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Study the Genetics of the Important Yield Attributing Traits and Identification of Potential Germplasm of Brinjal (*Solanum melongena* L.)

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ABSTRACT

Present experiment was conducted during October–April of 2021–22 and 2022–23 under the Department of Vegetable and Spice Crops, Uttar Banga Krishi Viswavidyalaya, Cooch Behar, West Bengal using forty-two brinjal germplasm on ten yield attributing traits to study the inheritance pattern for crop improvement. Experiment was laid out in RBD and pooled data of two years were subjected to statistical analysis. Negligible difference among GCV and PCV for all the traits excepting yield and pedicel length indicated that there was less environment influence. Existence of high heritability coupled with genetic advance for all the traits indicated existence of additive gene action in their inheritance. Character association and path coefficient revealed that fruit diameter, fruits inflorescence^{-1}, inflorescence plant^{-1}, fruit length and fruit weight could be considered effective traits as a basis for selection. Principle factor analysis broadly categorised all the traits into three groups those cumulatively explained 74.74% of the variance where first factor (38.2%) represented by flowers inflorescence^{-1} (0.739), inflorescences plant^{-1} (0.877), fruits inflorescence^{-1} (0.885), fruits plant^{-1} (0.871) and fruit weight (-0.602); Second factor (20.04%) was explained by plant height (0.876), fruit length (0.765) and pedicel length (0.876); third factor (16.50%) was associated with fruit diameter (0.767), fruit weight (0.738) and yield hectare^{-1} (0.859). 2021/BRLVAR-9, Pundibari Chikon, Utkal Kesari, Utkal Anushree, Hija were considered most suitable for selection of narrow and multi fruited germplasm and 2019/BRLVAR-9, 2020/BRRVAR-2, 2019/BRRVAR-1, 2019/BRRVAR-7, 2019/BRRVAR-13 and Nawabganj were considered most suitable for selection of big sized and high yielding germplasm.

KEYWORDS: Brinjal, variability, correlation, path coefficient, principal factor analysis

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1. INTRODUCTION

Botanically Brinjal is named as *Solanum melongena* L., popularly known by different names like eggplant in African and European countries and Baigan in India (Ayub and Chopra, 2024; Ansari and Singh, 2015). Eggplant are botanically multi seeded berry fruit which are used as vegetable and different other processed products, rich source of vitamins, minerals, and antioxidants (Caruso et al. (2017); Kaushik (2019); Bhargava et al. (2019). China is the largest producer and India stands in the second position (Anonymous (2023). It can be grown different climatic conditions and cultivated all over India in different parts of the country. (Choudhary et al. (2023); Bhushan and Samnotra (2017); Reshmika et al. (2015) In India majorly grown states are West Bengal, Orissa, Gujarat, Chhattisgarh, Madhya Pradesh, Karnataka, Assam, Haryana, Bihar, Maharashtra, Andhra Pradesh, and Tamil Nadu (Kumar et al., 2011). This crop is widely grown for its varieties in shapes and colours. Tiwari et al. (2016); Younas et al. (2022); Rajan et al. (2020).

However, improvement in quality and productivity remains the key challenge. These challenges may be due to the genetic and environmental influences which effect the important traits leading lack of availability of sufficient variety as per the regional demand (Gramazio et al. (2023; Biradar et al. (2023). To boost the efficiency of any breeding programme it is very important to understand the genetic basis of variability in brinjal becomes very crucial. To completely understand the potentiality to exhibit diversity and inheritance pattern of the important economic traits study on genetic variability, Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of variation (GCV) is utilized (Uddin et al., 2021). PCV is used to measure the overall variability including environmental effects, while GCV measures the genetic variation alone (Shilpa et al., 2018; Bhanushree et al. (2019). Heritability is one of essential parameter in plant breeding which indicates the proportion of phenotypic factors which can attribute to the genetic factors. Genetic advance along with heritability gives the insight of the expected gain from the selection process of a particular trait (Vanniarajan et al., 1996).

