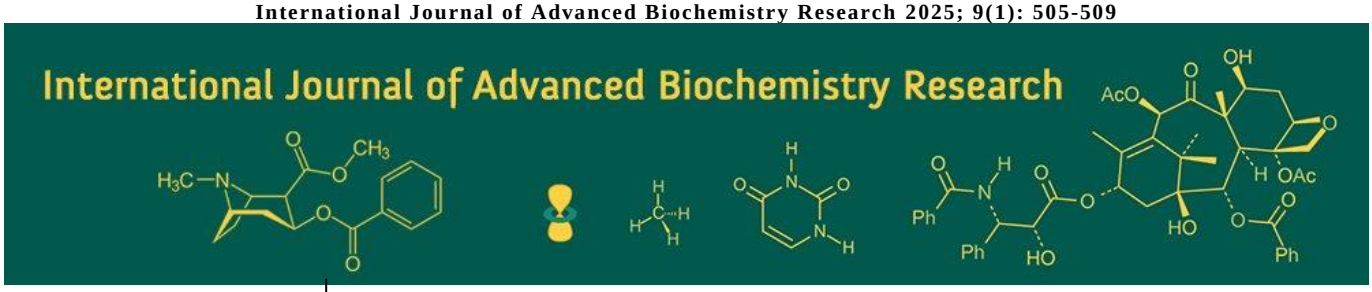

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2025; 9(1): 505-509
www.biochemjournal.com
Received: 17-11-2024
Accepted: 21-12-2024

SR Patel
Assistant Research Scientist, Regional Research Station, NAU, Vyara, Gujrat, India

RK Patel
Professor and Head, NM College of Agriculture, NAU, Navsari, Gujrat, India

VP Patel
Research Scientist, Regional Research Station, NAU, Vyara, Gujrat, India

VB Rana
Ph. D. Research Scholar, NM College of Agriculture, NAU, Navsari, Gujrat, India

Corresponding Author:
SR Patel
Assistant Research Scientist, Regional Research Station, NAU, Vyara, Gujrat, India

Genetic analysis of variability, heritability and genetic advance in F_2 segregating population of rice under drought condition

SR Patel, RK Patel, VP Patel and VB Rana

DOI: https://doi.org/10.33545/26174693.2025.v9.i1f.3561

Abstract
The study aimed to assess heritability, genetic variability, and genetic advance in the F_2 segregating population of a cross between drought-tolerant and drought-susceptible rice varieties (GNR-6 × NVSR-2272) for nine traits related to yield and drought tolerance. Experiments were conducted at the Regional Rice Research Station, Vyara, Gujarat, using 190 F_2 progenies during the summer of 2021. Traits were evaluated for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance. Days to flowering and productive tillers per plant exhibited low GCV and PCV, indicating limited variability and minimal environmental influence. Traits such as panicle length and spikelet fertility showed moderate to high PCV, reflecting environmental impact. Notably, filled grains per panicle displayed high GCV (48.04%) and heritability (71.11%), emphasizing significant genetic variability and potential for improvement through selection. Grain yield per plant had moderate GCV (16.15%) but high PCV (90.89%), highlighting environmental dominance in trait expression. Genetic advance estimates revealed that traits such as filled grains per panicle offer substantial scope for yield enhancement, while others like panicle length and days to flowering may require integrated breeding and environmental strategies. Overall, the study underscores the importance of combining genetic insights with agronomic interventions to improve rice yield and drought resilience effectively.

