

Boosting agronomic traits and enhancing water use efficiency in rice lines incorporated with qDTY3.1 and qDTY2.1

Vignesh Palani¹, Sunitha Selvaraj¹, Karthika Muthuswamy¹, Bharathkumar Srinivasan^{1*}, Selvaraj Jagannathan², Maghimaa Mathanmohun³

¹PG & Research Department of Botany, Kandaswami Kandar's College, Namakkal, India.

²Department of Microbiology, Pasteur Institute of India, Coonoor, India.

³Centre for Global Health Research, Saveetha Medical College and Hospital, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai, India.

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ABSTRACT

Continuously rising global temperature enhances drought stress in rain-fed low and upland areas by depleting the water level from the soil surface and plants by increasing the temperature of surface air. By this, seed formation is disturbed at the time of fertilization due to lack of enough water during flowering. Hence, the rate of grain yielding decreases significantly in drought susceptible rice genotypes. This study is to explore a rice variety ADT37 which is widely cultivated in the southern part of India incorporated with qDTY3.1 and qDTY2.1 linked with higher/ constant grain yield were evaluated under nonflooding conditions at field level during Rabi season of 2023–24 in Kandaswami Kandar's College campus, Namakkal district, Tamil Nadu. Here, rice lines with an increased number of fertile seeds are linked with a higher growth rate of plant height, root length, flag leaf length and width, number of tillers, and total plant biomass but not with panicle length, dry weight of panicle, total number of seed, 1,000 seed weight, seed length, and width. Thus, improved rice lines showed an increased grain yield of up to 36.4% over the parental line under nonflooding conditions. It reveals that the incorporated quantitative trait locus based on the selection of rice lines with positive and higher heterosis adapted to the genome of ADT37 rice variety and it is expressed well through many agronomic traits in order to increase the grain yields under nonflooding conditions. This variety having water use efficiency would be used under water-limited conditions following further evaluation.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is a semi-aquatic monocotyledon domesticated annual crop. It is well-adapted to the Asian continent and has become a dominant crop over there because of the prevailing warm and humid conditions [1]. Its grain called caryopsis contains higher levels of carbohydrate content, vitamins, and minerals. Therefore, it is cultivated immensely in most Asian countries where about 90% of the people consume rice as a primary food in their daily lives. As the world's population rises continuously, the rate of rice production has to be increased at a higher level because the population rate is predicted to be 9.7 billion in 2050 from the current 8 billion and it could peak at nearly 10.4 billion in the mid-2080s [2]. Already, rice yield stagnation has been initiated by Green Revolution technologies, and along with, the global warming caused by greenhouse gases [3] has become a hard challenge for rice scientists around the world [4]. The impact of drought stress on global rice production in rain-fed low

Bharathkumar Srinivasan, PG & Research Department of Botany, Kandaswami Kandar's College, Namakkal, India. E-mail: bharathkumar76kkc @ gmail.com and upland regions is very significant because of the decreasing water supply and increasing intensity of the changing climatic conditions. Growth of rice is hampered by limited leaf growth, reduced leaf area, leaf rolling, leaf drying, thickened leaf size, early senescence, stomatal closure, and cutinized layer on the leaf surface due to water stress [5-8]. Shah et al. [9] explored the development of drought-resistant rice varieties, focusing on the identification of genes that regulate responses to varying water conditions, and the usage of submergence-tolerant strains in flood-prone lowland areas. The study also underscores the important role of physiological, biochemical, and molecular adaptations in strengthening rice's resilience to drought stress. The paper highlights the significance of marker-assisted breeding and farming practices in semi-arid and rainfed regions to cultivate more drought-resilient strains [9]. Han et al. [10] improved the crop yield of RoLe1 by increasing seed setting rates under moderate drought. Genomic evolution analysis identified a new beneficial allelic variant, proRoLe1-526 [10].

