

Original Research

DOI : <http://doi.org/10.22438/jeb/43/3/MRN-1990>

Genetic variability, character association and path analysis for different traits in white onion genotypes under short day condition

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Received: 20.05.2021

Revised: 03.09.2021

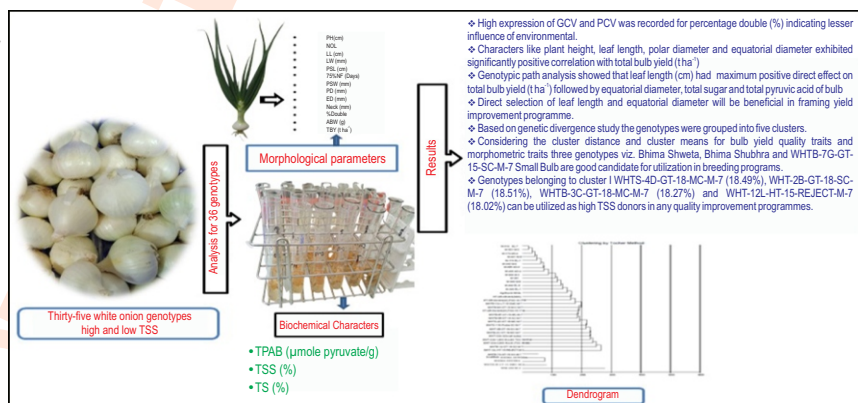
Accepted: 01.11.2021

Abstract

Aim: To estimate the nature and magnitude of genetic diversity of white onion genotypes.

Methodology: The experiment was carried out for two consecutive years (2018-19 and 2019-20) at ICAR-DOGR, Pune. Thirty-five genotypes of white onion identified as low and high TSS genotypes were used to study their genetic variability, character association, path analysis and genetic diversity for different morphological and biochemical traits.

Results: Significant differences were observed among all the genotypes. High expression of GCV over PCV was recorded for percentage double indicating lesser influence of environment. The broad sense heritability values were higher (60%) for all the characters under study ranging from 62.10% in days to 75% neck fall to 98.38% in total sugar. Plant height, leaf length, polar diameter and equatorial diameter exhibited significant positive correlation with total bulb yield. Genotypic path analysis showed that leaf length (cm) had maximum positive direct effect on total bulb yield followed by equatorial diameter, total sugar and total pyruvic acid of bulb.



Interpretation: Considering the cluster distance and cluster means for bulb yield quality traits and morphometric traits three genotypes viz., Bhima Shweta, Bhima Shubra from cluster III and WHTB-7G-GT-15-SC-M-7 Small Bulb from cluster II were good candidates for utilization in breeding programs. Genotypes belonging to cluster I WHTS-4D-GT-18-MC-M-7 (18.49%), WHT-2B-GT-18-SC-M-7 (18.51%), WHTB-3C-GT-18-MC-M-7 (18.27%) and WHT-12L-HT-15-REJECT-M-7 (18.02%) can be utilized as high TSS donors in quality improvement programmes. This study also indicated that, direct selection of leaf length and equatorial diameter will be beneficial in framing yield improvement programme.

Key words: *Allium cepa*, Genetic divergence, Path analysis

How to cite : Singh, P.R., V. Mahajan, A. Verma, B. Lalramhlimi, Y.P. Khade, P. Gedam, N. Shukla, O. Sogam and M. Singh: Genetic variability, character association and path analysis for different traits in white onion genotypes under short day condition. *J. Environ. Biol.*, **43**, 401-411 (2022).

Introduction

One of the most important commodities for export is the onion (*Allium cepa* L.) which belongs to family Alliaceae. It is a widely cultivated crop and regarded as single most important vegetable in the world after tomatoes (Kale *et al.*, 2015). The importance lies beyond its great export as voluminous literature on numerous usages and nutritional properties of various parts of onion are documented. Onions are consumed in variety of ways throughout the world because of its nutritional and medicinal value (Dhanya *et al.*, 2014). It is used for flavoring or seasoning the food items besides being used as salad and pickle (Sidhu *et al.*, 2005). A single bulb provides 2.0 g protein 72 mg calcium and 54 mg phosphorus (Ado, 2001). Raw onion juice is used for reducing hair loss traditionally. Onion leaves and bulbs are nutritionally rich in minerals like calcium, potash and phosphorus (Ullah *et al.*, 2005). Onion comes in different colors such as red, dark red, yellow, brown and white. White-skinned onion cultivars are used for dehydration purpose as they have high dry matter content and processed into dehydrated products like flakes, powders, rings, half slices, chopped onion, granulated onion, kibbled onion etc. Globally production of dried onion is more than 124.93 million tonnes under 6.32 million hectares area (FAOSTAT, 2019). The value of globally exported onions was accelerated by 12.2% from 2018 to 2019. Onion has 6% share in the overall production of vegetables in India and about 93% of the total export of fresh vegetables from India (Singh *et al.*, 2006).

The production in India for 2019-20 is estimated to be 267.15 lakh tonnes with Maharashtra as leading producer (113.63 lakh tonnes) contributing about 42.53% share. Though India ranks first in area and second in production after China, the productivity (18.71 t ha⁻¹) is far below as compared to USA (60.54 t/ha), Netherlands (36.63 t ha⁻¹) and China (22.11 t ha⁻¹) (FAOSTAT, 2019). This could be due to the lack of use of improved genotypes and optimum fertilizer dose (Shamima and Hossain, 2000) inadequate certified seeds, poor seed replacement ratio (< 20%), absence of investment in farm mechanization / improved farming practice, limited improved varieties suitable for different seasons with resistance to biotic and abiotic factors. The production of white onion has gained popularity among producers and consumers. It is widely used as fresh and processed onion for export purpose, however, previously the major focus was paid on improving the yield of red skin varieties, contribution of improved open pollinated varieties (OPVs) and hybrids almost doubled the production potential of cultivated onion in last five decades (Brewster, 2008), however research on white onions for its yield improvement and genetic studies is very scanty.