Beyond heritability and variability estimates it is crucial to understand the associationship between the traits at genotypic and phenotypic level along with path analysis is done (Ramjattan and Umaharan (2021); Dhaka and Soni (2014) to determine the effective selection basis. In the correlation analysis the relationship between traits is established. Sujin, et al. (2017); Prabakaran et al. (2015); Singh et al. (2024). However, it does not give us the clear view of how the trait effects the dependent trait. It is path analysis which gives us the clear view of the direct and the indirect effects of traits to the dependent trait.

Additionally factor analysis is used simplify the trait selection for breeding programme by grouping the traits based on underlying genetic control and interdependence of the traits. The main aim of factor analysis is to explain as much variance as possible in a data set by using the smallest number of factors and the smallest number of variables within each factor (Howard (2016); Imsong et al. (2023). By categorizing major traits into clusters or factors, it helps in prioritizing key attributes that contribute most to yield and adaptability (Denis and Adams (1978). Considering the importance of genotypic evaluation present investigation was laid out to study the inheritance pattern for establishing the basis of selection and to identify the potential genotype for crop improvement.

2. MATERIALS AND METHODS

Present experiments were conducted during October–April of 2021–22 and 2022–23 at the Instructional Farm under the Department of Vegetable and Spice Crops, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, West Bengal, India. The soil of the experimental plot was sandy clay soil with pH around 5. There were no significant differences in weather in both the experimental seasons but there was a more rainfall during the second year of experiment. During the experiment the maximum temperature was 32°C and minimum temperature 9°C with mean relative humidity of around 80%. The experimental material consisted of 42 genotypes of brinjal among which 23 were collected from All India Coordinated Research Project, 8 from West Bengal, 3 Odissa, 3 from Nagaland, 3 from Arunachal Pradesh and 1 each from Tripura and Manipur. For the experiment randomized block design was followed with three replication and the plants were planted maintaining spacing of 100×75 cm^2 consisted of 25 plants in each replication. The brinjal seeds were sown in nursery bed and transplanted 40 days after sowing to the main field. Recommended dose of fertilizer was applied in the field. Irrigation was done just after transplanting and following irrigation were done 10 days interval. Weeding was done every month till the crop were done till the last harvest of the crop. Ten randomly selected healthy plants were used for recording the observation on the yield and its attributing traits namely plant height (cm), Numbers of flowers inflorescence^{-1}, numbers of Inflorescence plant^{-1}, numbers of fruits inflorescence^{-1}, numbers of fruits plant^{-1}, pedicel length (cm), fruit length (cm), fruit diameter (mm), individual fruit weight (g) and yield (t ha^{-1}). The pooled data of two years observations for each character or trait was subjected to statical analysis. Heritability in broad sense was calculated as per formula given by Burton and Devane (1953) and Allard (1960). Expected genetic advance (GA) was worked out as

Table 1: Estimates of phenotypic and genotypic coefficients of variability, heritability, genetic advance and genetic gain of different characters in brinjal

Character	Grand mean	Range	GCV	PCV	Heritability (h^2) broad sence (%)	Genetic advance	Genetic advance as % of mean
PH	64.95±2.88	40.63-94.05	15.91	17.66	81.12	19.17	29.51
FlIn	3.21±0.25	1.02-7.14	34.47	37.00	86.78	2.12	66.15
InP	10.29±0.74	4.41-19.48	27.39	30.09	82.83	5.29	51.35
FrIn	1.83±0.23	1.00-5.21	45.17	50.17	81.05	1.53	83.77
FrP	9.20±1.62	2.02-50.34	87.62	92.78	89.19	15.68	170.47
PL	6.00±0.55	2.96-10.12	21.61	26.93	64.44	2.15	35.74
FL	19.92±1.55	8.93-44.06	33.30	35.93	85.91	12.69	63.59
FD	62.14±4.41	21.20-126.76	52.69	54.11	94.84	65.69	105.71
FW	221.76±12.09	23.79-751.12	67.47	68.31	97.56	305.53	137.77
YPH	18.18±2.26	8.21-34	20.83	32.05	42.25	0.34	27.89