Keywords: Genetic variability, heritability, genetic advance, f_2 segregating population, drought tolerance in rice

1. Introduction
Rice (*Oryza sativa* L.) is a cornerstone of global agriculture, serving as the primary staple for over half of the world's population. Its cultivation spans 115 countries, predominantly in Asia, which accounts for 90% of global production (Asati & Yadav, 2020) [7]. In India, rice is integral to both diet and economy, with the nation being a leading producer and exporter. India's rice production for the 2023/2024 period was estimated at a record 137.8 million metric tons, harvested from 47.828 million hectares, resulting in a yield of 4.32 tons per hectare (Anonymous, 2024a) [5]. This achievement is attributed to favorable monsoon rains, improved agricultural practices, and government support. The increase in paddy sown area from 40.45 million hectares in 2023 to 41.45 million hectares in 2024 indicates a positive trend in rice cultivation (Anonymous 2024b) [5]. In the 2023/2024 marketing year, global rice production reached a record 522.65 million metric tons. The top producers were China (144.62 million metric tons), India (137.83 million metric tons), and Bangladesh (37 million metric tons) (Anonymous 2024c) [6]. This production level represents a 1% increase from the previous year, reflecting ongoing efforts to enhance rice cultivation practices worldwide. Agriculture is the backbone of the economy, providing food security, raw materials, and livelihoods to a significant portion of the global population (Dodiya and Barad, 2022) [10]. Its cultivation and improvement are of paramount importance for ensuring food security. Agriculture, especially rice cultivation, is crucial as rice serves as a staple food for more than half of the world's population, underpinning food security and rural livelihoods (Dodiya *et al.*, 2023) [11]. Modern breeding programs aim to enhance rice productivity, quality, and resilience to biotic and abiotic stresses. Genetic variability refers to the diversity in gene frequencies within a species, providing the foundation for adaptation and improvement. In

rice, traits such as plant height, grain size, yield components, and stress tolerance exhibit significant variability. Studies have shown substantial phenotypic and genotypic variation among rice genotypes for these traits, indicating the potential for selection and breeding (Anbanandan & Eswaran, 2018) [3].

2. Materials and Methods

In present study, the estimates of heritability, coefficient of variability, genetic advance were computed in F_2 segregating population of one cross and its two parents for 9 characters, parental screening (in pipe experiment) for various physio-morphological traits imparting drought tolerance at reproductive stage development of F_1 was done during summer 2020. In *Kharif* 2020 development of F_2 generation by selfing selective F_1 and in summer-2021 phenotyping of F_2 mapping population was carried out for yield and contributing traits at, Regional Rice Research Station, Vyara, (Gujarat). The planting material consist of 190 F_2 plant progenies of a cross between GNR-6 × NVSR-2272. Three plants of F_2 progeny are planted in each pipe. The field trials for F_2 generation of cross GNR-6 as female (susceptible) and NVSR-2272 as male (tolerant) were conducted in pipe during summer season 2021. The plant material was sown in pots on 5th February 2021 and transplanted to pipe after 20 days of sowing. The data was recorded for days to flower, Productive tillers per plant, Panicle length (cm), Filled grains per panicle, Unfilled grains per panicle, Spikelet fertility (%), 100 seed weight (g), Grain yield per plant (g), Straw yield per plant (g). The mean data after computing for each trait was subjected to analysis of variance and genetic parameters of variation.

The experimental data were analyzed statistically to estimate various genetic parameters and trait relationships. The following approaches were employed: The Genotypic Coefficient of Variation (GCV), calculated as per Burton (1952) [9], quantified the variability attributed to genetic factors. The Phenotypic Coefficient of Variation (PCV), also determined using Burton's (1952) [9] method, assessed the total variation, encompassing both genetic and environmental influences. Broad-sense heritability (hb2h^2_bhb2) was estimated using the formula by Hanson *et al*. (1956) [13] to evaluate the proportion of phenotypic variation due to genetic effects. Genetic advance (GA), representing the expected improvement through selection, was computed based on the procedure described by Johnson *et al*. (1955) [15].

3. Results and Discussion

3.1 Measures of variability

Genotypic Coefficient of Variation (GCV) reflects the variation that is solely attributed to genetic factors. It indicates the proportion of variation in a trait caused by the genotypic constitution of individuals. A higher GCV signifies a greater potential for genetic improvement through selection. Phenotypic Coefficient of Variation (PCV)**,** on the other hand, measures the total variation in a trait, which includes both genetic and environmental effects. While PCV tends to be higher than GCV due to the influence of environmental factors, the degree of difference between them provides insight into the extent of environmental influence on a trait. Estimates of variability parameters for various quantitative characters in F_2 generation of GNR-6 × NVSR-2272 in rice is presented in Table 1.

