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Genetic Variability for Quantitative in Brinjal (*Solanum melongena* L.)

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ABSTRACT: For assessing the variability among thirty brinjal genotypes the present investigation was carried out at Horticulture complex, Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.). Wide variability was recorded among the thirty genotypes studied. The PCV was higher than the GCV for almost all the characters. Both the PCV and GCV were high for traits LAI, the number of long-styled flowers, Number of short-styled flowers, Number of fruits per plant, Girth of fruit, Seed weight per fruit, Pulp: seed ratio, and total phenol content. High heritability accompanied by high GA or GA as % of mean was noted for characters LAI, and seed weight per fruit, indicating the involvement of additive gene action. Direct selection therefore could be effective for the improvement of these traits. The genotypes found superior for most economic traits were 2017/BRLVAR-7, 2017/BRRVAR-10, 2017/BRLVAR-9, 2017/BRRVAR-4, 2016/BRLVAR-5, JB 64, 2017/BRRVAR- 9 and 2016/7BRLVAR-8. The genotype could be utilized as a parent in a hybridization breeding program. Brinjal production is facing major constrain of high input costs which could be resolved through developing yield superior varieties.

Keywords: Variability, GCV, PCV, Heritability, GA, Brinjal, Hybridization.

INTRODUCTION

Brinjal, eggplant, or aubergine (*Solanum melongena* L.) is the most popular and widely cultivated warm-season vegetable crop in central, southern, and South-East Asia and some African countries. India is the major producer of brinjal in the world and it is grown in an area of 688.70 thousand hectares with 12399.90 thousand tonnes production and 18.54 million tons per hectare productivity (Anonymous, 2017a). In Madhya Pradesh, the annual production is 918.78 thousand metric tonnes from 50.57 thousand ha area and 18.17 metric tonnes per hectare productivity (Anonymous, 2017b). Major Brinjal-producing states are Odisha, Bihar, Karnataka, West Bengal, Andhra Pradesh, Maharashtra, and Uttar Pradesh. It is an important vegetable for diet, consumed in a variety of ways, and also has considerable medicinal properties. It is considered to be the king of vegetables. Brinjal fruits are a fairly good source of Calcium, Phosphorus, Iron, and Vitamins, particularly the `B' group. According to USDA (2018) analysis of edible parts of fruit gave the following values (per 100 g fresh weight): Protein 1g, Fat 0.19 g, Dietary fiber 3.40 g. The mineral constituents per 100 g edible portions was: Ca (9 mg), Copper (0.08 mg), Mg (14 mg), Iron (0.24 mg), Sodium (2.0 mg), Potassium (230.0 mg), Zinc (0.16 mg) and Mn (0.25 mg). The vitamins present per hundred gram edible portions are vitamin A 124 IU; Thiamin (B1) 0.4 mg; riboflavin (B2) 0.11 mg; nicotinic acid (niacin) 0.9 mg; vitamin C 12 mg and Chlorine 25 mg (Singh and Kalda, 2001). Its highest production potential and availability of the product to consumers, it is also termed as poor man's vegetable. Although Brinjal contributes a good share in the Indian economy its yield is reducing day by day due to many biotic and abiotic stress such as phomopsis blight, frost, etc, thus screening for variability become an asset for future enhanced production of brinjal. Hence, all the above reasons influenced the researcher to focus on this vegetable.

Genetic variability analysis significantly contributes a major role in the recognition of differences in genetic composition and the environment in which individuals were raised. This would help in a selection based on superior performance (Tiwari *et al.*, 2019). The variability is a prerequisite for any successful crop improvement program as it provides a spectrum of variants for effective selection, which can be achieved through the processes of hybridization, recombination, mutation, and selection (Nair and Mehta, 2014). Planning and execution of a breeding program for the improvement of the various quantitative attributes depend, to a great extent, upon the magnitude of genetic variability and divergence existing in the population. Hence Co-efficient of variation is useful in the assessment of genetic variability for the particular characters (Srivastava *et al.*, 2019). The current investigation aimed at extracting the elite genotypes contributing to effective variations. The quantitative traits depicting immense polymorphism indicate a better scope for selection and developing high-yielding genotypes in Brinjal. The diversion observed is needed for the development of hybrids, which shows higher productivity per day along with good quality traits (Tiwari *et al*., 2021).

