Genetic variability and divergence analysis in sweet cherry (*Prunus avium* L.)

K.K. Srivastava*, M.K. Verma**, N. Ahmad, S.M. Razvi and Shabeer Ahmad
Central Institute of Temperate Horticulture, Old Airfield, Rangreth, Srinagar 190007, J&K

ABSTRACT

Twenty one sweet cherry (*Prunus avium* L.) cultivars were used to study genetic variability and diversity using Mahananobis D^2 statistics. Most of the traits showed low to moderate heritability, while only four traits *viz.*, fruit length, TSS, annual extension growth and trunk girth showed high heritability of 71, 68, 65 and 74%, respectively. The grouping of genotypes using Tocher's method revealed that these cultivars grouped into six clusters, with Cluster-I having maximum number of genotypes (9) followed by 8 in Cluster-II. Whereas, rest of the clusters were monogenotypic with one cultivar each. Cluster-II had the maximum intra-cluster distance, while inter-cluster distance was highest between Cluster-III and VI. Maximum contribution towards divergence came from trunk girth (19.52%), while minimum from fruit diameter (1.43). Cluster means indicated that none of the clusters were superior for all the characters studied. Therefore, hybridization between genotypes belonging to different clusters is suggested for development of superior genotypes.

Key words: Variability, genetic diversity, multivariate statistics, *Prunus avium*.

INTRODUCTION

Sweet cherry (*Prunus avium* L.) belongs to the family Rosaceae sub-family Prunoideae cultivated typically in temperate zone (Wunsch and Hormaza, 14). It is one of the most important temperate fruits cultivated at higher elevation. In India, cherry is mainly cultivated in Jammu and Kashmir, and Himachal Pradesh and very little acreage in Uttarakhand. The cultivation is mainly confined to high altitudes due to prevalence of high chilling varieties. Majority of cherry varieties hence originated from European countries and introduced in India some hundred years back. Over the period of time variations took place due to natural mutations. Central Institute of Temperate Horticulture, Srinagar initiated survey, identification, documentation and collection of natural variation which exists throughout this region. Twenty one selections obtained from different cultivars like 'Bigarreau Noir Grosse' (Mishri), 'Bigarreau Napoleon' (Double), 'Guigne Pourpeara Prece' (Awal Number), 'Guigne Noir Hative' (Makhmali), 'Lambert' and 'Lapins' were collected and planted for evaluation for various growth and quality attributes. Therefore, recognition and measurement of the nature and magnitude of such diversity is beneficial in breeding. Several researchers also reported the estimates of the diversity in sweet cherry (Christensen, 1; Hjalmarsson and Ortiz, 2; Rodrigues *et al.*, 11) utilized in the improvement programmes. Multivariate

*Corresponding author's E-mail: kanchanpom@gmail.com
**Division of Fruits and Horticultural Technology, IARI, New Delhi

statistical techniques were suggested for analysis of genetic diversity in crop plants as a useful tool (Mohammadi and Prasanna, 6). Mahalanobis D^2 statistic provided measure of the generalized distance in case of multiple measurements. It helps in the identification of genetically divergent genotypes that facilitated grouping and characterization by using both quantitative and qualitative characteristics (Susandarini *et al.*, 13). The multivariate D^2 analysis has been favoured as a tool in estimating genetic divergence for use in plant breeding, since it helps in the choice of parental combinations. Therefore, the this study was conducted to study general variability, correlation and assessment of genetic diversity within sweet cherry selections maintained at CITH Srinagar, for the identification of diverse parents to be used in improvement programme.

MATERIALS AND METHODS

The present investigation was carried out during 2009 to 2012 at Central Institute of Temperate Horticulture, Srinagar. The experimental site was situated at latitude of 34°45'N and longitude of 74°5'0 E and an elevation of 1,649 m amsl. Twenty one cultivars collected from different places across the valley (Table 1) were planted at 2.5 m × 2.5 m spacing. The budwood of collected selections were budded on seedling rootstock of sour cherry (*Prunus cerasus*). Three plants from each selection were selected for recording the observations. Twenty ripened fruits were randomly collected from each

Table 1. List of the germplasm accessions used in the study.

