Review article **Oryza Vol. 54 No. 1, 2017 (1-12)**

Rice breeding strategies of North Eastern India for resilience to biotic and abiotic stresses: A review

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Received : 20 February 2017 Accepted : 08 May 2017 Published : 19 May 2017

ABSTRACT

In north eastern region, rice is grown in diverse agro-climatic conditions viz., upland, jhum, terraces, lowland and deep water. The region is considered to be a hot spot for rice diversity and have reported to have valuable landraces, wild rice and primitive cultivars. The major rice production constraints in the region are large acreage under traditional cultivars, biotic and abiotic stresses, and lack of wide scale technological intervention. Among abiotic stresses, soil acidity, iron toxicity, aluminium toxicity, low light intensity, low temperature, flooding and moisture deficit stress are the major problems that lead to lower productivity of rice. Under biotic stress, rice blast is the major disease that ultimately affects rice in all the rice growing ecosystem of the region and cause huge economic loss. Hence, it would be logical to prioritize the rice research on the basis of prevailing constraints under rainfed areas of north eastern India.Breeding of suitable rice varieties by exploitation of landraces and local cultivars adapted to the regions would be the most sustainable strategy to boost rice production. A systematic collection, conservation, characterization and documentation of rice germplasms for resistance to stresses, grain quality and other agronomic important traits will accelerate the successful utilization of the germplasms in classical and innovative rice breeding work.

Key words: *Rice, germplasm, stress, breeding, diversity*

The north east (NE) region of India constitutes eight states (Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura). The region is consider as a hot spot for agro-biodiversity and is reported to have 9650 cultivars of rice, 15 races and 3-sub races of maize, 300 of taros, 230 of yams, 17 species and 52 cultivars of citrus, 16 taxa of banana, 700 taxa of orchids and 19 taxa of sugarcane (Satpathy and Sarma 2001). Rice is the principal staple food crop of the NE region and occupying maximum area under cultivation (Kuotsuo *et al.* 2014). The total rice production of NE region is estimated to be ~5.5million tones with average productivity of 1.57 t/ha, which is much below the national average of 2.08 t/ha (Pattanayak *et al.* 2006). In NE region, rice is grown mainly under four ecosystem, *viz.*, direct seeded rainfed upland, transplanted in terraced land, low lying wet land areas and flood prone valley areas. The production constraints of rice are widely related with certain abiotic and biotic stresses endemic to the region. The productivity of rice could be enhanced by systematic planning and designing of effective breeding system related with various aspect of rice. Except in some part of Assam and Tripura, rice is usually grown in only one season (mono-cropping). Rainy seasons in the NE region prevails for 7-8 months and hence there is opportunity to take two crop of rice by selection of appropriate varieties in *pre-kharif* and main *kharif* season. Traditional landraces are of long duration in nature and hence only one crop is grown during main *kharif* season (Kumar *et al.* 2016c). Systematic planning could execute cultivation of two crop of rice *i.e.*, cultivation of short duration variety during *pre-kharif* and medium duration variety during main *kharif* season. Development of short duration rice varieties having cold tolerance at reproductive stage could be most appropriate for post-flood seasons (Viraktamath *et al.* 2010). The current review paper highlight the richness of rice genetic diversity, specialty rice and breeding varieties for various biotic and abiotic stresses encountered by rice plants in the region.

