Short Communication

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Genetic diversity of 23 indigenous almond (*Prunus amygdalus*) genotypes under North West Himalayan region of India

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Almond [*Prunus amygdalus* Batsch (syn. *P. dulcis* (Mill.) D A Webb)] is a species in the Rosaceae family with 2n = 16 chromosome. It is the most important tree nut crop in terms of production and is one of the most polymorphic fruit species. It is also an important nut crops of temperate region of India and mainly grown as rain fed crop in Kashmir valley. It is a native to Mediterranean region and is considered as one of the oldest tree in the world which is closely related to peach and is probably evolved from the same ancestral species in South Central Asia. Its cultivation spread from Central Asia to the Mediterranean region by the Phoenicians or Greeks (Godini 2005). In India, it was first introduced to Kashmir during 16th century by Persian settlers but in spite of its great potential in the region, the crop could not gain momentum on commercial scale as that of apple.In India it is grown over an area of 0.021 mha with an annual production of 0.013 mt and productivity 0.62 t/ha (Anon 2014-15). Almond kernels are concentrated sources of energy with a significant share of fat, protein and fibre. Fats are primarily non saturated, mostly oleinic and linoleic fatty acids which is important in maintaining low cholesterol levels in the blood (Aslant *et al*. 2001).

Although seed propagation resulted in the proliferation of a large number of highly variable local genotypes, their origin from a restricted germplasm often limited their genetic diversity. Thus, the North West Himalayan region is considered as a wide diversity centre for almond and setup a germplasm collection bank (De Giorgio and Stelluti 1995). Genetic variability is the prerequisite for any plant breeding program (Khush 2002). For identification of desirable nut and kernel characters, the conservation and utilization of germplasm is important. These traits are in common use for elucidation of wide genetic diversity in different field and horticultural crops (Blazek 2007). The kernel taste is heredity character of almond genotype (Vargas *et al*. 2001). Morphological traits could feasibly be used for parental selection and along with molecular techniques are of highly appreciated procedures for description and germplasm classification of plants. The morphological and pomological evaluation of almond varieties was done in India by Kumar and Ahmed (2015), Colic and Zee, (2007) in Slankamen hill and Colic *et al*. (2012) in selected almond; 52 genotypes of almond was evaluated by De Giorgio *et al*. (2007) in Apulia region of South Italy and Damvar and Hassani (2006) in Karaj region. To safe guard the almond germplasm and to develop new improved varieties which will be well adopted to the environmental conditions of different growing areas, the current study was undertaken to investigate the diversity among the various horticultural traits in 23 indigenous almond genotypes under North West Himalayan region of India.

The current investigation was carried at ICAR-Central Institute of Temperate Horticulture, Old Air Field, Rangreth, Srinagar, Jammu and Kashmir during year 2013-15 to study the performance of almond genotypes (collected from north west Himalayan region of India). The experimental site at Srinagar was situated at a latitude of 34° 05'N, longitude of 74° 50'E and an altitude of 1640 m above msl. The soils of this experimental site was silty loam (39.60% sand, 24.0% Silt and 36.40% clay; 7.5 soil pH, 0.50% soil organic carbon, 462 kg N/ha, 9.59 kg P/ha and 279 kg K/ha) with poor drainage. The primary selection criterion was based on fruit and yield attributes of the genotypes. The experimental farm falls under temperate region having cold conditions from November to February. The mean maximum and minimum temperature of Srinagar climate during experimental period indicated that average maximum 30°C in August and minimum -2.1°C in December month. The average annual precipitation is 650 mm distributed erratically throughout the year during growing season.

