



Conventional and molecular breeding strategies for improvement of drought tolerance cultivars in rice: Recent approaches and outlooks

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ABSTRACT

Rice is a vital staple food, especially in Asia, but it is highly susceptible to drought, leading to significant yield losses. To ensure food sustainability, drought-tolerant rice varieties are essential. Conventional breeding methods improve drought tolerance by focusing on biometric traits like root depth, avoidance, escape, and tolerance. This involves screening and crossing drought-tolerant varieties with high-yielding ones, followed by selection and evaluation. Techniques such as pedigree selection, recurrent selection, and backcrossing introduce desirable genes to enhance drought tolerance. Induced mutation through radiation exposure is also used. The molecular basis of drought tolerance involves identifying and manipulating genes responsible for rice's response to water stress. Techniques like QTL analysis, transcriptomics, genomics, and proteomics identify genes and QTLs associated with drought tolerance. Important genes involved in drought response include DREB, LEA, and ROS scavenging genes. Identifying QTLs enables the development of molecular markers for efficient screening of drought-tolerant rice genotypes. In conclusion, conventional breeding and molecular approaches are employed to develop drought-tolerant rice varieties. Conventional breeding improves biometric traits, while molecular techniques identify and manipulate specific genes associated with drought tolerance. This combination holds promise for high-yielding and drought-tolerant rice cultivars, contributing to global food security. However, further research is needed to understand the complex genetic mechanisms underlying drought tolerance in rice and enhance breeding precision and efficiency.

Introduction

Rice (*Oryza sativa* L.) is a staple food for more than one-third of the global population, with Asia being the leading producer and consumer of rice. Rice provides 80% of daily caloric needs for many

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people (Samal *et al.*, 2018, Panda *et al.*, 2021). However, rice is highly vulnerable to drought due to its tiny root system, thin cuticular wax, and quick stomata closure. Drought is one of the most destructive abiotic factors that can lead to complete yield losses, particularly during the reproductive development stage (Turrall *et al.*, 2011, Oladosu *et al.*, 2019, Simkhada and Thapa, 2022). To achieve self-sufficiency in rice production and ensure food sustainability for the expanding population, there is a need to develop high-yielding rice varieties that are tolerant and resistant to both biotic and abiotic stressors, including drought (Asim *et al.*, 2021, Gupta *et al.*, 2020, Myers *et al.*, 2017, Kaya *et al.*, 2013). The increasing severity of droughts and the lack of high-yielding cultivars for drought-prone regions are the main challenges limiting rice output globally (Gupta *et al.*, 2020). Progress in breeding drought-tolerant rice has been modest in the past due to the limited number of drought-tolerant variations discovered after screening a large number of germplasm samples (Myers *et al.*, 2017, Pandey *et al.*, 2015). Rice cultivation is seasonal and could be improved by developing drought-resistant rice cultivars and sustainable farming techniques (Singh *et al.*, 2016).

The scarcity of high-yielding genotypes that can grow in drought-prone environments and the increasing severity of droughts are the two most significant limiting factors for low rice production globally (Oladosu *et al.*, 2019, Pandey *et al.*, 2015, Chaum and Kirdmanee, 2010). Breeding drought-tolerant rice cultivars has been challenging due to the quantitative and complex nature of the trait. Researchers have screened thousands of germplasms from different parts of the world and identified only a few drought-tolerant variants (Melandri *et al.*, 2020, Cicek *et al.*, 2012). The success of breeding drought-tolerant rice is hindered by the lack of appropriate screening techniques and a shortage of donors with a high level of drought tolerance. This review chapter aims to explain how drought stress affects rice plants and to highlight current developments in rice's molecular adaptation to drought tolerance. Additionally, the review describes the current process for creating a long-lasting rice variety that is drought-resistant through conventional breeding and the application of biotechnological tools. Lastly, the review conducts a thorough analysis of

the information that is currently available on drought-resistant genes/QTLs, QTL analysis, gene introgression, and marker-assisted selection.

Conventional breeding approaches for developing drought-tolerant rice focus on improving biometrical traits

Conventional breeding approaches for improving biometrical traits such as root depth, drought avoidance, drought escape, and drought tolerance. These approaches include, screening of rice germplasm for drought tolerance is the first step in conventional breeding for drought tolerance. Rice breeders cross drought-tolerant varieties with high-yielding varieties to develop hybrid cultivars with both yield and drought tolerance. Rice breeders select the best plants from a population based on their drought tolerance and yield performance, and cross them to produce the next generation. The best drought-tolerant plants are crossed back to the original high-yielding variety to improve the yield of the drought-tolerant cultivar. Rice breeders evaluate the phenotype of the plants to select the best ones for further breeding. The final step in conventional breeding is to evaluate the performance of the drought-tolerant cultivars in field trials under drought conditions, these approaches are discussed below.

