



## Genetic Improvement of Rainfed Shallow-lowland Rice for Higher Yield and Climate Resilience

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### SUMMARY

In India, 16 million ha area is under rainfed lowland rice cultivation. The rainfed shallow lowland is characterized by water accumulation of 0-50 cm and faces frequent drought and flash floods. Rice crop faces several challenges when grown under shallow lowland ecology. Simultaneous incorporation of drought and submergence tolerance besides imparting lodging resistance, anaerobic germination ability, seed dormancy and tolerance to major biotic and abiotic stresses becomes very crucial for developing rice varieties for shallow lowlands. Well-characterized genes and QTLs are available for majority of traits to be deployed in suitable combinations for resilient breeding. Updated information on genetic improvement of shallow lowland rice for attaining higher productivity has been discussed in this chapter.

### 1. INTRODUCTION

In India, rice is grown in 43 Mha, and approximately 50% of these areas are under rainfed ecology with low productivity due to various abiotic and biotic stresses. The severity of biotic and abiotic stresses is changing frequently due to the effects of climate change. The rainfed lowland ecologies cover around 16 Mha of which 92% are located in the eastern region of the country. Depending upon the water depth and duration of water logging in the lowland ecology during growth period of rice, it has been classified into rainfed shallow lowland, semi-deep, deep and very deep water or floating type ecosystem. The rainfed shallow lowland is characterized by water accumulation of 0-50 cm that face frequent drought and flash flood. As these areas are not suitable for growing most of the other economically important crops, developing high yielding climate resilient varieties of rice under those difficult ecologies becomes very important. In future, production of rice needs to be increased from lesser land area. In fact with the increasing scarcity of water for rice cultivation, the future thrust for growing rice must focus with such ecologies.

Rice crop faces several challenges when grown under shallow lowland ecology. Many rice growers under rainfed shallow lowlands adopt direct seeding of rice. These direct seeded fields usually not properly leveled before seed sowing. After sowing the plots get severe rain water accumulation frequently and resulting in heavy seedling mortality and hence low yield. Presence of stagnant water for more than 10 days period is very common in most areas under this ecology. Although by its name, the



ecology seems to possess sufficient amount of water and stagnant water seems to create problems, occasional drought spells are also observed. As the crop is grown almost completely under rainfed conditions, scope for supplementary irrigation is very much limited. Besides, the genotypes suitable for shallow lowland ecologies have longer maturity duration (140 days or more) and comparatively higher plant heights. In the eastern part of the country where these varieties are grown, frequent incidences of untimely rainfall and storms during grain maturity lead to heavy crop loss caused by lodging and pre-harvest germination of seeds. Biotic stresses like stem borer, brown plant hopper, gall midge, leaf folder, bacterial blight, bacterial sheath blight and false smut are significantly affecting rice grain yield. Simulation studies have clearly shown that, in future the distribution pattern of rains or associated wind is expected to show more erratic behavior (Turner and Annamalai, 2012). Moreover, disposal of paddy straw biomass is now-a-days become a burning issue and environmental concern. Keeping the context of the country in terms of utilization of straw, it will also be necessary to develop lodging resistant cultivars without compromising feed quality and biodegradability. Thus, there is an urgent need of region specific climate smart breeding in mega rice varieties with stacking of various stress tolerance genes through multipronged approaches. Hence, simultaneous incorporation of drought and submergence tolerance besides imparting lodging resistance, anaerobic germination ability, seed dormancy and tolerance to major biotic and abiotic stresses becomes very crucial for developing future rice varieties for shallow lowlands.

Fortunately rice researchers have already discovered many such useful genes and QTLs. A major QTL *Sub1* is very useful for conferring submergence tolerance for 12 days. Many yield QTLs have been reported which works well under drought stress. Pyramiding of these QTLs is expected to increase grain yield in rice under drought stress. Though no host plant resistance genes are identified for stem borer, but more than 30 resistance genes/QTLs are reported for brown plant hopper host plant resistance. Till date, 42 resistant genes have been reported for controlling bacterial blight disease in rice. Many yield enhancing QTLs have already been cloned in rice. Two genes controlling anaerobic germination are already known. Now it will be interesting to see how these QTLs or genes will behave when they are all taken together in a single background.

