Research Article

VARIATION IN SEED AND SEEDLING TRAITS OF MAHANEEM (*AILANTHUS EXCELSA* ROXB)

KAUSHIK N.*[1], DESWAL R.P.S.[1], JAKHAR V.[1] AND ARYA S.[2]

[1]Regional Research Station, Bawal, 123501, Chaudhary Charan Singh Haryana Agricultural University, Hisar, 125004, Haryana, India
[2]Department of Forestry, Chaudhary Charan Singh Haryana Agricultural University, Hisar, 125004, Haryana, India
*Corresponding Author: Email - nk20025@rediffmail.com

Abstract: *Ailanthus excelsa* Roxb (tree of heaven), is a fast growing multipurpose tree species for arid and semi-arid areas with vide variability. It is, therefore, necessary to identify the plus trees for its improvement. Therefore, the present studies were conducted to evaluate the performance of progenies of *A. excelsa* for germination and seedling characters. Thirty plus trees were identified from states of Haryana and Rajasthan, India and sufficient quantities of mature pods were collected from these plus trees individually. Observations on seed and seedling traits were recorded. Thirty progenies showed significant (P>0.05) variability for all the characters studied. Higher magnitude of phenotypic coefficient of variation (PCV) than corresponding genotypic coefficient of variation (GCV) was registered for all the characters. Highest heritability (99.50%) was shown by germination. The genetic advance as per cent mean varied from 12.62% (diameter) to 62.20% (fresh root weight). The clustering showed that progenies collected from different geographical regions were grouped in one cluster as evident from cluster III. Therefore, the pattern of divergence was not dependent upon geographical locations. Maximum intra-cluster distance (4.63) shown by cluster IV indicated wide divergence with in cluster itself. Maximum inter-cluster distance between cluster I and IV (7.44) indicated greater divergence between genotypes belonging to these clusters.

Keywords: *Ailanthus excels, Heritability, Plus Tree, Progeny*

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Introduction

Ailanthus excelsa Roxb commonly known as Mahaneem (tree of heaven), is a fast-growing tree species for dry areas and suitable for industrial forestry due to its adaptation to less moisture and high temperature conditions Seth *et al*. [1], Bhimaya *et al*. [2]. It is indigenous to India, found throughout the drier tropical and sub-tropical parts up to 1000 m altitude. It is fairly common in central Sudan and is found planted on reverie and sandy soils. The timber of *A. excelsa* is considered good for manufacturing plywood as its timber is ranked of Grade III and Grade IV category. The pulp is used in paper industry as a substitute for aspen and printing papers. It improved the surface quality of paper. *A. excelsa* was found suitable making laminated veneer lumber (LVL) using thickness of veneer 5.0 mm [3]. It is very light in weight, soft and not durable and used for packing cases, match box and sticks, fishing floats, catamarans, sword handles and toys [4]. The tree species have several medicinal properties for example antispasmodic, antiseptic etc. Asthma and bronchitis are also cured through this tree species [5]. *A. excelsa* is used in Indian system of medicine for a variety of purposes [6] and considered to be the main therapeutic constituents for amebic and bacterial dysentery and diarrhea; intestinal worms and internal parasites; malaria; as an astringent to stop internal bleeding (stomach ulcers, hemorrhages) and externally for wounds and in viral infections [7-9] and Kumar *et al*. [10]. *A. excelsa* bark is used to treat diarrhea and dysentery in Chinese system of medicine especially when there is a blood in stool [11, 12]. *A. excelsa* under agroforestry systems have been found to be soil organic carbon improver along with meeting the needs of farmers for fodder, fuel and timber [13], [14]. Moreover, its cultivation with low inputs and in harsh climatic conditions is an additional advantage [15-17]. It is a moderately salt tolerant species and grows well on dry lands [18]. Clayey soils with poor drainage and waterlogged conditions are not suitable for this tree. *A. excelsa* is an important species with vide variability, which can exploit for its improvement in different agro-