In Asia, approximately 42 million hectares of rice are affected by occasional or frequent drought stress [11]. The rate of yield loss depends on the growth stage, duration, and severity of drought stress. Particularly, significant yield loss is caused by the abortion of the

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^{*}Corresponding Author

fertilization process due to poor pollen grain germination and pollen tube elongation in the presence of drought stress at the time of flowering [12,13]. Various models and quantitative trait locus (QTL) mapping techniques are employed to identify the location of QTLs within marker intervals. QTL mapping serves as an effective method for uncovering genetic interactions related to disease resistance in plants. In rice, QTL mapping has been performed using F2, recombinant inbred lines, near iso genic lines (NILs), backcross populations, and double haploids to analyze the behavior of specific QTLs, their genetic expression related to grain yield, and additional yield-related traits such as biotic and disease resistance [14]. Fortunately, the continuous efforts of rice scientists of International Rice Research Institute (IRRI) are yielded many major QTL (qDTY 1.1, qDTY 2.1, qDTY 2.2, qDTY 2.3, qDTY 3.1, qDTY 3.2, qDTY 4.1, qDTY 6.1, qDTY 6.2, qDTY 9.1, qDTY 10.1, and qDTY 12.1) associated with increased grain yield in the presence of water scarcity. Among these, qDTY 1.1 [15], qDTY 2.2 [16-18], qDTY 3.1 [11,15], qDTY3.2 [19], qDTY4.1 [18], qDTY6.1 [15], and qDTY 12.1 [12,15,16,19–22] have been reported for its large effects under both lowland and direct seeded upland. In this study, rice varieties, ADT37 incorporated with qDTY3.1 and qDTY2.1 through conventional methods were evaluated for their efficiency of grain yield under nonflood conditions.

2. MATERIALS AND METHODS

2.1. Source of Rice Seeds

A small quantity of rice seeds of ADT37 from Tamilnadu Rice Research Institute, Aduthurai, Tamil Nadu state, and IR81869-B-B-195 from National Rice Research Institute, Cuttack, Odisha state were borrowed. In this study, the ADT37 rice variety was used as a female parent (recipient) for improving drought tolerance at the reproductive stage and IR81869-B-B-195 harboring qDTY3.1 and qDTY2.1 as a male parent (Donor).

2.2. Evaluation of NILs Under NonFlooding Conditions

Here, 32 rice lines of NIL-1 (F1-9.4.3.2) from BC₂F₂ generation which was incorporated with qDTY3.1 and qDTY2.1in the genetic background of ADT37 through marker-assisted backcrossing method (MABC) (data not shown) were evaluated at field level under moisture conditions. This experiment was carried out in an upland area located within the campus of Kandaswami Kandar's College, Velur, Namakkal District, Tamil Nadu State, INDIA (11.1121°N 78.0044°E) during Rabi season, 2023-24. Before the commencement of this evaluation, seeds of parental line and NIL were kept at 50°C for 5 days to break dormancy. Seeds were surface sterilized with 70% alcohol for 2 minutes and 2% Clorox for 30 minutes. Then, seeds were kept for incubation at 35°C for 7 days under dark conditions. Germinated seeds were planted in trays for 2 weeks. A 21-day-old 32 seedlings of NIL-1 (F1-9.4.3.2.1-33) were transplanted to the rice field with flooding for 5 cm at a 20×20 cm distance. Fertilizers were applied at rates of Urea 50 kg/ha, TSP 62.5 kg/ha, and MOP 50 kg/ha at sowing time. Urea at a rate of 37.5 kg/ha was also applied as a top dressing after 2 and 4 weeks of planting [23]. After 10 days of seedling establishment, the experimental field was water irrigated to avoid water stagnation (nonflooding) for 5 days once until harvesting (Fig. 1).

After the maturation of seeds, plants were uprooted carefully and growth rate of rice plants of NIL-1 and parental line in terms of plant height (PH) (measured height from the base of the plant to the top of the latest spikelet on the panicle, excluding awn), root length (RL), flag leaf length (FLL) (measured length from the leaf base to the leaf tip of the fully expanded leaves), flag leaf width (FLW) (measured at the widest point of the leaf), number of tillers (NTs) (counted tillers at the maturity stage), panicle length (PL) (measured from the base of the lowest spikelet to the tip of the latest spikelet on the panicle, excluding awn), panicle dry weight (PDW), number of fertile seeds (NFSs) (counted filled grains in sampled panicles), number of chaff (NC), total number of spikelet (TNS) (counted total number of spikeletes in sampled panicles), 1,000 seeds weight (1,000 SW) (1,000 grains were counted from 5 plants of each replicate and weighed), Single seed length (SSL) (measured using Venire caliper), single seed width (SSW) (measured using Venire caliper), and total plant biomass (TPB) were measured [23]. Seed setting percentages (SS%) were calculated in these NILs, according to IRRI's scale [24] (Scale 1-More than 80%; 3-61-80%; 5-41-60%; 7-11-40%; 9-Less than 11%).