The impact of the Green Revolution has sidelined the eastern Indian rainfed shallow lowlands. Sizeable rice areas of eastern India are under shallow lowlands with low production. We have to feed the burgeoning population in near future. The irrigated ecology has shown symptoms of yield plateauing. Thus, this traditionally neglected ecosystem has got tremendous potential to increase the yield level and total production as a whole.

Keeping these factors in mind, this chapter deals with the up-to-date information on genetic improvement of shallow lowlands rice for attaining higher productivity. Prominent genetic approaches for obtaining higher productivity against various abiotic and biotic stresses in this ecology namely submergence, drought, anaerobic



germination, brown plant hopper, gall midge, leaf folder, bacterial leaf blight, bacterial sheath blight, false smut, lodging resistance, dormancy, yield etc. are discussed here.

## 2. STATUS OF RESEARCH

Submergence and drought are two major abiotic stresses in rainfed rice cultivation. Rice plants tolerant to complete submergence usually exhibit very limited elongation during submergence and often show tolerance to complete flooding, a strategy known as quiescence. The mechanistic understanding of molecular regulation of true submergence tolerance/ quiescence in rice has been advanced through functional characterization of key genes responsible for acclimatization to submergence stress in rice (Xu et al. 2006). Limited number of rice genotypes possess inherent mechanism to tolerate a deep transient flash flood through economization of energy reserves (quiescence strategy) (Fukao and Xiong 2013). Quantitative trait locus (QTL) analysis and map-based cloning revealed that the *SUBMERGENCE1* (*SUB1*) locus, encoding a variable cluster of two or three tandem-repeated group VII of *ETHYLENE RESPONSIVE FACTOR* (*ERF-VII*), regulate the quiescence response (Xu et al. 2006). Most of the reported rice accessions found to contain *SUB1B* and *SUB1C* genes at the *SUB1* locus, whereas *SUB1A* was reported to contribute ~70% of submergence tolerance to some *indica* and *aus* rice varieties. The major QTL, *Sub1A* has been fine mapped on chromosome 9 in the submergence tolerant cultivar FR13A (Xu et al. 2000). Researchers at International Rice Research Institute (IRRI), Philippines used back crossing involving a double haploid derived from three tolerant parents (FR13A, IR49830-7-1-2-2 and IR67819F2-AC-61) and a *japonica* rice KDML105. They were able to develop new Jasmine rice carrying QTL for submergence tolerance retaining the quality traits of KDML105. Under considerable stagnation of water, no other cereals besides rice can survive and produce. This unique ability in rice is attributed to its ability to elongate rapidly with onset of water stagnation. Under both the situations ethylene responsive factor genes control the elongation but in opposite direction i.e. quiescence and elongation (expansion) (Hattori et al. 2009). Snorkel 1 (*SK1*) and Snorkel 2 (*SK2*) allow rice to elongate fast whereas Submergence1A-1 (*Sub1A-1*) allows rice to squeeze elongation for adaptation to water stagnation and flash floods conditions, respectively. Both *SK* genes and *Sub1A* encode ethylene-responsive factor, a specific group of transcription factor related to gibberellin biosynthesis or signal transduction. Several mega rice varieties, which were submergence sensitive were being converted to submergence tolerant types through introgression of *Sub1A-1* genes through marker-assisted backcrossing and released for commercial cultivation in different submergence prone areas of Asia and Africa.