climatic requirements, developing the elite seeds. It is necessary to identify the plus trees/ superior genotypes. However, performance of progenies of such superior genotypes needs to be evaluated at different stages from the seedling stage to at least one-third of the rotation of that crop for morphological and reproductive characters [19]. The effective tree improvement programme depends upon the nature and magnitude of existing genetic variability and also on the degree of transmission of the desired traits. The ultimate goal of tree breeding is to obtain genotypes that maximize the phenotypic performance so as to improve the production potential of an individual tree. The assessment of genetic variability is vital to tree improvement [20]. Partitioning of variability into heritable and non-heritable components facilitates the assessment of magnitude, nature and inter-relatedness of genotypic and non-genotypic variations. Knowledge about the nature and extent of source variation in relation to seed oil content, germination and seedling characters is very useful for the production of good quality planting stock. Present study is aimed at evaluation of different seed sources for estimation of genetic parameters for seed oil content and different growth characters. Progeny evaluation is one of the selection methods followed in tree improvement programmes, where superior genotypes are selected based on the performance of their respective progenies at an early age by providing similar environmental (growing) conditions to progenies of selected genotypes [21]. Individuals selected through this method are known to be superior with respect to their genetic characters. Therefore, the present studies were conducted to evaluate the performance of progenies of plus trees of *A. excelsa* for seed germination and seedling traits.

Materials and Methods
Survey and Seed collection
An intensive survey was conducted for plus tree selection in four districts of

Rajasthan and one district of Haryana. The healthy and superior phenotypes (trees) were selected as candidate plus trees on the basis of growth, straightness, clear bole height, less branching etc. and further confirmed to plus trees as per check tree method [22]. The plus trees were confirmed after comparing with five co-dominant trees within a radius of 50-100 m. Thirty plus trees were identified and sufficient quantities of mature pods were collected from these plus trees individually. The seeds were separated from pods manually and stored at room temperature for raising nursery.

Study site

The study was conducted at Chaudhary Charan Singh Haryana Agricultural University Regional Research Station, Bawal, Haryana, India (28.1°N, 76.5°E and 266 m above mean sea level). The site is characterized by inadequate and erratic precipitation (350-550 mm) during monsoon (July-September). The number of rainy days in a year varies between15 to 25. In general, May-June are the hottest (21-46°C temp.), whereas, December-January are the coldest (0-15° C temp.) months of the year. During summer, the maximum temperature reaches as high as 46°C. During peak winter months of December and January, the average minimum temperature is recorded around 4-5°C, which at times, reaches below 0°C. Between October and March, weather remains almost dry except occasional light showers. Thereafter, it is quite dry till June. The maximum evapo-transpiration rate of 14 mm/day is recorded in the month of June. The soil of the experimental site was loamy sand in texture (Typic Ustochrept) and the pH(1:2) and EC(1:2) were 8.14 and 0.19 dS/m respectively, The soil was low in organic carbon 0.18%, available N 108 kg/ha, available P 8.34 kg/ha and medium in available K 170 kg/ha.

Seedling parameters

The seeds were sown in the polybags filled with mixture of sand, soil and compost in equal proportion. The experiment was laid out in completely randomized design with five replications of 100 seeds each. Observations on germination, peak value, mean daily germination, speed of germination and germination value were recorded up to 21 days from date of sowing for each progeny as per the formulae given below. Height, collar diameter, no. of leaves, no. of branches, root length, shoot and root dry weight and shoot and root vigour index of seedlings of each progeny in nursery were also recorded after 90 days of sowing and analyzed statistically.

$$\text{Germination percent} = \frac{\text{Number of seeds germinated}}{\text{Number of seeds sown}} \times 100$$

Germination Value (GV) = PV × MDG
Where,
PV- Peak Value of germination.
MDG- Mean Daily Germination
Peak Value (PV) = Total germination percent / Total number of days

$$\text{Mean Daily Germination (MDG)} = \frac{\text{Final germination percent}}{\text{The number of days that took to reach Peak Germination}}$$

Shoot Vigour Index (SVI) = Germination percentage × Shoot length (cm)
Root Vigour Index (RVI) = Germination percentage ×Root length (cm).

Statistical analysis

Analysis of variance was carried out using complete randomized design as per the method suggested by Panse and Sukhatme [23]. Genotypic and phenotypic Coefficients of variations were estimated by the formula suggested by Burton [24] for each character as follows:
Genotypic coefficient of variance (GCV) = $\sqrt{\sigma^2 g} \times 100 / X$
Phenotypic coefficient of variance (PCV) = $\sqrt{\sigma^2 p} \times 100 / X$
Where X was mean of that particular character
Heritability in broad sense was calculated according to the formula as per Johnson *et al*. [25] for each character.