Accession	Growth habit	Cultivar	Growth habit
CITH-C-01	Spreading	CITH-C-12	Upright
CITH-C-02	Spreading	CITH-C-13	Upright
CITH-C-03	Spreading	CITH-C-14	Semi-spreading
CITH-C-04	Spreading	CITH-C-15	Upright
CITH-C-05	Semi-spreading	CITH-C-16	Spreading
CITH-C-06	Spreading	CITH-C-17	Spreading
CITH-C-07	Spreading	CITH-C-18	Semi-upright
CITH-C-08	Spreading	CITH-C-19	Spreading
CITH-C-09	Spreading	CITH-C-20	Spreading
CITH-C-10	Upright	CITH-C-21	Less spreading
CITH-C-11	Upright		

direction of the tree for recording observations on yield /plant, fruit weight, fruit length, fruit diameter, and other growth parameters at the termination of tree growth. The observation on annual extension growth, tree height, number of primary branches and total soluble solids content were also recorded. The data were subjected to pooled analysis. All the genotypes were grouped using Tocher's method as suggested by Rao (10).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among the genotypes for all the traits under study. The range of variation was high for annual extension growth (67.66-112.15 cm) followed by yield (1.45-6.60 kg/plant) and TSS (11.31-17.18%). A better idea can be gained by comparing the relative magnitude of phenotypic and genotypic co-efficient of variations for the actual strength of variability. The estimates of phenotypic coefficient were observed to be higher in magnitude than their corresponding estimates of genotypic coefficient of variations for all the traits, which indicates the influence of additive effect of the environment on the expression of these traits (Table 2). The estimates of PCV and GCV indicated the presence of fairly high degree of variability for yield per plant, trunk girth, annual extension growth and number of secondary branches. Moderate variability was observed for fruit weight, fruit length, TSS, tree height and number of primary branches, while for rest of the traits the estimates of PCV and GCV were relatively low. The difference between PCV and GCV was minimum for yield per plant, annual extension growth and trunk

Table 2. Range, standard error, grand mean, coefficient of variation, GCV, PCV, heritability and genetic advance for various qualitative and quantitative traits in sweet cherry.

Trait	Range		SE	Grand mean	GCV	PCV	Heritability (h^2)	Expected genetic gain
	Minimum	Maximum						
Yield (kg/tree)	1.45	6.66	1.08	3.65	32.98	34.41	0.66	28.59
Fruit weight (g)	4.42	6.31	0.37	5.31	12.89	14.07	0.24	6.96
Fruit length (mm)	16.80	22.84	0.72	19.26	17.12	19.67	0.71	40.81
Fruit diameter (mm)	17.31	21.86	0.85	19 .14	6.97	9.74	0.37	7.56
Total soluble solids (%)	11.31	17.18	0.87	14.41	20.21	24.65	0.68	44.65
Annual extension growth (cm)	67.66	112.15	8.44	89.37	21.72	22.69	0.65	32.44
Trunk girth (cm)	18.11	27.77	1.17	22.36	31.89	33.46	0.74	34.96
Tree height (m)	1.55	2.08	0.07	1.93	8.75	9.94	0.35	5.86
No. of primary br./plant	4.22	6.66	0.51	5.39	18.44	18.55	0.20	7.92
No. of secondary br./plant	7.11	15.88	1.95	10.30	26.22	36.58	0.19	14.82

girth suggesting that these traits were least affected by environment. These observations draw support from the high value of heritability recorded for these traits.

The amount of heritable portion of variation cannot be predicted with the help of PCV and GCV alone, but by estimating heritability along with genetic advance which inturn helps in predicting the resultant effect of selection on phenotypic expression. Estimates of heritability in broad sense were high for trunk girth, fruit length, yield per plant, annual extension growth and total soluble solids; whereas, these estimates for fruit weight and number of primary and secondary branches were low. Similar results have been reported by (Lacis and Rashal, 4; Rodrigues *et al*., 11). Main objective of any improvement programme is yield which is the outcome of interaction of a number of inter-related or correlated traits. Hence, the correlation coefficients among different traits were worked out in all possible combination at both the phenotypic and genotypic levels (Table 3). In general, the magnitudes of genotypic correlation coefficients were higher than their corresponding values at phenotypic level. Seed yield/plant exhibited significant and positive correlation with fruit weight, TSS, tree girth, and tree height at both phenotypic and genotypic levels. The positive association indicated that the selection for these traits would result in increased yield per plant. The interrelation of these characters with another character may provide likely consequences of selection for simultaneous improvement of desirable traits. The rate of influence of one component character over another can be studied by estimating the inter-correlation among different components of total yield per plant. Fortunately, fruit weight, fruit length and tree height had significant positive association with yield per plant and were also found to be significant and positively associated with each other. Similarly, TSS and tree height were significant and positively correlated with each other and had positive and significant association with yield per plant. The correlation between annual extension of growth and yield per plant was non-significant and negative. These results suggested that these characters could be considered as major yield contributing traits in cherry, indicating improvement in the characters, *i.e.* fruit weight, fruit length, TSS and tree height, would bring an enhancement in yield per plant. Fruit weight and diameter were significant and positively associated with each other at both the levels. Similarly, fruit length and tree height were also positive and significantly associated with each other.