Rice diversity and its utilization

NE region of India is a reservoir of large amount of rice germplams including wild rice. NE region is also being considered as the secondary centre of origin and enriched with landraces and primitive cultivars of special importance (Durai *et al.* 2015). The rice germplams grown in higher altitude of Arunachal Pradesh are intermediate between *indica* and *japonica*. Kampti cultivar of Arunachal Pradesh is rich in aroma with soft glutinous type endosperm (Durai *et al.* 2015). In Manipur, rice is grown in variable environment ranging from higher altitude, jhum cultivation to deep water rice. The state is enriched with very special black rice (Chakhao) along with other short grain indigenous rice. In Meghalaya genetic diversity are widely distributed in *Khasi*, *Garo* and *Jaintia* hills. In upland and jhum cultivation, farmers prefer mostly the local genotypes of special local taste. Most of these indigenous rice landraces are medium to longer duration (130-170 days). Sikkim is a high altitude hill state of NE India where agriculture is practiced only in~11.7% of geographical area. The majority of the local landraces of the state have been reported for cold tolerant. Tripura is covered by diverse topography and rice ecosystem includes *jhum*, wetland and deep water rice. In Assam, rice is cultivated in diverse ecology ranging from, flood prone areas of the Brahmaputra, Barak valley of Assam and also in upland *jhum*. Aromatic rice varieties of Assam are known as *Joha*. There are two variants of *Joha* rice available in Assam *viz., Kala Joha* and *Amru Joha*. Along with cultivated *Oryza* species, five wild species along with their different forms occurs in NE region. *Oryza nivara* and *O. sativa f. spontanea* are frequently observed in rice field as these are morphologically very similar with cultivated rice. Other species of *Oryza* reported in the region are *O. officinalis*, *O. granulata*, *O. rufipogon* and *O. meyeriana* (Hore 2005). Apart from species of *Oryza* several other related taxa of *Oryza viz., Hygrorhiza aristata*, *Leersia hexandra*, *Porteresia coarctata* and *Zizania latifolia* are commonly found in the region. *Zizania latifolia* is mostly observed in Loktak lake of Manipur. Several intermediate forms or weed like species are also found *i.e.*,Tulsibaon, bogibaon and Kenkubaon in deep water and water logged conditions in the region (Hore 2005).

Breeding for disease resistance in rice

The unique ecosystem of NE region provides a suitable environment for many fungal, bacterial and viral diseases in rice due to the favourable weather conditions congenial for the disease development and spread. Among various diseases recorded in the region, rice blast (*Magnaporthe oryzae*), sheath blight (*Rhizoctonia solani*), sheath rot (*Sarocladium oryzae*), false smut (*Ustilaginoide avirens*) and bacterial leaf blight (*Xanthomonas oryzae* pv. *oryzae*) holds economic significance. Rice blast is economically most important and prevalent disease of rice in whole NE region, resulting in the huge economic losses. Due to high rainfall and relative humidity, high incidence of leaf and neck blast was reported from the NE region (Ngachan *et al.* 2014). Screening of a large array of rice germplasm under uniform blast nursery and artificial inoculation has led to identification of nine germplasm lines *viz.*, Meghalaya Lakang, KumtaMah, KemenyaPepeu, Wainem, Thekrulaha, Vishkv, PhouralUtlou, MesaoTsuk and Gum Dhan resistant to both leaf and neck blast under Manipur conditions (Anonymous 2015). An analysis of virulence spectrum of rice blast pathogen indicated that race profile of rice blast pathogen in NE region is highly diverse and distinct compared to other rice growing regions of India. Akhanaphou, a unique rice landrace of NE India, having its origin in Manipur has been reported to exhibit high field resistance to leaf and neck blast. Recently two novel quantitative trait loci (QTLs), *qLNBL-5* and *qLNBL-7* were identified conferring resistance to leaf and neck blast diseases (Aglawe *et al.* 2017). Employing the data generated on virulence spectrum of rice blast pathogen, now the breeding focus has been on gene deployment/pyramiding based durable management strategy. Sheath blight is another economically important disease affecting rice in NE region of India. The disease is most prevalent in pockets where the relative humidity is very high (>95%), the temperature is moderate (28-32°C) and N application is high. The disease is more prevalent in the lowlands of NE region where water stagnation is common, however under upland conditions; sheath blight is not a severe problem. At present the management of sheath blight in the region relies on the use of chemicals. Studies conducted at various parts of world have suggested that partial or quantitative resistance exists in different varieties to *Rhizoctonia solani* (Liu *et al.* 2009). A major QTL conferring resistance to sheath blight was identified to be located at chromosome 9 (Liu *et al.* 2009). QTLs responsible to sheath blight pathogen of rice in NE region needs to be defined/validated and employed for breeding resistance. Sheath rot disease has its sporadic occurrence in the region, particularly in lowlands and high yielding; nitrogen responsive cultivars are most susceptible to the disease. Availability of resistance to sheath rot disease is limited due to its complex nature (Bigirimana *et al.* 2015). A high pathogenic variability was reported to exist among the *S. oryzae* isolates (Ayyadurai *et al.* 2005); hence breeding efforts needs to be focused keeping in view this pathogenic variability. False smut is an emerging disease of rice in NE region of India, recorded to have its high incidence during last five years. Different popular varieties and local landraces of NE region were having various level of susceptibility to false smut disease. Hybrids are more susceptible to the disease. Resistance mechanism to false smut in rice is not fully understood. Two major genes having equivalent additive and polygenes model for explaining inheritance of false smut resistance was proposed (Li *et al.* 2012). Once the genetic locus responsible for false smut resistance is identified, they can be transferred to popular varieties of NE region. Bacterial leaf blight (BLB) is a disease occurring in the pockets of NE region of India receiving little higher temperature with high relative humidity. Marker assisted pyramiding of these resistance genes into popular rice cultivars of NE region and identification of novel résistance genes against BLB from the germplasm of region will help devising a durable location specific management strategy for BLB.