Heritability (broad sense) in percent = $h^2 = \sigma^2 g / \sigma^2 p \times 100$
Where $\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance
Estimates of appropriate variance components were substituted for the parameters to predict the expected genetic gain as suggested by Lush [26]. The expected genetic gain was calculated at 5% selection intensity for each character as:
Genetic advance (%) of mean = K × σp × h^2 / X
Where:
K = selection differential (2.06)
σp = phenotypic standard deviation
h^2 = heritability in broad sense
X= general mean
The genetic divergence was calculated by using non- hierarchical Euclidian cluster analysis [27].

Results and Discussion

Germination and seedling characters

Thirty progenies showed significant (P>0.05) variability for all the characters studied [Table-1]. The germination percentage varied from 21. 93 (P 28) to 88.42 cm (P 13). Progeny 13 showed maximum mean daily germination (6.32), while minimum mean daily germination was recorded in P 28 (1.57). Maximum numbers of days to reach the peak germination were taken by P 8 (18 days). Peak value of germination varied from 1.46 (P 28) to 6.32 (P13). Wide variability was also recorded for germination value. P 28 showed minimum value (2.29) whereas, maximum was recorded in P13 (39.89). Shoot vigour varied from 745 to 3715.4 and root vigour varied from 438.6 to 2122.1 in P 28 and P13, respectively.

Maximum plant height (46.37 cm) was recorded in P 23 and minimum in P 30 (33.92 cm) [Table-2]. Progeny 23 showed maximum diameter (5.52 mm) followed by P 28 (5.51 mm) and P1 (5.50 mm). Numbers of leaves per plant varied from 22.67 (P1) to 34.42 (P29). Maximum height (36.60) to first leaf was recorded in P 2 followed by P 7 (34.85cm). Number of branches showed significant variability from 3.90 (P1) to 6.15 (P27). Progeny 16 showed maximum shoot weight (14.88 g) followed by P7 (14.80 g). Minimum shoot weight (8.51 g) was recorded in P9 followed by P24 (8.66 g). Dry shoot varied from 1.41 (P12) to 3.71 g (P 23). Maximum root length (26.66 cm) was reported in P 30 and minimum in P6 (12.33 cm). Number of secondary roots varied in the range of 8.66 (P24) to 13.33 (P11, P18 and P28). Fresh and dry root weight also varied significantly [Table-2]. Fresh root varied from 1.26 (P 29) to 4.65 g (P 23), while dry root weight varied from 0.62 (P25 and 29) to 1.13 g (P23).

Improvement of trees has become important part of forestry with the adoption of agroforestry by the farmers on their farm lands. Therefore, seed production areas have been recommended as an interim measure for immediate gain. Usually, progeny trials are used to predict the genetic worth of plus trees. Based on the superiority of the individuals, seedling or clonal seed orchards are established [19]. In the present study, wide variability recorded between 30 progenies of plus trees for germination and seedling traits can be tapped for future improvement of this species.

Progeny (P13) showed maximum germination percentage, mean daily germination, germination value, shoot and root vigour, whereas maximum plant height, diameter, height to first leaf, fresh and dry weight of shoot and root was recorded in P 23. The variability might be due to genotype differences as the progenies were raised under same environment. This type of variability for seed germination and seedling traits have already been recorded by Vasav *et al*. [28] and Kumar and Kaushik [29] in *Pongamia pinnata*; Kaushik [30] in *Azadirachta indica* and Chillar *et al*. [31] in *Acacia nilotica* Mishra *et al*. [32] in *Pterocarpus marsupium* and Berka eat al. [33].

Genetic variability and association studies

PCV and GCV can be used for judging the variation expressed by germination and seedling characters. PCV were higher than the GCV of all the characters studied. Higher magnitude of PCV than corresponding GCV was registered for all the characters.

Table-1 *Germination percentage and other germination traits in A. excelsa progenies after 21 days of sowing*