The plants were given uniform cultural treatment and irrigated through drip irrigation on daily basis during summer. Canopy volume (CV) was estimated for each individual tree using a geometrical model referred to as the contour method (CV = $[(1/4)\ \pi\ a\ b\ h) / (m(x) + m(y) + 1]$. The dimensions a and b were width of the tree at the base

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of the canopy, perpendicular and parallel to the tree row orientation, respectively. The height of the canopy (h) was measured from the lowest branch to the apex. The functions m (x) and m(y) were derived to accommodate the contour of the tree (Wright *et al.* 2006). Canopy volume measurements were made after harvest in October 2014 and 2015. Tree trunk girth was recorded before the execution and at the end of experiment during both the years of study. A ring was made with red paint at a height of 15 cm above the ground level in each selected tree to record the trunk girth from same point each year. The trunk cross-sectional area (TCSA) of tree was calculated by using formula TCSA= Girth^2/4л. Fruits were harvested at maturity, hulled, dried and nut weight in gram and yield/tree was recorded. For recording observations on nut and kernel characters, 10 nuts/ replication/genotype were used. Nut and kernel size was determined by observing the length and diameter by digital vernier calliper and thickness of shell was measured by digital screw gauge and both were expressed in millimetre. The experiment was conducted under randomised complete block design (RCBD) with three replications and pooled data of two years of experimentations were analyzed statistically as per Steel and Torrie (1986). To find out significant level, ANOVA performed using PROC GLM and clustering of genotypes into similar group was performed using the method tree procedure PROC CLUSTER based on average distance. In order to identify the patterns of morphological variations and contribution of traits, Principal component analysis (PCA) was conducted as PROC PRINCOP in the SAS 9.3 software (SAS Institute, Cary, NC).

Data on trunk cross sectional area (TCSA), plant height, canopy spread and volume of 23 genotypes have been presented in Table 1. The TCSA ranged from 37.49-290.45 cm^2 with mean value of 158.7 and standard deviation of 73.38. Maximum TCSA of 290.45 cm^2 was recorded in the genotype CITH-Almond-19 followed by CITH-Almond-23 (261.40 cm^2) and CITH-Almond-20 (255.06 cm^2) while minimum was recorded in CITH-Almond-10 (37.49 cm^2). Similarly plant height ranged from 3.40-5.10m with mean value (4.25) and standard deviation (0.49), the maximum plant height (5.10m) was recorded in CITH-Almond -19 which was at par with CITH-Almond-20 (5.0m) and

Table 1 Evaluation of genotypes for growth, flowering, fruit set and productivity efficiency in almond

Genotype	TCSA (cm^2)	Plant height (m)	Canopy spread (m)	Canopy volume (m^3)	Number of flowers (/tree)	Nut number (/tree)	Fruit set (%)	PE (g/cm^2 TCSA)
CITH-A-1	245.24	4.80	3.60	13.12	4558	2582	56.64	23.07
CITH-A-2	215.28	4.90	3.40	13.01	4322	2182	49.56	22.62
CITH-A-3	70.70	4.30	3.50	7.88	3011	1256	41.71	38.18
CITH-A-4	94.76	4.20	3.30	9.25	2988	1145	38.32	17.83
CITH-A-5	157.66	4.00	3.80	6.37	2218	1085	48.92	17.12
CITH-A-6	47.79	4.20	3.40	9.25	5889	2392	40.62	65.91
CITH-A-7	186.50	4.10	3.25	8.84	8462	1875	22.15	14.36
CITH-A-8	57.61	3.90	2.85	6.39	468	356	76.07	18.05
CITH-A-9	183.43	4.90	3.55	13.07	9315	4656	49.98	33.14
CITH-A-10	37.49	3.40	2.35	3.65	37	10	27.02	13.87
CITH-A-11	154.14	3.60	3.25	7.52	2652	1380	52.04	13.75
CITH-A-12	121.09	3.80	3.20	7.81	2382	1280	53.74	23.20
CITH-A-13	143.13	3.70	3.55	9.29	2076	1145	55.15	14.95
CITH-A-14	207.08	3.90	3.05	7.32	4281	2156	50.36	22.79
CITH-A-15	92.03	3.60	3.05	6.86	2432	1250	51.39	31.51
CITH-A-16	127.38	4.50	3.00	8.84	2077	846	40.73	17.66
CITH-A-17	226.18	4.65	3.50	11.94	4330	2341	54.06	16.18
CITH-A-18	94.76	4.00	3.38	8.97	2468	1560	63.21	30.39
CITH-A-19	290.45	5.10	3.60	13.93	3594	1760	48.92	10.15
CITH-A-20	255.06	5.00	3.40	11.99	5062	2345	46.35	12.38
CITH-A-21	187.28	4.10	3.20	8.58	3417	450	13.16	6.30
CITH-A-22	194.29	4.80	3.75	14.24	6250	3160	50.56	26.04
CITH-A-23	261.40	4.20	3.70	11.46	6500	3759	57.83	22.99
CD (P= 0.05)	25.15	0.52	0.74	3.15	1215.25	935.25	14.14	12.85
Range	37.49-290.45	3.40-5.10	2.35-3.80	3.65-14.24	37-9315	10-4656	13.16-76.07	6.30-65.91
Mean	158.7	4.24	3.33	9.54	3860.4	1781.3	47.33	22.28
Standard Deviation	73.38	0.49	0.32	2.80	2284.6	1090.5	13.33	12.29