Breeding for insect and pest

Brown plant hopper [*Nilaparvata lugens* (Stål.)] is one of the most destructive pests of rice in NE region which cause moderate to severe yield loss. Identification of resistant varieties is very important as the biotypes of the pest is changing its behaviour from time to time and the earlier released resistant rice varieties becomes susceptible to the pest. The Brown plant hopper (BPH) resistance genes have been identified in wild species *Oryza australiensis*, *Oryza officinalis*, *Oryza glaberima*, *Oryza eichengiri*, *Oryza rufipogon*, *Oryza minuta* and Indian cultivars (Zhang 2007). The use of resistant rice varieties is the most economical and efficient method for controlling the BPH as compared to chemical control. Therefore, it is imperative to identify BPH resistance genes from diverse sources and incorporate them into rice cultivars. Krishna *et al.* (1977) reported 69 resistant or moderately resistant lines from screening of 890 cultivars of NE region of India. Khush *et al.* (1985) found that resistance to brown plant hopper in rice cultivar, ARC10550 was governed by a single recessive gene which was designated as *bph5*. Li *et al.* (2010) evaluated 1200 accessions of common wild rice (*Oryza rufipogon*) and identified six accessions for broad spectrum resistance against several biotypes of BPH. Whorl maggot mainly infects the rice plant where stagnation of water occurs for longer duration and drainage of water is not adequate. The tolerant genotypes have the ability to compensate the loss occurred by whorl maggot by faster growth. The rice cultivar IR 40 and the wild rice *viz.*, *Oryza branchyantha* and *O. ridleyi* were identified as resistant to whorl maggot. In India, attempts were made to screen lines having resistance to whorl maggot and few lines such as RP 2418-5, RP 2418-10 and RP 2419-3 (Sain and Hakim 1988) and IR 9209-48-3-2 and UPR 82- 1-7, have been identified to be least susceptible to whorl maggot in Punjab. Gundhi bug has become a major problem in NE states, especially, Manipur since early 2000s (Krishnaiah and Varma 2012). It is one of the major pests responsible for crop damage at vegetative and reproductive stage particularly at milking stage. Both the adults and nymphs feed on grains at the milking stage and reduce yield by as much as 30%.