Progeny	Germination (%)	Mean Daily Germination	Days to reach peak germination	Peak Value	Germination value	Shoot Vigour	Root Vigour
P1	44.72	3.19	14	3.19	10.2	1808	730.3
P2	50.48	3.61	15	3.37	12.13	2253.9	908.6
P3	33.48	2.39	16	2.09	5	1480.8	636.1
P4	43.32	3.09	13	3.33	10.31	1685.1	620.8
P5	61.54	4.4	15	4.1	18.03	2372.4	943.4
P6	61.64	4.4	14	4.4	19.39	2471.8	760
P7	78.35	5.6	15	5.22	29.23	3502.2	1410.3
P8	58.56	4.18	18	3.25	13.61	2687.9	761.3
P9	53.31	3.81	17	3.14	11.94	1906.9	959.6
P10	38.38	2.74	16	2.4	6.58	1462.3	767.6
P11	49.95	3.57	14	3.57	12.73	2068.9	665.8
P12	68.49	4.89	15	4.57	22.34	2808.1	1072.6
P13	88.42	6.32	14	6.32	39.89	3715.4	2122.1
P14	85.1	6.08	15	5.67	34.49	3629.5	1872.2
P15	78.6	5.61	16	4.91	27.58	3132.2	1336.2
P16	86.56	6.18	14	6.18	38.23	3338.6	1731.2
P17	75.1	5.36	17	4.42	23.7	2624.7	1502
P18	73.47	5.25	13	5.65	29.66	2597.2	1469.4
P19	85.1	6.08	16	5.32	32.33	3252.5	1588
P20	78.32	5.59	14	5.59	31.3	3363.8	1696.4
P21	78.44	5.6	15	5.23	29.3	3354.9	1882.6
P22	66.89	4.78	15	4.46	21.31	2729.1	1582.6
P23	73.61	5.26	14	5.26	27.65	3413.3	1790.9
P24	66.43	4.75	16	4.15	19.7	2428	1350.5
P25	53.17	3.8	14	3.8	14.42	2018.9	921.4
P26	36.53	2.61	15	2.44	6.35	1442.9	657.5
P27	88.15	6.3	17	5.19	32.65	3311.8	2056.5
P28	21.93	1.57	15	1.46	2.29	745	438.6
P29	65.25	4.66	14	4.66	21.72	2508.9	1011.4
P30	43.58	3.11	16	2.72	8.48	1478.2	1161.8
Mean	62.9	4.49	15.07	4.2	20.42	2497.46	1236.8
C. V.	5	8	7.54	6.23	8.23	10.25	11.56
CD (5%)	2.01	1.21	2.3	1.58	4.32	544.78	359.63

Table-2 *Seedling performance of plus tree progenies of Ailanthus excelsa*

Progeny	Plant Height (cm)	Collar Diameter (mm)	Number of leaves	Height of first leaf (cm)	Number of branches	Fresh shoot weight (g)	Dry shoot weight (g)	Root length (cm)	Number of secondary roots	Fresh root weight (g)	Dry root weight (g)
P1	40.43	5.5	22.67	33.3	3.9	13.26	2.39	16.33	12	3.89	0.91
P2	44.65	5.4	28.7	36.6	4.82	14.73	2	18	13.16	2.62	0.74
P3	44.23	5.48	29.7	31.15	5.05	10.32	2.41	19	12.66	2.96	0.73
P4	38.9	5.03	27.45	31.07	5.27	13.86	2.41	14.33	11.66	2.72	0.81
P5	38.55	5.1	22.02	32.32	4.02	12.49	3.07	15.33	10.66	3.38	1
P6	40.1	5.17	28.37	30.8	4.9	9.74	1.93	12.33	10	2.11	0.71
P7	44.7	5.02	30.95	34.85	5	14.8	2.09	18	11	2.7	0.69
P8	45.9	4.65	24.75	33.5	4.8	10.17	2.35	13	12.33	3.05	0.88
P9	35.77	4.52	26.25	27.15	4.8	8.51	2.09	18	12.66	3.1	0.83
P10	38.1	4.65	27.72	31.5	5.15	9.94	2.03	20	13	3.74	0.98
P11	41.42	5.15	30.12	31.37	5.02	12.5	2.27	13.33	13.33	2.9	0.76
P12	41	5.25	33.05	30.37	5.32	12.66	1.41	15.66	11.33	2.02	0.88
P13	42.02	4.65	25.52	31.42	4.35	13.68	3	24	12	4.12	1
P14	42.65	4.65	29.32	33.82	4.9	10.76	2.31	22	13	3.12	0.87
P15	39.85	4.2	28.95	30.62	5.27	13.03	2.85	17	12	3.95	0.97
P16	38.57	4.17	28.42	28.4	5.35	14.88	3.03	20	11	3.56	0.94
P17	34.95	4.57	29.82	27.1	5.25	9.53	2.18	20	12.33	2.61	0.64
P18	35.35	4.57	32.92	28.6	5.57	13.85	2.65	20	13.33	2.73	0.9
P19	38.22	4.55	32.42	29.57	5.87	10.95	3.54	18.66	11	3	0.95
P20	42.95	4.9	31.62	31.42	4.94	11.66	2.61	21.66	9	2.61	0.73
P21	42.77	4.97	28.72	33.07	5.2	9.19	2.84	24	12.66	2.91	0.86
P22	40.8	5	28.27	34.01	5.17	10.99	2.56	23.66	10	2.71	0.71
P23	46.37	5.52	31.4	28.12	4.95	16.37	3.71	24.33	15	4.65	1.13
P24	36.55	4.42	30.67	29.4	5.77	8.66	2.98	20.33	8.66	3.62	1
P25	37.97	4.2	28.85	28.07	5.4	10.03	2.04	17.33	12	3.77	0.95
P26	39.5	4.55	27.52	30.92	5.1	11.15	1.89	18	10.66	2.23	0.62
P27	37.57	4.6	33.52	28.92	6.15	10.72	2.41	23.33	12.33	3.35	0.98
P28	33.97	5.51	31.55	27.45	5.17	13.85	2.35	20	13.33	3.73	0.9
P29	38.45	5	34.42	29.02	5.95	10.09	2.36	15.5	9.5	1.26	0.7
P30	33.92	4.5	33.75	25.17	6.5	9.86	2.62	26.66	10.33	2.43	0.62
Mean	39.87	4.79	29.46	30.66	5.16	10.47	2.59	19.03	11.9	3.3	0.894
C. V.		5.03	6.96	5.1	6.32	14.21	11.85	10.92	12.58	9.34	12.48
C.D.5%		0.39	3.36	2.56	0.53	2.43	0.93	3.45	3.22	1.04	0.4