The knowledge of genetic variability is of paramount importance to frame any breeding improvement programme. Moreover, phenotype is often not a true indicator of its genotype due to the masking effect of environment and other factors (Hosamani *et al.*, 2010), the effective selection can be achieved through genetic component study such as genotypic coefficient of variation phenotypic coefficient of variation heritability

genetic advance character association ship and the nature of yield contributing characters that influence the bulb yield of white onion. Evaluation of a large number of germplasm for genetic diversity enables to identify important source of a particular trait belonging to diverse genotypes for further selection of parents for hybridization programme.

Cluster analysis is a useful tool for grouping genotypes in clusters on the basis of weighted means and provides a way for breeders in selection of parents (Dangi *et al.*, 2018). Genetic diversity of various white onion types under Indian conditions is not yet known. It is an established fact that genetically diverse parents are likely to contribute desirable segregants and/or to produce high heterotic cross. In view of the above, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity of white onion genotypes so that their subsequent use in onion improvement programmes can be achieved.

Materials and Methods

The present investigation was conducted at the research farm of ICAR- Directorate of Onion and Garlic Research, Pune, Maharashtra, India. Thirty-five genotypes were used for the study which comprised of 33 genotypes and two varieties selected based on TSS properties. The layout of the experiment followed randomized block design with three replications and the size of plot was 2 × 3 m with a plant spacing 15 × 10 cm. Standard cultural operation was followed as per recommended cultural practices by ICAR-DOGR, Rajgurunagar, Pune. Five plants from each genotype per replication were randomly selected to record 16 quantitative and qualitative characters.

Observations were recorded on plant height (scale), number of leaves, leaf length (scale), leaf width (mm), pseudostem length (cm) (Scale), pseudostem width (mm), 75% neck fall, polar diameter(mm), equatorial diameter (mm), neck thickness (cm), percentage of doubles (%), pyruvic acid, total sugar (%), average bulb weight (gm) and total yield per hectare. A 1 m steel ruler scale was used to measure the plant height, pseudostem length and leaf length while Vernier caliper was used to measure the leaf width, pseudostem width, polar diameter, equatorial diameter and neck thickness. Pyruvic acid content was estimated according to method suggested by Ketter and Randle (1998). Total soluble solute was measured from five samples of each genotype per replication with hand refractometer (0-30) and mean value was presented. Total sugar was estimated by the method of Somogyi (1952).

Genetic variability parameters correlation and path analysis were analyzed as proposed by Johnson *et al.* (1995) and Dewey and Lu (1958) respectively. Genetic diversity was calculated using Mahalanobis generalized distance (D₂) extended by Rao (1952) while grouping of the population was conducted as per Tocher's method as described by Rao (1952). Hierarchical cluster analysis was performed with the same genotypes to observe degree of association according to

characteristics expressed in a dendrogram (Ward, 1963). Statistical analyses were carried out by using IndoStat computer software (INDOSTAT.exe Hyderabad).

Results and Discussion

Analysis of variance showed significant differences for all quantitative and qualitative traits of white onion genotypes indicating the presence of genetic differences among genotypes under study during both the years. The magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all characters (Table 2) indicating the effect of environment on genotypic expression. A high proportion of GCV to PCV is desirable in selection because it indicates that the traits are under genetic rather than environmental control (Kaushik *et al.*, 2007). The proportion of GCV in PCV observed in this study varied from 78.57% in 75% neck fall to 99.20% in total sugar of bulb which were high in

most of the traits. The traits which exhibit high proportion of this value are reliable for selection in genetic improvement of onion genotypes. High expression of GCV and PCV was recorded for percentage double (%) indicating lesser influence of environment. Moderate to high GCV and PCV values were recorded for characters like number of leaves, total soluble solids (%), total sugar, total pyruvic acid of bulb ($\mu\text{mole pyruvate g}^{-1}$) and total bulb yield (t ha^{-1}).

Our results are in agreement with earlier studies where high GCV and PCV were reported in total pyruvic acid of bulb and conversely low in TSS (Chattopadhyay *et al.*, 2013) and number of leaves (Hosamani *et al.*, 2010; Porta *et al.*, 2014; Pujar *et al.*, 2019). These characters showed greater genetic variability among the genotypes and offered good opportunity for crop improvement through selection. However genetic variability along with heritability should be considered for obtaining the maximum and accurate effect of selection (Burton 1952). The