Coarse-grain and bearded cultivars are resistant to the rice bug. Rice stem borers damage crop plants in nursery stage, vegetative stage and reproductive stage leads to drastic reduction in yield. Several species of rice stem borers are reported from NEH region and yellow stem borer is considering as predominant. Progress on the development of rice varieties with high level of resistance to stem borers in India and other part of the world is very much slow due to lack of suitable germplasm, screening techniques and a poor understanding of the genetics of resistance. In the recent years some efforts have been made at national and international levels to decipher genes from moderately resistant genotypes. Several landraces from the NE collection have been identified for moderate level of resistance that includes, ARC 6107, ARC 6044, RYT 2908 (vegetative stage), ARC 6215, ARC 6579, ARC 5757 (heading stage), and ARC 5500 (Kalode *et al.*1989). Gall midge (*Orseolia oryzae*) is one of the major pests which are causing significant yield loss of rice (Murlidharan and Pasalu 2005). In India, gall midge damage causes an average annual yield loss of ~ 477 thousand tons of grain or 0.8% of the total production amounting to US$ 80 million (Bentur *et al.* 2003). Currently, a total of 13 biotypes of the Asian rice gall midge are reported. The Indian biotypes have been identified and characterized on the basis of differential reactions to genetically defined host plants (Sardesai *et al.* 2001). A new gall midge biotype existing in Manipur was identified as biotype 6 (Singh 1996), which differs from the other six biotypes in India (Lakshmi *et al.* 2006). Breeding of resistant rice varieties has proved to be a viable and ecologically sound approach for management of this pest. Through a special germplasm collection and screening program, 6730 landraces from NE states were screened, out of which 43 accessions were identified as tolerant to gall midge (Sastry *et al.* 1971). Sain and Kalode (1994) reported 337 lines as primary donors, out of which a large proportion come from the landraces of NE states of Assam (34%) and Manipur (7%), followed by those from Madhya Pradesh (20%), Tamil Nadu (8%), Odisha (5%) and Kerala (4%). Besides, cultivated rice, several of the accessions of wild species of *Oryza*, like *O. brachyantha*, *O. eichingeri*, *O. granulata*, and *O. ridleyi* were also reported to be gall midge resistant (Israel *et al.* 1959).

Breeding for weed tolerance

Weed is a great problem especially in upland rice ecosystem of NE region (Kumar *et al.* 2016a; Chatterjee *et al.* 2016; Prasad *et al.* 2013). Weeds are among the most important biological constraints for rice production in the region (Kumar *et al.* 2017). For effective weed control, proper herbicide application, timing and method are required which are often not met thereby resulting in poor weed control (Mandal *et al.* 2011a). Therefore, attention must be paid for alternative technologies which offer sustainable and economical weed control method in rice (Kumar *et al.* 2015; Roy *et al.* 2011). Genetic variation among diverse range of genotypes in their ability to compete with weeds has been documented for many crops, including rice (Kumar *et al.* 2016b). Crop competitiveness against weeds is composed of tolerance to weed infestation (Kumar *et al.* 2016c), which is the ability to maintain high yields under weedy conditions (Kumar *et al.* 2016d). A better understanding of genetic mechanisms by which a rice genotype becomes more competitive to weeds would not only serve to assist plant breeders in developing competitive cultivars more quickly and effectively but would also justify the use of plant breeding to increase crop-competitive ability. Competitive ability of rice genotypes is a much complex trait and could not be justified by selection of one or few characteristics. Plant height, specific leaf area index, tillering ability, dry matter portioning of leaves, crop duration, root biomass and shoot biomass at an early stage will be important traits while selecting the weed tolerant rice genotypes under upland rice ecosystem (Kumar *et al.* 2016d). In NE region, farmers prefer to grow traditional tall type varieties despite of low yield due to fast initial growth and exhibit weed tolerant ability under upland and jhum rice cultivation. Early seedling vigor is desirable trait under direct seeded rice (DSR) for enhancing the initial crop establishment and the ability to compete against weeds. Recently, Singh *et al.* (2017) phenotype a set of 253 BC_3F_4 lines derived from cross between Swarna and Moroberekan and identified several QTLs (*qEV3.1*, *qEUE3.1*, *qSHL3.1*, *qSL3.1*, *qSFW3.1*, *qTFW3.1*, *qRDW3q*, *EV5.1*, *qEUE5.1*, *qSHL5.1*, *qSL5.1*, *qSFW5.1*, *qSDW5.1*, *qTDW5.1*) for early seedling vigor and related traits under direct seeded system. Further, there is need to explore a range of diverse genotypes and design an effective breeding methodology for weed tolerant in order to achieve reasonable yield in upland rainfed dry land ecosystem.