Days to flowering: The F2 population exhibited low phenotypic coefficient of variation (PCV, 8.81%) and genotypic coefficient of variation (GCV, 6.45%), reflecting limited variability in flowering time. The minimal difference between GCV and PCV suggests that genetic factors primarily control this trait, with environmental influence being minimal. While flowering time impacts the crop lifecycle, its low variability indicates limited potential for improvement in this trait within this population. The same kind of result for low PCV and GCV value was observed by Ratnakar *et al*. (2012) [24]; Krishna *et al*. (2014) [18]; Allam *et al*. (2015) [2]; Bhati *et al*. (2015) [8]; Kahani and Hittalmani (2015) [16] and Balat (2018) [34] and Tiwari *et al*. (2019) [33].

Productive tillers per plant displayed low GCV (4.83%) and PCV (4.91%), indicating low variability and minimal environmental influence. This suggests stability in the expression of productive tillers and limited scope for genetic improvement. However, this trait contributes significantly to overall grain yield, as more tillers generally result in increased grain production. The present result showed resemblance with findings of Allam *et al.* (2015) [2]; Bhati *et al.* (2015) [8]; Kahani and Hittalmani (2015) [16]; Sumanth *et al.* (2017) [17] and Balat (2018) [34] for low PCV and GCV value. Panicle length showed low GCV (1.28%) and moderate PCV (8.93%), highlighting limited genetic variability and moderate environmental influence. The narrow gap between GCV and PCV underscores that improvement through selection may be possible, albeit with a focus on environmental optimization. As panicle length directly correlates with grain numbers, its role in yield improvement remains notable. The similar results for low GCV and PCV is in accordance with Ratnakar *et al*. (2012) [24]; Sravan *et al.* (2012) [31]; Idris and Mohamed (2013) [14]; Kumar *et al*. (2015) [20] and Sumanth *et al*. (2017) [17].

Filled grains per panicle: This trait demonstrated high GCV (48.04%) and PCV (59.55%), reflecting substantial genetic variability. High variability suggests this trait is highly amenable to improvement through selection. Since filled grains per panicle have a direct and significant impact on grain yield, this trait offers considerable potential for enhancing productivity. The present result of high GCV and PCV showed resemblance with findings of Krishna *et al.* (2014) [18]; Shaikh *et al*. (2017) [29]; Balat (2018) [34]. Unfilled grains per panicle exhibited high GCV (33.73%) and PCV (46.77%), indicating significant variability. This trait, inversely related to grain yield, is critical for improving overall productivity. Breeding efforts aimed at reducing the number of unfilled grains can significantly enhance yield.

Spikelet fertility (%): Spikelet fertility showed low GCV (4.98%) and high PCV (61.10%), revealing high environmental influence and limited genetic variability. While spikelet fertility is an essential contributor to grain yield, its improvement may require focused environmental management rather than genetic manipulation.

100-seed weight (g): The GCV (13.55%) and PCV (27.40%) values for 100-seed weight indicate moderate variability and a high environmental influence. Although the

genetic contribution is moderate, this trait impacts grain yield significantly, as heavier seeds generally contribute to higher overall yield. Improvement can be achieved through combined genetic and environmental interventions. The same kind of moderate PCV and low GCV value was observed by Akinwale *et al.* (2011) [1]; Ratnakar *et al.* (2012) [24]; Kahani and Hittalmani (2015) [16]; Mallimar *et al.* (2015) [22]; Kumar *et al*. (2017) [20]; Sumanth *et al*. (2017) [17] and Balat (2018) [34].