Table 1: Detailed sources of collection of thirty-five white onion genotypes

Variety/ Accession Number	Source of collection
WHT-23A-1Big BULBS TSS 15-17.8	ICAR-DOGR Breeding Lines
WHTS-11K-Pickle-SC-M-7	ICAR-DOGR Breeding Lines
WHT-23A-3(Small bulbs)	ICAR-DOGR Breeding Lines
WHTB-3C-GT-18-MC-M-7	ICAR-DOGR Breeding Line
WHTB-7G-GT-15-SC-M-7 Small Bulb	ICAR-DOGR Breeding Line
WHTB-10J-LT-15-SMC-M-7	ICAR-DOGR Breeding Lines
WHTB-9I-LT-15-SMC-M-7	ICAR-DOGR Breeding Lines
WHTB-8H-GT-15-M-C-M-7	ICAR-DOGR Breeding Lines
WHT-12L-HT-15-Reject-M-7	ICAR-DOGR Breeding Lines
W-340 EL-7	NHRDF Nasik Maharashtra
Agrifound White	NHRDF Nasik Maharashtra
WHTB-6F-GT-15-MC-M-7	ICAR-DOGR Breeding Lines
W-361	NHRDF, Nasik
WHTB-5E-GT-15-SC-M-7	ICAR-DOGR Breeding Lines
WHT-2B-GT-18-SC-M-7	ICAR-DOGR Breeding Lines
WHTS-4D-GT-18-MC-M-7	ICAR-DOGR Breeding Lines
W-444 EL-6	Bhavnagar, Gujarat
WHTB-1A-GT-18-SC-M-7	ICAR-DOGR Breeding Lines
WHT-23A(P)	ICAR-DOGR Breeding Lines
HT-GR-5A-M-6(SC)TSS-15-17.8	ICAR-DOGR Breeding Lines
HT-GR-2B-M-6(SMC)	ICAR-DOGR Breeding Lines
WHT-23A-2BIG BULB (TSS 18-20)	ICAR-DOGR Breeding Lines
W-172-AD-4	ICAR-DOGR Breeding Lines
W-441 M-8	Bhavnagar, Gujarat
W-414 EL-7	Parbhani, Maharashtra
W-085 AD-4	ICAR-DOGR Breeding Lines
W-402 AD-4	Akola, Maharashtra
W-174 EL-7	Pune, Maharashtra
W-545 M-6	Adilabad, Andhra Pradesh
W-521 M-3	Karimnagar, Andhra Pradesh
WM-504 M-4	Bhavnagar, Gujarat
W-340 M-6	NHRDF, Nasik
W-504 M-3	Bhavnagar, Gujarat
Bhima Shweta	ICAR-DOGR Pune Maharashtra
Bhima Shubhra	ICAR-DOGR Pune Maharashtra

Table 2: Genetic parameters of variation for yield and its components in white onion genotypes for quantitative and qualitative traits during the year 2018-19 and 2019-20 (pooled data)

Characters	Grand mean	Range		GCV (%)	PCV (%)	GCV: PCV	Hbs (%)	GA	GA as % of Mean
		min	max						
PH	53.43	47.17	59.41	4.30	5.15	83.50	69.74	3.95	7.40
NOL	10.85	8.87	15.83	11.32	11.67	97.00	94.15	2.45	22.63
LL (cm)	45.73	40.83	52.34	4.80	5.32	90.23	81.49	4.08	8.92
LW (mm)	6.54	5.67	7.73	7.46	7.95	93.84	88.23	0.94	14.44
PSL (cm)	8.09	6.24	9.47	8.45	9.07	93.16	86.81	1.31	16.21
PSW (mm)	14.94	12.65	17.71	5.41	6.63	81.60	66.60	1.36	9.10
75%NF (Days)	101.13	92.93	104.79	2.09	2.66	78.57	62.10	3.44	3.40
PD (mm)	38.28	34.71	43.31	5.92	6.11	96.89	93.82	4.52	11.80
ED (mm)	52.04	48.24	56.82	4.39	4.58	95.85	91.90	4.52	8.68
Neck (mm)	4.18	3.60	5.45	7.14	8.48	84.20	70.81	0.52	12.37
%Double	6.11	0.00	10.81	36.96	38.01	97.24	94.55	4.52	74.04
TPAB ($\mu\text{mole pyruvate g}^{-1}$)	2.97	1.99	3.76	15.53	15.99	97.12	94.34	0.92	31.07
TSS (%)	15.80	12.19	18.50	11.67	11.78	99.07	98.23	3.76	23.83
TS (%)	5.16	3.46	7.07	19.87	20.03	99.20	98.38	2.10	40.60
ABW (g)	60.25	51.64	70.99	8.87	9.02	98.34	96.66	10.82	17.96
TBY (t ha^{-1})	25.71	18.95	32.82	12.37	13.18	93.85	88.11	6.15	23.92

Note: GCV- Genotypic Coefficient of Variation; PCV- Phenotypic Coefficient of Variation; Hbs- Broad sense heritability; GA- Genetic advance; PH-Plant height(cm) NOL-Number of leaf LL-Leaf length (cm) LW-Leaf width (mm) PSL-Pseudostem length (cm) PSW-Pseudostem width (mm) 75%NF- 75% Neck fall (days) PD-Polar diameter (mm) ED-Equator diameter (mm) NT-Neck thickness (mm) %D-Percentage double TPAB-Total pyruvic acid bulb ($\mu\text{mole pyruvate/g}$) TSS-Total soluble solid of bulb (%) TS-Total sugar of bulb (%) ABW-Average bulb weight (g) and TBY-Total bulb yield (t/ha).

broad sense heritability values were higher (more than 60%) for all the characters under study ranging from 62.10% in days to 75% neck fall to 98.38% in total sugar. High heritability indicates that the environmental influence is minimal on traits; those traits can be used for selection due to maximum genetic variation. These observations are in concordance with the results of Chattopadhyay *et al.* (2013), except for polar diameter. Singh *et al.* (2011) also reported high heritability in plant height percentage doubles gross yield and bulb diameter. Leaf length and soluble solids content was also reported to exhibit high heritability (Galmarini *et al.*, 2001; Maia *et al.*, 2008; Porta *et al.*, 2014). Since heritability is also influenced by environment, the information on heritability alone may not be helpful in selecting the characters. Johnson *et al.* (1955) suggested that heritability estimates in conjunction with the predicted genetic gain is much reliable. Heritability provides information on the magnitude of inheritance of quantitative traits, while genetic advance helps in formulating suitable selection procedures (Brunda *et al.*, 2014).