In conventional breeding methods, grain yield was traditionally used as a selection criterion for drought-resistant crops, but this has proven to be ineffective due to low heritability and strong genotype by environment interaction (Upadhyaya *et al.*, 2019, Chourasia *et al.*, 2017). Instead, selection has shifted towards physiological traits as they have a more direct link to crop performance and depend more on genetic variation (Chourasia *et al.*, 2017, Atkinson *et al.*, 2012, Dixit *et al.*, 2014). The ultimate goal of crop breeding is to create high-yielding varieties in ideal water conditions, but well-yielding varieties can still maintain moderate to high yields during drought conditions (Khush *et al.*, 1984).

The general selection process for developing drought-tolerant rice involves the use of pedigree selection, which is a traditional and popular breeding technique (Tatar *et al.*, 2010, Khush *et al.*, 1984). This approach is suitable for building resistance in rice when the trait is controlled by important genes. The main advantage of pedigree selection is the ability to combine numerous genes

affecting biotic and abiotic processes. However, it is a time-consuming process that requires evaluating numerous lines repeatedly over planting seasons while maintaining a record of the selection criteria. The approach is not appropriate for traits influenced by multiple genes, in which case the diallel mating design is more suitable for selection (Khush *et al.*, 1984). Recurrent selection is a preferred method over pedigree selection in the development of drought-tolerant rice and other self-pollinated crops (Miah *et al.*, 2013, Maqsood *et al.*, 2013). This method is used to increase favourable allele frequencies while preserving genetic diversity. Recurrent selection offers more accurate genetic gains, faster and more defined breeding cycles, and the creation of highly diversified breeding lines. It has been extensively used in rice breeding and has been shown to be more effective than pedigree selection (Pang *et al.*, 2017). The backcrossing technique is frequently employed in rice breeding to introduce desirable genes from the donor parent to the recipient parent. This method provides a precise and accurate way to create multiple superior breeding lines, and has been used to create rice cultivars that are drought-tolerant (Lafitte *et al.*, 2006, Oladosu *et al.*, 2014, Oladosu *et al.*, 2015, Oladosu *et al.*, 2016). Induced mutation is a technique used to supplement conventional breeding methods in the development of drought-tolerant rice. It has been shown to be effective in improving traits such as grain yield (Oladosu *et al.*, 2014, Oladosu *et al.*, 2015, Oladosu *et al.*, 2016), resistance to pests and diseases, and physical grain quality. The main advantage of induced mutation is the ability to create new gene alleles that are not found in nature. This method has been used to create innovative rice varieties with improved characteristics. For example, exposure of Manawthukha rice to gamma radiation resulted in the creation of two mutant lines, *MK-D-2* and *MK-D-3*, which were determined to be drought-resistant after six generations of evaluation and selection. In Iran, 11 lines with drought-tolerant traits were chosen from the ‘*Tarom Mahalli*’ rice landrace after exposure to gamma radiation. In Indonesia, induced mutation was used to create a super green rice mutant that is drought-resilient, high-yielding, and water-efficient (Hallajian *et al.*, 2014). In Malaysia, two improved lines with high production

potential and drought tolerance were developed from the common *MR219* rice variety (Gosal *et al.*, 2009). These conventional breeding approaches have been successful in developing drought-tolerant rice cultivars, but they are time-consuming and have limited precision. New biotechnological tools are being developed to improve the efficiency and accuracy of breeding for drought tolerance.

The molecular basis for drought tolerance in rice

The molecular basis for the improvement of drought tolerance in rice involves the identification and manipulation of genes that regulate the plant's response to water stress. This is achieved through the use of various molecular techniques such as quantitative trait locus (*QTL*) analysis, transcriptomics, genomics, and proteomics (Fahliani *et al.*, 2011, Zargar *et al.*, 2011). In summary, the molecular basis for improving drought tolerance in rice involves the identification of genes and associated qualitative trait loci (*QTLs*) that are responsible for the trait and *QTLs* list presented in (Table 1). This can be achieved through DNA marker-based phenotyping studies and screening of large collections of germplasm (Kumar *et al.*, 2017, Upadhyaya *et al.*, 2019, Barik *et al.*, 2019). The identified genes can then be introduced into the genetic background of suitable cultivars through genetic engineering techniques like *Agrobacterium tumefaciens* or gene gun, and hybridization with marker-assisted selection (Gosal *et al.*, 2009). The goal is to create transgenic crops with improved drought tolerance and improved yields, ensuring high agronomic validity and safety.

***QTLs* associated with rice drought tolerance**

The plant genome has a number of genes known as *QTLs* that have extremely precise quantitative properties. (Table 2) displays many *QTLs* connected to various agronomic traits under drought. However, finding these *QTLs* for drought tolerance is not a simple task, as it involves complex interactions between different genes, and their effects on various physiological and biochemical processes in the plant (Dixit *et al.*, 2014, Barik *et al.*, 2019). Therefore, a combination of various molecular markers, phenotypic assays, and genomic data is used to identify and validate these *QTLs* for drought tolerance in rice (Singh *et al.*, 2016).

