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Assessment of Genetic Variability, Heritability and Genetic Gain for Yield and Quality Traits in Onion (*Allium cepa* L.)

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ABSTRACT

The experiments were undertaken at 'C' Block Farm of Bidhan Chandra Krishi Viswavidyalaya, Kalyani, Nadia, West Bengal, India during 2017–18 and 2018–19 to study the genetic variability, heritability and genetic gain of 23 onion genotypes. Twenty open-pollinated varieties, two hybrid varieties were taken under consideration with one variety taken as standard check. Characters like number of leaves at 30 DAT and 90 DAT, neck thickness, number of scales per bulb, bolters, average weight of 10 bulbs, vitamin C content, dry matter, TSS, phenol content, severity of purple blotch disease, total yield and marketable yield expressed high heritability along with high genetic gain. These traits were least influenced by environmental effect, so, additive genetic effect might be the influential factor for expression of such traits. Traits with such high heritability values gives clear indication that the variability observed was mainly under genetic control and offers ample scope and opportunities to conduct selection based on phenotypic performances for improvement in future onion breeding programme. For traits with moderate heritability viz., double bolters, pyruvic acid, total sugar, storage loss, selection would be less effective in these traits but can still be taken up. Characters plant height at 90 DAT and unmarketable yield, which expressed low heritability are governed by non-additive genes and therefore, hybridization between diverse parents will be the best strategy for their improvement.

KEYWORDS: Genetic variability, genetic gain, heritability, quality, yield

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1. INTRODUCTION

In India, onion (*Allium cepa* L.) is grown as one of the most important commercial vegetable cum spice crop. It belongs to the family Alliaceae and has got 8 gametic and 16 somatic chromosomes. The plants have hollow scape with completely flat leaves and require cool season, long days for its growth and development. The color of red onions is primarily due to presence of anthocyanins in the epidermal cells of the scale leaves (Pavlovic et al., 2003) of the bulb, and the pigment is reported to be due to cyanidin 3-glucoside (Lee et al., 2015). The unique pungency is mainly attributed to the sulphur containing compound (allyl propyl disulphide) (Gurjar and Sighania, 2006). Quercetin, a flavanoid compound in onion, is known to possess anti-cholesterol, anticancer and antioxidant properties (Bal et al., 2019). Its phenolic compounds can offer significant anti-mellitus atherogenic protection by inhibiting the oxidation of low density lipoproteins (LDLs) (Benkeblia, 2005). Major onion crop is grown during *rabi* or winter season (60%) and rest is grown during *kharif* or monsoon season (20%) and late *kharif* or late monsoon season (20%) (Singh et al., 2013). In terms of area and production of onion India ranks next to China (Sidhu et al., 2019). Among the different states, Maharashtra is leading in terms of area and production (Bal et al., 2019). Other major onion states are Gujarat, Karnataka, Orissa, Uttar Pradesh, Andhra Pradesh, Tamil Nadu and Rajasthan. From the export of fresh vegetables, onion accounts for 60 percent of total foreign exchange (Ram et al., 2011). Being protandrous in nature, onion is highly cross-pollinated crop, thus, high variation in genetic component can be observed (Rajalingam and Haripriya, 2000). Genetic variation forms the basis of plant breeding (Dangi et al., 2018) and is the "*sine qua non*" of any such crop improvement programme (Mallor et al., 2011a). Research studies related to genetic variation in onion have been reported (Mohanty, 2004, Khosa and Datt, 2015, Singh et al., 2013, Arya et al., 2017, Dhotre et al., 2010). Inspite of having tremendous genetic variation, the crop still stands forfeited in terms of their genetic potential (Manjunathagowda and Anjanappa, 2021) which happens due to the cloaking of environmental effects over genotype and thus the inheritance pattern of various characters turns an important consideration for determining the most appropriate breeding mechanisms applicable for any given crop (Hosamani et al., 2010). The discerned way to start any breeding programme is to survey the variation in the available materials (Mohanty, 2001). Such genetic potential can be escalated by assessing variability parameters viz., heritability, genetic gain, genotypic (GCV) and phenotypic coefficient of variation (PCV) of different qualitative and quantitative traits for any given crop (Panse, 1957). Besides, knowledge of heritability of a trait assists in development of efficient breeding strategies by assessing the degree of transmissibility of a character (Porta et al., 2014; Netrapal and Chowdhary, 1988; Singh et al., 2010) and enables selection for enhancing the genetic progress (Ghodke et al., 2020; Gedam et al., 2021), whereas, genotypic and phenotypic coefficient of variation helps in estimating the magnitude of genetic variation present in a population (Mallor et al., 2011b), furthermore, estimates of heritability in conjugation with genetic advance have to be contemplated in order to find the expected genetic gain in following generations (Mohanty, 2002; Singh et al., 2020). Thus, through this investigation, little attempt had been taken to analyze the magnitude of different components of heritability and genetic parameters present among the genotypes of onion.