Breeding for abiotic stresses

Rice cultivation in the NE region of India is exposed to different abiotic stresses that include problematic soil (acid soil), low temperature, metal toxicity (Fe & Al), low light intensity, intermittent flooding and drought (Ngachan *et al.* 2014). Recently researchers are using geostatistics and krigging tools to study the spatial variability of soil physico chemical properties to achieve a better understanding of complex relations between soil properties and environmental factors (Tripathi *et al*. 2015). Rice plant encounter several abiotic stresses right from nursery, vegetative to reproductive stage causing significant loss in yield depending upon intensity and severity of stresses. Identification and introgression of target genes/QTL(s) conferring high level of resistance/tolerance to agronomically desirable varieties through marker assisted selection (MAS) would be the most efficient strategy to achieve potential yield under stress environment. Soil quality is one of the important issue responsible for widespread yield stagnation and productivity declines in the rice cropping system (Shahid *et al*. 2013).

Breeding for low-Phosphorous (P) tolerance

In NE India, rice productivity is less than 40% of the national average due to acidic soils and poor availability of phosphorus (Anonymous 2012). Deficiency of phosphorous in acid soils are usually tackled by application of adequate amount of suitable phosphatic fertilizer and other management practices (Kumar and Meena 2016; Bhattacharyya *et al.* 2015). Several researchers has reported considerable genotypic variation for P uptake in diverse traditional varieties of rice and these traditional varieties are likely to possess genes/QTLs for high P acquisition. Phosphorus uptake1 (Pup1), a major quantitative trait locus (QTL) derived from Kasalath is reported to exhibit 78.8% phenotypic variance for P-uptake and the only available QTLs for maker assisted selection in rice (Wisuwa *et al.* 2002). Tyagi *et al*. (2012) have identified four genotypes containing *Pup1*, Sahbhagidhan, Dagaddeshi, Pynthor and Paijong, adapted to north eastern and eastern part of India, as potential donors for rice breeding for P deficiency tolerance. A major candidate gene *OsPSTOL1* (Phosphorus starvation tolerance 1) in the Pup1 QTL has been cloned and gene based makers are available for maker assisted gene pyramiding in different genetic background of rice (Pariasca-Tanaka *et al.* 2014). Recent years, a specific group of rice (aus-type varieties) that originates from NE region of India with poor and problematic soils has been recognized as a valuable source for novel genes/QTLs for tolerance to P and other nutrient deficiency.

Breeding for iron toxicity

Fe toxicity is one of the most emerging abiotic stress constraints in valley (low land) area of NE region. However, exact area and annual loss incurred due to iron toxicity is not yet fully studied in the region. Fe toxicity is commonly characterized by high amounts of reducible Fe, low pH, low redox potential, low cation exchange capacity (CEC) and low exchangeable potassium content (Ottow *et al*. 1982). Rice cultivars differs in their ability of iron toxicity tolerance and selection of rice cultivars with superior iron tolerance has paramount importance in the view of breeding of high yielding varieties with inbuilt iron toxicity tolerance (Shahid *et al*. 2014). Genetic differences in adaptation and tolerance for iron toxicity have been exploited for development of iron toxic tolerant cultivars (Nozoe *et al*. 2008).Therefore, pyramiding of genes/QTLs from different sources could result in higher level of tolerance in new varieties. Physiological mechanism of tolerance, such as root exclusion, iron compartmentalization within organs or true tissue tolerance, have been proposed but remain unexplored in diverse gene pool of rice (Matthus *et al*. 2015). Sahrawat and Sika (2002) reported African cultivated rice (*O. glaberrima*) could be a good source of tolerance to Fe toxicity as compared to Asian cultivated rice (*Oryza sativa*). Therefore, there is need to exploit genetic variability available among the different accession of *O. glaberimma* for tolerance to iron toxicity. Identification and incorporation of Fe toxicity tolerance QTL(s) in elite genetic background would be beneficial in order to get higher productivity of rice in iron toxic soils. Currently, application of DNA markers in breeding for tolerance to Fe toxicity by marker-assisted selection is very much limited because QTLs reported are for small effects and even for the few major ones, large confidence intervals and/or lack of validation in other genetic backgrounds and environment (Sikirou *et al*.