In breeding programs, MABC is considered an effective tool, free from the ethical concerns associated with transgenic crops. Unlike genetically modified crops, this method relies on molecular markers [25]. MABC is extensively applied in crop improvement, particularly in rice, where it has been instrumental in developing new varieties with resistance to both biotic and abiotic stresses, including bacterial blight, blast, brown planthopper, green leafhopper, gall midge, viral infections, salinity, submergence, drought, cold, semi-dwarfism, and grain quality issues. This technique enables the efficient identification and selection of genes linked to these stresses. Additionally, it is wellaccepted by rice farmers due to its ability to recover the recurrent parent genotype within three generations [26]. At the IRRI in the Philippines, rice scientists have identified several key DTY QTLs (qDTY1.1-qDTY12.1) for reproductive-stage drought tolerance, which have been incorporated into popular rice varieties such as IR64, MTU1010, Swarna, Sabitri, TDK1, and Vandana [27].

2.3. Statistical Analysis

Statistical analysis was done for these agronomic characters evaluated in this experiment using mean, standard deviation, and standard error.

3. RESULTS

In this study, we explored 32 NIL-1 rice lines, each incorporated with qDTY3.1 and qDTY2.1, under moisture conditions to assess their growth and water use efficiency. The water use efficiency of these 32 lines impacted the variation in their agronomic traits (Table 1 and Figs. 1 and 2).

3.1. Plant Height

For PH character, we noted variations from 47.0 cm (plant 24) to 90.1 cm (plant 10) with a 69.5 cm mean value. The values of variance, standard deviation, standard error, and coefficient variance % were noted to be 161.72%, 2.24%, 0.38%, and 0.03%, respectively.

3.2. Root Length

RL of 32 rice lines varied from 8.0 cm (plant 21) to 19.8 cm (plant 1) with a mean value of 13.5 cm. Here, we noted variance (6.9), standard deviation (0.46), standard error (2.64), and coefficient variance % (0.06%).

3.3. Flag Leaf Length

The length of the flag leaf of 32 rice lines varied from 14.0 cm (plant 4) to 31.5 cm (plant 16) with a mean value of 23.0 cm. The level of variance, standard deviation, standard error, and coefficient variance % of these lines were 19.06%, 0.77%, 0.13%, and 0.03%, respectively.



Figure 1. Evaluation of rice lines of NIL-1 under nonflooding conditions.

 Table 1. Statistical analysis of agronomic characters of rice lines of NIL-1 under nonflooding conditions.

Agronomic characters	Mean value	Range	Variance	Standard deviation	Standard error
PH	69.5	47.0–90.1	161.7	2.24	0.38
RL	13.5	8.0-19.8	6.9	0.46	2.64
FLL	23.0	14.0-31.5	19.06	0.77	0.13
FLW	1.2	0.7-1.5	0.14	0.06	0.01
NT	6.1	4-8	1.30	0.20	0.03
PL	19.0	16.0-21.5	2.02	0.25	0.04
PDW	6.6	4.6-8.24	6.8	0.16	0.02
TNS	122.1	102-149	88.2	1.7	0.28
NC	19.9	4–54	114.11	1.88	0.32
NFS	102.2	72–124	204.2	2.52	0.24
1000SW	3.5	3.24-4.0	0.09	0.05	0.008
SSL	0.68	0.6-0.7	38.93	1.10	0.19
SSW	0.28	0.2-0.4	0.001	0.006	0.001
TPW	13.4	5.6-19.8	8.95	0.52	0.09

PH, Plant height; RL, Root length; FLL, Flag leaf length; FLW, Flag leaf width; NT, Number of tiller; PL, Panicle length; PDW, Panicle dry weight; TNS, Total number of spikelet; NC, Number of chaff; NFS, Number of fertile seed; 1000SW, 1000 seed weight; SSL, Single seed length; SSW, Single seed width; TPW, Total plant biomass.

3.4. Flag Leaf Width

In the case of FLW, we noted variations in the range of 0.7 cm (plant 19)—1.5 cm (plants 1 and 6) with a mean value of 1.2 cm. The level of variance, standard deviation, standard error, and coefficient variance % of these lines were 0.14%, 0.06%, 0.01%, and 0.05%, respectively.

3.5. Number of Tiller

In 32 rice lines, a NTs ranged from 4 (plants 5, 9, 24, and 25) to 8 (plants 29,31, 32) with mean value, variance, standard deviation, standard error, and coefficient variance % of 6.1%, 1.30%, 0.20%, 0.03%, and 0.03%, respectively.