2. MATERIALS AND METHODS

The study was carried out at 'C' Block Farm of Bidhan Chandra Krishi Viswavidyalaya, Kalyani, Nadia, West Bengal, India. The soil of the farm was fine sandy-loam in texture, neutral in reaction with good water holding capacity. The meteorological observations taken during the experimental period of 2017–18 and 2018–19.

The experiment was laid out in a Randomized Block Design with three replications during *rabi* (winter) seasons of 2017-2018 and 2018-2019. The plants were spaced 15 cm row to row and 10 cm plant to plant. Optimum plot size was 2×1 m^2. Twenty-three onion genotypes were used in the present investigation among which twenty genotypes are open-pollinated varieties (Arka Bheem, Arka Niketan, Akola Safed, Agrifound Light Red, Bhima Dark Red, Bhima Kiran, Bhima Raj, Bhima Red, Bhima Safed, Bhima Shakti, Bhima Subhra, Bhima Super, Bhima Sweta, Hisar-2, Hisar-4, Kalyanpur Red Round, L-28, Onion HO-3, PRO-6 and Punjab Naroya), two hybrid varieties (Arka Kirtiman and Arka Lalima) and one genotype (Sukhsagar) had been taken as standard check. The observations were recorded for plant height and the number of leaves at 30 DAT, 60 DAT and 90 DAT; neck thickness (mm), number of scales bulb^{-1}, bolter and double bolter (%), polar diameter and equatorial diameter (mm), number of bulbs^{-1}, average weight of ten bulbs (kg), days to maturity, vitamin C (mg g^{-1}), pyruvic acid (μmole g^{-1}), which was estimated by following the procedure of Anthon and Barrett (2003), total sugar percentage which was calculated using Anthrone method as per Dubois et al. (1956), dry matter %, TSS (°Brix), phenol (mg g^{-1}), severity of purple blotch disease (%) using 0-5 scale as given by Bhangale and Joi (1985), storage loss (%), total yield (kg plot^{-1}), marketable yield (kg plot^{-1}) and unmarketable yield (kg plot^{-1}) and severity of purple blotch disease (%) (Sandhu et al., 1981).The statistical analysis for each observed character was carried out using MS-Excel and OPSTAT.

3. RESULTS AND DISCUSSION

In order to study variability present in a population a breeder needs to have diversified breeding population. The success of any plant breeding programme is dependent on amount of variability present in the available germplasm and the degree of transmission of that character from one generation to next generation. The component of genetic variation includes phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), genetic gain *i.e.,* genetic advance as percent over mean. The idea of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is useful in predicting the amount of variation present in any given number of genotypes. GCV helps in measuring range of genetic variability and provides a way to compare genetic variability among the characters under study (Sanghi et al., 1964). However, genotypic coefficient variation alone cannot measure the heritable variation. For correct estimation of the genetic makeup and its contribution to phenotypic expression of the character, it is necessary that the evaluation or analysis of the characters to be performed in different locations and seasons. This suggests that selection would be effective on the basis of characters having high genotypic coefficient of variation. To understand the extent of variation observed due to genetic factors, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), genetic gain were worked out for twenty six traits and are represented in Table 1. The observed variations in the characters studied among all the genotypes are described hereunder.