Genetic advance as percent of mean for different characters ranged from 3.40 to 74.04% (Table 2). The number of leaves, percentage double, total pyruvic acid of bulb, total soluble solids, total sugar and total yield exhibited high genetic advance as percent of mean. Moderate to high genetic variability coupled with high heritability and high genetic advance were recorded in number of leaves, percentage double, total soluble solids, total sugar total pyruvic acid of bulb and total bulb yield. These characters are controlled by additive genes and selection based

on these characters are most reliable. Characters showing high heritability along with moderate or low genetic advance were plant height, leaf length, leaf width, pseudostem length, pseudostem width, days to 75% neckfall, polar diameter, equatorial diameter, neck thickness and average bulb weight. These can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadia, 2005).

The correlation coefficients at the genotypic level were greater than the corresponding phenotypic ones in magnitude (Table 3). The higher values of genotypic as compared to phenotypic correlation indicated that the genotypic effects were more important than environmental factors. Characters like plant height ($r_g = 0.733$ $r_p = 0.558$) leaf length ($r_g = 0.580$ $r_p = 0.461$) polar diameter ($r_g = 0.692$ $r_p = 0.626$) and equatorial diameter ($r_g = 0.709$ $r_p = 0.630$) exhibited significantly positive correlation with total bulb yield. This indicated that increase in plant height, leaf length, polar diameter and equatorial diameter will result in higher total bulb yield. Strong positive association between total bulb yield with plant height (Chattopadhyay *et al.*, 2013; Dewangan and Sahu, 2014; Nikhil *et al.*, 2016; Santra *et al.*, 2017) polar and equatorial diameter (Golani *et al.*, 2006; Haydar *et al.*, 2007; Santra *et al.*, 2017) were reported earlier. Whereas the total bulb yield exhibited significant negative association with TSS ($r_g = -0.672$ $r_p = -0.619$) and total sugar ($r_g = -0.354$ $r_p = -0.342$) indicating an increase of bulb yield with decrease in quality, *i.e.*, TSS and total sugar. As quality parameters gain importance among the masses breeding for high yield combined with

Table 3: Phenotypic (above diagonal) and genotypic (below diagonal) correlation co-efficient between different traits in white onion genotypes (pooled data)

Characters	PH (cm)	NOL	LL (cm)	LW (mm)	PSL (cm)	PSW (mm)	75%NF Days	PD (mm)	ED (mm)	Neck (mm)	% Double	TPAB (µmole pyruvate g ⁻¹)	TSS (Bulb)	TS (Bulb)	ABW (g)	TY (t ha ⁻¹)
PH (cm)	1	-0.049	0.863**	-0.003	0.169	0.071	-0.092	0.422**	0.439**	-0.172	-0.008	0.118	-0.537	-0.291	0.308	0.558**
NOL	-0.069	1	0.044	-0.067	0.032	0.798**	0.149	0.076	0.126	-0.072	-0.189	-0.122	0.018	-0.093	0.074	-0.28
LL (cm)	0.954**	0.045	1	0.122	0.114	0.157	-0.184	0.396*	0.402*	-0.151	0.109	-0.03	-0.422**	-0.193	0.325*	0.461**
LW (mm)	-0.01	-0.072	0.162	1	0.02	-0.053	-0.356*	-0.325*	-0.334*	0.244	0.555**	0	0.413*	0.559**	-0.221	-0.129
PSL (cm)	0.167	0.044	0.092	0.022	1	0.096	-0.011	0.162	0.064	-0.49	-0.119	0.169	-0.15	-0.1	0.061	0.214
PSW (mm)	0.071	0.902**	0.156	-0.025	0.145	1	-0.011	0.244	0.274	-0.055	-0.312	-0.153	-0.184	-0.147	0.099	-0.033
75%NF Days	-0.058	0.227	-0.176	-0.452**	-0.035	-0.01	1	0.092	0.081	-0.188	-0.293	0.148	-0.164	-0.164	0.236	-0.033
PD (mm)	0.541**	0.081	0.437**	-0.357*	0.171	0.272	0.166	1	0.878**	0.061	-0.308	0.083	-0.763**	-0.630**	0.261	0.626**
ED (mm)	0.578**	0.133	0.470**	-0.391*	0.076	0.341	0.165	0.915**	1	0.049	-0.459**	0.042	-0.837**	-0.670**	0.366*	0.630**
Neck (mm)	-0.185	-0.106	-0.188	0.307*	-0.647	-0.103	-0.272	0.023	0.012	1	0.069	-0.145	0.194	0.269	-0.358*	-0.089
%Double	-0.01	-0.2	0.126	0.585**	-0.122	-0.402	-0.395*	-0.328*	-0.506**	0.09	1	-0.048	0.484**	0.407*	-0.482**	-0.174
TPAB (µmole pyruvate g ⁻¹)	0.146	-0.13	-0.022	-0.008	0.216	-0.152	0.213	0.093	0.044	-0.175	-0.052	1	-0.108	-0.199	0.043	0.193
TSS (%)	-0.647	0.015	-0.479**	0.447**	-0.161	-0.253	-0.233	-0.799**	-0.880**	0.224	0.493**	-0.111	1	0.682**	-0.507**	-0.619**
TS (%)	-0.359	-0.091	-0.225	0.618**	-0.099	-0.173	-0.2	-0.656**	-0.703**	0.335	0.421**	-0.211	0.693**	1	-0.3	-0.342*
ABW(g)	0.369*	0.076	0.378*	-0.241	0.062	0.132	0.309	0.272	0.387*	-0.445**	-0.507**	0.048	-0.522**	-0.308	1	0.26
TBY (t ha ⁻¹)	0.733**	-0.331*	0.580**	-0.157	0.242	-0.073	-0.071	0.692**	0.709**	-0.147	-0.189	0.212	-0.672**	-0.354*	0.267	1

