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Genetic divergence study among the progenies of plus trees in *Peltophorum pterocarpum*

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ABSTRACT

In the present study, twenty half-sib progenies of *Peltophorum pterocarpum* were collected from different geographic regions of Bihar and compared for their morphological and biomass traits. The genetic divergence study revealed that twenty PPTs yielded five and seven clusters under greenhouse and open field conditions respectively using non-hierarchical Clusters VI and VII (30.79) in open field conditions and had the greatest inter-cluster distances resulting in a broad spectrum of variability in following generations due to hybridization/crossing. Seedling biomass was the main contribution for genetic divergence under both the environments. Based on the observed diversity, Giriyak and Sathopur in Nalanda district of Bihar were found most suitable for collecting diverse germplasm lines and also for future hybridization programmes.

Keywords: D^2 analysis; *Peltophorum pterocarpum*; cluster analysis; plus tree

INTRODUCTION

Peltophorum pterocarpum, often known as yellow-flamboyant, is a very elegant tree with a spreading crown and is a popular decorative tree that is planted all over the world (Sukumaran et al 2011). It is a fast growing tree with several applications. Because of its dense spreading crown, *P pterocarpum* is a popular shade tree. It has reforestation potential as well as the capacity to fix nitrogen and serves as a source of green manure. Despite the fact that it is not a commercial timber species, the wood is utilized locally for light building, cabinet making and as fuelwood. It is an excellent source of green manure (Singh et al 2016).

The genetic divergence analysis determines the variation pattern in the collection of genotypes, identifies the characters and differentiates the genotypes into different groups that could be used in the crop improvement programmes. Genetic variety is significant because hybrids between lines with different genetic backgrounds tend to have more heterosis than hybrids between closely related parents, which might result in broad-spectrum genetic variety in separate generations. Therefore, breeders always look for genetic divergence among traits to select desirable types. Hence, the present study was planned to estimate the genetic diversity through Mahalanobis D^2 technique (Mahalanobis 1936), among twenty genotypes of *P pterocarpum* in respect of ten characters to identify potential parents for tree improvement programmes.

MATERIAL and METHODS

An intensive survey was made in various regions of Bihar and twenty candidate plus trees (CPTs) were selected and marked based on comparison/check tree selection method using the morphological features viz height, girth, number of branches and incidence of pests and diseases. The geographical locations and salient features of the PPTs are presented in Table 1. The investigations were carried out at the research farm of College of Forestry, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh in greenhouse and open field conditions. Mature pods were collected from different parts of the crown of an individual plus tree selected from twenty different locations. Observations on pod characters and the morphological and biomass data were recorded.

Table 1. Details of plus trees of *Peltophorum pterocarpum* collected from different locations of Bihar