Table 3. Estimates of genotypic and phenotypic correlation coefficients for yield and yield contributing attributes in sweet cherry.

Trait	Yield (kg/tree)	Fruit weight (g)	Fruit length (mm)	Fruit dia. (mm)	TSS (%)	Annual extension growth (cm)	Trunk girth (cm)	Tree height (m)	No. of primary branches/plant	No. of secondary branches/plant
Yield (kg/ tree)	1.00	0.86	0.23	-0.08	0.88	-0.28	-0.45	0.65	0.14	0.02
Fruit weight (g)	0.39	1.00	0.48	0.58	0.60	0.15	-0.14	0.67	0.45	-0.004
Fruit length (mm)	0.17	0.32	1.00	0.42	-0.26	-0.42	-0.50	0.38	0.12	-0.48
Fruit diameter (mm)	0.07	0.36	0.34	1.00	-0.22	-0.53	-0.31	0.55	0.41	-0.46
Total soluble solids (%)	0.50	0.34	0.19	0.83	1.00	0.18	0.06	0.73	-0.22	0.30
Annual extension growth (cm)	-0.23	-0.23	-0.38	-0.18	0.16	1.00	0.46	-0.13	0.06	0.02
Trunk girth (cm)	-0.39	-0.14	-0.30	0.15	0.04	0.38	1.00	0.38	0.24	0.62
Tree height (m)	0.63	0.45	0.32	0.003	0.40	-0.17	0.36	1.00	0.21	0.64
No. of primary branches/ plant	0.62	-0.04	0.11	0.26	-0.13	0.04	0.24	0.15	1.00	0.36
No. of secondary branches/ plant	0.23	-0.06	-0.19	-0.34	0.26	0.12	0.30	0.30	0.34	1.00

Correlation studies alone are not adequate to establish clear-cut associations among the traits as more variables need to be considered. Hence, the knowledge of actual contribution of individual characters towards yield per plant becomes essential. The path coefficient analysis was carried out which provides an idea of direct and indirect effects of certain characters on correlation. The path coefficient analysis (Table 4) revealed appreciable amount of direct positive effect of fruit diameter, tree height, TSS and annual extension of growth on yield per plant. Significant genotypic correlation coefficients of TSS, tree height and fruit diameter and number of secondary branches contributing maximum towards yield per plant and are having no significant positive association with yield per plant and would also be reliable in the process of selection for higher yield per plant. Overall results indicated that the greater emphasis should be given to traits like, fruit diameter, TSS, plant height and number of secondary branches. The direct effect of remaining component traits on yield per plant was either negligible as that of number of primary branches or negative as that of fruit length.

The pooled divergence of all the characters within the cultivars tested by Wilk's criterion χ^2 and was found significant. Hence, the analysis of genetic divergence among genotypes used in the study was considered relevant. On the basis of relative magnitude of D^2 values , 21 genotypes were grouped by using Tocher's method into 6 clusters with maximum number of genotypes (9) in Cluster-I and 8 in Cluster-II (Table 5); while, rest of the clusters were monogenotypic. Murty and Arunachalam (7) described heterogeneity, genetic architecture of the populations and developmental traits as possible reasons for the prevalent of diversity. The intra-cluster distance was maximum (16.76) in Cluster-II followed by in Cluster-I (11.62) (Table 6). The mean inter-cluster distance was highest between clusters III and VI (41.22), followed by Cluster-III and V (37.76), Cluster-III and VI (37.58) and cluster V and VI (36.28). Since, these clusters have more inter-cluster distances among themselves, hence, the selection of parents for hybridization from such clusters would helps to evolve novel hybrids. The parents for hybridization could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Inter-cluster distance was minimum between clusters III and IV indicating close relationship and similarly for most of the traits in these genotypes. Hence, selection of parents from such clusters should be avoided. Similar findings in sweet cherry were also

Table 4. Direct (bold) and indirect effects (genotypic level) of yield and its attributes in sweet cherry cultivars.