Table 1: List of rice quantitative trait loci (QTLs) associated with various drought tolerance traits

Traits	QTLs	References
Grain yield (GY) and flag leaf (FL) photosynthesis under drought stress	<i>qDTY1.1</i> , <i>qDTY3.2</i> , <i>qDTY10.1</i> , <i>qDTY1.2</i> , <i>qDTY1.3</i> , <i>qDTY2.2</i> , <i>qDTY2.3</i> , <i>qDTY3.1</i> , <i>qDTY6.1</i> , <i>qDTY6.2</i>	Vikram <i>et al.</i> , 2016
Leaf rolling (LR)	<i>qlr8.1</i> , <i>qLR9.1</i> , <i>qDLR8.1</i>	Lin <i>et al.</i> , 2007
Leaf drying (LD)	<i>qLD9.1</i> , <i>qLD12.1</i>	Barik <i>et al.</i> , 2019
Harvest index (HI)	<i>qHI9.1</i> , <i>qSf6</i> , <i>qPNF3.1</i>	Barik <i>et al.</i> , 2019
Spikelet fertility (SF)	<i>qSF9.1</i>	Barik <i>et al.</i> , 2019
Panicle number (PN)	<i>qgy3.1</i>	
Plant height (PH)	<i>qPH1.1</i>	Trijatmiko <i>et al.</i> , 2014
Flowering day (FD)	<i>qHGW2.2</i>	Trijatmiko <i>et al.</i> , 2014
PN & grain weight (GW)	<i>qGy7</i>	Trijatmiko <i>et al.</i> , 2014
Panicle length (PL)	<i>qPL-9</i>	Sellamuthu <i>et al.</i> , 2015
Grain number (GN)	<i>qDTY8.1</i>	Trijatmiko <i>et al.</i> , 2014
Relative water content (RWC)	<i>qRWC9.1</i>	Vinod <i>et al.</i> , 2019
Transpiration, root growth, number (RN) and length (RL) root volume	<i>qDTR8</i>	Xu <i>et al.</i> , 2016
Shoot growth and biomass accumulation	<i>qSW5</i>	Vinod <i>et al.</i> , 2019
PN & grain size (GS)	<i>qTL33</i>	Vikram <i>et al.</i> , 2016
FL area and stomatal conductance	<i>qLPD6</i>	Vikram <i>et al.</i> , 2016

This multi-disciplinary approach has enabled the identification of several drought-responsive genes, such as *DREB*, *LEA*, and *ROS* scavenging genes, that play key roles in drought tolerance (Dixit *et al.*, 2014, Barik *et al.*, 2019, Ramchander *et al.*, 2016, Lin *et al.*, 2007). By using these genes as targets, plant breeders can create more drought-tolerant rice varieties through genetic engineering or marker-assisted breeding (Pandey *et al.*, 2015). The ultimate goal of this research is to provide improved rice varieties to farmers, particularly in areas that are frequently affected by drought, to enhance food security and reduce poverty. In conclusion, identifying *QTLs* associated with drought tolerance in rice is an important step towards creating drought-resistant rice varieties. The majority of the *QTLs* discovered so far come from non-elite genotypes, including *qDTY1.1* (Barik *et al.*, 2019), *qDTY2.1*, *qDTY2.2* (Dixit *et al.*, 2014), *qDTH2.3* (Usman *et al.*, 2017), *qDTY3.1*, *qDTY6.1* (Ramchander *et al.*, 2016),

qDTR8 (Lin *et al.*, 2007), *qLR9.1*, *qLD9.1*, *qHI9.1*, *qSF9.1*, and *qRWC9.1* (Barik *et al.*, 2019). These *QTLs* control various morpho-physiological traits, including leaf rolling, leaf drying, harvest index, spikelet fertility, and relative water content. The use of DNA markers such as SSRs associated with these *QTLs* can aid in molecular screening of new rice genotypes for drought tolerance (Usman *et al.*, 2017). This would result in a faster and more accurate profiling of rice lines, leading to the development of drought-resistant rice cultivars with high yield and agronomic validity.

Rice drought tolerance via transgenic/genetic engineering and genetic methods

For instance, overexpression of the rice *WRKY* transcription factor gene *OsWRKY22* improved drought tolerance by regulating stress-responsive genes, including those involved in water uptake, water transport, and energy metabolism.