MATERIALS AND METHODS

The present investigation was conducted during 2018-19 at Horticulture complex, Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) during 2018-2019. The experimental material for the present investigation comprised of 30 genotypes of brinjal collected from IVRI Varanasi and JNKVV Jabalpur and laid out in Randomized Block Design with three replications. Jabalpur (M.P.)is situated on the Kymore Plateau and Satpura Hills Agro and Climatic Region at 23°10″N latitude, 79°59″E longitude, and at an altitude of 411.78 meters above the mean sea level. Analysis of variance was carried out as per methods suggested by Panse and Sukhatme (1967) for twenty - six growth, yield and its attributing characters viz., plant height (cm), number of branches per plant, Plant spread(cm), Leaf area index, Days to flower initiation, Days to 50 percent flowering, Number of flowers per cluster, Number of long-styled flowers, Number of short-styled flowers, Number of fruits per plant, Days taken to fruit set, Percent fruit set, Number of days to first picking, Number of days to the last picking, Fruiting span, Number of fruits per cluster, Length of fruit, Girth of fruit, Weight of fruit, Seed weight per fruit, Test weight, Yield per plant, Yield (quintal per hectare), Pulp seed ratio, Dry matter percent in fruit and Total phenol content**.** The phenotypic and genotypic coefficient of variation (expressed in %) was calculated by using the formula given by Burton (1952). Estimation of heritability was done as per the formula given by Hanson et al. (1956). The expected genetic advance was calculated by using the method suggested by Johnson *et al.*, (1955) at 5% selection intensity.

RESULTS AND DISCUSSION

From the experimental analysis, the ANOVA revealed that highly significant variation among all the traits studied (Table 1). The estimated genetic variability parameters for twenty-six characters in brinjal are depicted in Table 2. Number of branch per plant, days to flower initiation, days to 50% flowering, number of flowers per cluster, number of long-styled flowers, number of fruit per plant, percentage of fruit set, number of fruit per cluster, the weight of fruit, and yield per plant were found to be a most economic trait. The direct selection of genotype contributing to these traits could provide better yield.

Table 1: Analysis of variance (ANOVA) for various characters understudy.

Mean sum of squares											
Sr. No.	**Source of variation**	**d.f.**	**Plant height (cm)**	**No. of branches per plant**	**Plant Spread (cm)**	**LAI**	**Days to flower initiation**	**Days to 50% flowering**	**No. of flowers per cluster**	**No. of long-styled flower per cluster**	**No. of short-styled flower per cluster**
1.	**Replication**	2	26.81	2.34	77.07	2.20	.54	1.45	1.25	0.33	0.206
2.	**Treatments**	29	513.652	6.944	545.038	14.547	163.318	178.987	3.863	1.590	1.338
3.	**Error**	58	15.267	0.350	15.190	0.437	2.313	0.471	0.115	0.040	0.062

Sr. No	**Source of variation**	**d.f.**	**Mean sum of squares**								
			No. of fruits per plant	**Days take to fruit set**	**Percent fruit set**	**No. of days to first picking**	**No. of days to last picking**	**Fruit span**	**No. of fruits per cluster**	**Length of fruit (cm)**	**Girth of fruit (cm)**
1.	**Replication**	2	1.41	1.08	1.28	5.54	111.04	67.35	0.38	0.04	1.34
2.	**Treatments**	29	162.508	3.977	81.365	122.651	357.648	281.248	0.690	20.651	15.520
3.	**Error**	58	.693	0.171	2.462	2.627	79.401	54.613	0.088	2.320	0.351

Sr. No	**Source of variation**	**d.f.**	**Weight of fruit (g)**	**Seed weight per fruit (g)**	**Test weight (g)**	**Yield per plant (kg)**	**Yield q/ha**	**Pulp: seed ratio**	**Dry matter % in fruit**	**Total phenol content mg/100g**
1.	**Replication**	2	54.64	0.13	0.22	0 .005	6026.5	0 .008	2.07	11.85
2.	**Treatments**	29	1,649.537	10.072	1.464	0.183	20,725.260	0.400	21.623	17,413.354
3.	**Error**	58	32.494	0.144	0.245	0.005	2,069.743	0.004	0.638	26.580