3.6. Panicle Length

In 32 rice lines, the length of the panicle was noted in a range of 16.0 cm (plant 1)–21.5 cm (plant 4) with mean value, variance, standard



Figure 2. Growth of improved rice lines incorporated with qDTY3.1 and qDTY2.1 under nonflooding conditions. (a) Mean value; (b) Variance; (c) Standard deviation; (d) Standard error.

deviation, standard error, and coefficient variance % of 19.0 cm 2.02%, 0.25%, 0.04%, and 0.01%, respectively.

3.7. Panicle Dry Weight

The rate of the dry weight of panicle in 32 rice lines varied from 4.57 g (plant 9) to 8.24 (plant 33) with mean value, variance, standard deviation, standard error, and coefficient variance % of 6.6 g 6.8%, 0.16%, 0.02%, and 0.02%, respectively.

3.8. Number of Spikelet (NS)

In the case of a TNS, variation was from 102 (plant 22) to 149 (plant 3) with mean value, variance, standard deviation, standard error, and coefficient variance % of 122.1%, 88.2%, 1.7%, 0.28%, and 0.01%, respectively, among 32 rice lines.

3.9. Number of Chaff

A NC of 32 rice lines varied in the range of 4 (plant 30)—54 (plant 25) with mean value, variance, standard deviation, standard error, and coefficient variance % of 19.9%, 114.11%, 1.88%, 0.32%, and 0.09%, respectively.

3.10. Number of Fertile Seed

A NFSs of 32 rice lines was in the range of 72 (plant 24)—124 (plant 2) with mean value, variance, standard deviation, standard error, and coefficient variance % of 102.2%, 204.2%, 2.52%, 0.24%, and 0.02%, respectively.

3.11. 1,000 Seed Weight

In case of 1,000SW of 32 rice lines, we found variation in the range of 3.24 g (plants 2, 4, 5, 6, 7, 8, 9, 10, 13, 15, 16, 18, 19, 20, 21, 25, 27, 29, 30)—4.0 g (plants 11, 12, 17, 22, 24, 26, 31, 33) with mean value, variance, standard deviation, standard error, and coefficient variance % of 3.5 g, 0.09%, 0.05%, 0.008%, and 0.01%, respectively.

3.12. Length of Single Seed (LSS)

LSS of 32 rice lines ranged from 0.6 cm (plant 1, 2, 3, 4, 5, 6, 7, 8, 9,11, 12, 13, 14,16, 17, 18, 19, 20, 21, 23, 24, 25, 26, 28, 29, 30, 31, 32) to 0.7 cm (plant 10, 5, 22, 27, 33) with mean value, variance, standard deviation, standard error and coefficient variance % of 0.68 cm, 38.93%, 1.10%, 0.19%, and 0.02%, respectively.



Table 2. Rice lines with increased grain yield and their linkage with other agronomic characters under nonflooding conditions (Black box indicates the correlation of morphological character with grain yield).

PH, Plant height; RL, Root length; FLL, Flag leaf length; FLW, Flag leaf width; NT, Number of tillers; PL, Panicle length; DWP, Dry weight of panicle; TNS, Total number of seeds; NFS, Number of fertile seed; NC, Number of chaff; 1000SW, 1000 seed weight; SSL, Single seed length; SSW, Single seed width; TPB, Total Plant biomass.

3.13. Single Seed Width

The width of a single seed of 32 rice lines varied from 0.2 cm (plant 6, 7, 14, 15, 16, 17) to 0.4cm (plant 32) with mean value, variance, standard deviation, standard error, and coefficient variance % 0.28 cm, 0.001%, 0.006%, 0.001%, and 0.02%, respectively.

3.14. Total Plant Biomass

The TPB of 32 rice lines was noted in the range of 5.6 g (plant 1)—19.8 g (plant 7) with mean value, variance, standard deviation, standard error, and coefficient variance % of 13.4 g, 8.95%, 0.52%, 0.09%, and 0.03%, respectively. Rice lines with enhanced grain yield and their association with other agronomic traits under nonflooding conditions (Table 2).