Drought is a major yield limiting factor in rainfed lowlands. Progress in drought breeding is very slow. The recent scenario in climate change indicates more unpredictable drought intensity in the eastern region of the country directing us for developing drought-resilient varieties. Fukai and Cooper (2001) have summarized the complexity of drought tolerance and emphasized strategies that influence yield under drought stress. The use of grain yield under drought stress is a selection criterion



which is useful for developing high-yielding rice cultivars for rainfed rice-growing areas. Several major quantitative trait loci (QTLs) showing effects under drought need to be pyramided together to develop drought-tolerant versions of popular drought-susceptible varieties. Three QTLs namely *qDTY1.1*, *qDTY2.1* and *qDTY3.1* are showing yield improvement under drought stress (Dixit et al. 2014). The QTL, *qDTY1.1*, shows a consistent effect on grain yield under lowland drought. Two large-effect QTLs influencing grain yield (*qDTY2.1* and *qDTY3.1*) show  $R^2$  values of 16.3% and 30.7%, respectively, under lowland drought. Another QTL, *qDTY12.1* shows consistent additive effects of 45% under drought, is mapped within the physical interval of 2.7MB between two microsatellite markers RM28048-RM28166 (Dixit et al. 2014). A large effect QTL (*qDTY3.2*) shows positive effect on yield under drought stress which co-localizes with *Hd9*, a locus which is related to days to flowering.

*Dro1* is negatively regulated by auxin and is involved in cell elongation in the root tip that causes asymmetric root growth and downward bending of the root in response to gravity. Higher expression of *Dro1* increases the root growth angle, whereby roots grow in a more downward direction. Introducing *Dro1* into a shallow-rooting rice cultivar by backcrossing enabled the resulting line to avoid drought by increasing deep rooting, which maintained high yield performance under drought conditions relative to the recipient cultivar. Root growth angle (RGA) is an important trait that influences the ability of rice to avoid drought stress. *DEEPER ROOTING 1 (Dro1)*, which is a major quantitative trait locus (QTL) for RGA, is responsible for the difference in RGA between the shallow-rooting cultivar IR64 and the deep-rooting cultivar Kinandang Patong (Uga et al. 2013). Natural variation in RGA in rice cultivars carrying functional *Dro1* alleles may be controlled by a few major QTLs and by several additional minor QTLs (Kitomi et al. 2015).

Rice is usually grown as direct seeded crop in the rainfed shallow lowlands of eastern India, which frequently coincides with heavy rainfall in a poorly leveled and with poorly drainage field resulting in poor plant stand. Submergence just after sowing imposes stress by creating hypoxic condition (3% Oxygen) during germination as well as during vegetative stage. Interestingly, mode of overcoming hypoxic stress by rice plants seems to be different during germination and vegetative stages. The genes and QTLs reported for vegetative stage submergence tolerance are of no use to tolerate germination stage submergence and *vice-versa*. Being adapted to aquatic ecology, rice has developed the unique mechanism to germinate and extend its coleoptile under water even in complete absence of oxygen - a phenomenon termed as anaerobic germination (AG). In general, rice coleoptile under water has been found to elongate about 1 mm h<sup>-1</sup> to reach the atmosphere by rapid elongation of basal cells (up to 200  $\mu$ m in 12 h) immediately after emerging from embryo (Narsai et al. 2015). However, anaerobic germination potential (AGP) varies greatly among different rice genotypes, which ultimately provide an edge to a few genotypes to perform better under oxygen deficient conditions over others.

Anaerobic respiration usually yields much less energy as compared to the aerobic mode of respiration. Here, the energy requirement is largely fulfilled by glycolysis followed by alcoholic fermentation. Transcriptome analysis data also revealed up-



regulation of genes related to starch and glucose metabolism, glycolysis and fermentation during germination under anaerobic condition/submergence (Narsai et al. 2017). Starch degrading enzymes like  $\alpha$ -amylase, aldolase and sucrose synthase are up regulated in germination stage oxygen deficiency (GSOD) tolerant cultivars greatly compared to susceptible cultivars with higher *RAmy 3D* gene expression as well as greater up-regulation of rice cytosolic hexokinase *OsHXX7* (Kim et al., 2016). The work of mapping QTLs imparting high anaerobic germination potential (AGP) has been initiated and one of the identified QTL, *qAG-9.2* has been fine-mapped to *OsTPP7* gene which encodes trehalose-6-phosphate phosphatase involved in starch mobilization during germination (Kretzschmar et al. 2015). Recent studies showed effective operation of anaerobic respiration and nitrogen metabolism in tolerant rice genotypes led to more energy efficient metabolic system under oxygen limiting GSOD condition resulting in better ROS handling and cellular pH maintenance (Vijayan et al. 2018).