Among 30 genotypes of brinjal, 2017/BRLVAR-7 was exhibiting the highest value for most of this trait i.e., number of flowers per cluster, number of long-styled flowers, the weight of fruit, and yield per plant. For traits days to flower initiation, days to 50% flowering genotype 2017/BRRVAR-10 depicting greater mean values and for Number of branch per plant, 2017/BRLVAR-9 was reporting maximum values as per mean. Fruiting span is the difference between the first fruit harvest and the final picking, thus the short span would affect the yield negatively while large or wide fruiting duration would enhance the yield. Genotype 2017/BRRVAR-4 was articulating the highest value of fruiting span with a sufficient yield of 424.50q/ ha. Therefore, all the above genotypes could be further utilized as good yielder parents in hybridization programs.

Table 2: Estimate of the genetic parameter of variation for the various character in brinjal.

Sr. No.	Character	Grand mean	Range		Coefficient of Variance		Heritability	GA% of Mean
			MIN	MAX	GCV	PCV		
1.	**Plant height (cm)**	75.62	41.50	99.00	17.01	17.17	91.58	33.54
2.	**Number of branches per plant**	10.94	08.26	13.64	13.55	14.59	86.25	25.92
3.	**Plant Spread (cm)**	75.99	44.00	102.88	17.47	18.21	92.08	34.55
4.	**Leaf Area Index (LAI)**	06.10	03.12	12.48	35.56	37.70	91.50	70.08
5.	**Days to flower initiation**	40.97	33.44	58.55	17.87	18.25	95.86	36.05
6.	**Days to 50% flowering**	50.95	41.70	69.00	15.13	15.19	91.21	31.06
7.	**No. of flower per cluster**	04.58	02.15	09.00	24.40	25.49	91.58	48.10
8.	**No. of long-styled flower**	01.68	00.60	03.33	42.17	45.38	86.34	80.73
9.	**No. of short-styled flower**	01.78	00.57	03.06	36.44	38.99	87.35	70.16
10.	**No. of fruits per plant**	09.03	2.08	45.29	79.93	81.28	96.71	15.03
11.	**Days take to fruit set**	11.05	9.39	13.26	10.19	10.87	87.90	19.69
12.	**Per centage of fruit set**	57.98	40.00	63.83	08.84	09.20	91.43	10.10
13.	**No. of days first picking**	59.66	46.00	73.48	10.60	10.94	93.84	21.15
14.	**No of days last picking**	191.57	150.13	205.5	04.96	06.80	53.27	07.46
15.	**Fruit span**	131.91	93.50	142.16	06.58	08.64	58.03	10.34
16.	**No of fruit per cluster**	01.62	01.03	02.73	27.52	33.03	69.40	47.23
17.	**Length of fruit (cm)**	13.38	08.57	17.95	29.65	30.76	92.91	58.88
18.	**Girth of fruit (cm)**	06.48	03.49	11.26	34.69	35.88	93.51	69.12
19.	**Weight of fruit (g)**	94.45	24.00	144.76	24.56	25.29	94.31	49.13
20.	**Seed weight per fruit (g)**	03.70	01.13	08.70	48.015	49.048	95.83	96.82
21.	**Test weight (g)**	04.49	03.06	05.80	14.18	17.96	62.38	23.08
22.	**Yield per plant (kg)**	0.90	00.45	01.31	26.34	27.38	92.60	52.23
23.	**Yield q/ha**	330.10	167.30	489.00	23.51	27.14	75.02	41.56
24.	**Pulp: seed ratio**	0.70	0.12	1.85	51.70	52.47	97.10	42.57
25.	**Dry matter % in fruit**	10.09	06.29	16.55	26.20	27.37	91.64	51.67
26.	**Total phenol content mg/100g**	133.04	38.16	318.83	52.09	57.48	82.21	97.29

A high significant difference was observed for all the characters indicating high genetic variation among the genotypes. Maximum variation was observed for trait Fruit yield in quintal per hectare varied from 167.30 to 489.00 quintal per hectare with an average yield of 335.36 quintals per hectare and fruit weight was observed maximum in genotype 2016/BRLVAR-5 (142.58 g) and was minimum in JB 64 (23.55 g). The maximum leaf area index (12.49) was recorded in JB-64, Days to first flowering varied from 33.44 to 58.55 days with an average of 40.98 days, Days to fifty percent flowering was recorded to be early in genotype 2016/7BRLVAR-8 (41.70 days), while it was late in the genotype 2017/BRRVAR9 (69 days). The average days for 50 percent flowering were 50.95 days.