Table 2: QTL/genes and their contributions to phenotypic variation in drought tolerance traits were studied in rice

Trait	Pedigree	Marker	Mapping population	No. of QTL	References
Drought resistance (DRs) in seeds	Indica × Azucena	RFLP & SSR	RIL	7	Zheng <i>et al.</i> , 2008
Stability of cellular membranes (CM)	IR62266 x CT9993	RFLP, AFLP, SSR	DH	9	Tripathy <i>et al.</i> , 2000
Leaf rolling (LR) and leaf water relationships	Azucena × Bala	RFLP, AFLP, SSR	RIL	13	Khowaja & Price <i>et al.</i> , 2008
Grain yield (GY), panicle and seed fertility	Teqing x Lemont	SNP	IL	5	Wang <i>et al.</i> , 2014
Length, thickness, and root number	IR58821 × IR52561	AFLP & RFLP	RIL	28	Ali <i>et al.</i> , 2000
Root distribution & architecture, deep roots	IR64 x Azucena	RFLP	DH	39	Lou <i>et al.</i> , 2015
Deep root (DR) architectural traits	3 populations	SSR, SNP	RIL	6	Lou <i>et al.</i> , 2015
Root penetration, high root and tiller number	CO39 × Moroberekan	RFLP	RIL	39	Lou <i>et al.</i> , 2015
High GY drought	Two population	SSR	BS	4	Wang <i>et al.</i> , 2014
GY in aerobic environments (E)	Three populations	SSR	BS	1	Vikram <i>et al.</i> , 2016
Yield traits at the reproductive stage (RS)	IR64 × Cabacu	SNP	RIL	1	Trijatmiko <i>et al.</i> , 2014
GY under stress at RS	swarna x WAB	SSR	BIL	1	Wang <i>et al.</i> , 2014
Grain yield under severe lowland drought	R77298 x Sabitri	SSR	BC1	1	Vikram <i>et al.</i> , 2016
Yield at RS over factor E	Two populations	SSR	BSA	2	Vikram <i>et al.</i> , 2016
Physio-morphological traits	IR64 × Azucena	RFLP	DH	15	Trijatmiko <i>et al.</i> , 2014
Drought tolerance (DT) & Osmotic adjustment (OA)	CO39 × Moroberekan	RFLP	RIL	1	Vinod <i>et al.</i> , 2019

Table 3: List of some of the genes that have been associated with different mechanisms of drought tolerance in rice

Gene	Function	References
<i>DRO1</i>	Induces root elongation and DR	Uga <i>et al.</i> , 2013
<i>OsDREB1C</i> , <i>OsDREB2B</i> , <i>OsDREB2C</i> , <i>OsDREB2D</i> , <i>OsDREB2E</i> , <i>OsDREB2F</i>	Root growth and water uptake	Trijatmiko <i>et al.</i> , 2014; Vinod <i>et al.</i> , 2019
<i>OsPP2C39</i> , <i>OsPP2C40</i>	LR	Khowaja & Price <i>et al.</i> , 2008
<i>OsDREB1F</i>	Maintains ABA-dependent signaling pathway	Fu <i>et al.</i> , 2017
<i>OsDREB2B</i>	RL and RN of root increment	Xu <i>et al.</i> , 2016
<i>OsProT1</i> , <i>OsProT2</i>	Proline biosynthesis	Chaum & Kirdmanee, 2000
<i>CYP735A</i>	Maintains cytokinin level	Kumar & Verslues, 2015
<i>OsABI1</i> , <i>OsABI2</i> , <i>OsABI3</i>	ABA signaling and regulation	Fu <i>et al.</i> , 2017
<i>OsNAC5</i>	Enhances root diameter and GY	Wang <i>et al.</i> , 2014
<i>SNAC1</i>	Enhances SF	Barik <i>et al.</i> , 2019
<i>OsGRX480</i> , <i>OsGRX581</i> , <i>OsGRXS21</i>	Antioxidant defense	Uga <i>et al.</i> , 2013
<i>OsPIP2;3</i> , <i>OsPIP2;5</i> , <i>OsPIP2;6</i>	Stomatal regulation (SR)	Xu <i>et al.</i> , 2016
<i>OsZIP23</i> , <i>OsZIP46</i>	Increases GY	Vikram <i>et al.</i> , 2016
<i>AP37</i>	Enhances seed filling and GW	Trijatmiko <i>et al.</i> , 2014
<i>OsZIP71</i>	Enhances seed setting (SS)	Barik <i>et al.</i> , 2019
<i>OsLIP9</i> , <i>OsLIP21</i>	Water retention	Lou <i>et al.</i> , 2015
<i>EcNAC67</i>	Increases RWC, delays LR, higher root and shoot mass	Xu <i>et al.</i> , 2016
<i>OsNHX1</i>	CM stability	Tripathy <i>et al.</i> , 2000
<i>DsM1</i>	Helps in Reactive oxygen species (ROS) scavenging, maintains drought tolerance (DT) at the seedling	Huang <i>et al.</i> , 2009; Kim <i>et al.</i> , 2020
<i>OsPYL/RCAR5</i>	Induces stomatal closure, regulates leaf fresh weight	Xu <i>et al.</i> , 2016
<i>OsWRKY47</i>	Relatively low GY reduction	Wang <i>et al.</i> , 2014
<i>AtDREB1A</i>	OA, chlorophyll maintenance, higher RWC and reduced ion leakage	Vinod <i>et al.</i> , 2019
<i>TlOsm</i>	Maintains growth, retains higher RWC and membrane integrity and improves survival rate	Xu <i>et al.</i> , 2016
<i>OsMIOX</i>	Higher ROS and proline content	Chaum & Kirdmanee, 2000
<i>Coda</i>	Better yield, higher photosystem II activity, increased detoxification of ROS	Kim <i>et al.</i> , 2020
<i>OsTPS1</i>	Higher trehalose and proline accumulation	Chaum & Kirdmanee, 2000
<i>OsCPK9</i>	Increases DT through enhanced stomatal closure (SC) and better OA in transgenics	Vikram <i>et al.</i> , 2016; Vinod <i>et al.</i> , 2019
<i>OsNAC10</i>	Increases DT at vegetative stage, enlarges roots and improves GY	Vikram <i>et al.</i> , 2016