PH: Plant height (cm); FlIn: Flowers inflorescence^{-1}; InP: I inflorescences plant^{-1}; FrIn: Fruits inflorescence^{-1}, FrP: Fruits plant^{-1}, PL: Pedicel length (cm); FL: Fruit length (cm); FD: Fruit diameter (mm); FW: Fruit weight (g); YPH: Yield (t ha^{-1})

suggested by Burton and Devane (1953) and Johanson et al. (1955). Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953). Correlation coefficients of were estimated as suggested by Al-Jibouri et al. (1958). Path coefficient analysis was done as suggested by Wright (1921). To know the direct and indirect effects of the important quantitative traits path coefficient analysis was carried out following Dewey and Lu (1959). The principal factor analysis was done according to Harman (1976). As suggested by Cattell (1965) the highest correlation was taken as an estimate of Communality (h^2). The maximum likelihood method was followed as suggested by Lawley (1940); Rao (1952). For the analysis software like R version 4.4.2, OriginPro 2024 and SPSS version 26.0 were utilized.

3. RESULTS AND DISCUSSION

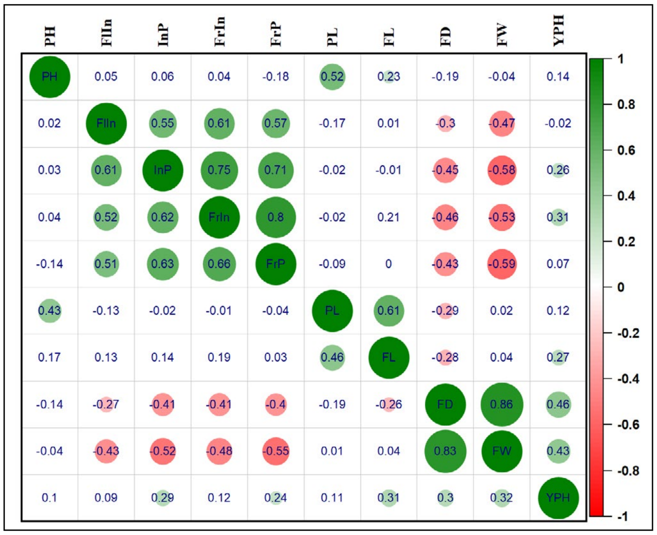
3.1. Variability study

Variability, heritability, and genetic advance are key parameters in any kind of crop improvement programme in plant breeding and genetics to assess the potential for genetic improvement in a population (Sangam et al. (2020) High value of GCV and PCV as per Karak et al. (2012) in Table 1 were observed number of fruits plant^{-1} (87.62% and 92.78%), individual fruit weight (67.47% and 68.31%), fruit diameter (52.69% and 54.11%), fruits inflorescence^{-1} (45.17% and 50.17%), flowers inflorescence^{-1} (34.47% and 37.00%), fruit length (33.30% and 35.93%), inflorescence plant^{-1} (27.39% and 30.09%), pedicel length (21.61% and 26.93%) and yield (20.83% and 32.05%) except for plant height (15.91% and 17.66%) which exhibited moderate PCV and GCV. The PCV values were slightly higher than the corresponding GCV values excepting yield and pedicel length indicated that there was less influence of environment to the traits under study. Whereas pedicel development and yield were much influenced by the environmental factors. The results were similar with Golani et al. (2007); Tirkey et al. (2018); Tabasum et al. (2024).