CITH-Almond-02 (4.90m), CITH-Almond-09 (4.90m), CITH-Almond-22 (4.80m) and CITH-Almond-17 (4.65m), respectively and significantly superior to other genotypes. The canopy spread ranged from 2.35 to 3.80m with mean value of 3.33 and standard deviation of 0.32, the maximum canopy spread (3.80m) was recorded in CITH-Almond-05 followed by CITH-Almond-22 and CITH-Almond-23 (3.70m). The canopy volume varied from 3.65-14.24m^3 with mean value of 9.54 and standard deviation of 2.80, maximum canopy volume 14.24m^3 was recorded in CITH-Almond-22 followed by CITH-Almond-19 (13.93m^3) and CITH-Almond-01(13.12m^3), respectively. The variations in vegetative characters such as TCSA, plant height, canopy spread and canopy volume might be due to differences in their genetic makeup and prevailing agro-climatic conditions under which the plants are growing. Similar findings were reported by Kumar and Ahmed (2015) while working on almond varieties.

Data on number of flowers, nut number, fruit set and productivity efficiency is presented in Table 1. The number of flowers and nut number varied from 37 to 9315 and 10 to 4656 /tree respectively, the highest flower and nut number/ tree (9315 and 4656/tree respectively) were recorded in genotype CITH-Almond-09 while, lowest (37 and 10/ tree) was in CITH-Almond-10. Whereas, maximum fruit set (76.07%) was recorded in genotype CITH-Almond-08 followed by CITH-Almond-18 (63.21%) and CITH-Almond-23 (57.83%). The productivity efficiency varied from 4.80 to 90.19 g/cm^{2}TCSA, the maximum value (90.19 g/cm^2 TCSA) was recorded in genotype CITH-Almond-06 followed by CITH-Almond-CITH-Almond-03 (58.56g/cm^2 TCSA) and CITH-Almond-09 (49.99 g/cm^2 TCSA). The highest number of flower and nut number might be due to heredity character and favourable agro-climatic conditions for CITH-A-09 genotype. The genotype CITH-Almond-08 retained maximum fruit set may be due to favourable environmental conditions during fruit setting stage. The highest productivity efficiency was calculated in CITH-Almond-06 might be due to all the favourable agro-climatic factors governed for productivity efficiency. Similar results were reported by Kumar *et al.* (2008).

The data on nut and kernel yield in almond genotypes is presented in Fig 1.The nut and kernel yield per tree varied from 0.52 to 6.08 kg/tree and 0.12 to 2.75 kg/tree respectively, and maximum yield (6.08 kg/tree) was recorded in CITH-Almond-09 followed by CITH-Almond-23 (6.01 kg/tree) and CITH-Almond-01(5.66 kg/tree). The highest kernel yield more than 2 kg/tree was recorded in the genotype CITH-A-23,CITH-A-22 and CITH-A-09 while 1-2 kg/tree were recorded in CITH-A-01, CITH-A-02,CITH-A-06,CITH-A-14 and CITH-A-19 and remaining 15 genotypes having less than1kg/tree kernel yield. The highest kernel yield in CITH-A-23 might be due to genetic makeup of the genotype and favourable environmental conditions for kernel filling stage. The results are inconformity with the findings of by Kumar and Ahmed (2015).