4. DISCUSSION

Over the past two decades, many mega rice varieties such as IR64, MTU1010, Swarna, Sabitri, TDK1, PB1, and Vandana have been improved for drought tolerance at reproductive stage incorporating major drought yield QTLs (qDTY 1.1, qDTY 2.1, qDTY 2.2, qDTY 2.3, qDTY 3.1, qDTY 3.2, qDTY 4.1, qDTY 6.1, qDTY 6.2, qDTY 9.1, qDTY 10.1, and qDTY 12.1) [12,15–17,19–21, 25–30] through MABC method worldwide. In the present study, 32 rice lines of NIL-1 incorporated with qDTY3.1 and qDTY2.1 were evaluated under moisture conditions to check their growth and water use efficiency.

In this evaluation, 14 plants (plants 1, 2, 3, 7, 8, 10, 21, 22, 23, 26, 29, 30, 31, 32) were taller than the parental line (ADT37) (78.1 cm) in range of 1.08%-15.29%. A higher rate of PH indicates the water use efficiency of drought-tolerant rice lines and it gets sufficient water and promotes the cell elongation process very fast under stress conditions [31]. Growth of RL is increased in 15 rice lines (plants 1, 2, 5, 6, 9, 11, 15, 18, 25, 26, 27, 28, 29, 31, 32) from 1.3% (plant 27) to 43.3% (plant 1) over the parental line (13.82 cm). Elongation of RL in drought-tolerant rice lines increases due to well adaptation in soil by production of abscisic acid in response to insufficient water [32] and it leads to increased grain yield [33]. In 25 rice lines (plants 1, 2, 3, 6, 7, 8, 10, 11, 12, 13, 15, 16, 18, 19, 20, 21, 22, 23, 26, 27, 28, 29, 30, 31), FLL is increased from 0.96% (plant 29) to 51.4% (plant 16) when compared to the parental line (20.8 cm). In 14 rice lines (plants 1, 6, 7, 8, 9, 12, 13, 16, 17, 21, 23, 24, 28, 31), the rate of FLW increased over the parental line (1.4 cm) in the range of 7.1% (plants 1 and 6)-14.3% (plant 17). In previous studies, the increased rate of flag leaf area along with leaf relative water and leaf pigment content has played a significant role in the drought tolerance of rice lines [6,7,34]34]. Supportively, Kumar et al. [35] reported that the length and width of flag leaves become longer and wider, respectively, in drought-tolerant rice varieties under drought conditions. NT is increased in 24 rice lines (plant 1, 2, 6, 7, 10, 11, 12, 14, 15, 16, 17, 18, 20, 21, 22, 23, 26, 27, 28, 29, 30, 31, 32) from 20.0% (plant 1, 2, 10, 11, 12, 18, 20, 23, 28, 30) to 60.0% (plant 29, 31, 32) over the parental line (5). The NTs increases with

the increasing rate of plant growth and photosynthesis in droughttolerant genotypes promoting the NTs in the presence of sufficient water [8,36,37]. In 17 rice lines (plant 2, 3, 4, 6, 7, 10, 15, 16, 18, 19, 23, 26, 28, 29, 30, 31, 32), PL is increased from 2.16% (plant 23) to 16.21% (plant 4) over the parental line (18.5 cm). The incident of decreased number of panicles and PL occurs significantly in drought-intolerant rice genotypes under drought stress conditions [38]. PDW is found to be increased in 6 rice lines (plant 2, 4, 18, 19, 31, 32) which is superior to the parental line (7.33 gms) in the range of 6.54% (plant 32)-12.41% (plant 33). The rate of NS is higher in 6 rice lines (plant 2, 3, 5, 23, 25, 32) than that of the parental line (130) in the range of 0.7% (plant 23, 25)-14.61% (plant 3). In these, 4 rice lines (plant 23, 24, 25, 26) showed more NS sterility over the parental line (34) up to 58.82% (plant 25). Spikelet sterility is associated with the inability of pollen grains to germinate on dried stigma due to the interruption of phloem loading to ovules by lack of sufficient water [39].

In drought-tolerant genotypes, the rate of grain yield increases with an increasing rate of photosynthesis due to stomatal opening, increased turgor pressure, leaf gas exchange, and CO assimilation under lack of sufficient water [5,34,40]. In this study, NFS is increased in 22 rice lines (plants 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 13, 15, 16, 18, 19, 20, 27, 29, 30, 31, 32) when compared to parental line (96) in the range of 2.08% (plant 13)-36.45% (plant 3). In 13 plants (plant 1, 3, 7, 11, 12, 14, 17, 22, 23, 24, 26, 28, 31), rate of 1,000SW is increased over the parental line (3.24 g) in the range of 11.41% (plant 1, 2, 7, 24, 23, 28)-23.45% (plant 11, 12, 14, 17, 22, 26, 31, 33). Increased 1,000SW over the parental line indicates the drought tolerance ability of rice lines under drought stress conditions [41]. Moreover, increased activity of antioxidant enzymes such as Peroxidase, Catalase, and Superoxide dismutase in drought-tolerant rice genotypes during drought stress leads to increase grain weight by preventing reactive oxygen species accumulation in plant tissues [42,43].