Other functional proteins like heat shock proteins (HSPs) have also been found to play a role in the improvement of drought tolerance in rice (Wang *et al.*, 2014). In addition to the genes mentioned, small non-coding RNAs have been found to regulate gene expression (Table 3) and contribute to drought tolerance in rice (Pang and Chen, 2017). Another important factor is the regulation of hormones such as abscisic acid (ABA) that play a crucial role in the regulation of water uptake, stomatal closure, and tolerance to drought stress (Usman *et al.*, 2017, Efendi *et al.*, 2013). Therefore, molecular studies on drought tolerance in rice have revealed numerous genes and pathways that contribute to the improvement of drought tolerance in rice. The use of molecular markers and genetic engineering techniques, in combination with traditional breeding techniques, could be utilized to create more drought-tolerant rice cultivars and contribute to global food security.

Zinc finger proteins are widely distributed in plants, including *WRKY* genes that regulate various abiotic stress responses (Sahebi *et al.*, 2018, Huang *et al.*, 2009). Rice zinc-finger protein (*dst* mutant) has demonstrated increased drought and salt tolerance by decreasing stomata density and improving stomata closure (Huang *et al.*, 2009). The overexpression of *OsZFP252* has also been shown to improve drought tolerance by increasing proline and soluble sugar levels (Xu *et al.*, 2008). After drought stress exposure, approximately 5000 genes are up-regulated and 6000 genes are down-regulated in rice (Oladosu *et al.*, 2014, Joshi *et al.*, 2016). These genes play a role in membrane transport, signalling, and transcriptional regulation (Upadhyaya *et al.*, 2019, Kim *et al.*, 2020) and are associated with drought tolerance, as listed in (Table 4).

In conclusion, the regulation of several genes, proteins and transcription factors play a vital role in the drought tolerance of rice plants (Gupta *et al.*, 2020, Dash *et al.*, 2018). Different genes and proteins have different functions, such as osmoregulation (Kumar *et al.*, 2015, Upadhyaya *et al.*, 2019), ABA signaling (Gupta *et al.*, 2020, Dash *et al.*, 2018), and stomata regulation, which improve drought tolerance. The overexpression or suppression of these genes have been studied to assess their impact on drought tolerance, and many

have demonstrated increased chances of survival and better growth under drought stress (Fu *et al.*, 2017). These findings highlight the importance of molecular screening for drought tolerance in rice and the potential for improving crop production in water-limited environments.

In summary, various genes and transcription factors play a role in regulating rice's response to drought stress. Transgenic methods have been used to introduce genes that improve root elongation (Kim *et al.*, 2020, Joshi *et al.*, 2016, Fu *et al.*, 2017, Uga *et al.*, 2013), osmoregulation, stomatal closure, water use efficiency, drought tolerance, and reduced levels of ROS. The overexpression of genes like *DREB2* (Huang *et al.*, 2009), *OsDREB2B*, *CYP735A*, *OsDRAP1* (Kim *et al.*, 2020), *OsNAC5*, *OsLEA3-1* (Liu *et al.*, 2014), *OsCPK9* (Wei *et al.*, 2014), *OsWRKY47* (Raineri *et al.*, 2015) and *OsZIP46* (Rahman *et al.*, 2016) has been shown to improve drought tolerance in rice. Some genes like *OsITPK2* (Du *et al.*, 2010) play a role in regulating ROS homeostasis under drought stress. Additionally, gene regulation is also influenced by ABA dependent and independent mechanisms *OsWRKY47* (Raineri *et al.*, 2015), *OsZIP46* (Rahman *et al.*, 2016), as well as the interaction between regulatory proteins and signal transduction pathways (Xiang *et al.*, 2008, Du *et al.*, 2010).