All the characters viz. individual fruit weight (97.56% and 137.77%), fruit diameter (94.84% and 105.71%), fruits plant^{-1} (89.19% and 170.47%), flowers inflorescence^{-1} (86.78% and 83.77%), fruit length (85.91% and 63.59%), inflorescence plant^{-1} (82.83% and 51.35%), plant height (81.12% and 29.51%), fruits inflorescence^{-1} (81.05% and 83.77%) and pedicel length (64.44% and 35.74%) and exhibited high heritability coupled with high genetic advance as a percentage of mean except for yield (t ha^{-1}) (42.25% and 27.89%) which exhibited moderate heritability coupled with high genetic advance as a percentage of mean. Present outcome showed that all these characters were inherited through additive gene action, thus could be improved by simple selection methods. These findings agreed with Chaudhary and Kumar (2014); Sujin et al. (2017); Kumar et al. (2023); Soumya et al. (2023).

3.2. Genotypic and phenotypic correlation coefficient

Estimation of character association at genotypic and phenotypic level was performed to understand the inter relationship among the growth and yield attributing traits for standardization the basis of selection (Kushwah and Bandhyopadhya, 2005). Experiment clearly exhibited (Figure 1) existence of significant and positive correlation among plant height and pedicel length (rg=0.52 and



	PH	FlIn	InP	FrIn	FrP	PL	FL	FD	FW	YPH
	PH	0.05	0.06	0.04	-0.18	0.52	0.23	-0.19	-0.04	0.14
	0.02	FlIn	0.55	0.61	0.57	-0.17	0.01	-0.3	-0.47	-0.02
	0.03	0.61	InP	0.75	0.71	-0.02	-0.01	-0.45	-0.58	0.26
	0.04	0.52	0.62	FrIn	0.8	-0.02	0.21	-0.46	-0.53	0.31
	-0.14	0.51	0.63	0.66	FrP	-0.09	0	-0.43	-0.59	0.07
	0.43	-0.13	-0.02	-0.01	-0.04	PL	0.61	-0.29	0.02	0.12
	0.17	0.13	0.14	0.19	0.03	0.46	FL	-0.28	0.04	0.27
	-0.14	-0.27	-0.41	-0.41	-0.4	-0.19	-0.26	FD	0.86	0.46
	-0.04	-0.43	-0.52	-0.48	-0.55	0.01	0.04	0.83	FW	0.43
	0.1	0.09	0.29	0.12	0.24	0.11	0.31	0.3	0.32	YPH

Figure 1: Plot for genotypic and phenotypic correlation of coefficient of different characters of Brinjal; *Circle and Colour indicated level of significance at 5%. **PH: Plant height (cm); FlIn: Flowers inflorescence^{-1}, InP: I inflorescences plant^{-1}; FrIn: Fruits inflorescence^{-1}; FrP: Fruits plant^{-1}; PL: Pedicel length (cm); FL: Fruit length (cm); FD: Fruit diameter (mm); FW: Fruit weight (g); YPH: Yield (t ha^{-1})