2015). Dufey *et al.* (2015) constructed an integrated map with the previous QTLs identified using the annotated physical map of the rice reference variety Nippon bare and highlighted four candidate regions (CR), with a high QTL density. Chrisanawati *et al.* (2016) identified three STS markers *i.e.*, OsIRT1, OsIRT2 and OsFRO2 associated with iron toxicity tolerance in double haploid lines of rice. Nugraha *et al.* (2016) identified SNPs markers, TBGI380435 related to heavy metal transport detoxification and marker, TBGU313277 associated with proline transporter, probably associate with tolerance to iron toxicity in rice. Identification of several small effects QTLs for Fe toxicity tolerance showed that mechanism of tolerance may involve additive/cumulative effects of several minor genes. Manipulation of several major and minor QTLs/ genes may have a significant impact on phenotype. Acidic soils with iron toxicity often lead to zinc toxicity. Therefore, identification of QTLs associated with zinc toxicity tolerance is equally important while breeding for iron toxicity tolerance. Recently, Liu *et al.* (2016) identified a unique QTL, *qFRSDW11* associated with iron and zinc toxicity tolerance. NE regions has a rich reservoir of germplasm in form of landraces, primitive cultivars, wild rice and these untapped potential germplasm could be targeted for identification of some novel QTLs for iron toxicity.

Breeding for Aluminum toxicity

Aluminum toxicity in acid soils can be managed by application of lime, that is expensive, ineffective in sub-soil and in some cases may have a deleterious effect on the soil structure (Rao *et al.* 1993). Development of aluminum toxicity tolerant cultivars is most effective and sustainable approach to manage the problem. Genetics of aluminum tolerance revealed a complex multi-genic trait and therefore, for characterization of aluminum tolerance traits, composite screening methods could be much reliable than single screening method. Exploitation of natural variation and mapping of QTL through association mapping are most impressive tools for development of Al-stress tolerant cultivars. Kumar *et al.* (2016*) identified few rice cultivars *viz.,* Posimot, Epyo, Aaha and VR-14 having aluminum toxicity tolerance under acid soil conditions of Meghalaya. Tolerant genotypes could be used in hybridization programme for development of high yielding genotypes with inbuilt tolerance of aluminum tolerance. The identification of DNA markers that are linked for aluminum tolerance loci in particular gene pools provides an important starting point for transferring and pyramiding genes that may contribute to the sustainable improvement of crop productivity in aluminum-rich soils (Nguyen *et al.* 2001). The isolation and characterization of genes responsible for aluminum tolerance is likely to be necessary to gain a comprehensive understanding of this complex trait. STAR1/2, the major Al tolerance gene identified in rice has conferred a basal Al tolerance in rice which is probably because, unlike temporary environmental stresses such as water and temperature stresses, Al toxicity is continuous in soil (Pattanayak and Pfukrei 2013). Recent progress in genomic research may lead to identification of more number of tolerant genes/QTLs and accelerate development of rice varieties having inbuilt tolerance to Al toxicity.