Data on nut and quality character such as nut weight, nut size, shell thickness, kernel weight, kernel size have been presented in Table 2. The nut weight ranged from 1.54-3.95g and maximum value of 3.95g was recorded in CITH-Almond-02 followed by CITH-Almond-01 (3.31g) and CITH-Almond-13 (3.28g). Nut size, i.e. length and diameter ranged from 28.20-39.05mm and 15.10-21.54mm, maximum nut length (39.05 mm) was recorded in CITH-Almond-08 followed by CITH-Almond--21 (37.90 mm) and CITH-Almond-22 (34.07 mm) whereas, maximum diameter 21.54mm was recorded in CITH-Almond-21. The shell thickness ranged from 0.82-3.45 mm, maximum value 3.45mm was recorded in CITH-Almond-18 and minimum value (0.82 mm) was in CITH-Almond-08. Kernel weight ranged from 0.65-0.99g, maximum value 0.99g was recorded in CITH-Almond-09 followed by CITH-Almond-19 (0.95g) and CITH-Almond-22 (0.94g) and minimum (0.65g) in CITH-Almond-17 genotype. The kernel size (Length and diameter), maximum length 24.37 mm was recorded in CITH-Almond-21 and minimum 17.31 mm in CITH-Almond-18, whereas, diameter was maximum in CITH-Almond-04 (12.53 mm) and minimum in CITH-Almond-22 (10.07 mm). The softness of shell varied from soft to hard shell, the genotype CITH-Almond-08 was soft and CITH-Almond-09,CITH-Almond-19, CITH-Almond-21, CITH-Almond-22 and CITH-Almond-23 were semi-hard and rest of the genotypes were hard. The better nut weight, size and kernel size might be due to genetic makeup of particular genotypes. Similar findings were reported by Kumar and Ahmed (2015) and De Giorgio *et al.*2007 while working on almond varieties/genotypes and apricot and plum genotypes (Kumar *et al.* 2015, Kumar *et al.* 2016).

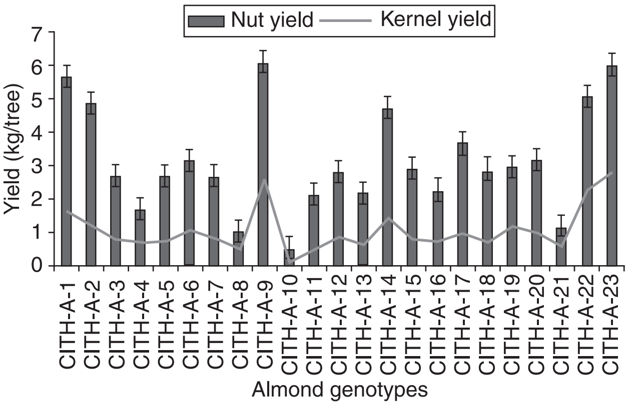

Fig 1 Performance of almond genotypes for nut and kernel yield.

Data on kernel recovery indicated that it ranged from 24.05 to 50.0 % and maximum kernel recovery (50%) was recorded in CITH-Almond-08 followed by CITH-Almond-21 (48.38%), CITH-Almond-23(45.85%) and CITH-Almond-22 (43.72%) while the minimum kernel recovery (24.05%) was recorded in CITH-Almond-02 genotype. The maximum kernel recovery in elite genotype might be due to their genetic makeup and favourable agro-climatic conditions.