Phosphorus is a limiting nutrient in the direct seeded rice ecology. Due to high cost of phosphatic fertilizers, farmers are not applying required quantity of the fertilizer. A major QTL *Pup1*, located on chromosome 12 exhibiting 78.8 % of the total phenotypic variance for phosphorus uptake has been found to be associated with tolerance to P deficiency and efficient P uptake in low phosphorus soil (Wissuwa et al. 2002). Kasalath, a *Pup1* donor variety has a 278 Kb INDEL and near isogenic lines with the QTL exhibited an increase P uptake and also 2-to 4- fold increase in grain weight per plant (Chin et al. 2010). Therefore, the development of P-efficient crop varieties that can grow and yield better with low P supply is a key to improve rice production.

Studies have showed that after flowering, lodging one day earlier causes yield loss to the tune of 2.6-2.7% per day in best *japonica* varieties grown at China. Through systematic studies on lodging resistance from last 25 years; researchers from Japan were able to demonstrate that lodging resistance can be significantly improved in rice without any compromise on grain yield. In fact they were able to identify mechanisms which simultaneously improve yield and lodging resistance and the genes were further cloned and characterized (Yano et al. 2015). Typhoon causes major damage to rice crop in Japan especially at maturity stage. Researchers were able to develop QTL-NILs by transfer of a genomic region from an Indian landrace Kasalath in the background of *japonica* cultivar Koshihikari which could survive two or more moderate typhoons in a particular year without any reduction in yield (Ishimaru 2008). The same research group was also able to identify another functional QTL which could improve lodging resistance through prevention of factors which lead to culm strength deterioration after grain lling (Kashiwagi et al. 2016). The prospect of combining high biomass production and lodging resistance was demonstrated through development of a long-culm rice forage cultivar named as 'Leaf Star' which was a low-lignin producing lodging resistant rice cultivar suitable for feed and bioenergy production (Ookawa et al. 2014). The important QTLs/genes responsible for lodging resistance in rice are presented in Table 1. The possibility of effective utilization of lodging resistance in rice while addressing the concern of yield and feed quality in Indian rice breeding programme need to be considered.



**Table 1. List of QTLs/ genes identified to confer lodging resistance in rice.**

QTL/ Gene	Feature	Population	Reference
<i>bsuc11</i> (Breaking strength upper culm 11)	Present in Chromosome 11. Improves Breaking strength of upper culm through thickening of cortical bre tissues in internode and raising the level of holocellulose.	Chromosome Segment Substitution Lines (CSSLs) developed from 'Koshihikari' and 'Kasalath'	Kashiwagi 2014
<i>pr15</i> (Pushing resistance lower 5)	Present in chromosome 5. Improves pushing resistance of lower plant parts ( <i>pr15</i> ) by delaying senescence and increasing carbohydrate reaccumulation in stems.	CSSLs developed from 'Koshihikari' and 'Kasalath'	Kashiwagi and Ishimaru 2004
<i>lrt5</i> (Lodging resistance in atyphoon 5)	Plants carrying this QTL circumvent domino effect. Starch content of upper culm in <i>lrt5-NILs</i> was 4.8 times when compared with recurrent parents	CSSLs developed from 'Koshihikari' and 'Kasalath'	Ishimaru et al. 2008
<i>SCM2</i> (Strong Culm 2) QTL/ Aberrant Panicle Organization1 ( <i>APO1</i> ) gene	The gene simultaneously improves section modulus of culm along with grain number per panicle.	CSSLs derived from Sasanishiki and Habataki	Ookawa et al. 2010
<i>SCM3</i> (Strong Culm 3) QTL/ Teosinte Branched1 ( <i>OsTB1</i> ) gene	The gene simultaneously improves section modulus of culm along with grain number per panicle. NILs of <i>SCM2</i> + <i>SCM3</i> further improves both traits	Backcross Inbred Lines (BILs) of Koshihikari and Chugoku117	Yano et al. 2015