Table-3 *Estimates of genetic parameters for germination percentage and seedling traits in A. excelsa*

Characters	Variance		Coefficient of variation (%)		Heritability (Broad Sense)	Genetic Advance as % of Mean (5%)
	Genotypic	Phenotypic	Genotypic	Phenotypic		
Plant Height (cm)	12.11	13.67	8.79	9.33	88.60	17.04
Diameter (mm)	0.13	0.18	7.41	8.96	68.40	12.62
Number of leaves	9.98	14.19	10.72	12.78	70.30	18.51
Height of first leaf (cm)	6.14	8.60	8.08	9.56	71.40	14.07
Number of branches	0.27	0.38	10.02	11.85	71.05	17.46
Germination (%)	332.60	334.11	28.96	29.03	99.50	59.53
Fresh shoot weight (g)	6.33	8.54	24.00	27.90	74.00	42.54
Dry shoot weight (g)	0.58	0.90	29.33	36.57	64.30	48.44
Root length (cm)	14.72	19.20	19.82	22.63	76.70	35.75
Number of secondary roots	4.94	8.84	18.68	24.98	55.90	28.79
Fresh root weight (g)	1.31	1.72	34.59	39.64	76.20	62.20
Dry root weight (g)	0.08	0.14	32.19	42.32	57.80	50.42

Table-4 *Genotypic (G) and phenotypic (P) correlation coefficient between germination and seedling characters in A. excelsa*

Characters		Plant height (cm)	Diameter (mm)	No. of leaves	Height of first leaf (cm)	No. of branches	Germination (%)	Fresh shoot weight (g)	Dry shoot weight (g)	Root length (cm)	No. of secondary roots	Fresh root weight g	Dry root weight (g)
Plant ht. (cm)	G		0.273	-0.371	0.69	-0.482	0.382	-0.102	-0.25	-0.2.8	-0.085	-0.255	-0.28
	P		0.27	-0.229	0.657	-0.394	0.355	-0.093	-0.199	-0.126	-0.049	-0.22	-0.199
Diameter (mm)	G			-0.209	0.623	-0.422	-0.248	-0.35	-0.572	-0.257	-0.126	-0.379	-0.516
	P			-0.065	0.501	-0.293	-0.26	-0.26	-0.391	-0.172	-0.095	-0.305	-0.342
No. of leaves	G				-0.519	0.871	0.148	-0.406	-0.038	0.115	-0.173	-0.269	-0.356
	P				-0.427	0.824	0.12	-0.233	-0.043	0.145	-0.127	-0.177	-0.197
Ht. of first leaf (cm)	G					-0.562	0.076	-0.036	-0.207	-0.062	0.029	-0.034	-0.058
	P					-0.52	0.063	-0.114	-0.174	-0.027	0.033	-0.068	-0.056
No. of branches	G						0.123	-0.412	0.203	0.144	-0.308	-0.044	0.002
	P						0.105	-0.201	0.149	0.177	-0.182	0.022	0.045
Germination (%)	G							0.096	0.302	0.282	-0.262	0.224	0.251
	P							0.084	0.246	0.244	-0.199	0.203	0.2
Fresh shoot weight (g)	G								0.412	0.127	0.31	0.334	0.437
	P								0.387	0.11	0.185	0.386	0.404
Dry shoot weight (g)	G									0.207	-0.12	0.89	0.921
	P									0.222	-0.143	0.678	0.723
Root length (cm)	G										-0.162	0.258	0.293
	P										-0.106	0.208	0.254
No.of secondary roots	G											-0.01	0.01
	P											-0.03	-0.027
Fresh root weight (g)	G												0.974
	P												0.727