rp=0.43) which was in accordance with the finding of Thomas et al. (2022). Flowers inflorescence^{-1} was significant and positively correlated with inflorescences plant^{-1} (rg=0.55 and rp=0.61), fruit inflorescence^{-1} (rg=0.61 and rp=0.52) and fruits plant^{-1} (rg=0.57 and rp=0.51); significant and negative correlation was exhibited with fruit weight (rg=-0.47 and rp=-0.43). Inflorescences plant^{-1} positively and significantly correlated with fruits inflorescence^{-1} (rg=0.75 and rp=0.62), number of fruits plant^{-1} (rg=0.71 and rp=0.63) and yield (rp=0.29), but were significantly negatively correlated with the fruit diameter (rg=-0.45 and rp=-0.41) and fruit weight (rg=-0.58 and rp=-0.52). Fruits inflorescence^{-1} had significant positive correlation with number of fruit plant^{-1} (rg=0.80 and rp=0.66) and yield (rg=0.31), but was associated with significant negative correlation with fruit diameter (rg=-0.46 and rp=-0.41) and fruit weight (rg=-0.53 and rp=-0.48). Similarly, fruits plant^{-1} also exhibited significant and negative correlation with fruit diameter (rg=-0.43 and rp=-0.40) and fruit weight (rg=-0.59 and rp=-0.55) along with positive significant association with yield (rp=0.24). Pedicel length exhibited significant correlation in both direction with fruit length (rg=0.61 and rp=0.46) and fruit diameter (rp=-0.19). Fruit length showed positive correlation with the yield (rp=0.31). Whereas, fruit diameter exhibited significant positive correlation with individual fruit weight (rg=0.86 and rp=0.83) and yield (rg=0.46 and rp=0.30), but negative correlation with the fruit length (rp=-0.26) and similar findings were reported by karak et al. (2012). Fruit weight had positive and significant association with the fruit yield (rg=0.43 and rp=0.32). This finding was in accordance with Jhangta et al. (2017) who reported with the increased magnitude of fruit weight, automatically yield increased. In the contrary, in the present experiment it was clear evident that the magnitude of traits attributed fruit quantity were strongly in negative direction with the fruit weight, suggested consideration of either factor could be rewarding in reduction of selection complexity. Present findings were strongly supported by the earlier research work of Kowalska (2006), Kousalya et al. (2024) Gangadhara et al. (2023) and Rameshkumar et al. (2021).

3.3. *Path coefficient*

Yield is a very complex character which is affected by different characters and path analysis is one of the tools which further divides the correlation coefficient with yield into direct and indirect component for better understanding

Table 2: Path coefficient analysis showing the direct (diagonal bold) and indirect effect of different characters on yield plant^{-1}

Characters	PH	FlIn	InP	FrIn	FrP	PL	FL	FD	FW	Gen. Cor (RYPH)
PH	0.118	-0.015	0.033	0.026	0.034	0.06	0.088	-0.21	0.005	0.14
FlIn	0.006	-0.296	0.288	0.357	-0.106	-0.02	0.005	-0.328	0.071	-0.02
InP	0.007	-0.163	0.524	0.441	-0.132	-0.003	-0.002	-0.497	0.088	0.26
FrIn	0.005	-0.179	0.392	0.590	-0.149	-0.003	0.08	-0.506	0.08	0.31
FrP	-0.022	-0.168	0.371	0.47	-0.187	-0.011	0.001	-0.472	0.089	0.07
PL	0.061	0.052	-0.013	-0.014	0.018	0.116	0.229	-0.323	-0.003	0.12
FL	0.028	-0.004	-0.003	0.125	-0.001	0.071	0.375	-0.311	-0.005	0.27
FD	-0.023	0.088	-0.237	-0.272	0.08	-0.034	-0.106	1.098	-0.13	0.46
FW	-0.004	0.138	-0.305	-0.312	0.11	0.003	0.013	0.939	-0.152	0.43

*Residual: 0.1079; **PH: Plant height (cm); FlIn: Flowers inflorescence^{-1}; InP: I inflorescences plant^{-1}; FrIn: Fruits inflorescence^{-1}; FrP: Fruits plant^{-1}; PL: Pedicel length (cm); FL: Fruit length (cm); FD: Fruit diameter (mm); FW: Fruit weight (g); YPH: Yield (t ha^{-1})