Trait	Fruit wt. (g)	Fruit length (mm)	Fruit dia. (mm)	TSS (%)	Annual extension growth (cm)	Trunk girth (cm)	Tree height (m)	No. branches/ plant	No. of sec. branches/ plant	Genotypic correlation coefficient with yield/plant
Fruit weight (g)	**0.06**	-0.77	0.58	0.53	0.02	0.19	0.40	0.03	-0.005	0.65
Fruit length (mm)	0.03	**-0.58**	0.25	-0.03	-0.06	0.67	0.23	0.008	-0.05	0.23
Fruit dia. (mm)	0.03	-0.64	**0.98**	-0.10	-0.08	0.42	0.33	0.03	-0.05	-0.08
TSS (%)	0.07	0.107	-0.22	**0.47**	0.03	-0.08	0.56	-0.01	0.05	0.98
Annual extension in growth (cm)	0.01	0.66	-0.52	0.08	**0.16**	-0.62	-0.08	0.004	0.002	-0.28
Tree girth (cm)	-0.009	0.79	-0.31	0.03	0.07	**-0.34**	0.20	0.006	0.097	-0.45
Tree height (m)	0.044	0.60	0.54	0.44	-0.02	-0.44	**0.60**	0.001	0.08	0.65
No. of primary branches	0.030	0.19	0.40	-0.10	0.01	-0.12	0.12	**0.07**	0.03	0.14
No.of secondary branches	-0.003	0.76	-0.45	0.21	0.03	-0.40	0.45	0.02	**0.119**	0.02

Table 5. Distribution of 21 sweet cherry genotypes in to different clusters .

Cluster No.	No. of genotype (s)	Genotype (s)
I	9	CITH-C-12, CITH-C-13, CITH-C-15, CITH-C-14, CITH-C-11, CITH-C-9, CITH-C-9, CITH-C-6, CITH-C-8, CITH-C-5.
II	8	CITH-C-2, CITH-C-4, CITH-C-3, CITH-C-16, CITH-C-17, CITH-C-1, CITH-C-21, CITH-C-19
III	1	CITH-C-10
IV	1	CITH-C-18
V	1	CITH-C-07
VI	1	CITH-C-20

Table 6. Average intra- and inter-cluster distance (D^2) values of 21 sweet cherry genotypes.

Cluster	I	II	III	IV	V	VI
I	**11.62**	31.33	19.73	20.76	20.71	31.29
II		**16.76**	28.13	27.65	25.32	37.58
III			**0.00**	9.72	37.76	41.22
IV				**0.00**	28.00	35.26
V					**0.00**	36.28
VI						0.00

reported by Lacis *et al.* (3), Singh *et al.* (12) in pomegranate; Rai and Mishra (9) in *bael*; Lal *et al.* (5) in fennel and Nagar and Fageria (8) in *lehsua* suggested selection of distant parents based on D^2 analysis.

The diversity in the present germplasm was also evident by the considerable amount of variation among cluster means for different traits (Table 7). Cluster-III showed the highest mean for annual extension growth, trunk girth and tree height, Cluster-V for yield per plant, fruit weight and number of primary branches and Cluster-II for fruit length and fruit diameter. This indicates that these clusters had genotypes with the respective desirable traits. Hence, for the improvement of any particular trait should be selected from their respective genotypes cluster showing highest cluster mean for those traits. The experimental observations further revealed that character trunk girth contributes

Table 7. Cluster means for morphological, yield and yield attributing traits and their relative contribution towards divergence of 21 sweet cherry genotypes.

Trait	Cluster						Times ranked I[st]	% contribution towards divergence
	I	II	III	IV	V	VI		
Yield (kg/tree)	4.14	3.31	2.04	1.92	6.66	2.39	11	5.24
Fruit weight (g)	5.40	5.30	4.59	5.37	6.14	4.51	4	1.90
Fruit length (mm)	18.15	20.68	10.09	19.12	19.33	17.62	25	11.90
Fruit diameter (mm)	18.10	20.52	18.97	19.25	19.37	17.31	3	1.43
TSS (%)	15.52	13.58	13.90	13.30	15.44	11.83	31	14.76
Annual extension in growth (cm)	98.28	78.82	108.99	78.81	67.66	106.34	40	19.05
Trunk girth (mm)	23.22	20.94	27.67	26.33	21.00	18.11	41	19.52
Tree height (m)	1.96	1.94	2.02	1.90	2.00	1.55	30	14.29
No. of primary branches	5.17	5.49	5.78	5.11	6.56	5.44	17	8.10
No. of secondary branches	10.67	8.79	13.33	14.55	13.78	8.44	8	3.81

maximum towards the genetic divergence (19.52%) followed by annual extension growth (19.05%). Thus, importance of these traits is emphasized as principal contributors to genetic diversity prevalent in such germplasm.

The main conclusion arising from this study is that GCV, PCV, heritability, correlation, path analysis and genetic divergence are of paramount importance for selecting parents for initiating hybridization programme than eco-geographical isolation. Genotypes from the Cluster-II within group and between Clusters-III and VI may be selected as better recombinants for yield if chosen for hybridization. Furthermore, for the improvement of traits like fruit length and fruit diameter selection of parents should be made from Cluster-II.

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