* ** significant at P ≤ 0.05 or P ≤ 0.01 respectively.

Table 4: Direct and indirect effects of sixteen characters on total bulb yield of white onion genotypes at genotypic level (pooled data)

Characters	PH (cm)	NOL	LL (cm)	LW (mm)	PSL (cm)	PSW (mm)	75%NF Days	PD (mm)	ED (mm)	NT (mm)	% Double	TPAB (µmole pyruvate/g)	TSS (%)	TS (%)	ABW (g)	Correlation co-efficient with yield
PH (cm)	-2.358	0.163	-2.251	0.025	-0.394	-0.167	0.136	-1.277	-1.363	0.436	0.024	-0.345	1.526	0.848	-0.870	0.733**
NOL	0.035	-0.512	-0.023	0.037	-0.023	-0.462	-0.116	-0.042	-0.068	0.054	0.102	0.067	-0.008	0.047	-0.039	-0.331*
LL (cm)	2.566	0.120	2.689	0.434	0.248	0.419	-0.473	1.175	1.264	-0.505	0.339	-0.058	-1.288	-0.606	1.016	0.580**
LW (mm)	0.005	0.036	-0.081	-0.499	-0.011	0.012	0.225	0.178	0.195	-0.153	-0.292	0.004	-0.223	-0.308	0.120	-0.157
PSL (cm)	0.045	0.012	0.025	0.006	0.271	0.039	-0.010	0.046	0.020	-0.175	-0.033	0.059	-0.044	-0.027	0.017	0.242
PSW (mm)	-0.009	-0.119	-0.021	0.003	-0.019	-0.131	0.001	-0.036	-0.045	0.014	0.053	0.020	0.033	0.023	-0.017	-0.073
75%NFdays	0.000	0.000	0.000	0.0001	0.000	0.000	-0.0002	0.000	0.000	0.0001	0.0001	0.000	0.000	0.000	-0.0001	-0.071
PD (mm)	-0.093	-0.014	-0.075	0.061	-0.029	-0.047	-0.029	-0.172	-0.157	-0.004	0.056	-0.016	0.137	0.113	-0.047	0.692**
ED (mm)	0.475	0.110	0.386	-0.321	0.062	0.281	0.136	0.752	0.822	0.009	-0.416	0.036	-0.723	-0.578	0.318	0.709**
NT (mm)	-0.002	-0.001	-0.002	0.003	-0.006	-0.001	-0.003	0.000	0.000	0.010	0.001	-0.002	0.002	0.003	-0.004	-0.147
%Double	0.002	0.039	-0.025	-0.115	0.024	0.079	0.078	0.064	0.099	-0.018	-0.196	0.010	-0.097	-0.083	0.100	-0.189
TPAB (µmole pyruvate g ⁻¹)	0.076	-0.067	-0.011	-0.004	0.112	-0.079	0.110	0.048	0.023	-0.091	-0.027	0.518	-0.057	-0.110	0.025	0.212
TSS (%)	0.374	-0.009	0.277	-0.259	0.093	0.146	0.135	0.462	0.509	-0.129	-0.285	0.064	-0.578	-0.401	0.302	-0.672**
TS (%)	-0.208	-0.053	-0.130	0.358	-0.057	-0.100	-0.116	-0.379	-0.407	0.194	0.244	-0.122	0.401	0.578	-0.178	-0.354*
ABW(g)	-0.175	-0.036	-0.179	0.114	-0.029	-0.063	-0.147	-0.129	-0.183	0.211	0.241	-0.023	0.247	0.146	0.474	0.267

*Residual effect=0.4247

Table 5: Cluster classification of thirty-five white onion genotypes

Cluster number	Number of genotypes	Genotypes
I	30	W-414 EL-7, W-521 M-3, W-172-AD-4, W-441 M-8, W-174 EL-7, W-340 M-6, W-085 AD-4, W-402 AD-4, W-504 M-3, W-361, W-545 M-6, W-444 EL-6, W-340 EL-7, Agrifound White, HT-GR-2B-6(SMC), WHT-23A(P), WHTB-10J-LT-15-SMC-M-7, WHTB-8H-GT-15-M-C-M-7, HT-GR-5A-6(SC)TSS-15-17.8, WHTB-6F-GT-15-MC-M-7, WHTB-5E-GT-15-SC-M-7, WHTS-4D-GT-18-MC-M-7, WHTS-11K-Pickle-SC-M-7, WHT-2B-GT-18-SC-M-7, WHTB-3C-GT-18-MC-M-7, WHT-23A-3(Small bulbs), WHT-23A-1BIG BULBS (TSS 15-17.8), WHT-23A-2 BIG BULB (TSS 18-20), WHTB-1A-GT-18-SC-M-7, and WHT-12L-HT-15-REJECT-M-7
II	1	WHTB-7G-GT-15-SC-M-7 Small Bulb
III	2	BHIMA SHWETA, BHIMA SHUBRA
IV	1	WHTB-9I-LT-15-SMC-M-7
V	1	WM-504 M-4