3.1. Plant height (cm) at 30 DAT

Significant variation was observed among all the genotypes for this character. The overall mean of this character was 27.56 cm and the range varied from 21.72 to 34.93 cm. The estimates of PCV and GCV were found moderate (17.69 and 13.86 respectively) and high heritability (61.35%) associated with moderate genetic gain (19.28%) were observed for this trait.

3.2. Plant height (cm) at 60 DAT

For this parameter, the range varied from 37.84 to 64.52 cm with overall mean of 53.49 cm. The PCV and GCV values were found moderate (10.87 and 10.08 respectively) and high heritability (85.95%) along with moderate genetic advance as percent over mean (19.25%) value was observed.

3.3. Plant height (cm) at 90 DAT

The performances of the genotypes taken under study exhibited significant variation for this trait. The range of this character varied from 53.90 to 79.00 cm and the overall mean was 64.35 cm. The values of PCV and GCV were found high (36.27 and 22.56 respectively) along with low heritability (38.67%) and high genetic gain (23.07%) was observed. The results were validated with the findings of Yaso, (2007a) and Santara et al., (2017).

3.4. Number of leaves at 30 DAT

A perusal of data (Table 1) showed that the number of leaves at 30 DAT varied from 3.26 to 4.46 with an overall mean of 3.87. The estimates of PCV and GCV were found moderate (13.68 and 11.90 respectively) and high heritability (75.87%) coupled with very high genetic advance as percent over mean (147.65%) were observed.

3.5. Number of leaves at 60 DAT

The performances of the genotypes taken under study exhibited significant variation for this trait. The range of this character varied from 4.60 to 6.06 with an overall mean of 5.25. Low PCV and GCV values (7.70 and 6.06 respectively) were observed for this trait. The heritability for this trait was high i.e., 61.90% and genetic gain was found low (9.83%).

3.6. Number of leaves at 90 DAT

Based on the data appended on Table 1 it was found that the all the genotypes taken under study had shown significant variation with respect to this character. The range of this character varied from 6.20 to 8.66 with an overall mean of 6.94. Furthermore, moderate PCV (10.52) and low GCV (8.31) were observed for this parameter. Besides, high heritability (62.50%) coupled with high genetic advance as percent over mean (60.45%) were also observed for this trait. The results were corroborated with findings of Santara et al. (2017).

3.7. Neck Thickness (mm)

All the genotypes differed significantly for neck thickness. The overall mean for this character was 7.44 mm with range varying from 5.49 to 9.25 mm. The estimates of PCV and GCV were found moderate (12.87 and 12.24 respectively) along with high heritability (90.50%) and high genetic gain (89.88%). The findings were corroborated with findings of Khosa and Datt (2015).

3.8. Number of scales bulb^{-1}

A perusal of data (Table 1) showed that the number of scales per bulb varied from 6.11 to 10.44 with an overall mean of 15.04. The estimates of PCV and GCV values (19.01 and 18.57 respectively) were found moderate but the heritability (95.42%) along with genetic advance as percent over mean was observed high (37.38%). The result finds support from the findings of Yaso (2007a), Ijeomah et al. (2020) and Dangi et al. (2018).