Grain yield per plant, the primary focus of this study, exhibited moderate GCV (16.15%) and very high PCV (90.89%), indicating a substantial environmental influence on yield expression. The large difference between GCV and PCV underscores the predominant role of environmental factors over genetic factors in determining yield. To maximize productivity, breeding strategies should be complemented by agronomic practices that mitigate environmental variability. Low and high GCV and PCV was obtained by Krishna *et al*. (2014) [18]; Shaikh *et al*. (2017) [29] and Balat (2018) [34]. Straw yield per plant showed moderate GCV (16.59%) and PCV (31.31%), suggesting that both genetic and environmental factors influence this trait. While straw yield is not directly linked to grain yield, optimizing this trait can enhance overall plant health and productivity. Ratnakar *et al.* (2012) [24]; Kiran *et al.* (2012) [17]; Kahani and Hittalmani (2015) [16]; Sumanth *et al*. (2017) [17] and Balat (2018) [34] obtained similar result of high PCV and moderate GCV.

3.2 Heritability and Genetic Advance

Genetic advance refers to the expected improvement in a trait under selection, expressed either in absolute terms or as a percentage of the mean. It is influenced by three factors: the selection intensity, heritability, and genetic variability of the trait. In rice breeding, genetic advance provides insights into the potential effectiveness of selection programs. Heritability is a measure of the proportion of phenotypic variance that is attributable to genetic variance. In rice, heritability can be broadly categorized into broad-sense heritability (which includes all types of genetic effects: additive, dominance, and epistasis) and narrow-sense heritability (which focuses only on additive genetic variance). High heritability values indicate that a trait is primarily governed by genetic factors and can be reliably passed on to the next generation. Estimates of genetic parameters for various quantitative characters in F_2 generation of GNR-6 × NVSR-2272 in rice is presented in Table 1.

Days to flowering: Moderate heritability (53.72%) and low genetic advance (9.75%) suggest that days to flowering is influenced by a significant non-additive gene action and genotype × environment interactions. Improvement in this trait through selection might be challenging as environmental factors play a significant role. The similar result for low and moderate genetic advance as per cent of mean was in conformation with the result of Kahani and Hittalmani (2015) [16] and Tiwari *et al*. (2019) [33].

Productive tillers per plant: This trait exhibited low heritability (29.14%) and moderate genetic advance (19.03%), highlighting a considerable environmental influence. The preponderance of non-additive gene action indicates limited effectiveness of direct selection. However, as productive tillers are a critical determinant of grain yield, efforts must integrate breeding with environmental management. Kumar *et al.* (2015) [21]; Kahani and Hittalmani (2015) [16]; Sumanth *et al.* (2017) [17] and Tiwari *et al*. (2019) [33] obtain same kind of result for low and moderate genetic advance as per cent of mean.

Panicle length (cm): Low heritability (14.54%) and minimal genetic advance (2.67%) underscore the dominant role of environmental factors in shaping panicle length. Direct selection for this trait would likely be ineffective, as its expression is highly environment-dependent. The result for low genetic advance as per cent of mean is in accordance with Kumar *et al*. (2015) [21]; Sumanth *et al.* (2017) [17] and Mamata *et al.* (2019) [23].

Filled grains per panicle: This trait demonstrated high heritability (71.11%) and genetic advance (87.23%), suggesting that additive gene effects dominate its expression. High genetic variability indicates that selecting for filled grains per panicle can significantly improve grain yield. This trait represents one of the most promising targets for breeding programs focused on enhancing yield. The same result of high heritability was found by Satya & Jebaraj (2013) [27]; Savitha and Usha (2015) [28] and Mallimar *et al.* (2015) [22]; Balat (2018) and Saha *et al.* (2019) [25].

Unfilled grains per panicle: Moderate heritability (52.01%) and high genetic advance (50.11%) suggest that this trait is also influenced by additive gene effects. Improvement through selection is feasible, making it another critical factor in optimizing yield, as reducing unfilled grains directly increases productivity.

Spikelet fertility (%): Low heritability (1.09%) and minimal genetic advance (1.37%) indicate a strong environmental influence on spikelet fertility. Non-additive gene action predominates, making genetic improvement through selection ineffective. Environmental interventions may better enhance this trait. The 100-seed weight exhibited moderate heritability (31.63%) and genetic advance (17.85%), indicating a balance between genetic and environmental factors. While non-additive effects dominate, moderate variability suggests partial potential for improvement through careful breeding combined with environmental optimization. The findings are in confirmation with Krishna *et al.* (2014) [18]; Mallimar *et al.* (2015) [22]; Sumanth *et al*. (2017) [17] and Balat (2018) [34].