Table 6: Intra and inter- cluster distances of thirty-five white onion genotypes

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	14.18a	18.39	20.95	16.8	20.79
Cluster II		0	32.54	13.66	27.68
Cluster III			8.61	25.85	19.09
Cluster IV				0	25.14
Cluster V					0

^aBold diagonal values indicate intra-cluster distance; the remainder of values indicate the inter cluster distances

quality traits is a challenge. Thus, selection based on quality traits (TSS and total sugar) will not be effective for improvement in bulb yield. In contrast, Chattopadhyay *et al.* (2013) reported a weak positive correlation between bulb yield and TSS.

The total correlation coefficient is partitioned into direct and indirect effects to study the cause and nature of independent variables on total bulb yield. The genotypic path analysis (Table 4) showed that, leaf length had maximum positive direct effect (2.689) on total yield followed by equatorial diameter (0.822), total sugar (0.578), total pyruvic acid of bulb (0.518) and average bulb yield (0.474). High positive direct effect of bulb yield with bulb girth (Golani *et al.*, 2006) and equatorial diameter (Nikhil *et al.*, 2016) were also reported. This indicates the true relationship of these traits and direct selection of leaf length and equatorial diameter will be effective since these characters showed highly significant correlation with total bulb yield. Similar results were also reported by Trivedi *et al.* (2006) and Porta *et al.* (2014), whereas, the highest negative direct effect on total bulb yield was observed in plant height followed by total soluble solids (-0.578), number of leaves (-0.512) and leaf width (-0.499). Selection of these characters exhibiting high negative direct effect with bulb yield may not be beneficial for yield improvement. Indirect contribution for total bulb yield also showed high positive indirect effect among plant height and leaf length; equatorial diameter and leaf length and average bulb weight and leaf length. The residual effect in this study was 0.43 which explains inclusion of a reasonable proportion of independent characters influencing bulb yield of onion.

A systemic study on genetic divergence based on different traits is important for targeted breeding programme. Tocher's method (Rao, 1952) was used to group the genotypes into different clusters based on D2 values. Cluster analysis has also been regarded as an efficient tool of varietal classification (Tsukazaki *et al.*, 2010). Thirty-five genotypes were grouped into five clusters (Table 5), whereas other researchers had grouped onion genotypes into three clusters (Akter *et al.*, 2015), four (Nikhil and Jadhav, 2017), five (Rashid *et al.*, 2012; Singh *et al.*, 2020 and Ahmad *et al.*, 2021) and eight clusters (Bal *et al.*, 2019). In this study, cluster I consisted of thirty genotypes, cluster II, IV and V with one genotype each, while cluster III had two genotypes (Table 4). Little to no work was done to study genetic divergence on white onion whereas the same has been studied in the other onion genotypes through cluster analysis by many workers (Rashid *et al.*, 2012; Akter *et al.*, 2015; Nikhil and Jadhav, 2017 and Bal *et al.*, 2020).

Genotypes belonging to one cluster do not necessarily belong to same geographical region. There was no parallel relationship found between genetic and geographic divergence which may be due to continuous exchange of germplasm from one place to another (Rashid *et al.*, 2012). The absence of relationship between genetic diversity and geographical distance indicated that forces other than geographical origin such as exchange of genetic stock, genetic drift, spontaneous mutation, natural and artificial selection were responsible for genetic diversity (Lalramhlimi *et al.*, 2019). The monotypic genotypes in cluster II, IV and V indicated that the genotypes from these

Table 7: Cluster means of 35 genotypes of white onion

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Contribution% towards divergence
PH (cm)	53.42	49.2	58.1	54.21	47.71	0%
NOL	10.66	10.83	11.73	9.77	15.83	3.70%
LL (cm)	45.64	42.41	50.94	46.07	40.93	0%
LW (mm)	6.57	6.7	5.99	7.14	5.72	0.84%
PSL (cm)	8.09	8.47	8.03	7.92	7.85	1.51%
PSW (mm)	14.79	15.09	15.67	15	17.71	0%
75%NFDays	101.04	99.99	104	96.54	103.73	0%
PD (mm)	38.2	35.69	42.07	36.09	37.88	3.19%
ED (mm)	51.82	48.61	56.67	50.72	54.31	0%
Neck thickness (mm)	4.19	3.94	4.08	4.4	3.97	0.17%
% Double	6.56	5.92	3.85	3.36	0	2.35%
TPAB (μ mole pyruvate/g)	3.03	2.52	2.58	2.53	2.81	7.06%
TSS (%)	15.96	18.5	12.27	15.73	15.16	17.65%
TS (%)	5.2	7.07	3.64	6.87	3.65	42.69%
ABW (g)	59.36	54.15	69.27	68.07	67.04	16.64%
TBY (t/ha)	25.66	25.17	29.9	26	18.95	4.20%