PCV was greater than GCV for all the traits indicating the interaction of genotypes with the environment. The coefficient of variation ranged from the number of days last picking PCV (6.8 %) & GCV (4.96%) to the number of fruit per plant PCV (81.28%) & GCV (79.93%) respectively for the twenty-six characters under study. High phenotypic & genotypic coefficient of variation was observed for characters like the length of fruit, number of fruits per cluster, the girth of fruit, leaf area index, number of short-styled flowers, number of long-styled flowers, seed weight per fruit, pulp: seed ratio, total phenol content mg/100g, and number of fruit per plant. The findings are in close harmony with those of Manpreet *et al.*, (2013); Milli *et al.*, (2014) for seed weight per fruit; Milli *et al.*, (2014) for pulp seed ratio; Bansal (2007) for leaf area index; Manpreet *et al.*, (2013) for number of long-styled flower and number of short-styled flower per cluster; PCV & GCV was low for the number of days to the last picking, fruiting span, percent fruit set, days take to fruit set, number of days first picking, number of branch per plant, days to 50 percent flowering, plant spread, plant height, test weight, days to flower initiation, yield quintal per ha, the weight of fruit, yield per plant, number of flower per cluster and dry matter in fruit. The findings are in close harmony with Madhavi *et al.*, (2015); Sujin *et al.*, (2017) for percent of fruit set; Manpreet *et al.*, (2013); Milli *et al.*, (2014) for the number of days to first picking; Naik *et al.*, (2010) for dry matter in fruit and Gavade and Ghadage (2015) for plant height.

High heritability in the broad sense helps identify appropriate characters for selection and enables the breeder to select superior genotypes based on phenotypic expression of quantitative characters. High yield can be achieved by the selection of characters that have high heritability coupled with genetic advances. Selection of one trait invariably affects several associated traits which evoke the necessity of determining interrelationships of various yield components among them and with yield. (Konyak *et al.*, 2020).

The estimated values of heritability in the broad sense were classified as high (more than 90%), medium (70-90%), and low (less than 70%). High values of heritability were recorded for days to 50 percent flowering, leaf area index, plant height, number of flowers per cluster, dry matter percent in fruit, plant spread, yield per plant, length of fruit, a girth of fruit, number of days to first picking, the weight of fruit, days to flower initiation, percent fruit set, Pulp: seed ratio. The results were in close proximate to that of Nair and Mehta (2009); Chattopadhya *et al.*, (1011); Kumar and Arumugam (2013).

Result of genetic advance in % of mean is classified as low (less than 20%), medium (20-70%), and high (more than 70%) genetic advance in % of mean ranged from 7.46% (number of days last picking) to 97.29% (total phenol content), for different characters studies. The girth of fruit (69.12%), leaf area index (70.08%), number of short-styled flowers (70.16%), number of long-styled flowers (80.73), seed weight per fruit (96.82%), and total phenol content (97.29%) recorded high genetic advance. While moderate genetic advance was noted for characters viz., number of days first picking (21.15%), test weight (23.08%), number of branch per plant (25.92 %), 50 percent flowering (31.06%), plant height (33.54%), plant spread (34.55), days to first flower initiation (36.05%), yield quintal per ha (41.46%), number of fruit per cluster (47.23%), number of flower per cluster (48.16%), the weight of fruit(51.07%), dry matter in fruit (51.67%), yield per plant (52.23%), pulp: seed ratio (57.44%), and length of fruit (58.88%). However, the low values of genetic advance were observed in the number of days to last picking (7.46%), percent of fruit set (10.10%) fruiting span (10.34), the number of fruit per plant (15.03%), and days taken to fruit set (19.69%).