Grain yield per plant showed low heritability (8.08%) and moderate genetic advance (15.14%), emphasizing the predominant role of environmental factors. This low heritability limits the efficacy of selection-based breeding for this trait. Instead, yield improvement might require indirect selection through correlated traits, such as filled grains per panicle. Sanghera and Kashyap (2012) [26]; Shet *et al.* (2012) [30]; Gangashetty *et al.* (2013) [12]; Kumar and Senapati (2013) [19]; Savitha and Usha (2015) [28] and Mamata (2018) [23] exhibited same kind of result for moderate genetic advance as per cent of mean. Straw yield per plant exhibited moderate heritability (31.41%) and high genetic advance (20.26%), indicating that while non-additive gene effects predominate, improvement potential exists. However, as this trait is less directly linked to grain

yield, its impact on overall productivity is indirect. Results of present study was in conformation with the findings of Sravan *et al.* (2012) [31]; Kahani and Hittalmani (2015) [16]; Sumanth *et al*. (2017) [17] and Balat (2018) [34], Sanghera and Kashyap (2012) [26]; (2018) and Mamata *et al.* (2018) [23] obtained similar result of high genetic advance as per cent of mean.

This study highlights the importance of a balanced approach combining genetic selection with environmental optimization to achieve significant gains in grain yield. Future research should focus on stabilizing high-yielding genotypes across diverse environmental conditions and exploiting additive genetic effects to maximize the impact of breeding efforts. The traits examined in this study can be broadly categorized into: Traits with High Potential for Selection: Filled grains per panicle and unfilled grains per panicle showed high heritability and genetic advance, indicating that additive gene effects dominate. These traits have a direct and substantial impact on yield and represent primary targets for breeding programs. Traits with Limited Genetic Improvement Potential**:** Traits such as spikelet fertility, panicle length, and days to flowering exhibited low heritability and genetic advance, reflecting a significant environmental influence. For these traits, genetic selection is unlikely to yield substantial improvements. Traits Moderately Amenable to Selection**:** Productive tillers per plant, 100-seed weight, and straw yield per plant displayed moderate heritability and genetic advance, indicating a blend of genetic and environmental influences. These traits can be improved through a combination of breeding and agronomic practices.

Table 1: Estimates of variability parameters for various quantitative characters in F_2 generation of GNR-6 × NVSR-2272 in rice

Characters	Mean	σ^2p	σ^2e	σ^2g	GCV%	PCV%	h^2 (b)%	GA	GAM%
Days to flowering	55.70	24.08	11.16	12.92	6.45	8.81	53.72	5.43	9.75
Productive tillers per plant	5.73	3.30	2.44	0.86	16.21	31.70	29.14	1.09	19.03
Panicle length (cm)	24.75	4.89	4.79	0.10	1.28	8.93	14.54	0.66	2.67
Filled grains per panicle	49.55	870.58	303.95	566.63	48.04	59.55	71.11	43.22	87.23
Unfilled grains per panicle	105.62	2440.68	1171.59	1269.09	33.73	46.77	52.01	52.93	50.11
Spikelet fertility (%)	33.81	426.78	423.95	2.84	4.98	61.10	1.09	0.46	1.37
100-seed weight (g)	1.63	0.20	0.15	0.05	13.55	27.40	31.63	0.29	17.85
Grain yield per plant (g)	2.22	4.09	3.96	0.13	16.15	90.89	8.08	0.34	15.14
Straw yield per plant (g)	22.33	48.90	35.17	13.73	16.59	31.31	31.41	4.52	20.26
Root length (cm)	52.07	179.35	145.64	33.71	11.15	25.72	19.46	5.37	10.31
Root volume (cm^3)	51.67	188.64	116.67	71.98	16.42	26.58	38.35	10.85	21.00
Root dry weight (g)	4.43	1.46	1.41	0.05	5.02	27.23	3.78	0.09	2.12
Shoot length (cm)	90.46	172.76	29.78	142.98	13.22	14.53	82.95	22.46	24.83
Root to shoot ratio	21.79	85.40	20.76	64.63	36.89	42.40	75.84	14.44	66.24
Relative water content (%) (72 hour)	29.14	534.02	438.52	95.51	33.53	79.29	18.90	9.00	30.87
Relative water content (%) (20 days)	23.53	375.99	317.33	58.66	32.55	82.42	20.96	8.37	35.59
Water use efficiency (%)	12.15	16.84	4.59	12.26	28.81	33.78	73.17	6.19	50.91
Photosynthesis (µM $CO^2/m^2/s$)	116.19	6108.30	5872.28	236.02	13.22	67.27	4.55	7.33	6.31
Stomatal conductance (M H2O/m^2/s)	130.38	6246.61	6102.38	144.23	9.21	60.62	2.40	3.91	3.00
Transpiration (mM H2O/m^2/s)	12.42	134.74	40.94	93.79	77.96	93.44	69.62	16.65	134.01