clusters might have originated across the geographical location in breeding programs. Intra and inter cluster distances among genotypes (Table 6) indicated that cluster I had the most intra-cluster value which means thirty genotypes were included in the cluster viz., W-414 EL-7, W-521 M-3, W-172-AD-4, W-441 M-8, W-174 EL-7, W-340 M-6, W-085 AD-4, W-402 AD-4, W-504 M-3, W-361, W-545 M-6, W-444 EL-6, W-340 EL-7, Agrifound White, HT-GR-2B-M-6(SMC), WHT-23A(P), WHTB-10J-LT-15-SMC-M-7, WHTB-8H-GT-15-M-C-M-7, HT-GR-5A-M-6(SC)TSS-15-17.8, WHTB-6F-GT-15-MC-M-7, WHTB-5E-GT-15-SC-M-7, WHTS-4D-GT-18-MC-M-7, WHTS-11K-Pickle-SC-M-7, WHT-2B-GT-18-SC-M-7, WHTB-3C-GT-18-MC-M-7, WHT-23A-3(Small bulbs), WHT-23A-1BIG BULBS TSS 15-17.8, WHT-23A-2 BIG BULB (TSS 18-20), WHTB-1A-GT-18-SC-M-7 and WHT-12L-HT-15-REJECT-M-7 which were extremely diverse (Fig.1). Cluster III had the least intra-cluster value. Genotypes belonging to clusters with maximum intra-cluster distance are genetically more divergent and hybridization between divergent clusters is likely to produce wide variability with desirable segregant (Maloo and Bhattacharjee, 1999). Cluster II, IV and V are solitary clusters as they show zero intra-cluster distance.

The inter-cluster level minimum values occurred between cluster I and IV (13.66) indicated close relationship among genotypes in those clusters. The greatest inter-cluster values were observed between cluster II and III (32.54) followed by the distance between cluster II and V (27.68) indicating that the genotypes in those clusters had the greatest divergence. It is expected to obtain greater heterotic segregants by crossing genotypes belonging to distant and diverse clusters. The minimum inter-cluster distance was recorded between cluster II and IV (13.66), therefore the genotypes from these clusters should not be used for crossing with each other. Kalloo *et al.* (1980) stated that crosses between selected varieties from widely separated clusters were most likely to give desirable recombinants.

The cluster means of genotypes presented in Table 7 showed mean values of clusters varying in magnitude for all the characters in plant height (49.2- 58.1 cm), number of leaves (9.77- 15.83), leaf length (40.93- 50.94 cm), leaf width (5.72- 7.14 mm), pseudostem length (7.85- 8.47 cm), pseudostem width (14.79- 17.71mm), days to 75% neckfall (96.54- 104), polar diameter (35.69- 42.07mm), equatorial diameter (48.61- 56.67mm), neck thickness (3.94- 4.4mm), percentage double (0- 6.56%), total pyruvic acid in bulb (2.52- 3.03 μ mole pyruvate g^{-1}), total soluble solids (12.27- 18.5%), total sugar (3.64- 7.07%), average bulb weight (54.15- 69.27g) and total bulb yield (18.95- 29.9t ha^{-1}). Earlier studies have reported wide variability among the clusters for yield and its contributing traits. (Rashid *et al.*, 2012; Kale *et al.*, 2015; Nikhil and Jadhav, 2017; Bal *et al.*, 2019) and Singh *et al.* (2020).

The maximum cluster mean values for plant height (58.1 cm), leaf length (50.94 cm), polar diameter (42.07 mm), equatorial diameter (56.67 mm), average bulb weight (69.27 g) and total bulb yield (29.9 t ha^{-1}) were recorded in cluster III, while the maximum total pyruvic acid in bulb (3.03 μ mole pyruvate g^{-1}) was recorded maximum in cluster I. Cluster V showed the maximum mean values for number of leaves (15.83) and pseudostem width (17.71 mm) with no percentage double, and the maximum cluster mean values for leaf width (7.14 mm) along with minimum days to 75% neckfall (96.54) were recorded in cluster IV, while cluster II had maximum mean values for pseudostem length (8.47 cm), total soluble solids (18.5%), total sugar (7.07%) and minimum neck thickness (3.94 mm). A high bulb yielding early types with long leaves and bigger bulbs could be bred by utilizing genotypes from cluster III and cluster IV as parents. Moreover, genotypes in cluster III and cluster II can be bred to develop high bulb yielding genotypes rich in total soluble solids total sugar in bulb and small neck thickness which could render them suitable for processing