Table 3 depicted the high variability coupled with high genetic advance for traits Leaf Area index, Seed weight per fruit. The research aligned with Chandra *et al.*, (1998) for seed weight per fruit. The high heritability accompanied with moderate genetic advance was found for traits Plant height, number of branch per plant, days to flower initiation, days to 50% flowering, number of flower per cluster, number of days to first picking, length of fruit, the girth of fruit, weight of fruit, yield per plant, pulp seed ratio, dry matter percent in fruit. The result is in propinquity with of Kabir and Som (1993) for plant height. Patel *et al.*, (1999) for trait seed to pulp ratio. High heritability with the low genetic advance exhibited by traits Number of fruits per plant and percent of fruit set indicates that these characters are governed by non-additive gene action and the presence of high genotype x environment interaction. The heritability is being exhibited due to the favorable influence of environment rather than genotype and simple selection would not be rewarding. Thus, they can be improved by the development of hybrid varieties and the utilization of transgressive segregants in heterosis breeding programs. The exploitation of diversity is needed for the development of hybrids, which shows higher productivity per day along with good quality traits (Tiwari *et al*., 2021). These findings are in agreement with, Chaudhary and Pathania (1999); Negi *et al*., (2002).

Table 3: Heritability estimated with genetic advance.

High heritability coupled with high genetic advance	Leaf Area index, Seed weight per fruit
High heritability coupled with moderate genetic advance	Plant height, number of branches per plant, days to flower initiation, days to 50% flowering, number of flower per cluster, number of days to first picking, length of fruit, girth of fruit, weight of fruit, yield per plant, pulp seed ratio, dry matter percent in fruit
High heritability Coupled with low genetic advance	Number of fruits per plant, percent of fruit set

CONCLUSION

The investigation declared significant variation and genotypes found superior for most of the economic traits were 2017/BRLVAR-7, 2017/BRRVAR-10, 2017/BRLVAR-9, 2017/BRRVAR-4, 2016/BRLVAR-5, JB 64, 2017/BRRVAR- 9 and 2016/7BRLVAR-8. These genotypes could be utilized in future hybridization breeding programs. Both GCV and PCV were high for traits LAI, the number of long-styled flowers, Number of short-styled flowers, Number of fruits per plant, Girth of fruit, Seed weight per fruit, Pulp: seed ratio, and total phenol content. The selections on basis of these traits have scope for selections and improvement of traits, while the lowest variability depicted the need for generation of variability. The traits days to 50 percent flowering, Leaf Area index, and Seed weight per fruit reported major heritable portion and thus guide plant breeder in adopting appropriate breeding procedure.

FUTURE SCOPE

The present experiment would create a base stone for future researchers willing to work in the varied breeding program. The elite varieties obtained could be used as donor parents for economic traits. Also, the found trait could be further validated through molecular characterization.

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Conflict of Interest. None.

REFERENCES

Anonymous (2017a). Horticultural statistics at a glance 2017, Horticulture statistics Division, Dept. of Agriculture Cooperation Farmers Welfare, *GoI :* 149.

Bansal, S. (2007). Study of genetic divergence in brinjal (*Solanum melongena* L.) genotypes. M.Sc. Thesis, JNKVV, Jabalpur: 55-69.

Burton, G. W. (1952). Quantitative inheritance in grasses. Proc. *6th Int. Grassland Cong., 1:* 227-283.

Chandra, A., Dhurvey G.S., Verma, B.K. (1998) Abstract silver jubilee national emerging scenario in vegetable research and development PDVR Varanasi India 12-14.

Chattopadhya, A., Dutta, S., & Hazra, P. (2011). Characterization of genetic resources and identification of selection indices of brinjal (*Solanum melongena* L.). *Vegetable Crops Research Bulletin, 74:* 39-49.

Chaudhary, D. R. & Pathania, N. K. (1998). Variation studies in some genetic stocks of eggplant. *Himachal J. Agric. Res., 24*(1-2): 67-73.

Gavade, R. T., & Ghadage, B. A. (2015). Genetic variability, heritability, and genetic advance in segregating generation of Brinjal (*Solanum melongena* L.). Bioinfolet - *A Quarterly Journal of Life Sciences 12*(1C): 325-328.

Hanson, C. H., Robinson, H. F., Comstock, R. E. (1956). Biometrical studies of yield in segregating population of Korean Lespedsa. *Agronomy Journal, 48*(2): 268-272.

Johnson, H. W., Robinson, H. F, Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal, 47*: 314-318.