4. Conclusion

The evaluation of genetic parameters in the F_2 population revealed significant variability for key traits, offering insights into the genetic architecture of rice under drought conditions. Traits such as filled grains per panicle exhibited high genetic variability and heritability, suggesting their potential as selection targets for yield improvement. Conversely, traits influenced heavily by environmental factors, such as grain yield per plant, necessitate integrated approaches combining genetic and environmental management. These findings emphasize the importance of targeted breeding programs aimed at enhancing drought resilience and productivity in rice.

5. References

1. Akinwale MG, Gregorio G, Nwilene F, Akinyele BO, Ogunbayo SA, Odiyi AC. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). Afr J Plant Sci. 2011;5(3):207-212.
2. Allam CR, Jaiswal HK, Qamar A, Venkateshwarlu C, Reddy YS. Variability, heritability and genetic advance studies in some indigenous genotypes of basmati rice (*Oryza sativa* L.). Electron J Plant Breed. 2015;6(2):506-511.
3. Anbanandan V, Eswaran R. Genetic variability studies in rice genotypes. Eur J Biotechnol Biosci. 2018;6(5):74-75.
4. Anonymous. Data retrieved from https://www.infomerics.com/publication-detail/indian-rice-industry-outlook-for-2024. 2024a.
5. Anonymous. Data retrieved from Foreign Agricultural Service, U.S. Department of Agriculture. Usda.gov/data/production/commodity/0422110. 2024b.
6. Anonymous. Data retrieved from https://www.InternationProductonAssessmentDivision.fas.usda.gov/countrysummary-2024. 2024c.
7. Asati R, Yadav RK. Genetic Variability Studies in F2 Generation of Rice (*Oryza sativa* L.). Int J Curr Microbiol Appl Sci. 2020;Special:2548-2554.
8. Bhati M, Babu GS, Rajput AS. Genetic variability, correlation and path coefficient for grain yield and quantitative traits of elite rice (*Oryza sativa* L.) genotypes at Uttar Pradesh. Electron J Plant Breed. 2015;6(2):586-591.
9. Burton GW. Quantitative inheritance in grasses. Proceedings of the 6th International Grassland Congress. 1952;1:277-283.
10. Dodiya RD, Barad AH. Effectiveness of biopesticides against Spodoptera litura infesting groundnut under