the importance of the effect (Gal et al. (2023)) (In the present investigation (Table 2) maximum direct effect towards yield was shown through fruit diameter (1.098) followed by number of fruits inflorescence^{-1} (0.590), Number of Inflorescence plant^{-1} (0.524), fruit length (0.375), plant height (0.118) and pedicel length (0.116). Direct negative effect towards yield was found through individual fruit weight (-0.152), Number of fruits plant^{-1} (-0.187) and number of flowers inflorescence^{-1} (-0.296). Similar findings were given by Naliyadhara et al. (2007); Bansal and Mehta (2008) and Nazir et al. (2022). Fruit diameter had positive indirect effect on yield via Number of flowers Inflorescence^{-1} (0.880), Number of fruits plant^{-1} (0.080) Number of fruits inflorescence^{-1} had positive indirect effect on yield ha^{-1} via plant height (0.007), Number of flowers inflorescence^{-1} (0.441) and individual fruit weight (0.088). Fruit length had positive indirect effect on yield via plant height alone (0.028). Plant height had had positive indirect effect on yield via Number of Inflorescence plant^{-1} (0.033), Number of fruits inflorescence^{-1} (0.026), Number of fruits plant^{-1} (0.034), pedicel length (0.060), fruit length (0.088) and Individual fruit weight (0.005). Pedicel length had positive indirect effect on yield via Number of flowers Inflorescence^{-1} (0.052), Plant height (0.061) Number of fruits plant^{-1} (0.018) and fruit length (0.229). These findings were similar with; Neha et al. (2017); Gal et al. (2023); and Chaudhary et al. (2024). Residual effect indicated traits under study contributed approximately 90% towards yield, strongly justified the incorporation of traits for the present experiment.

Hence, fruit diameter, fruits inflorescence^{-1}, inflorescence plant^{-1} and fruit length could be considered effective traits as a basis for selection to enhance the yield parameters due to having high direct effect on yield through these traits with positive and high character associationship. In the contrary, fruit weight exhibited high positive correlation with yield with negligible indirect effect on yield suggested for restricted simultaneous selection model to nullify the undesirable effect (Singh and Kakar, 1977).

3.4. Principle factor analysis

In the present experiment mean data of 10 traits were subjected to principal factor analysis through principal component analysis method based on correlation matrix using varimax rotation. Factors had eigen value greater than unity was taken under consideration as proposed by Kaiser (1960). In the present investigation three principal factors exhibited eigen value greater than unity those cumulatively explained 74.74% of the variance (Table 3 and Figure 1) suggested sufficiency of these factors to explain maximum variation in the population for the selected traits and their complex inter relationship. Communality data suggested that all the traits could possibility be explained by these three principal factors excepting the plant height (0.47) where proportion of variability explained by the three factors to the total variability was insufficient. First factor explained most to the variation (38.20%) with eigen value of 3.82 which was mainly due to traits responsible for

Table 3: Eigen values, percentage of variance, cumulative variance percentage of three principal factors based on 10 traits of the 42 brinjal genotypes

Factor	F_1	F_2	F_3
Eigenvalue	3.82	2.00	1.65
Variance (%)	38.20	20.04	16.50
Cumulative variance (%)	38.20	58.24	74.74

Table 4: Factor load matrix (varimax rotation) of ten characters on three principal factors

Characters	Factor 1	Factor 2	Factor 3	Communality
PH	-0.044	0.682	-0.051	0.47
FlIn	0.739	-0.075	-0.087	0.56
InP	0.877	0.052	-0.023	0.77
FrIn	0.885	0.109	-0.019	0.80
FrP	0.871	-0.093	-0.091	0.78
PL	-0.103	0.876	-0.054	0.78
FL	0.127	0.765	0.136	0.62
FD	-0.450	-0.345	0.767	0.91
FW	-0.602	-0.020	0.738	0.91
YPH	0.293	0.245	0.859	0.88
Proportion of variance explained by the model				0.75

**PH: Plant height (cm); FlIn: Flowers inflorescence^{-1}; InP: I inflorescences plant^{-1}; FrIn: Fruits inflorescence^{-1}; FrP: Fruits plant^{-1}; PL: Pedicel length (cm); FL: Fruit length (cm); FD: Fruit diameter (mm); FW: Fruit weight (g); YPH: Yield (t ha^{-1})