Breeding for cold tolerance

Low temperature is a major limiting factor for rice productivity in high altitudes of NE region of India. Cold stress affects rice plants by causing seedling mortality, spikelet sterility and eventually significant yield losses (Shimono *et al.* 2002). Identification of new genetic sources of cold tolerance is very much crucial for rice breeders to develop cold-tolerant rice cultivars in temperate and high altitude regions. There is a significant amount of genetic variability available for cold tolerance among rice gene pools and this variability often reflect the place of origin, natural selection as well as breeding history. Dissecting cold stress-mediated physiological, biochemical and genetic causes will facilitate in breeding of rice varieties for cold tolerance. The booting stage is found to be the most critical and cold sensitive stage for rice plants. On cold damage/injury at the booting stage, many evaluation methods were proposed in past such as, long cold water irrigation (Han and Koh 2000), constant temperature deep cold water irrigation (Futsuhara and Toriyama 1964), short-term low temperature management (Tsumoda *et al.* 1968), natural low temperature treatment (Dai *et al.* 2002) and identification of artificial climate chamber (Farrell *et al.* 2006). Cold-tolerant genetic resources have been identified and being used as a donor material for incorporating cold tolerance into new high yielding varieties (Abe *et al.*1989). Cruz *et* *al.* (2006) reported that reduction rate in spikelet fertility in response to low temperature can be used for evaluating cold tolerance per se. The ICAR Research Complex for NEH Region Umiam has identified Upper Shilong (1900 MSL) a site for cold tolerance research work, where temperature is quite low during reproductive stage (flowering and seed formation stage) of rice growth. About 1000 cultures of rice and segregating populations were screened at Upper Shillong and cultivar, Khonorullo was found to be the best followed by DuIlo-6, Ryllo Red 2, Ryllo Red 5, IR 3941-23, Jungruh *etc*. (Ngachan *et al*. 2014).The identified genotypes have low yield potential but possess unique adaptive cold tolerance traits and these traits could be targeted for development of high yielding cold tolerant rice variety. Many cold-tolerance related QTL have been identified in the past 20 years for reproductive stage, germination stage and vegetative growth. The QTL *Ctb1*, *qCTB2a*, *qPSST-3*, *qLTB3* are related to cold tolerance at the reproductive stage; *qCTP11* is related to cold tolerance at the germination stage; and *qCtss11* and *qCTS4a* are related to cold tolerance at the seedling stage (Zhang *et al*. 2014).

Breeding for low light intensity

Light intensity is one of the most vital environmental factors that affect growth and development of rice. The solar radiation requirements of a rice crop differ at various growth phases (Yoshida and Parao 1976). Cloudy weather during the vegetative growth phase slightly affects rice growth and development, while shading during reproductive phase has a pronounced effect on spikelet fertility and grain quality. There has been several report that increasing light intensity will lead to increase in total number of tillers, number of effective tillers (Emmanuel and Mary 2014) and plant height and leaf area (Liu *et al*. 2009). Rice crop suffers from low light intensity in NE India and ~50% of the total requirement *i.e.*, 1600 bright sunshine hours during growth period. Rice cultivars adapted to various geographical conditions in the NE India differ in their light tolerant capacities. Cultivars that are traditionally being grown are supposed to have greater tolerance for low-light stress than recently introduced cultivars. Therefore, identification of such rice cultivar will be essential in breeding for low light tolerant high yielding varieties of rice. Hence, in the future, new research should focus on strengthening the tolerance of rice plants to low light intensity.