Correlation coefficient among different traits studied was also estimated in all possible combinations for growth,

Table 2 Evaluation of genotypes for nut quality contributing characters in almond

Genotype	Nut wt. (g)	Nut size (mm)		Shell thickness (mm)	Kernel wt. (g)	Kernel size (mm)		Softness of shell
		Length	Dia.			Length	Diameter	
CITH-A-1	3.31	29.67	20.20	2.75	0.97	17.90	11.71	Hard
CITH-A-2	3.95	29.42	19.25	2.41	0.95	19.56	12.23	Hard
CITH-A-3	2.71	31.11	20.20	2.52	0.77	21.11	12.30	Hard
CITH-A-4	2.12	29.45	20.58	2.35	0.86	20.86	12.53	Hard
CITH-A-5	2.52	28.95	19.83	2.38	0.70	19.38	12.29	Hard
CITH-A-6	2.24	30.73	19.29	2.35	0.74	21.32	10.87	Hard
CITH-A-7	2.78	30.89	21.90	2.74	0.88	21.23	12.52	Hard
CITH-A-8	1.54	39.05	19.54	0.82	0.77	27.41	11.55	Soft
CITH-A-9	2.28	29.31	20.01	2.26	0.99	16.68	10.15	Semi hard
CITH-A-10	2.94	28.20	18.90	2.12	0.73	18.46	10.14	Hard
CITH-A-11	2.35	31.52	16.51	2.31	0.62	20.37	10.13	Hard
CITH-A-12	2.57	31.78	21.35	2.73	0.77	17.89	12.06	Hard
CITH-A-13	3.28	31.41	18.40	2.48	0.96	22.24	10.98	Hard
CITH-A-14	3.07	30.74	21.19	2.73	0.90	18.24	12.49	Hard
CITH-A-15	3.06	31.53	20.82	2.55	0.85	21.21	12.70	Hard
CITH-A-16	2.66	36.78	15.10	3.17	0.87	20.02	11.89	Hard
CITH-A-17	2.48	36.19	21.11	2.68	0.65	22.42	11.36	Hard
CITH-A-18	2.98	29.22	19.57	3.45	0.74	17.31	10.77	Hard
CITH-A-19	2.43	29.60	21.02	2.16	0.95	17.68	11.33	Semi hard
CITH-A-20	3.11	30.46	17.33	2.21	0.96	21.91	10.48	Hard
CITH-A-21	1.86	37.90	21.54	2.65	0.90	24.37	12.19	Semi hard
CITH-A-22	2.15	34.07	19.05	2.52	0.94	19.99	10.07	Semi hard
CITH-A-23	1.81	33.47	18.82	1.27	0.83	17.54	12.35	Semi hard
CD (P = 0.05)	0.17	2.81	1.65	0.48	0.12	1.99	1.04	
Ranged	1.54-3.95	28.20-39.05	15.10-21.54	0.82-3.45	0.62-0.99	17.31-24.37	10.07-12.70	
Mean	2.61	31.80	19.63	2.41	0.83	20.22	11.52	
Standard Deviation	0.55	3.02	1.65	0.53	0.11	2.51	0.90	

yield and quality parameters (Table 3). The positive and significant correlation was observed between trunk cross sectional area and plant height (0.651), canopy spread (0.585), canopy volume (0.735), flowers per tree (0.506), nut number (0.554), nut yield (0.606) kernel yield (0.551) and kernel weight (0.485). Similarly plant height exhibited positive significant association with canopy spread (0.614), canopy volume (0.890), number of flowers (0.540), nut number (0.592), nut yield (0.567), kernel yield (0.562) and kernel weight (0.535). The canopy spread and canopy volume (0.795), flower number (0.585), nut number (0.686), nut yield (0.653) and kernel yield (0.627) were also showed positive significant relationship. Likewise the positive correlation observed between canopy volume and number of flowers (0.636), nut number (0.739), nut yield (0.706), kennel yield (0.680) and kernel weight (0.560). The number of flowers and nut number (0.860), nut yield (0.712) and kernel weight (0.749) was found positively associated as nut number and nut yield (0.916) and kernel yield (0.924). Positive significant correlation was also noticed between nut weight and shell thickness (0.501) and nut length and kernel length (0.674) and kernel recovery (0.528). Whereas, significantly negative correlation coefficient was observed between nut number and kernel length (-0.472), nut weight and nut length (-0.552), shell thickness (0.501),kernel recovery (-0.790), shell thickness and kernel recovery (-0.551).