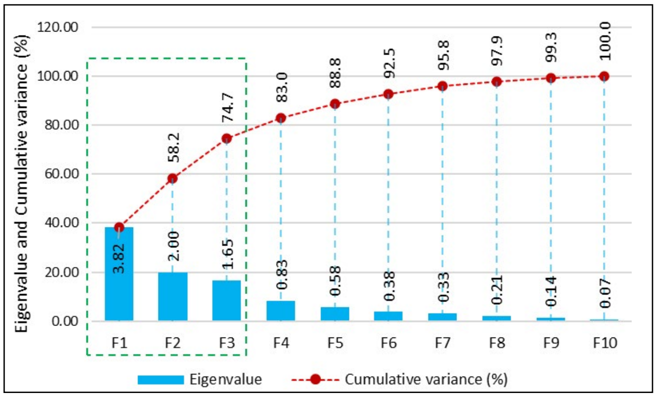


Figure 2: Scree plot showing eigen value and cumulative variability with their respective factors

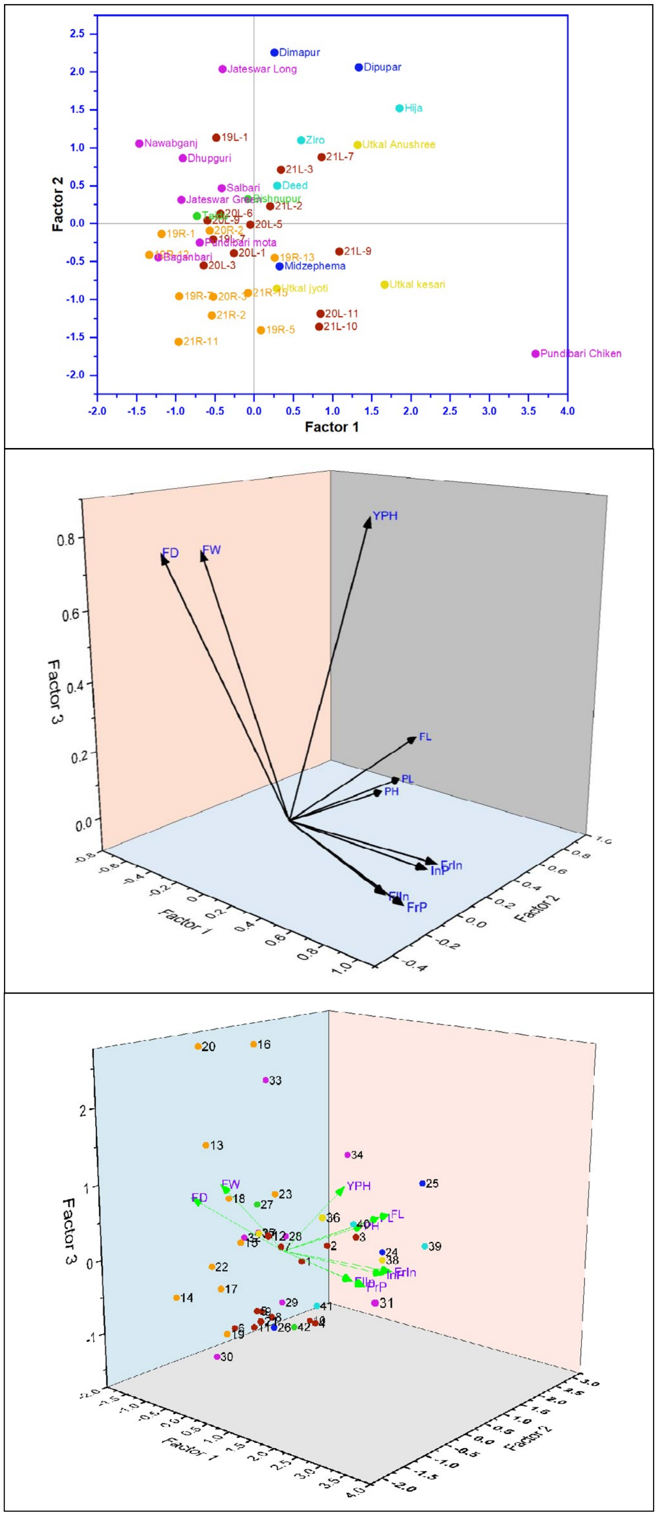


Figure 2: Loading plot, score plot and biplot 3-D model for distribution of ten traits to the three principal factors; **PH: Plant height (cm); FlIn: Flowers inflorescence^{-1}; InP: I inflorescences plant^{-1}, FrIn: Fruits inflorescence^{-1}, FrP: Fruits plant^{-1}, PL: Pedicel length (cm); FL: Fruit length (cm); FD: Fruit diameter (mm); FW: Fruit weight (g); YPH: Yield (t ha^{-1}) and Pundibari chicken: Pundibari chickon

Table 5: Distribution of elite genotypes that contribute to each factor from factor load matrix (varimax rotation)

Factor	Characters	Category	Genotypes
Factor 1	No. of flowers inflorescence^{-1}, No. of inflorescences plant^{-1}, No. of flowers in florescence^{-1} and No. of fruits plant^{-1}	Quantity of yield traits	2021/ BRLVAR-9, Pundibari Chikon, Utkal Kesari, Utkal Anushree, Hija
Factor 2	Plant height, fruit length and pedicel length	Growth	2021/ BRLVAR-2, 2021/ BRLVAR-3, 2021/ BRLVAR-7, Dimapur, Dipupar, Salbari, Jateswar Long
Factor 3	Fruit diameter, fruit weight and yield ha^{-1}	Yield	2019/ BRLVAR-9, 2020/ BRRVAR-2, 2019/ BRRVAR-1, 2019/ BRRVAR-7, 2019/ BRRVAR-13 and Nawabganj

quantity of yield traits like number of flowers inflorescence^{-1} (0.739), number of inflorescences plant^{-1} (0.877), number of fruits inflorescence^{-1} (0.885), Number of fruits plant^{-1} (0.871) and fruit weight (-0.602) (table 3, 4 and 5; figure 2). Second factor explained 20.04% variation with eigen value of 2.0 which was mainly associated with the growth-related traits like plant height (0.876), fruit length (0.765) and