Seed source	Location	Latitude	Longitude	Tree height (m)	Tree girth (m)	Pod length (cm)	Seed length (cm)	100-seed weight (g)
PPT$_{1}$	Akhara Par Talaab, Bihar Sharif	25.59°N	85.51°E	7.62	0.30	5.78	1.0	6
PPT$_{2}$	Praranchak, Nalanda	25.56°N	85.29°E	8.53	0.38	6.69	0.6	6
PPT$_{3}$	Araut, Nalanda	25.02°N	85.45°E	9.14	1.38	6.05	1.0	6
PPT$_{4}$	Muraura, Nalanda	25.27°N	85.91°E	9.82	0.91	6.93	1.0	7
PPT$_{5}$	Kisanbag, Nalanda	25.11°N	85.o4°E	10.66	1.09	6.40	1.0	6
PPT$_{6}$	Nari (Makanpur), Nalanda	25.99°N	85.13°E	8.12	0.45	7.56	0.7	6
PPT$_{7}$	Rajgirkund, Nalanda	25.87°N	85.50°E	15.24	1.82	6.55	0.9	5
PPT$_{8}$	Bakrabihar, Nalanda	25.51°N	85.37°E	13.71	1.21	5.67	0.9	4
PPT$_{9}$	Giriyak, Nalanda	25.44°N	85.97°E	12.12	0.55	5.92	0.9	7
PPT$_{10}$	Kalyanbigah, Nalanda	25.31°N	85.70°E	10.28	1.23	6.85	1.0	7
PPT$_{11}$	Tulsigarh, Nalanda	25.96°N	85.83°E	8.36	0.68	6.73	0.9	6
PPT$_{12}$	Rajgir Park, Nalanda	25.26°N	85.28°E	18.89	1.92	5.87	1.1	7
PPT$_{13}$	Sathopur, Nalanda	25.44°N	85.93°E	17.67	1.37	6.91	1.0	5
PPT$_{14}$	Chandi, Nalanda	25.90°N	85.69°E	12.23	1.82	6.53	0.6	5
PPT$_{15}$	Ramdiha, Nalanda	25.54°N	85.84°E	11.58	1.39	6.82	0.8	3
PPT$_{16}$	Bihar Sharif, Nalanda	25.52°N	85.04°E	12.92	1.56	7.01	0.9	5
PPT$_{17}$	Madhopur, Nalanda	25.09°N	85.38°E	15.57	1.30	6.66	0.8	6
PPT$_{18}$	Budh Vihar, Patna	25.65°N	85.76°E	11.88	1.10	6.50	0.8	6
PPT$_{19}$	Sarmera, Nalanda	25.04°N	85.96°E	14.12	1.13	5.62	0.9	6
PPT$_{20}$	Sharifganj, Katihar	25.18°N	87.60°E	18.28	1.82	6.29	0.8	7

Genetic divergence was calculated by using non-hierarchical euclidean cluster analysis (Beale 1969, Spark 1973) and genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

RESULTS and DISCUSSION

In the present study, a total of ten biometric traits were considered and significant variations were observed among the progenies performance for shoot length, root length, seedling height, collar diameter, shoot fresh weight, shoot dry weight, root fresh weight, root dry weight and seedling biomass which indicated that substantial amount of genetic variability existed among the 20 plus tree progenies. The clustering pattern of 20 plus trees for green house and field atmosphere is given in Table 2. Under greenhouse and field context they were grouped into five and seven clusters, respectively. The variation under greenhouse and field situations for total number of clusters could be attributed mainly to the environmental differences as the range of day and night temperature and humidity are were wide in greenhouse and field conditions.

Plus tree progenies PPT$_{1}$, PPT$_{2}$, PPT$_{3}$, PPT$_{4}$, PPT$_{5}$, PPT$_{6}$, PPT$_{7}$ and PPT$_{8}$ consistently occupied the same cluster in two different environments indicating that they were relatively stable and could be used in hybridization programmes to evolve stable genotypes.

Table 2. Distribution of superior trees in different clusters under open field conditions

Cluster	Number of seed sources		Notation of clusters	
	Open field	Greenhouse	Open field	Greenhouse
I	10	7	1, 2, 3, 4, 5, 6, 7, 8, 14, 17	1, 2, 3, 4, 5, 12, 18
II	2	2	10, 16	16, 17
III	2	2	18, 20	14,15
IV	2	8	15, 19	6, 7, 8, 9, 10, 11, 13, 19
V	2	1	11, 12	20
VI	1	-	9	-
VII	1	-	13	-

The present results are supported by the findings of Bhat and Ahmad (2012) in *Grewia optiva* and Gupta et al (2020) in *Acacia nilotica.*

On the basis of morphological and biomass traits, inter-cluster distance was found highest between clusters VI and V (7.43) in greenhouse condition (Table 3). Under field condition, maximum inter-cluster distance was found between clusters VI and VII (30.79). Maximum intra-cluster distance was found in clusters IV (4.43) and V (6.20) under greenhouse and open field conditions respectively showing genetic closeness. Genotypes having maximum inter-cluster distances may perhaps result in wide spectrum of variability in the subsequent generations by hybridization/crossing.

Among the different clusters, the clusters VII showed high mean performance for most of the characters in open field conditions (Table 4). Hence, the trees belonging to these clusters were divergent as well as had higher means most of important seedling attributes which were economically valuable. The preset results are supported by the findings of Yadav et al (2011) in *Madhuca longifolia*.