Table 1: Estimates of phenotypic and genotypic coefficients of variability, heritability and genetic gain for different traits in onion

Traits	Mean	Range	Coefficients of variability (%)		Heritability (%)	Genetic gain (%)
			Phenotypic	Genotypic		
Plant height (cm) at 30 DAT	27.56	21.72-34.93	17.69	13.68	61.35	19.28
Plant height (cm) at 60 DAT	53.49	37.84-64.52	10.87	10.08	85.95	19.25
Plant height (cm) at 90 DAT	64.35	53.90-79.00	36.27	22.56	38.67	23.07
No. of leaves at 30DAT	3.87	3.26-4.46	13.68	11.90	75.87	147.65
No. of leaves at 60DAT	5.25	4.60-6.06	7.70	6.06	61.90	9.83
No. of leaves at 90DAT	6.94	6.20-8.66	10.52	8.31	62.50	60.45
Neck thickness (mm)	7.44	5.49-9.25	12.87	12.24	90.50	89.88
No. of scales bulb^{-1}	15.04	6.11-10.44	19.01	18.57	95.42	37.38
Bolters (%)	2.47	0.67- 4.66	55.35	48.14	73.31	46.58
Double bolters (%)	6.71	3.12-8.97	135.15	80.77	35.72	579.06
Polar diameter (mm)	53.19	43.48-57.33	9.03	7.39	67.04	12.48
Equatorial diameter (mm)	50.18	43.58-56.95	9.92	8.07	66.31	13.55
No. of bulbs plot^{-1}	89.27	64-109	16.31	15.30	87.93	8.16
Average weight (kg) of 10 bulbs plot^{-1}	0.55	0.42-0.67	15.00	14.48	93.19	28.80
Days to maturity	129.04	116-137.33	5.61	5.39	92.10	10.66
Vitamin C (mg g^{-1})	0.35	0.12-0.71	55.94	54.34	95.00	109.50
Pyruvic acid (µmole g^{-1})	1.48	0.78-3.16	45.39	30.96	45.51	43.50
Total sugar (%)	1.73	0.81-3.48	45.03	27.13	36.30	33.68
Dry matter (%)	11.51	0.21-34.56	81.07	79.57	96.34	160.90
Total soluble Solids (˚B)	9.46	6.37-14.14	31.12	29.55	90.16	57.81
Phenol content (mg g^{-1})	5.00	2.61-8.20	40.51	40.18	98.38	82.11
Severity of Purple blotch disease (%)	16.18	1.23-28.49	57.01	55.13	93.49	109.80
Storage loss (%)	1.07	0.27-8.27	111.82	77.37	47.87	593.49
Total yield (kg plot^{-1})	3.02	1.08-7.15	60.97	60.70	99.38	124.50
Marketable yield (kg plot^{-1})	2.58	1.03-5.49	63.51	62.72	97.38	617.48
Unmarketable yield (kg plot^{-1})	0.18	0.03-0.68	150.46	73.75	24.05	32.53

3.9. Bolters (%)

The performances of the genotypes taken under study exhibited significant variation for this trait. The range for this character varied from 0.67 to 4.66% with an overall mean of 2.47%. The estimates of PCV and GCV for this character were found high (55.35 and 48.14 respectively) coupled with high heritability (73.31%) and high genetic gain (46.58%).

3.10. Double bolters (%)

For this parameter, the range varied from 3.12 to 8.97% with an overall mean of 6.71. In addition, high PCV and GCV values (135.15 and 80.77 respectively) were observed for this trait. The heritability was found moderate i.e., 35.72% coupled with high genetic advance as percent over mean (579.06%).

3.11. Polar diameter (mm)

Based on the data appended in Table 1 it was found that the all the genotypes taken under study had shown significant variation with respect to polar diameter. The range of this character varied from 43.48 to 57.33 mm with an overall mean of 53.19 mm. The estimates of PCV and GCV were found low (9.03 and 7.39 respectively) for this trait. In addition, high heritability (67.04%) and low genetic gain (12.48%) were also observed. The results find support from the findings of Hosamani et al. (2010).