pedicel length (0.876). Whereas, third factor explained 16.50% variation with eigen value of 1.65 which was mainly associated with yield components like fruit diameter (0.767), fruit weight (0.738) and yield ha^{-1} (0.859). These findings were in accordance with Solaimana et al. (2014); Kumar et al. (2016). Data clearly revealed contradictory existence of attributes related to fruit weight and fruit quantity (Kumar et al. (2016). From the figure 2 it was clear that germplasm collected from the West Bengal and Nagaland exhibited high degree of variability than any other sources. Based on the magnitude of the loading through 42 diversified germplasm (Table 5; Figure 2), first factor was represented by 2021/BRLVAR-9, Pundibari Chikon, Utkal Kesari, Utkal Anushree, Hija; second factor was represented by 2021/BRLVAR-2, 2021/BRLVAR-3, 2021/BRLVAR-7, Dimapur, Dipupar, Salbari, Jateswar Long; third factor was represented by 2019/BRLVAR-9, 2020/BRRVAR-2, 2019/BRRVAR-1, 2019/BRRVAR-7, 2019/BRRVAR-13 and Nawabganj. Hence, further breeding strategy for crop improvement from these genotypes for the three separated desired trait group could be rewarding.

4. CONCLUSION

Present experiment suggested simple selection breeding method based on fruit diameter, fruits inflorescence^{-1}, inflorescence plant^{-1}, fruit length and fruit wight could be rewarding. 2021/BRLVAR-9, Pundibari Chikon, Utkal Kesari, Utkal Anushree, Hija were considered most suitable for selection of narrow and multi fruited germplasm and 2019/BRLVAR-9, 2020/BRRVAR-2, 2019/BRRVAR-1, 2019/BRRVAR-7, 2019/BRRVAR-13 and Nawabganj were considered most suitable for selection of big sized and high yielding germplasm.

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