Breeding for submergence/deep water

NE region of India falls under high rainfall zone and during monsoon, flood is one of the major problems occurring in low lying areas of Assam, Tripura, Manipur and Meghalaya. Rice is a reasonably flooding-tolerant crop but water logging for longer duration significantly affect the crop growth and survival. Flooding of rice field may be flash or intermittent or stagnant prolonged flooding. Flash-floods or submergence are highly unpredictable and may occur at any growth stage of the rice crop and the yield loss may range between less than 10 and 100% depending on associated factors such as water depth, duration of submergence, temperature, turbidity of water, nitrogen fertilization, light intensity and age of crop (Mohanty *et al*. 2001). Several local landraces generally grow in low-laying areas where water stagnation beyond 50 cm for more than a month in the season. These local landraces are slightly tolerant to deep water conditions due to inherent internodal elongation ability. The important local cultivars of north eastern region suitable for deep water rice are Padmapani, Panikekoa, Panindra, Padmanath, Sabita, Rayada B3, Maguribao, Negheribao (Bhowmick *et al*. 2000). Screening of the elite germplams for flood tolerance and its utilization in hybridization programme is one of the major objectives of conventional plant breeding for development of flood tolerance rice variety. In the past breeders have concentrated on using tall traditional cultivars such as FR13A and Kurkaruppan to incorporate strong submergence tolerance in modern varieties. At International Rice Research Institute (IRRI), Phillipines, submergence tolerance gene "*Sub1-A*" has been identified in FR-13 and successfully transferred in breeding lines, IR 49830-7-1-2-3 and IR-40931-33 using conventional breeding approaches (Sarkarung *et al*. 1995). Xu *et al*. (2006) reported clusters of three genes at Sub1 locus encoding putative ethylene response factors, which includes three ethylene responsive factors (ERF) like genes, *Sub1A*, *Sub1B* and *Sub1C*. *Sub1A-1* was later reported to be tolerance specific allele and a primary determinant of submergence tolerance. There is also possibility of novel gene/QTL in tolerant cultivars of NE accessions and therefore exploring elite germplasms for submergence or deep water rice has to be taken in priority.

Breeding for drought tolerance

Drought is one of the major abiotic constraints, affecting rice production and yield stability in a wider range of rainfed ecosystem. The water requirement by conventional transplanted rice varies from 1300-1900 mm of water (Kumar *et al*. 2017). In the present scenario, increasing water scarcity has threatened productivity and sustainability of irrigated rice systems; hence alternative water saving rice production technique has gained focus (Kumar *et al*. 2016). Although high rainfall occurs in NE region of India especially during monsoon season but short period of drought/intermittent drought is very much common in jhum or upper terraces due to low water retention capacity. The success of a drought breeding programme greatly depends on extent of available genetic variability in the population subjected to selection, the selection criterion, and availability of suitable selection protocol/screening. Selection for genotypes for drought resistance can be performed by measuring yield under stress and or measuring a secondary trait correlated to yield under stress. NE region of India is a rich reservoir of germplasm and these germplasm need to be well characterized for various morphological and physiological traits which are directly or indirectly contributing to drought tolerance.Several efforts have been made to identify major QTLs with a large and consistent effect on grain yield under drought (Bernier *et al.* 2007). At the International Rice Research Institute (IRRI), traditional and improved donors were used in developing mapping populations for the identification of major qDTYs (Swamy and Kumar 2011). *qDTY12.1* was the first reported large-effect QTL for grain yield under drought environment in a population of 436 random F_3-derived lines from a cross between upland rice cultivars Vandana and Way Rarem (Bernier *et al*. 2007). Anupam *et al.* (2017) identified seven droughts tolerant QTLs in 74 Tripura rice germplasms and observed *qDTY2.1*was present in the maximum number of germplasm while *qDTY1.1* was present in the least. Development of near isogenic lines (NILs) for vegetative and reproductive stage QTLs and pyramiding of these QTLs not only allow sustainable rice cultivation in areas affected by drought but also open a new way to grow rice in new areas.

Conclusion and future scope

The potential landraces and wild species of the region are source of valuable gene(s)/QTL (s) for several economic important traits. Therefore, it is utmost necessary for systemic collection, characterization and documentation of germplasm for its successful utilization in breeding programme. Farmers of the region are still conserving the germplam in their traditional way and hence there is need to keep balance between introduction of HYVs/Hybrids and cultivation of indigenous varieties in the view of protection of the traditional varieties of special value. The valuable landraces are reported to have gene(s) for several biotic and abiotic stresses and therefore these genes must be introgressed in the elite varieties through marker assisted selection. The nutritional dense cultivars could serve as a source materials for biofortification programme and these valuable cultivars should be quantified for several nutritional and biochemical characters. In future, there is need to prioritize the rice research on the basis of prevailing the local constraints under rainfed areas of NE India in order to achieve sustainable and profitable rice production.

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