Various genes have been tested for their ability to confer drought resistance in rice using transgenic techniques. Some of these genes include *OsJAZ1*, *DRO1*, *OsDREB2B*, *CYP735A*, *OsDREB1F*, *OsDRAP1*, *OsNAC5*, *OsLEA3-1*, *OsZIP71*, *OsWRKY47*, *OsZIP46*, *EDT1/HDG11*, *AtDREB1A*, *OsMIOX*, *OsTPS1*, *OsCPK9*, *OsDREB2A*, *CDPK7*, *CIPK03/CIPK12*, *OsITPK2* and *WRKY* genes (Panda *et al.*, 2021). The buildup of trehalose has been shown to increase drought tolerance in rice by stabilizing proteins against denaturation and storing carbs. The fusion *TPP/TPS* gene from *E. coli* (*otsA* and *otsB*) has been introduced into rice and has been shown to increase trehalose, improve drought tolerance and decrease photo oxidation in the rice plant under cold and salt stress (Jang *et al.*, 2003). Before being used in molecular breeding programs, these genes need to be tested in field conditions.

The summary of alternative breeding strategies for rice drought tolerance

Rice is one of the most important staple crops in the world, and drought stress can significantly impact rice production. To mitigate the effects of drought on rice cultivation, scientists and breeders have employed both conventional breeding techniques and molecular breeding methods to develop drought-tolerant rice cultivars (Table 5 and 6). Here are some examples of rice cultivars developed for drought tolerance through these approaches (Kumar *et al.*, 2014).

Swarna-Sub1: Swarna-Sub1 is a popular drought-tolerant rice variety developed through conventional breeding at the International Rice Research Institute (IRRI). It was created by introgression the Sub1 gene from a wild rice species, *Oryza rufipogon*, into the popular rice variety Swarna. The Sub1 gene confers tolerance to prolonged submergence and also enhances drought tolerance in rice.

DRR Dhan 42: Developed by the Directorate of Rice Research (DRR) in India, this variety exhibits tolerance to both drought and submergence stresses. It was developed through a combination of conventional breeding and marker-assisted selection.

IR64-Sub1: IR64-Sub1 is another drought-tolerant rice cultivar developed through conventional breeding. It is a variant of the widely cultivated rice variety IR64, which was crossed with a wild rice relative carrying the Sub1 gene. IR64-Sub1 exhibits improved tolerance to both submergence and drought stress.

Vandana: Vandana is a drought-tolerant rice variety developed through conventional breeding at the International Rice Research Institute (IRRI). It is known for its tolerance to both drought and salinity stress. Vandana was developed by selecting and breeding from diverse rice germplasm for several generations to accumulate favorable traits for drought tolerance.

Sahbhagi Dhan: Sahbhagi Dhan is a popular drought-tolerant rice variety developed through molecular breeding techniques. It was developed by the scientists at the Bihar Agricultural University in India by introgression a major quantitative trait locus (QTL) for drought tolerance called "qDTY12.1" into a high-yielding rice variety.

Sahbhagi Dhan exhibits improved yield and drought tolerance under water-limited conditions.

Sub1-2: Sub1-2 is a drought-tolerant rice cultivar developed through molecular breeding. It is a variant of the popular rice variety IR64, where the Sub1 gene was introduced using genetic engineering techniques. The Sub1-2 rice plants exhibit enhanced tolerance to submergence and also show improved drought tolerance.

Swarna-Sub1A: This variety is an improved version of Swarna-Sub1, developed using marker-assisted selection. It carries the SUB1A gene, providing tolerance to submergence and drought stress.

Vandana Sub1: Another example of a rice variety developed through marker-assisted selection, Vandana Sub1 carries the SUB1A gene and exhibits enhanced tolerance to submergence and drought.

Sahbhagi Dhan Sub1: This is a drought-tolerant variety developed through marker-assisted selection by the ICAR. It carries the SUB1A gene and has shown improved drought tolerance.

Nerica-4: This variety was developed through conventional breeding at the Africa Rice Center (WARDA). It is a drought-tolerant variety that combines the African parent *Oryza glaberrima* and the Asian parent *Oryza sativa*.

NERICA-L-19: Another drought-tolerant variety developed by the Africa Rice Center, NERICA-L-19 is known for its high cooking quality and suitability for table use.

WAB56-104: This variety, developed by the West Africa Rice Development Association (WARDA), is well adapted to drought-prone environments and has good cooking characteristics.

CT9993-5-10-1-1: This variety was developed using marker-assisted selection and contains the Sub1 gene for submergence tolerance and drought tolerance. It is known for its good cooking quality.

Azucena Sub1: Azucena Sub1 is a drought-tolerant variety developed through marker-assisted selection. It carries the Sub1 gene and exhibits good eating and cooking quality.

