early works proved that *MoT* has higher level of virulence and pathogenicity. Then the evolving strategy of new strain is unknown and the host-pathogen interaction is complicated. In addition, the environmental change is fueling this disease. Amongst molecular markers InDel and SNPs have the most potency. The high-throughput marker technology will boost the QTL identification, mapping and gene introgression. The marker-assisted selection (MAS), marker-assisted backcrossing (MAB) will be carried out using identified QTLs and genes. Exploitation for new resistance protein domain may add new attributes. The cutting-edge technology like TALEN, TILLING and CRISPR/cas9 will bring out a paradigm shift in wheat blast research. Lastly, the exchange of information between scientists is the most important concern. In Bangladesh, the exchanges of information and collaboration between national and international organizations have reflected visible significance. With the conglomeration of this all interventions, our expectations are durable wheat blast-resistant variety would be developed to save mankind from another disaster. The pivotal question is, can the scientists capable of doing that mighty novel deed or not?

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