Highest GCV (34.59) and PCV (42.32) were recorded for fresh and dry root weight, respectively [Table-3]. Highest heritability (99.50%) was shown by germination followed by plant height (88.60%). The genetic advance as per cent mean varied from 12.62% (diameter) to 62.20% (fresh root weight).

Plant height was positively correlated with diameter, height of first leaf and germination percentage at both genotypic and phenotypic levels [Table-4]. Diameter was found negatively correlated with all the characters except height of first leaf. Number of branches showed positive correlation with germination percentage, dry shoot weight, root length and dry root weight at both the levels, however, it was negatively correlated at genotypic level with fresh root weight. Germination percentage showed positive correlation with fresh shoot weight, dry shoot weight, root length, fresh and dry root weight at both levels. Fresh shoot weight was positively correlated with dry shoot weight, root length, number of secondary roots and fresh and dry root weight.

Genetic variability in trees forms the basis for selection and further improvement of species. The information on the genetic structure and diversity relationship of a progeny provides a basis for planning future utilization of genetic resources to realize the potentiality for maximizing growth and yield. The results of present study clearly indicated that for a majority of traits there is much scope for selection in *Ailanthus excelsa* for improvement. Variations among progenies are commonly used as an estimate of total genetic variation and to calculate the degree of genetic control for a particular trait. In the present study, for all traits the genotypic coefficient of variation (GCV) was found to be of a lower magnitude than the phenotypic coefficient of variation. This indicates that these traits are influenced by local environmental factors. Heritability has an important place in tree improvement programmes as it provides index of the relative strength of heredity versus environment [34]. Gains from tree improvement programmes depend on the type and extent of genetic variability. The best gains are for the characteristics that are strongly under genetic control and a wide range of variability [20]. In the present study, the heritability estimates were more than 70.00% for most of the characters with highest heritability for the germination (99.50%). In the present study, high magnitude of heritability (> 60.00%) for most of the characters also envisaged that environment has comparatively low influence on these characters. Johnson *et al.* [25] reported that heritability estimates along with expected genetic gain is more useful and realistic than the heritability alone in predicting the resultant effect for best genotypes. High heritability coupled with high genetic advance for germination, root length, fresh and dry weights of root and shoot suggested the presence of an additive gene effect for these characters. Thus, individual plant selection for these characters would be satisfactory. High heritability accompanied by moderate genetic advance for several growth parameters have earlier been reported in *Pongamia pinnata*[35].

Divergence studies
Six clusters were obtained on the basis of non- hierarchical analysis [Table-5]. Cluster III comprises of maximum numbers of progenies (10) followed of cluster II and V (6). Minimum progenies (2) were recorded in cluster I and VI. The clustering showed that progenies collected from different geographical regions were grouped in one cluster as evident from cluster III. Therefore, the pattern of divergence was not dependent upon geographical locations. The intra cluster distances [Table-6] varied from 2.78 (cluster VI) to 4.63 (cluster IV).