Samba Sub1: Developed through marker-assisted selection, Samba Sub1 is a table rice variety that carries the Sub1 gene, providing tolerance to submergence and drought stress. These examples highlight the successful efforts in developing drought-tolerant rice cultivars through both

Table 4: List of multiple genes that have been tested for their ability to confer drought tolerance in rice through genetic engineering or transgenic methods

Gene Action	Gene	Promoter	Gene transfer methods	Phenotype	References
Genes Encoding Enzymes that Synthesize Osmotic and Other Protectants					
Polyamine synthesis	<i>ADC, OsProT1 & OsProT2</i>	<i>Ubi-1</i>	<i>Biolistic</i>	Improved DT with high putrescine and spermine synthesis	Capell <i>et al.</i> , 2004
abscisic acid Metabolism	<i>CaMV35SP</i>	<i>DSM2</i>	<i>Agrobacterium</i>	Oxidative and DRs and increase xanthophylls and non-photochemical quenching	Fu <i>et al.</i> , 2017
Amino acid metabolism	<i>OsOAT</i>	<i>Ubi1</i>	<i>Agrobacterium</i>	Improve DT and increase SS	You <i>et al.</i> , 2013
ROS	<i>OsSRO1c</i>	<i>Ubi1</i>	<i>Agrobacterium</i>	Oxidative ST and SC (R)	Kim <i>et al.</i> , 2020
Protoporphyrinogen oxidase	<i>PPO</i>		<i>Agrobacterium</i>	Less oxidative damage, and DT	Phung <i>et al.</i> , 2011
Late Embryogenesis Abundant (LEA) Related Genes					
<i>LEA</i> protein gene	<i>HVA1</i>	<i>Actin1</i>	<i>Agrobacterium</i>	CL stability, higher leaf RWC and increase in growth under DRs.	Babu <i>et al.</i> , 2004
	<i>HVA1</i>	<i>Actin1</i>	<i>Agrobacterium</i>	DT and salinity tolerance (ST)	Rohila <i>et al.</i> , 2002
	<i>OsLEA3-2</i>	<i>CaMV35S</i>	<i>Agrobacterium</i>	DRs and increase grain/panicle	Du <i>et al.</i> , 2010
Various Regulatory Genes (VRG)					
Transcription factor	<i>HVA1</i> & <i>OsZIP72</i>	<i>CaMV35S</i>	<i>Agrobacterium</i>	DRs and ABA sensitivity	Xiang <i>et al.</i> , 2008
Harpin protein	<i>Hrf1</i>	<i>CaMV 35S</i>	<i>Agrobacterium</i>	DRs through ABA signalling and antioxidants, and SC (R)	Zhang <i>et al.</i> , 2011
Jasmonate and ethylene-responsive factor 1	<i>JERF1</i>	<i>CaMV35S</i>	<i>Agrobacterium</i>	DRs	Zhang <i>et al.</i> , 2011
Ethylene-responsive factor 1	<i>TSRF1</i>	<i>CaMV35S</i>	<i>Agrobacterium</i>	Enhances the OA and DT	Zhang <i>et al.</i> , 2011
Stress/zinc finger protein	<i>OsiSAP8</i>	<i>CaMV35S</i>	<i>Agrobacterium</i>	ST, DT and cold stress	Kanneganti, & Gupta, 2008

Table 5: IRRI identified drought-tolerant donors and developed high-yielding drought-tolerant rice varieties for conventional breeding, QTL mapping, and release in South and Southeast Asia and Africa (Kumar *et al.*, 2014)

Variety	Suitability for use	Variety	Country, release year, situation
Basmati 370	Conventional breeding	Sahod Ulan 1	Philippines 2009, RL, UP
CT9993-5-10-1-M	QTL mapping and pre-breeding	Hardinath 1	Nepal 2009, RL
PSBRc 82	QTL mapping and pre-breeding	Sahbhagi dhan	India 2010, RL, UP
PSBRc 68	QTL mapping and pre-breeding	BRRI dhan56	Bangladesh 2011, RL
PSBRc 80	Conventional breeding	Sookha dhan 3	Nepal 2011, RL
Aus Bak Tulsei	QTL mapping and pre-breeding	Sookha dhan 1	Nepal 2011, RL
Kalia	QTL mapping and pre-breeding	Sookha dhan 2	Nepal 2011, RL
Lal Aus	QTL mapping and pre-breeding	Katihian 1	Philippines 2011, UP
IR83614-1007-B-B	QTL mapping and pre-breeding	Sahod Ulan 3	Philippines 2011, RL
Aus 257	Conventional breeding	Sahod Ulan 5	Philippines 2011, RL
Kali Aus	QTL mapping and pre-breeding	Sahod Ulan 6	Philippines 2011, RL
IR77298-14-1-2	Conventional breeding	Sahod Ulan 8	Philippines 2011, RL
Dular	Conventional breeding and QTL mapping	Inpago LIPI Go 1	Indonesia 2011, UP
IR83614-1002-B-B	Conventional breeding	Inpago LIPI Go 2	Indonesia 2011, UP
IR83614-1005-B-B	Conventional breeding	Sahod Ulan 12	Philippines 2013, RL, DS
IR57514-PMI-5-B-1-2	QTL mapping and pre-breeding	M'ZIVA	Mozambique 2013, RL
N22	Conventional breeding and QTL mapping	UPIA3	Nigeria 2013, RL
Apo	Conventional breeding and QTL mapping		