3.12. *Equatorial diameter (mm)*

Significant variation was observed among all the genotypes for equatorial diameter. The range for this trait varied from 43.58 to 56.95 mm and the overall mean was of 50.18 mm. In addition, low PCV and GCV values (9.92 and 8.07 respectively) were observed for this trait. The heritability for this character was found high (66.31%) and low genetic advance as percent over mean (13.55%). The results were corroborated with results of Hosamani et al., (2010) and Porta et al., (2014).

3.13. *No. of bulbs plot^{-1}*

A perusal of data (Table 1) showed that the number of bulbs plot^{-1} varied from 64 to 109 with overall mean of 89.27. The estimates of PCV and GCV values (16.31 and 15.30 respectively) were found moderate for this trait. The heritability was found high (87.93%) and low genetic gain was observed (8.16%). The results find support from earlier works done by Hosamani et al., (2010) and Santara et al. (2017).

3.14. *Average weight of 10 bulbs (kg)*

All the genotypes differed significantly for average weight of 10 bulbs. The overall mean of this character was 0.55 kg and the range varied from 0.42 to 0.67 kg. The estimates of PCV and GCV were found moderate (15.00 and 14.48 respectively) for this parameter. In addition, high heritability (93.19%) and high genetic advance as percent over mean (28.80%) were found for this trait. The results were corroborated with the results of Santara et al. (2017).

3.15. *No. of days to maturity*

The performances of the genotypes taken under study exhibited significant variation for number of days to maturity. The range for this trait varied from 116 to 137.33 with an overall mean of 129.04. The values of PCV and GCV (5.61 and 5.39 respectively) were observed low for this trait. The heritability was found high (92.10%) coupled with low genetic gain (10.66%).

3.16. *Vitamin C (mg g^{-1})*

All the genotypes differed significantly for vitamin C content. The range of this character varied from 0.12 to 0.71 mg g^{-1} with an overall mean of 0.35 mg g^{-1}. The values of PCV and GCV values (55.94 and 54.34 respectively) were observed high for this trait. In addition high heritability (95.00%) along with high genetic advance as percent over mean (109.50%) was observed for this trait. The results find support from the findings of Hosamani et al. (2010) and Khosa and Datt (2015).

3.17. *Pyruvic acid (µmole g^{-1})*

Based on the data appended in Table 1 it was found that the all the genotypes taken under study had shown significant variation with respect to pyruvic acid content. The range of this parameter varied from 0.78 to 3.16 µmole g^{-1} with an overall mean of 1.48 µmole g^{-1}. The estimates of PCV and GCV values (45.39 and 30.96 respectively) were found high for this trait. The heritability for this trait was found moderate (45.51%) coupled with high genetic gain (43.50%). The results were corroborated with the results of Ijeomah et al. (2020).

3.18. *Total sugar (%)*

The range of this character varied widely from 0.81 to 3.48% with an overall mean of 1.73. The estimates of PCV and GCV were found high (45.03 and 27.13 respectively). In addition, moderate heritability (36.30%) and high genetic advance as percent over mean (33.68%) were observed. The results find support from the findings of Porta et al. (2014).

3.19. *Dry matter (%)*

All the genotypes differed significantly for dry matter. The range of this character varied from 0.21 to 34.56% with an overall mean of 11.51%. Moreover, high PCV and GCV values (81.07 and 79.57 respectively) along with high heritability (96.34%) coupled with high genetic gain (160.90%) were observed for this trait. The findings were corroborated with the findings of Ram et al. (2011), Porta et al. (2014).

3.20. *Total soluble solids (°B)*

A perusal of data (Table 1) showed that the total soluble solids varied from 6.37^{0} B to 14.14°B with an overall mean of 9.46 °B. The estimates of PCV and GCV were found high (31.12 and 29.55 respectively) coupled with high heritability (90.16%) and high genetic advance as percent over mean (57.81%). The results finds support from the findings of Maia et al. (2008), Porta et al. (2014) and Ijeomah et al. (2020).