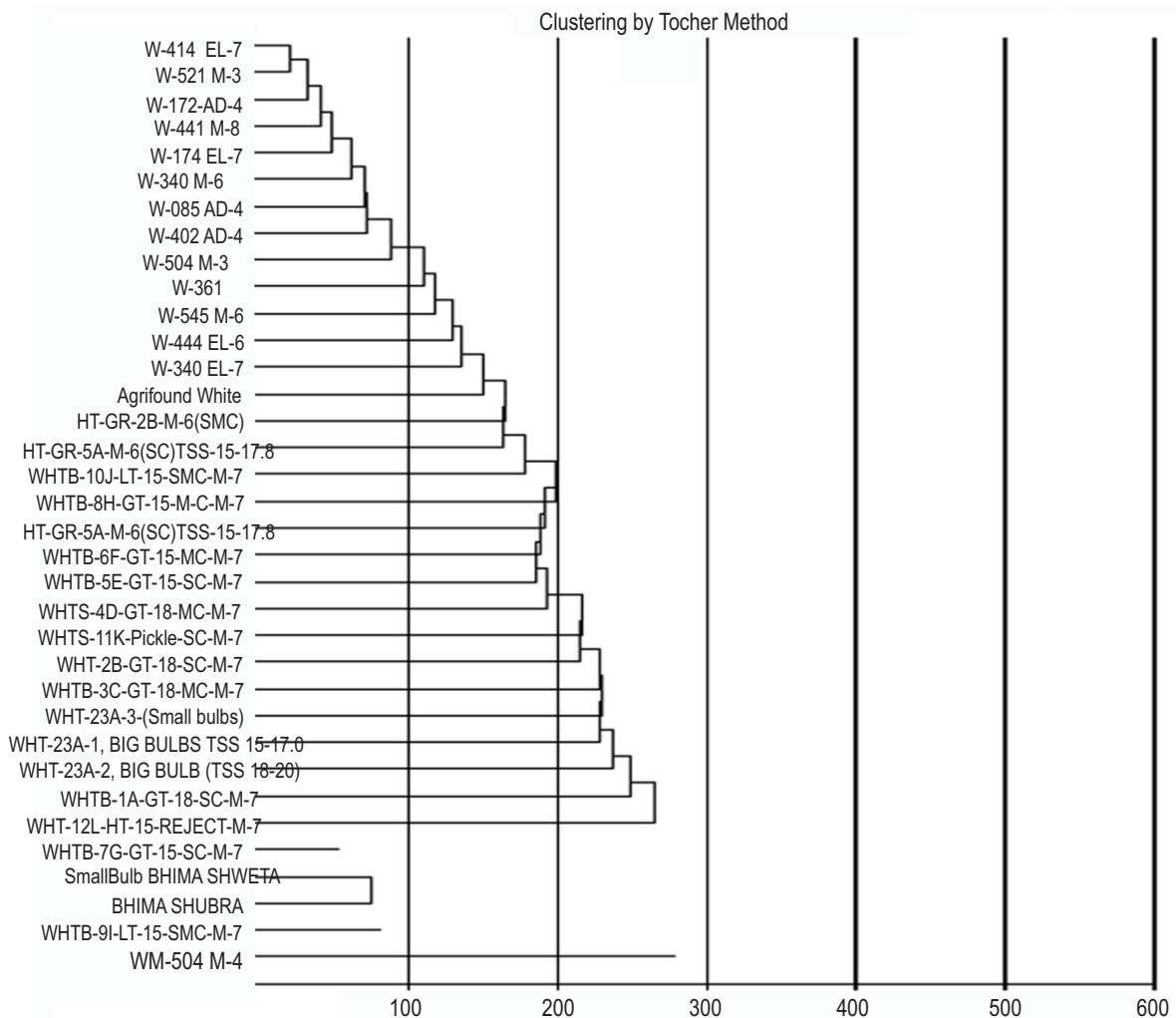


Fig 1: Dendrogram constructed based on UPGMA based on Tocher of 35 white onion genotypes.

Clusters that exhibited high mean value of traits may be used for hybridization program to get better segregates (Arya *et al.*, 2017; Singh *et al.*, 2017 and Singh *et al.*, 2020). Total sugar in bulb contributed maximum to genetic divergence followed by total soluble solids, average bulb weight, total pyruvic acid in bulb, total bulb yield, number of leaves, polar diameter, percentage double, pseudostem length, leaf width and neck thickness.

This indicated that the characters mentioned above are suitable for selection in any breeding programme. In white onion, quality parameters are as crucial as some morphological traits for determining genetic divergence. Generally, Indian white onion varieties have low TSS (10-14%) which is not suitable for dehydration (Lawande *et al.*, 2009). However, the genotypes belong to cluster I, II, IV and V have cluster mean values for total soluble solids ranging from 15.16% to 18.5% which were beyond average (10-14%). Earlier researchers had suggested neck diameter plant height and bulb yield (Rashid *et al.*, 2012); weight

of bulb and neck thickness (Mohanty and Prusti, 2002); total yield phenol and vitamin C (Bal *et al.*, 2019) as major characters that contributed predominantly to genetic divergence.

Total yield, plant height, TSS, A Grade bulb, polar diameter of bulb, resistance to purple blotch, thin neck thickness of bulb is also ideal for selection (Singh *et al.*, 2020). Based on the genetic diversity, cluster distance and cluster mean performance for bulb yield quality and morphometric traits, three genotypes viz. "Bhima Shweta", "Bhima Shubra" and "WHTB-7G-GT-15-SC-M-7 Small Bulb" belonging to cluster III and cluster II are recommended as good candidates for utilization in breeding programmes. Singh *et al.* (2021) had previously identified genotypes high in TSS through use of molecular markers such as WHTS-4D-GT-18-MC-M-7 (18.49%) WHT-2B-GT-18-SC-M-7 (18.51%) WHTB-3C-GT-18-MC-M-7 (18.27%) and WHT-12L-HT-15-REJECT-M-7 (18.02%). These genotypes belonging to cluster I are excellent materials for improvement of TSS in any onion breeding programme.

Acknowledgments

We earnestly acknowledge the Indian Council of Agricultural Research for providing the financial support and ICAR-Directorate of Onion and Garlic Research for their technical assistance towards this study.

Add-on Information

Authors' contribution: P.R. Singh: Execution, data compilation, analysis and manuscript preparation; M. Singh, V. Mahajan: Conceptualization, methodology, execution, data analysis, supervision and fund acquisition; Y.P. Khade: Conceptualization, execution, data analysis, supervision, review and editing; A. Verma, B. Lalramhlimi: Data execution, review and editing; P. Gedam, N. Shukla, O. Sogam: Data analysis, review and editing.

Research content: The research content of manuscript is original and has not been published elsewhere.

Ethical approval: Not applicable.

Conflict of interest: The authors declare that there is no conflict of interest.

Data from other sources: Not applicable.

Consent to publish: All authors agree to publish the paper in *Journal of Environmental Biology*.

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