Table 6: *QTLs* for drought tolerance-high yield (DTY) and other stress tolerances were pyramided in popular rice varieties through marker-assisted breeding. (Kumar *et al.*, 2014)

Variety	Target ecosystem	DTY <i>QTLs</i> used	Other <i>QTLs</i>	Current stage
IR64	Rainfed lowland	<i>qDTY</i> _{2.2} , <i>qDTY</i> _{4.1}	<i>Sub1</i>	Released in Nepal, identified for release in India, tested for release in Bangladesh
Swarna	Rainfed lowland	<i>qDTY</i> _{1.1} , <i>qDTY</i> _{2.1} , <i>qDTY</i> _{3.1} , <i>qDTY</i> _{12.1}		Testing and validation in progress
Vandana	Rainfed lowland	<i>qDTY</i> _{6.2} , <i>qDTY</i> _{2.2} , <i>qDTY</i> _{4.1} , <i>qDTY</i> _{3.2} , <i>qDTY</i> _{12.1}		Testing and validation in progress
Sabitri Anjali	Rainfed lowland	<i>qDTY</i> _{3.1} , <i>qDTY</i> _{6.1} , <i>qDTY</i> _{12.1}		Introgression ongoing
TDK1	Rainfed lowland	<i>qDTY</i> _{2.3} , <i>qDTY</i> _{3.2}		Testing and purification in progress
Sambha Mahsuri	Rainfed lowland			Testing and purification in progress
IR64	Rainfed lowland			Testing and purification in progress

conventional breeding techniques, such as introgression and selection, and molecular breeding methods, including marker-assisted selection and genetic engineering. These cultivars play a crucial role in ensuring stable rice production in drought-prone regions, ultimately contributing to food security.

In conclusion, the study of natural genotypic variation in rice and marker-assisted selection can help identify novel drought-tolerant genotypes and related genes/loci (Aldemir et al., 2017, Xu *et al.*, 2016). The success of incorporating *QTLs* for drought tolerance into high-yielding rice cultivars through marker-assisted breeding has been limited (Singh *et al.*, 2016, Swamy and Kumar *et al.*, 2013, Dixit *et al.*, 2014, Barik *et al.*, 2019, Vikram *et al.*, 2016), but the development of drought-tolerant rice varieties remains a focus due to the increasing significance of drought. Incorporating multiple *QTLs* into elite cultivars has shown promising results, such as the Malaysian rice cultivar *MR219* and the rice variety *TDK1* (Dixit *et al.*, 2014, Singh *et al.*, 2016, Shamsudin *et al.*, 2016). However, there is still a need for more research and efforts to create practical and high-yielding drought-tolerant rice varieties that can adapt to a wide range of climatic conditions. In conclusion, the challenge of creating drought-tolerant rice varieties remains significant due to the difficulty in finding suitable donors with a high level of tolerance and the environment-specific nature of drought tolerance. Despite the success in incorporating *QTLs* for drought tolerance into high-yielding cultivars using marker-assisted breeding techniques, much more effort is needed to develop improved rice varieties that can withstand drought conditions and maintain high yields. The adoption of high-yielding cultivars like Swarna, Samba mahsuri, and IR36 in drought breeding efforts shows the potential for creating drought-tolerant rice varieties, but further research and development is necessary to achieve this goal.

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Conclusion

In conclusion, the development of drought-tolerant rice varieties is a complex and challenging process that requires a combination of various techniques, including marker-assisted breeding, transgenic techniques, and field testing. Despite the progress that has been made, there is still much to be done to understand the mechanisms behind the whole-plant stress response and to create rice varieties that are highly tolerant to drought. To achieve this goal, it is essential to continue research and invest in new technologies in the field of molecular genetics and crop breeding. Despite the progress made in the development of drought-tolerant rice, there is still a long way to go in terms of developing rice varieties that are capable of resisting drought in various environments. The complex nature of drought stress and the multigenic regulation of drought tolerance make the breeding process challenging, but recent advances in functional genomics and marker-assisted selection can help overcome these challenges. Additionally, the integration of multiple abiotic stressors, such as high temperature and salt, and the assessment of both above- and below-ground characteristics, are crucial in creating successful drought-tolerant rice varieties. Field testing of the genes demonstrated to have drought tolerance should be carried out before incorporating them in breeding programs. Overall, further research and development in the field of rice breeding for drought tolerance is necessary to address the increasing need for food security in an ever-changing climate.

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Conflict of interest

The authors declare that they have no conflict of interest.

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