3.21. *Phenol (mg g^{-1})*

Significant variation was observed among all the genotypes for phenol content. The range of this trait varied from 2.61 to 8.20 mg g^{-1} with an overall mean of 5.00 mg g^{-1}. The PCV and GCV values were found high (40.51 and 40.18 respectively) along with high heritability (98.38%) and genetic gain (82.11%). The results were corroborated with the findings of Hosamani et al. (2010).

3.22. *Severity of purple blotch disease (%)*

Based on the data appended in Table 1 it was found that the all the genotypes taken under study had shown significant variation with respect to severity of purple blotch disease. The range of this trait varied from 1.23 to 28.49% with an overall mean of 16.18%. The estimates of PCV and GCV (57.01 and 55.13 respectively) were observed for high this trait. In addition, the heritability and genetic advance as percent over mean were found high i.e., 93.49% and 109.80% respectively for this trait.

3.23. *Storage loss (%)*

All the genotypes differed significantly for storage loss. The overall mean was 1.07% and the range varied from 0.27 to 8.27%. In addition, the estimates of PCV and GCV were high (111.82 and 77.37 respectively) along with moderate heritability (47.87%) and high genetic gain (593.49%) were observed for this trait.

3.24. *Total yield (kg plot^{-1})*

Significant variation was observed among all the genotypes for this character. The range of this character varied from 1.08 to 7.15 kg plot^{-1} with overall mean of 3.02 kg plot^{-1}. The estimates of PCV and GCV for this character were found high (60.97 and 60.70 respectively) coupled with high heritability (99.38%) and high genetic advance as percent over mean (124.50%). These results finds support from the findings of Santara et al. (2017).

3.25. *Marketable yield (kg plot^{-1})*

For this parameter, the range varied from 1.03 to 5.49 kg plot^{-1} with an overall mean of 2.58 kg plot^{-1}. The estimates of PCV and GCV (63.51 and 62.72 respectively) were observed high for this trait, in addition, the heritability was found high (97.38%) coupled with high genetic gain (617.48%). The findings were corroborated with the findings of Khosa and Datt (2015) and Santara et al. (2017).

3.26. *Unmarketable yield (kg plot^{-1})*

All the genotypes taken under study varied significantly for this trait. The range of this trait varied from 0.03 to 0.68 kg plot^{-1} with an overall mean of 0.18 kg plot^{-1}. For this trait both PCV and GCV estimates (150.46 and 73.75 respectively) were observed high. Furthermore, low heritability (24.05%) coupled with high genetic advance as percent over mean (32.53%) was observed for this trait.

In all of the above traits both phenotypic coefficient variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (0-10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Menon (1973), although the classification is not a rigid one. In this study high GCV and PCV values (>20%) was documented for plant height at 90 DAT, bolters, double bolters, vitamin C, pyruvic acid, total sugar, dry matter, TSS, phenol, severity of purple blotch disease, storage loss, total yield, marketable yield and unmarketable yield. In all of these traits the proportion of genetic contribution to the overall phenotypic expression of most traits was very high. Such high magnitude of GCV and PCV indicates ample scope for the improvement of the above-mentioned traits through normal selection. Moderate PCV and GCV values (10-20%) were observed in plant height at 30 DAT, plant height at 60 DAT, number of leaves at 30 DAT, neck thickness, number of scales bulb^{-1}, number of bulbs plot^{-1} and average weight of 10 bulbs. Whereas, low GCV and PCV estimates (0-10%) were observed in number of leaves at 60 DAT, polar diameter, equatorial diameter and number of days to maturity. These traits are largely under the environmental effect rather than genetic control. Such traits whose expressions are environmentally dependent may not be reliable descriptors for morphological characterization (Pandey et al., 2008). During *rabi* season, Golani et al. (2006) evaluated thirty two genotypes and revealed that the estimates of PCV were greater than the corresponding GCV for all the traits under study.