Kabir, J. & Soma, M. G. (1993). Studies on genetic variability in brinjal (*Solanum melongena* L.). *Haryana Journal of Horticultural Science, 22*(4): 334-336.

Konyak, W. L., Kanaujia, S. P., Jha, A., Chaturvedi, H. P., Ananda, A. (2020). Genetic Variability, Correlation, and Path Coefficient Analysis of Brinjal. *SAARC Journal of Agriculture, 18*(1): 13-21.

Kumar, R. S. & Arumugam, T. (2013). Variability, heritability, and genetic advance for fruit yield, quality, and pest and disease in eggplant. *Vegetable Science, 4*(1):111-113.

Madhavi, N., Mishra, A.C., Pushpavathi, Y., & Kumari, V. L. P. (2015). Genetic diversity in brinjal (*Solanum melongena* L.). *Plant Archives*, *15*(2). 1107-1110.

Manpreet, Dhatt, A. S., & Singh, B. (2013). Variability, heritability, and genetic advance in eggplant *(Solanum melongena L.*) during summer and rainy season. *Asian Journal of Bio Science, 8*(2): 200-204.

Mili, C., Bora, G., Das, B., Paul, S. K. (2014). Studies on variability, heritability, and genetic advance in brinjal (*Solanum melongena* L.) genotypes. *Direct Research Journal of Agriculture and Food Science, 2*(11): 192-194.

Naik, K., Sreenivasulu, G. B., Prashanth, S., Jayaprakashnarayan, R. P., Nataraj, S. K., & Mulge, R. (2010). Genetic variability in eggplant (*Solanum melongena* L.). *International Journal of Agricultural Science, 6*(1): 229-231.

Nair, R. & Mehta, A. K. (2014). Induced genetic variability in cowpea [*Vigna unguiculata* (L.) *Walp*] var. *pusakomal. The Bioscan., 9*(2): 829-833.

Nair, R. & Mehta, A. K. (2009). Genetic variability for some quantitative and qualitative traits in brinjal (*Solanum melongena* L.). *Indian Journal of Tropical Biodiversity, 17*(2): 191-196.

Negi, A. C., Baswana, K. S., Singh, A., Sanwal, S. K., & Batra, B. R. (2002) Studies on genetic variability and heritability in brinjal (*Solanum melongena* L.) under high-temperature conditions. *Haryana J. Hort. Sci., 29*(3-4): 205-206.

Panse, V. G. & Sukhatme, P. V. (1967). Statistical methods for Agricultural workers, ICAR, New Delhi.

Pate, l N. T., Bhalala, M. K., Kathiria, K. B., Doshi, K. M. (1999). Genetic variability for yield and its components in brinjal. *Gujarat Agric. Univ. Res. J., 25*(1): 77-80.

Singh, N. & Kalda, T. S. (2001). In: Textbook of Vegetables, Tuber crops, and spices. Eds.: Thamburaj S. and Singh N. ICAR, New Delhi : 29-30.

Srivastava, S., Saidaiah, P., Shivraj, N., & Ravinder Reddy, K. (2019). Study of genetic variability, heritability, and genetic advance for yield and yield-related components of Brinjal [*Solanum melongena* (L.)] genotypes. *Journal of Pharmacognosy and Phytochemistry, 8*(4): 917-919.

Sujin, G.S., Karuppaiah, P., & Saravanan, K. (2017). Genetic variability and correlation studies in brinjal (*Solanum melongena* L.). *Indian Journal Agricultural Research, 51*(2): 112-119.

Tiwari, S., Koutu, G. K., & Singh, Y. (2019). Genetic evaluation of rice restorer lines through variability, heritability and genetic advance analysis. *International Journal of Chemical Studies, 7*(6): 1934-1937.

Tiwari, S., Koutu, G.K., Pathak, N. (2021). Diversity Analysis of Grain Attributes in Restorer Lines of Rice (*Oryzae sativa*). *Biological Forum – An International Journal, 13*(2): 386-392.

Tiwari, S., Koutu, G.K., Singh, Y. & Pathak, N. (2021). Phenotypic Characterization of Diverse Rice Fertility Restorers. *JPSS, 33*(16): 220-231.

USDA. (2018). National Nutrient Database for Standard Reference. April 1, 2018. US Department of Agricultural https://ndb.nal.usda.gov/ndb/food

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