The dendrogram generated from the linkage cluster analysis based on average distance, classified 23 almond genotypes into two major groups (Fig 2) at normalized root mean square (NRMS) distance 1.73. The First group further categorized into two major clusters at 0.98 NRMS distance. Of these the first major cluster consisted of 9 genotypes contributing 20.7 % of the total genotypes (CITH-A-1, CITH-A-2, CITH-A-14, CITH-A-17,CITH-A-20, CITH-A-19, CITH-A-6, CITH-A-22, CITH-A-23). This first major cluster was further divided into two sub-sub-clusters at 0.62 NRMS distance and first sub-cluster included 6 genotypes (CITH-A-1, CITH-A-2, CITH-A-14, CITH-A-17,CITH-A-20, CITH-A-19,) and

Table 3 Correlation coefficient for 18 characters of almond genotypes

Particular	TCSA (cm^2)	Plant height (m)	Canopy spread	Volume (m^3)	Flower (Nos)	Nut number	Fruit set (%)	Nut yield (kg/tree)	Kernel yield (kg/tree)	PE (g/cm^2 TCSA)	Nut weight (g)	Nut size (mm)		Shell thickness (mm)	Kernel weight (g)	Kernel size (mm)		Kernel recovery (%)
												Length	Dia			Length	Dia	
TCSA	1.000	0.651*	0.585*	0.735*	0.506*	0.554*	0.053^{NS}	0.605*	0.551*	-0.424^{NS}	0.133^{NS}	-0.017^{NS}	0.092^{NS}	-0.006^{NS}	0.483*	-0.284^{NS}	0.047^{NS}	0.137^{NS}
Plant height		1.000	0.614*	0.890*	0.540*	0.592*	0.065^{NS}	0.567^{NS}	0.526*	0.013^{NS}	0.088^{NS}	-0.026^{NS}	-0.025^{NS}	0.051^{NS}	0.535*	-0.184^{NS}	-0.131^{NS}	0.213^{NS}
Canopy spread			1.000	0.795*	0.585*	0.686*	0.252^{NS}	0.653*	0.627*	0.191^{NS}	-0.031^{NS}	-0.102^{NS}	0.088^{NS}	0.084^{NS}	0.300^{NS}	-0.232^{NS}	-0.034^{NS}	0.165^{NS}
Volume				1.000	0.636*	0.739*	0.183^{NS}	0.706*	0.680*	0.029^{NS}	0.080^{NS}	-0.038^{NS}	0.014^{NS}	0.051^{NS}	0.560*	-0.262^{NS}	-0.197^{NS}	0.242^{NS}
Flower Nos					1.000	0.860*	-0.163^{NS}	0.712*	0.749*	0.275^{NS}	-0.070^{NS}	-0.146^{NS}	0.207^{NS}	0.040^{NS}	0.412^{NS}	-0.284^{NS}	-0.072^{NS}	0.261^{NS}
Nut number						1.000	0.242^{NS}	0.916*	0.924*	0.344^{NS}	-0.022^{NS}	-0.201^{NS}	0.043^{NS}	-0.064^{NS}	0.362^{NS}	-0.472*	-0.218^{NS}	0.204^{NS}
Fruit set							1.000	0.331^{NS}	0.260^{NS}	0.154^{NS}	-0.002^{NS}	0.069^{NS}	-0.174^{NS}	-0.306^{NS}	-0.112^{NS}	-0.057^{NS}	-0.142^{NS}	-0.007^{NS}
Nut yield								1.000	0.909*	0.301^{NS}	0.181^{NS}	-0.212^{NS}	0.081^{NS}	0.028^{NS}	0.407^{NS}	-0.553*	-0.009^{NS}	0.065^{NS}
Kernel yield									1.000	0.249^{NS}	-0.166^{NS}	-0.058^{NS}	0.051^{NS}	-0.194^{NS}	0.427*	-0.475*	-0.095^{NS}	0.414^{NS}
PE										1.000	-0.013^{NS}	-0.209^{NS}	0.033^{NS}	0.075^{NS}	-0.143^{NS}	-0.150^{NS}	-0.071^{NS}	-0.093^{NS}
Nut weight											1.000	-0.552*	-0.073^{NS}	0.501*	0.305^{NS}	-0.324^{NS}	0.064^{NS}	-0.790*
Nut size (Length)												1.000	-0.106^{NS}	-0.235^{NS}	-0.131^{NS}	0.674*	0.125^{NS}	0.528*
Diameter													1.000	0.053^{NS}	0.084^{NS}	-0.007^{NS}	0.454^{NS}	0.125^{NS}
Shell thickness														1.000	0.045^{NS}	-0.344^{NS}	0.048^{NS}	-0.551*
Kernel weight															1.000	-0.151^{NS}	0.093^{NS}	0.307^{NS}
Kernel size (Length)																1.000	0.113^{NS}	0.301^{NS}
Diameter																	1.000	0.019
Kernel recovery																		1.000