In the case of SSL, 4 plants (plant 10, 15, 22, 27) were noted for having a higher rate of seed length up to 16.7% when compared to the parental line (0.6 cm). For SSW, we noted only one plant (plant 32) with a wider than parental line (0.3 cm) at the rate of 33.4%. In 18 rice lines (plant 3, 4, 6, 7, 9, 12, 13, 15, 16, 18, 19, 22, 23, 24, 26, 29, 30), TPB is increased when compared to parental line (12.0 g) in the range of 3.87% (plant 13, 29)—53.48% (plant 7). Plant biomass is associated with increased leaf area and fast photosynthesis rate under drought conditions [44,45].

In this study, the rate of SS% in the improved lines with qDTY3.1 and qDTY2.1 is increased in the range of 2.1%-36.4% under nonflooding conditions with IRRI's scale 7 and 9. Moreover, an increased rate of fertile seed is detected to be linked with other trait of plants such as PH in plant 1, 2, 7, 8, 12, 29, 30, 31, 32, FLL in plants 1, 2, 3, 5, 6, 7, 8, 10, 12, 13, 14, 15, 18, 20, 27, 29, 30, and 31, NTs in plant 1, 2, 7, 8, 29, 31, and 32 and TPB in plant 3, 4, 6, 7, 8, 10, 15, 16, 18, 20, 27, 29, and 30. Among these, many rice lines having increased FLL are associated with grain yield trait followed by TPB rather than PH and NT (Table 2). Moreover, water use efficiency of rice lines influences on expression of agronomic traits differentially among 32 rice lines, for instance, increased rate of PH, FLL, NT, and TPB in plant 7, 8, and 29; PH, FLL, and NT in plant 1, 2, and 31; PH and FLL in plant 12; PH, FLL, and TPB in plant 30; PH and NT in plant 32; FLL and TPB in plant 3; FLL and TPB in plant 6; FLL and TPB in plant 10, 15, 18, 20, 27. It indicates the variations in the adaptive potential of qDTY3.1 and qDTY2.1 in the genetic background of the modern rice variety (ADT37). Very recently, it has been reported that the expression of microRNA (miRNA) affects various transcription factors and traits linked with drought tolerance [46]. In a previous study also, it has been pointed out that two miRNAs (miR2919 and miR156k) regulate the signaling gene of cytokinin and brassinosteriod growth hormone by targeting the genes in the major drought-responsive qDTYs such as qDTY3.1, qDTY1.1, qDTY12.1 associated with drought tolerance at reproductive stage [47]. Marker-assisted breeding, particularly using the backcross method, has been extensively used for introgressing genes governing resistance/tolerance biotic as well as abiotic stresses in rice [48]

5. CONCLUSION

The incorporation of qDTY3.1 and qDTY2.1 into the widely cultivated ADT37 rice variety has successfully improved drought tolerance, particularly at the flowering stage. The study revealed significant variation across agronomic traits among the 32 rice lines, with notable improvements in traits such as PH, RL, NTs, and TPB linked to increased grain yield. These drought-tolerant lines demonstrated up to 36.4% higher yield under nonflooding conditions, making them valuable for low-water farming systems. The enhanced water-use efficiency and adaptability of these lines offer practical benefits for farmers, particularly in drought-prone regions of Southern India, by providing higher yields, reduced reliance on irrigation, and increased economic returns, contributing to overall food security. For future breeding programs, targeting the genetic markers associated with root development, tiller production, and biomass accumulation will be critical for enhancing rice resilience against drought.

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7. AUTHOR CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work. All the authors are eligible to be an author as per the international committee of medical journal editors (ICMJE) requirements/guidelines.

8. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

9. CONFLICTS OF INTEREST

The authors report no conflicts of interest in this work.

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There is no funding to report.

11. DATA AVAILABILITY

Research data is available with the authors and shall be provided upon request.

12. PUBLISHER'S NOTE

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The authors declares that they have not used artificial intelligence (AI)-tools for writing and editing of the manuscript, and no images were manipulated using AI.

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