CONCLUSION

The present study revealed that grouping of twenty PPTs in different clusters had no relationship between genetic divergence and geographical distribution. The selection of genotypes from the cluster VI (PPT_9) and VII (PPT_{13}) in open field condition

Table 3. Inter- and intra-cluster distance of superior tree progenies of *Peltophorum pterocarpum* under open field and greenhouse conditions

Cluster	Condition	I	II	III	IV	V	VI	VII
I	Open field	5.84	5.25	5.51	5.28	5.98	19.16	22.01
	Greenhouse	3.28	2.51	3.04	4.12	6.58	-	-
II	Open field		1.93	2.87	3.86	6.21	19.03	24.83
	Greenhouse		1.72	2.27	3.40	6.26	-	-
III	Open field			2.51	3.93	5.45	20.56	24.52
	Greenhouse			1.79	3.66	7.42	-	-
IV	Open field				4.37	5.65	19.50	23.39
	Greenhouse				4.43	7.43	-	-
V	Open field					6.20	20.81	21.32
	Greenhouse					0.00	-	-
VI	Open field						0.00	30.79
VII	Greenhouse							0.00

Table 4. Mean cluster for various traits in different clusters for superior tree progenies of *Peltophorum pterocarpum* under open field and greenhouse conditions

Trait/cluster	Condition	Shoot length	Root length	Collar diameter	Seedling height	Shoot fresh weight
I	Open field	17.86	20.31	2.07	38.44	2.56
	Greenhouse	48.93	31.54	2.61	81.03	16.69
II	Open field	13.62	18.28	1.58	32.92	1.10
	Greenhouse	53.95	31.07	3.00	85.03	21.93
III	Open field	13.37	19.50	1.73	32.35	1.07
	Greenhouse	66.48	34.85	3.27	101.23	28.00
IV	Open field	5.18	7.05	0.82	12.23	0.67
	Greenhouse	65.43	35.65	3.60	98.82	42.95
V	Open field	18.05	24.95	2.35	45.47	3.08
	Greenhouse	16.00	8.93	0.97	24.90	1.77
VI	Open field	0.60	0.87	0.10	1.50	0.07
	Greenhouse	-	-	-	-	-
VII	Open field	46.63	37.47	5.30	82.93	12.40
	Greenhouse	-	-	-	-	-

Table 4. Contd…..

Trait/cluster	Condition	Root fresh weight	Shoot dry weight	Root dry weight	Shoot-root ratio	Seedling biomass
I	Open field	0.73	1.47	0.49	3.05	1.96
	Greenhouse	3.19	9.07	1.64	5.40	10.60
II	Open field	0.45	0.57	0.28	2.20	0.87
	Greenhouse	4.33	12.27	2.20	5.47	14.48
III	Open field	0.45	0.75	0.23	2.93	0.95
	Greenhouse	3.85	14.25	2.03	6.63	16.30
IV	Open field	0.27	1.18	0.30	4.45	1.50
	Greenhouse	8.33	25.94	4.63	5.58	30.61
V	Open field	0.80	1.60	0.45	3.45	2.00
	Greenhouse	1.70	0.93	0.93	0.70	1.77
VI	Open field	0.07	0.00	1.91	0.00	2.01
	Greenhouse	-	-	-	-	-
VII	Open field	3.60	7.23	1.90	3.93	9.10
	Greenhouse	-	-	-	-	-

exhibited maximum inter-cluster distance (30.79) and could be utilized as potential parents and crossing between these genotypes resulting in high heterotic expression for yield and its components. Plus tree progenies PPT$_1$, PPT$_2$, PPT$_3$, PPT$_4$, PPT$_5$, PPT$_6$, PPT$_7$ and PPT$_8$ consistently occupied the same cluster in two different environments indicating that they were relatively stable and could be used in hybridization programmes to evolve stable genotypes. The selection of genotypes from these clusters may perhaps result in wide spectrum of variability in the subsequent generations by hybridization/crossing in tree improvement programmes.

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