*, NS = Significant at 5% level and non-significant respectively.

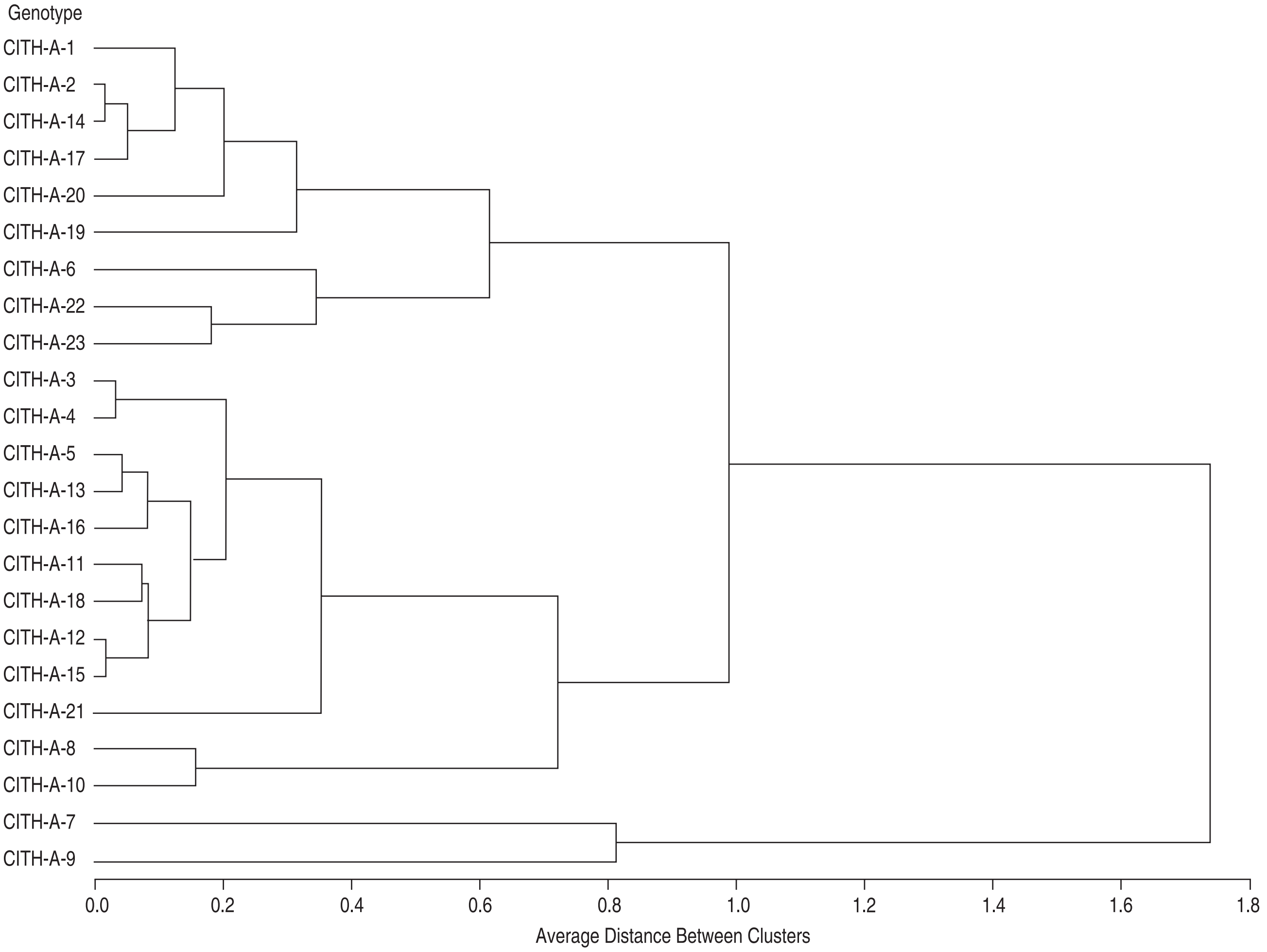

Fig 2 Dendrogram of 23 almond genotypes obtained by average distance between cluster analyses based on 18 plant growth, nut quality and yield traits.

characterized by higher TCSA and plant height. However, the second sub-cluster consisted, a total of 3 genotypes (CITH-A-6, CITH-A-22, and CITH-A-23) characterized by kernel yield. Further the second major cluster consisted of 12 genotypes contributing 27.06% of the total genotypes studied. This major cluster divided in to four sub clusters. The first sub-cluster consisted two genotypes (CITH-A-3 and CITH-A-4), whereas second sub cluster included seven genotypes (CITH-A-5, CITH-A-13, CITH-A-16, CITH-A-11, CITH-A-18, CITH-A-12, CITH-A-15, CITH-A-21), third sub cluster consisted only one genotype CITH-A-21 and fourth sub cluster included two genotypes CITH-A-8 and CITH-A-10. It had the maximum canopy spread, canopy volume, nut yield, productivity efficiency, nut weight, shell thickness and kernel weight. The second group further divided into two major clusters at 0.81. In each cluster only one genotype was found i.e. in first cluster CITH-A-7 and CITH-A-9 which possess higher kernel size, nut size, fruit set and kernel recovery.

SUMMARY

A field experiment was carried out at the ICAR-Central Institute for Temperate Horticulture, Srinagar during 2013-2015 to evaluate twenty three almond genotypes for important horticultural traits to detect similarities among morphological, nut yield and quality parameters. Genotypes differed significantly for observed traits. The 18 variables were scored and subject to multivariate analysis. Results showed a considerable phenotypic diversity among almond genotypes. The cluster analysis classified genotypes into two major groups according