Under shallow lowland condition, seed dormancy is a prerequisite for breeding of cultivars as it prevents pre-harvest sprouting of seeds which in terms significantly reduce the quality and storability of the harvest. Pre-harvest sprouting mostly happens when humidity and temperatures increase during grain filling and maturation, which are caused mostly by unseasonal rains. Several efforts for mapping QTLs/genes for seed dormancy have been taken by researchers of China and Japan using *indica* x *japonica* derivatives. Some of the significant findings have been listed in Table 2.

Bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is the most important disease of lowland rice in India. In some areas of Asia, it can reduce crop yield by up to 50% (Khush et al. 1989) or even up to 80% (Singh et al. 1977). In absence of effective chemical or other control agents against the pathogen, host plant resistance has gained enormous importance in controlling this disease. Using the gene pyramid approach, improved *indica* rice cultivars with broad spectrum durable BB resistance have been developed by combining different genes (Pradhan

**Table 2. List of QTLs/ genes identified to confer seed dormancy in rice.**

Genes/QTLs detected	Population	Reference
1. One QTL ( <i>Sdr1</i> ) for seed dormancy was identified which was very tightly linked to another QTL for heading date ( <i>Hd8</i> )	BILs from Nipponbare and Kasalath	Takeuchi et al. 2003
2. Four major QTLs and several minor QTLs were detected. <i>qSD-3</i> in chromosome 3 was most important.	Doubled haploid from indica x japonica	Guo et al. 2004
3. Three QTLs ( <i>Sdr6</i> , <i>Sdr9</i> and <i>Sdr10</i> ) were detected	CSSLs of Nona Bokra and Koshihikari	Marzougui et al. 2012
4. Four putative QTLs detected. <i>qSD-6.1</i> most effective among those.	BIL of Nipponbare x Kasalath	Sasaki et al. 2013
5. Eight additive effect QTLs for seed dormancy detected. Best combination for pyramiding also suggested.	RILs of japonica x indica	Wang et al. 2014
6. Several QTLs were mapped at 4, 5 and 6 weeks after heading in the same population	RILs of japonica x indica	Cheng et al. 2014
7. Sixteen and 38 loci significantly associated with dormancy in freshly harvested seeds and after ripened seeds were detected. There were three common QTLs among them.	Association mapping in global accessions of rice	Magwa et al. 2016
8. Six major additive effect QTLs ( <i>qSD3-2</i> , <i>qSD4-1</i> , <i>qSD7-1</i> , <i>qSD7-2</i> , <i>qSD7-3</i> and <i>qSD11-2</i> ) with contributions of more than or equal to 30 percent. Validated over seven cropping seasons	Single Segment Substitution Line of one indica rice with several donors	Zhou et al. 2017
9. Ten SNPs were identified which significantly affect Pre Harvest Sprouting and the alleles were validated using regression based model.	Resequencing of multiple accessions.	Lee et al. 2017

et al. 2015; 2016). A three-gene combination appeared to be the most effective; with *Xa21* contributing the largest component of resistance. Gall midge insect is an internal feeder of rice plant and it reduces rice yield severely. Till date, 11 gall midge resistant genes have been identified.

As overall grain yield of rice from a crop field is a very complex trait for direct improvement; efforts have been taken worldwide for utilizing the genes and QTLs for its component traits. *Gn1a*, a major QTL, has been cloned and characterized for grain number per panicle. The functional analysis shows that *Gn1a* encoded cytokinin oxidase/dehydrogenase (Ashikari et al. 2005). Ideal plant architecture1 (*IPA1*) changes rice plant architecture and enhances rice grain yield. This IPA1 encodes OsSPL14 (Jiao et al. 2010). The genes/QTLs associated with the yield enhancing traits are presented in Table 3.