field condition. The Pharma Innovation Journal. 2022;11(8):1601.
11. Dodiya RD, Barad AH, Pathan NP, Raghunandan BL. Trichogramma: a Promising Biocontrol Agent. Int J Econ Plants. 2023;10(3):192-199.
12. Gangashetty PI, Salimath PM, Hanamaratti NG. Association analysis in genetically diverse non-basmati local aromatic genotypes of rice (*Oryza sativa* L.). Mol Plant Breed. 2013;4.
13. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. Agron J. 1956;48(6):268-272.
14. Idris AE, Mohamed KA. Estimation of genetic variability and correlation for grain yield components in rice (*Oryza sativa* L.). Glob J Plant Ecophysiol. 2013;3(1):1-6.
15. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-318.
16. Kahani, Hittalmani. Genetic analysis and traits association in F3 intervarietal populations in rice under aerobic condition. J Rice Res. 2015;3:152.
17. Kiran KK, Rao MR, Rajanna MP, Rao AM, Mahadevu P, Siddegowda DK. Variability, heritability and genetic advance studies in F2 populations of two crosses of rice (*Oryza sativa* L.). 2012;917-919.
18. Krishna L, Raju CS, Kumar SS, Reddy SN, Bhave HV. Genetic variability studies for qualitative and quantitative traits in F2 generation of aromatic rice (*Oryza sativa* L.). 2014;26-30.
19. Kumar A, Senapati BK. Genetic parameters and association studies for important quantitative traits in advanced lines of Sambamahsuri derivatives. J Crop Weed. 2013;9:156-163.
20. Kumar A, Nayak AK, Pani DR, Das BS. Physiological and morphological responses of four different rice cultivars to soil water potential based deficit irrigation management strategies. Field Crops Res. 2017;DOI:10.1016/j.fcr.2017.01.026.
21. Kumar S, Dwivedi SK, Haris AA, Prakash VE, Mondal S, Singh SK. Screening and identification of rice genotypes for drought tolerance at reproductive stage under rainfed lowland condition. J AgriSearch. 2015;2(2):105-111.
22. Mallimar M, Surendra P, Hanamaratti NG, Jogi M, Sathisha TN, Hundekar R. Genetic variability for yield and yield attributing traits in F3 generation of rice (*Oryza sativa* L.). Res Environ Life Sci. 2015;9(1):24-28.
23. Mamata B, Bastia DN, Monalisa SP. Variability, heritability, genetic advance analysis in aerobic rice. Int J Chem Sci. 2018;2(2):48-52.
24. Ratnakar MS, Rajanna MP, Ramesh S, Sheshshayee MS, Mahadevu P. Genetic variability, correlation and path coefficient studies in F2 generation of aerobic rice (*Oryza sativa* L.). Electron J Plant Breed. 2012;3(3):925-931.
25. Saha SR, Hassan L, Haque MA, Islam MM, Rasel M. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. J Bangladesh Agric Univ. 2019;17(1):26-32.
26. Sanghera GS, Kashyap SC. Genetic parameters and selection indices in F3 progenies of hill rice genotypes. Not Sci Biol. 2012;4(4):110-114.
27. Satya R, Jebaraj S. Heritability and genetic advance estimates from three line rice hybrids under aerobic condition. 2013;69-74.
28. Savitha P, Usha Kumari R. Scope for exploitation of heterosis using traditional land races and cultivars in rice (*Oryza sativa* L.). 2015;151-157.
29. Shaikh SA, Umate SM, Deosarkar DB. Genetic divergence analysis in rice (*Oryza sativa* L.) genotypes under irrigated condition. Bioinfolet. 2017;14(2):156-159.
30. Shet RM, Rajanna MP, Ramesh S, Sheshshayee MS, Mahadevu P. Genetic variability, correlation and path coefficient studies in F2 generation of aerobic rice (*Oryza sativa* L.). Electron J Plant Breed. 2012;3(3):925-931.
31. Sravan T, Rangare NR, Suresh BG, Kumar SR. Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). J Rice Res. 2012;5(1):2.
32. Sumanth V, Suresh BG, Ram BJ, Srujana G. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). J Pharmacogn Phytochem. 2017;6(4):1437-1439.
33. Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Adv Agric. 2019;1:5975901.
34. El-Balat A, DeWilde RL, Schmeil I, Tahmasbi-Rad M, Bogdanyova S, Fathi A, Becker S. Modern myoma treatment in the last 20 years: a review of the literature. BioMed research international. 2018;2018(1):4593875.