to their potential characteristics. The biometric parameters indicated that maximum Trunk Cross Sectional Area (290.45 cm^2) and plant height (5.10m) were recorded in CITH-Almond-19. Highest canopy volume (14.24m^3) was recorded in CITH-Almond-22. Maximum flowers number (9315/tree), nut number (4656/tree) and kernel yield (2.75 kg/tree) were recorded in CITH-Almond-23. Highest productivity efficiency (65.91 g/cm^2 TCSA) was calculated in CITH-Almond-06. The nut weight (3.95g) was maximum in CITH-Almond-02. Kernel recovery above 40% was recorded in CITH-Almond-04, CITH-Almond-08, CITH-Almond-09, CITH-Almond-21, CITH-Almond-22 and CITH-Almond-33. The softness of shell were also observed in these genotypes and found to be semi hard to soft shell. The correlation coefficient among different characters was worked out in all possible combination. The

positive correlation between nut yield and TCSA, plant height, canopy spread, canopy volume, flower numbers and fruit set in almond genotypes. The current results will be very useful for conservation of indigenous almond genotypes and formulating future breeding strategies in almond. Based on overall performance, it may be concluded that there was significant genetic diversity among selected almond genotypes for the selected horticultural traits. The genotype, viz. CITH-Almond-23, CITH-Almond-22, CITH-Almond-09, CITH-Almond-01, CITH-Almond-15, CITH-Almond-02 and CITH-Almond-19 and CITH-Almond-06 found to be superior in respect to nut quality under north western Himalayan region of India. These genotypes could be multiplied and distributed for performance evaluation under different temperate growing region of India for productivity enhancement besides utilization as parents for almond breeding programme for desirable traits.

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