**Table 3. Useful genes/QTLs for pyramiding of yield component traits for increasing yield potential in rice.**

Yield Genes/QTLs	Traits	Chromosome location	Donor line/variety	Gene function	Reference
1. <i>Gn1a</i>	Grain number	1	Habataki	Cytokinin Oxidase/Dehydrogenase2	Ashikari et al. 2005
2. <i>SPL16</i>	Panicle branching	8	ST12	Squamosa Promoter binding protein like-14	Wang et al. 2012
3. <i>SCM2</i>	Culm diameter	6	Habataki	F-box containing protein	Ookawa et al. 2010
4. <i>Ghd7</i>	Delayed heading date and increased plant height and yield	7	Minghui63	CCT domain protein	Xue et al. 2008
5. <i>GS5</i>	Grain length	5	Zonhhua11	Serine carboxy peptidase	Li et al. 2011
6. <i>GW5</i>	Grain weight	5	Nipponbare	Unknown protein	Weng et al. 2008
7. <i>TGW6</i>	Test grain weight	6	Kasalath	IAA glucose hydrolase	Ishimaru et al. 2013
8. <i>DEP1</i>	Erect panicle, high grain number	9	Shenung265	Phosphatidylethanol-amine binding protein	Huang et al. 2009
9. <i>SPIKE1</i>	Grain number/panicle	4	IR68522-10-2-2	Polar auxin protein	Fujita et al. 2013
10. <i>GW2</i>	Grain weight	2	Oochikara	Ring-type E3 ligase protein phosphatase	Song et al. 2007
11. <i>GS3</i>	Grain length	3	Minghui63	Trans membrane protein	Fan et al. 2006

FR13A, a selection from landrace ‘Dhalaputia’ is a widely used submergence tolerance donor line in submergence breeding programme. This line is the source material for submergence tolerance QTL, *Sub1*. The variety Swarna in which *Sub1* has been introduced through marker-assisted breeding has become very popular in rainfed lowland ecologies in the country. This was the first ever submergence tolerant variety released in the country (Neeraja et al., 2007). Swarna-Sub1 was released by SVRC, Odisha and SVRC, Uttar Pradesh and notified by Dept. Of Agriculture and Cooperation, Ministry of Agriculture, Govt. of India. Many pyramiding works on bacterial blight has also been performed in the country in various superior backgrounds (Pradhan et al. 2015; 2016). Till date 11 gall midge resistance genes have





been identified (Dutta et al. 2014). Researchers of ICAR-Indian Institute of Rice Research developed drought tolerant variety DRR Dhan 42 through pyramiding of *qDTY1.1*, *qDTY2.1* and *qDTY3.1* in IR64 background. The donor germplasm line N22, CR143-2-2, Bala, Lalnakanda, Dagad Deshi, Moroberekan, Aus 276, Vandana, Apo and IR55419-04 are commonly used donors for drought tolerance breeding programme in the country.

The rice breeders in India have mostly depended upon dwarfing genes for improving lodging resistance coupled with phenotypic selection for stronger culm. The general perception remained that selection of high culm strength may have negative impact on yield besides its low acceptability among farmers due to reduced feed quality of straw. There is no significant research report about genetic studies on lodging resistance of rice from India in last 20 years especially for waterlogged ecologies. Only very recently a report for mapping QTLs associated with lodging resistance in dry direct-seeded rice have been published by researchers from IRRI, India hub (Yadav et al. 2017). Rathi et al. (2011) mapped two QTLs for seed dormancy and one for duration of seed dormancy in a smaller F<sub>2</sub> population derived from two *indica* genotypes.