The genotypic co-efficient of variation is the measure to estimate the variability of characters, but GCV alone cannot determine the amount of variation that is heritable. The GCV×selection differential, helps in estimating the maximum effectiveness of selection and heritability indicates how closely the goal can be achieved. Thus estimates of heritability stand here important (Pandey et al., 2008). Plant breeder find interests in heritability as it serves as an index of transmissibility of characters from one generation to next generation (Al-Jibouri et al., 1958). Heritability is essential to measure the relative magnitude of the effect of genes and environment on total phenotypic variability and thus fetch us a measure of genetic relationship between parent and progeny. Burton (1953) described heritability as the ratio of the variance due to hereditary difference (genotypic variance) to the total observed variance (phenotypic variance). In this study, heritability was classified as low (<30%), medium (30-60%) and high (>60%) (Johnson et al., 1955). Such high broad sense heritability was observed in plant height at 30 DAT and 60 DAT, number of leaves at 30 DAT, 60 DAT, neck thickness, number of scales bulb^{-1}, bolters, polar diameter, equatorial diameter, number of bulbs plot^{-1}, average weight of 10 bulbs, days to maturity, vitamin C, dry matter, TSS, phenol, severity of purple blotch disease, total yield and marketable yield. Such high heritability measures indicated that these characters are under genetic control and had lesser influence of environmental effect on the genotypes studied (Songsri et al., 2008).This aids plant breeders to conduct selection based on the phenotypic performance.

Improvement in the mean genotypic value of the selected families over base population is the genetic advance under selection and it depends mainly on the genetic variability, heritability and intensity of selection (*i.e.*, proportion of plants selected) (Charles and Smith, 1939). Heritability and genetic gain are complementary aspects, thus, estimates of heritability can be used for computing the expected genetic progress possible through selection (Hanson et al., 1956). In this study, selection differential has been kept constant (2.06) for 5% selection intensity. Genetic advance as percent of mean was categorized as suggested by Johnson et al., (1955a). Very high GA as % of mean (>100%) was recorded for number of leaves at 30 DAT, double bolters, vitamin C, dry matter, storage loss, severity of purple botch disease, total yield and marketable yield. High GA as % over mean (>20%) was recorded for the characters plant height at 90 DAT, number of leaves at 90 DAT, neck thickness, number of scales per bulb, bolters, average weight of 10 bulbs plot^{-1}, pyruvic acid, total sugar, TSS, phenol and unmarketable yield. Johnson et al. (1955) suggested that heritability in combination with substantial amount of genetic advance would be more reliable than heritability alone for predicting the effect of selection in segregating generation. In this study, high heritability coupled with high genetic advance as percent of mean was observed for traits viz. number of leaves at 30 DAT, number of leaves at 90 DAT, neck thickness, number of scales per bulb, bolters, average weight of 10 bulbs, vitamin C, dry matter, total soluble solids, phenol, severity of purple blotch disease, total yield and marketable yield. Thus, these characters can be regarded as most reliable for selection as these characters are controlled by additive genes (Panse, 1957) and selection of these traits would be rewarding for the improvement of these traits. Several researchers conducted experiments with different genotypes and environments. Maia et al. (2008) reported high heritability and genetic gain for different plant and qualitative parameters. Ram et al. (2011) reported high heritability in bulb weight and bulb diameter while working in different onion accessions. Porta et al. (2014) observed high broad sense heritability for the characters leaf length, dry matter and total soluble solids and other yield components. Ijeomah et al. (2020) observed genetic variation in 10 spring onion genotypes for different yield components in Nigeria.

4. CONCLUSION

The characters with high heritability and genetic gain were under genetic control and least affected by environmental conditions. Such traits would provide ample scope and opportunities to the breeders to undergo selection based on phenotypic performances for future breeding programmes. Traits with moderate heritability, selection would be less effective but can still be taken up. For traits with low heritability, hybridization between diverse parents would be the best strategy for improvement.

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