Table-5 *Clustering for genetic divergence of germination and seedling traits in A. excelsa*

Cluster	Number of progenies	Progenies
I	2	1, 5
II	6	2,7, 14, 21, 20,22
III	10	3, 28, 9,17, 4, 26, 10, 6, 11, 8
IV	4	12, 29, 23,30
V	6	13,16,15, 25,18, 27
VI	2	19, 24

Table-6 *Intra and inter cluster distances for germination and seedling traits in A. excelsa*

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	3.77	5.1	5.1	7.44	5.6	6.68
Cluster II		2.99	4.2	4.95	4.95	6.52
Cluster III			3.46	4.19	4.69	6.14
Cluster IV				4.63	6.1	6.87
Cluster V					3.79	4.87
Cluster VI						2.78

Table-7 *Cluster mean values for germination and seedling traits in A. excelsa*

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Plant Height (cm)	39.49	43.09	39.28	39.94	38.56	37.39
Diameter (mm)	5.3	5	4.93	5.07	4.4	4.49
Number of leaves	22.35	29.6	28.33	33.16	29.7	31.55
Height of first leaf (cm)	32.81	34.1	30.2	28.18	29.34	29.49
Number of branches	3.96	5.01	5.05	5.68	5.35	5.83
Germination (%)	53.13	72.93	47.23	62.74	78.4	75.77
Fresh shoot weight (g)	12.88	12.02	10.46	12.24	12.64	9.81
Dry shoot weight (g)	2.73	2.4	2.19	2.53	2.66	3.26
Root length (cm)	20.83	22.05	16.8	19.04	20.61	19.5
Number of secondary roots	11.33	11.47	10.76	11.54	12.11	9.83
Fresh root weight (g)	3.64	2.78	2.92	2.59	3.75	3.31
Dry root weight (g)	0.96	0.77	0.79	0.83	1.19	0.98

The Cluster I and IV showed maximum inter cluster distance (7.44) followed by cluster IV and VI (6.87), whereas minimum inter cluster distance was recorded between cluster III and IV (4.19). Maximum intra- cluster distance (4.63) shown by cluster IV indicated wide divergence with in cluster itself might be due to environmental factors and suggested that selection of parents for hybridization within cluster should be based on genetic diversity rather than geographic diversity. Maximum inter-cluster distance between cluster I and IV (7.44) followed by cluster IV and VI (6.87) indicated greater divergence between genotypes belonging to these clusters and an attempt to cross the genotypes/progenies in these clusters should bring out desirable gene combinations. The minimum inter cluster distance recorded between clusters III and IV suggested that seed sources originating from these clusters were not genetically much diverse and thus, selection of parents from these clusters should be avoided. It is therefore desirable for the tree breeder to select those clusters which are having more inter-cluster distance. Thus, it may be suggested that the crosses between clusters I and IV may result sufficient segregation and further progeny selection may help in the improvement of species. Variability was also recorded for cluster means [Table-7]. Maximum cluster mean was recorded in cluster VI for number of branches (5.83), dry shoot weight (3.26) and fresh root weight (3.31).

In this study, 30 progenies have been divided into 6 clusters and revealed that geographical diversity was not necessary to be related to genetic diversity. Such type of clustering for 24 accessions of *P. pinnata* on the basis of non-hierarchical euclidian cluster analysis into 6 clusters has been reported by Divakara and Das [34] (2011). Maximum inter-cluster distance between cluster I and IV (7.44) followed by cluster IV and VI (6.87) indicated greater divergence between genotypes belonging to these clusters and an attempt to cross the genotypes/progenies in these clusters should bring out desirable gene combinations. The minimum inter cluster distance recorded between clusters III and IV suggested that seed sources originating from these clusters were not genetically much diverse and thus, selection of parents from these clusters should be avoided. Similar results have been reported in *P. Pinnata* by [36] and [37].

Conclusion

Wide variability was observed for different characters studied. Higher magnitude of PCV than corresponding GCV indicated the predominance role of environment.

The clustering showed that progenies collected from different geographical regions were grouped in one cluster as evident from cluster III. Therefore, the pattern of divergence was not dependent upon geographical locations. Maximum intra- cluster distance (4.63) shown by cluster IV indicated wide divergence with in cluster itself. Maximum inter-cluster distance between cluster I and IV (7.44) indicated greater divergence between genotypes belonging to these clusters and an attempt to cross the genotypes/progenies in these clusters should bring out desirable gene combinations. The minimum inters cluster distance recorded between clusters III and IV suggested that seed sources originating from these clusters were not genetically much diverse and thus, these clusters should be avoided for selection of parents.

Application of research: Present material can be used for further improvement of *Ailanthus excelsa*, the valuable arid tree species

Research Category: Seed science

**Principal Investigator or Chairperson of research: Kaushik N.
University: CCS Haryana Agricultural University, Hisar, 125004, Haryana, India
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Author Contributions: All authors equally contributed

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