The submergence tolerance property of FR13A was first reported by NRRI and shared with other institutes, which was subsequently mapped as *Sub1* and used in rice breeding. The ICAR-NRRI has developed pyramided lines with *Xa21*, *xa13* and *xa5* resistance genes in the backgrounds of Swarna, Jalmagna, IR 64, Lalat and Tapaswini. The Institute also collaborated with IRRI for release of Swarna-Sub1 through SVRC, Odisha. Under ‘QTL to variety’ project, the Institute has stacked three abiotic stress tolerance genes viz., *Sub1+qDTY1.1+qDTY2.1* in the background of Swarna variety. Also, under IRRI-NRRI collaborative project, Swarna variety containing *Sub1*, *qDTY1.1*, *qDTY2.1* and *qDTY3.1* QTLs have been released for submergence and drought affected areas of Andhra Pradesh, Telangana, Odisha, Uttar Pradesh and West Bengal states of the country. A bacterial blight resistance genes pyramided line of Swarna has been released as CR Dhan 800 by SVRC, Odisha. Efforts are made to improve the popular lowland varieties like Gayatri, Sarala, Varshadha, Pooja and Pratikshya with submergence tolerance by incorporating “*Sub1*” gene through marker-assisted backcross breeding. Presently, the improved lines of these varieties are in the advanced stages of testing. Closely linked markers have been identified for gall midge resistance gene *Gm4* and QTL for BPH resistance (Mohanty et al. 2017) which can be used for pyramiding with other genes reported nationally and internationally. The Institute has released several varieties namely Pooja, Sarala, CR Dhan 500, CR Dhan 401, Gayatri, Savitri, Dharitri, Swarna-Sub1, CR Dhan 800, CR Dhan 801, CR Dhan 505, CR Dhan 506 and CR Dhan 508 for cultivation under shallow lowland ecosystem (Table 4).



**Table 4. Rice varieties developed by the institute for shallow lowland ecosystem.**

Variety name	Year of release	Maturity duration	Potential yield (t ha <sup>-1</sup> )	Grain type*	Special feature**	Recommended States
1. Anamika	1979	145	4.5	LB	-	Tamil Nadu
2. Ramakrishna	1980	130	4.0	MS	BLB, GM, tolerant to water logging, iron toxicity	Odisha
3. Samalei	1980	150	4.5	LS	GM, BL	Odisha
4. Savitri	1982	155	5.5	SB	BL, BB, MR	Andhra Pradesh, Odisha, Tamil Nadu
5. Dharitri	1988	150	5.0	SB	BI, BB, SB, GM	Odisha
6. Padmini	1988	145	4.0	ShS	BB	Odisha
7. Moti	1988	145	5.0	LS	BL, RTV, GLH	Odisha
8. CR 1002	1992	145	4.5-5.0	SB	ShB, GLH	West Bengal, Odisha, Bihar
9. Seema	1992	150	4.5-5.0	MS	Blast, BPH, GM, tolerant to water logging	Odisha
10. Pooja	2000	150	5.0	MS	BL	Odisha, Madhya Pradesh, West Bengal
11. Ketekijoha	2005	145	3.5	MS	BB, ShB, SB, GM	Odisha
12. Nua Kalajeera	2008	145-150	3.0	SB	YSB, BI, Sh.R, Black husk	Odisha
13. Nua Dhusara	2008	145-150	3.0	SM	NB, ShR, RTV, GM	Odisha
14. Swama-Sub1	2009	143	7.0	MS	Tolerant to complete submergence for two weeks	Odisha, Uttar Pradesh
15. Reeta	2010	150	7.5	MS	BL, NB, BS, ShB, ShR, SB, LF	Odisha, West Bengal, Tamil Nadu, Andhra Pradesh
16. Nua Chinikamini	2010	145-150	3.5	SB	RTV, SB, RGM, NB, Sh.R	Odisha
17. CR Dhan 500	2011	160	7.2	MS	MR to LB, NB, GM, SB, LF	Odisha, Uttar Pradesh
18. Sumit	2012	145-150	7.5	LB	LB, SB, LF	Odisha
19. Poorna Bhog	2012	140-145	5.2	LS	NB, GM, ShR, SB	Odisha
20. Jalamani	2012	160	4.9	MS	MR-LF, GLH, LB, NB, BS, G, SB	Odisha

Contd....



Variety name	Year of release	Maturity duration	Potential yield (t ha <sup>-1</sup> )	Grain type*	Special feature**	Recommended States
21. Jayantidhan	2012	160	5.3	MS	MR-LB, NB, ShB, ShR, RTV, GM, SB, LF, RT, WM	Odisha
22. CR Dhan 407	2014	150	5.8	LB	MR to leaf blast, neck blast	Odisha, West Bengal
23. CR Dhan 505	2014	162	7.1	MS	Submergence tolerance	Odisha, Assam
24. CR Dhan 408 (Chakaakhi)	2014	165	7.5	LB	MR-LB, NB, BB, Sh.R, SB, LF, WBPH	Odisha
25. CR Dhan 508	2016	160	8.5	LB	MR-NB, BS, ShR, SBR, LF, WM	Odisha, Assam West Bengal
26. Pradhandhan (CR Dhan 409)	2016	160	7.8	LS	MR-LB, NB, ShR, SBR, LF	Odisha
27. CR Dhan 507	2016	165	6.8	MB	MR-NB, BS, ShR, ShB, SBR, WM, LF	Odisha
28. CR Dhan 910	2016	140-145	5.6	MS	MR-BL, NBI, ShR, RTV, SB, LF, WBPH	Odisha
29. CR Dhan 909	2017	140	6.5	MS	Tolerant to LB, NB, Sh.R, RTD	Uttar Pradesh, Bihar, Assam, Maharashtra
30. CR Dhan 801	2017	140	7.8	MS	For submergence and drought prone areas	Uttar Pradesh, Bihar, Odisha, West Bengal

Note: \*SB-Short bold; LS-long slender; MS-Medium slender; MB-Medium bold; LB-Long bold\*\*Bl-blast; BB-Bacterial blight;BPH-brown plant hopper; BS-brown spot; GB-gundhi bug; GM-gall midge; GLH-green leaf hopper; LF-leaf folder; RTV-rice tungro virus; SB-stem borer; Sh.B-Sheath blight; Sh.R-Sheath rot; WBPH-white backed plant hopper; YSB-yellow stem borer; HS-Helmenthosporium

### 3. WAY FORWARD

Research need to be carried out to reduce the yield limiting factors of the rainfed lowland ecology. Efforts to increase yield potential of the shallow lowland rice may further be expedited to get a quantum jump in yield from a vast neglected area of eastern India. As the rainfed areas of the country are highly affected by climate change effects, the high yielding varieties of the ecology need to be stacked with stress tolerance gene(s)/QTLs for making them climate smart. Effects of the QTLs/ gene(s) need to be segregated out first and then combination effects need to be studied so that proper pyramiding as well as stacking combinations can be identified. Study on development of host plant resistance for the emerging diseases and insect pests need to be taken up in an environment friendly manner. Translocation of elements like heavy metals from soil to grains and straw need to be in a safer level. Genetic enhancement of the materials for toxic and other problematic soils need more attention



in future. Trait combinations in superior background should lead to development of high and sustainable performing varieties with higher benefits to the producers. Thus, in popular varieties, multiple tolerance genes for submergence, anaerobic germination, yield QTLs under drought, bacterial blight resistance genes, gall midge resistance genes, seed dormancy and yield enhancing QTLs need to be stacked to make them highly resilient to the climate change.

In future, production of rice needs to be increased from lesser land area. For this purpose there is effort towards increasing per plant yield though higher grain number per panicle and grain weight. This will definitely increase the weight of upper part of the rice plant and thereby increasing the chance of lodging with current plant types of *indica* rice. The problem is further coupled by increasing climatic vagaries like erratic rainfall, increase in extreme weather events and uncharacteristic wind flow especially in eastern and southern coasts of the country. Lodging related losses in semi dwarf varieties still remains to the extent of 35% and at some specific locations even >85% where traditional cultivars are grown. There is a need for systematic studies for improving lodging resistance of rice in our country. More so, understanding the mechanism and devising strategies for improvement of lodging resistance to *indica* rice would be important to breed future rice with high biomass coupled with higher harvest index. Further it will be necessary to save rice in climate vulnerable regions where incidences of sudden heavy rain or wind during maturity of crop cause severe production losses.

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