

## Genetic divergence for seed and seedling characteristics in *Grewia optiva* Drummond in Himachal Pradesh, India

Sheeraz Saleem Bhat\*, H. P. Sankhyan and N. B. Singh

Department of Tree Improvement and Genetic Resources, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan 173 230

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*Grewia optiva* Drummond is the best quality fodder provider in the subtropical Western Himalayas from Jammu and Kashmir to Nepal up to an elevation of 2,000 m above mean sea level. It grows on types of soil. The species possesses wide variability for different traits of concern, thus inviting the breeders for selection and hybridization to achieve more economic gains. Divergence studies enable the breeder to select the most diverse parents for inter-mating and thus, help the breeder in gainful hybridization [1]. Many other workers have also studied divergence pattern in trees for different traits of concern [2-4].

A Seedling Seed Orchard of *Grewia optiva* Drummond collected was established at the Nauni Campus of Dr. Y.S. Parmar University of Horticulture and Forestry during July 2000 from various districts of Himachal Pradesh (Table 1). It had three replications at a spacing of 2m x 2m in three blocks. Evaluation of genetic divergence among the different open pollinated families of this orchard for various seed and seedling parameters was carried out in 2008-09. The experiment was carried out in RBD to investigate clustering pattern among these thirty five families in order to undertake intensive breeding work for the production of heterotic hybrids.

Data was subjected for analysis of variance. Genetic divergence was estimated by Mahalanobis  $D^2$  statistics [5] and the families were grouped on the basis of minimum generalized distances using Tocher's method as described by [6].

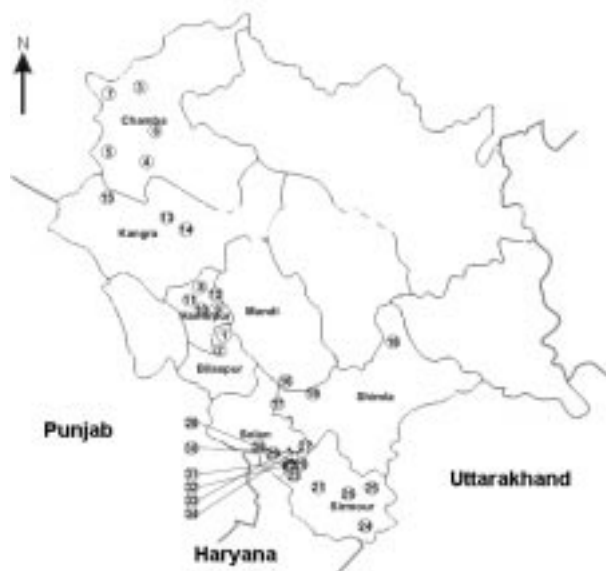
Upon analyzing the genetic divergence, the families were clustered into four clusters: Cluster I-(CH-2, HA-4, SH-5, SI-13, SI-15, SO-9, SO-10, SO-12), Cluster II-(CH-5, CH-6, HA-5, SH-1, SH-3, SO-2, SO-5, SO-11), Cluster III-(BI-4, BI-5, CH-1, HA-1, HA-3, KA-2, MA-2, SI-6, SO-1, SI-10) and Cluster IV-(CH-3, HA-2, KA-1, KA-3, SI-3, SI-5, SI-7, SO-6, SO-8). Cluster means are given in Table 2. The average intra and inter cluster D values are presented in Table 3. The generalized inter cluster distances were 5.665 (between I and IV), 4.486 (between I and II), 3.276 (between III and IV), 3.103 (between I and III), 2.941 (between II and III) and 2.217 (between II and IV). The relative divergence of each cluster from other clusters (inter cluster distance) indicated high order of divergence between I and IV, followed by I and II, III and IV, I and III, II and III and II and IV.

Since the trees were selected from the different eco-geographical regions of the state (Fig. 1), they showed varied differences among each other. Besides, the genetic constitution of the species must be the cause of huge variation in these traits. Therefore, the variation observed may be due to the different genetic architecture as a result of breeding system, level of heterogeneity and adaptation to diverse environmental conditions. This was in line with the results obtained earlier [2, 7]. The clustering of families from same eco-geographical location into different clusters indicates the genetic similarity among the germplasm coming from

\*Corresponding author's e-mail: shrzhat@gmail.com

**Table 1.** Description of different families of *Grewia optiva*, undertaken for divergence studies from Himachal Pradesh

District	Family	Code	
Bilaspur	Kuthira	BI-4	
	Talvano	BI-5	
Chamba	Chanad	CH-1	
	Shahu	CH-2	
	Balu	CH-3	
	Rajpura	CH-5	
	Saru	CH-6	
Hamirpur	Bharari	HA-1	
	Patta Balakhar	HA-2	
	Bassi	HA-3	
	Hamirpur Kanal	HA-4	
	Ghahar	HA-5	
Kangra	Dharamshala	KA-1	
	Bhalun	KA-2	
	Varal	KA-3	
Mandi	Bachhwan	MA-2	
Shimla	Daugi	SH-1	
	Jeury	SH-3	
Shimla	Sunni	SH-5	
Sirmour	Deothal	SI-3	
	Deyoltikkeri	SI-5	
	Kalaghat	SI-6	
	Nandel	SI-7	
	Seenaghat	SI-10	
	Sarpadol	SI-13	
	Madhobag	SI-15	
	Solan	Gaura	SO-1
		Nauni	SO-2
		Badhlech	SO-5
Amberkothi		SO-6	
Kailar		SO-8	
Deothi		SO-9	
Jaunaji		SO-10	
Mishuar		SO-11	
Kasholi		SO-12	

**Fig. 1.** Map showing the source of different families undertaken for divergence studies for seed and seedling parameters of *Grewia optiva* Drummond in Himachal Pradesh, India (Map not in scale)**Table 2.** Means of seed and seedling parameters of different families of *Grewia optiva* included in clusters

Parameter	Mean values			
	Cluster I	Cluster II	Cluster III	Cluster IV
Germination capacity (%)	43.00	59.83	52.13	59.70
Germination energy (%)	26.67	38.83	35.47	38.52
100-seeds weight (g)	8.73	11.60	10.18	11.30
Seed length (mm)	5.81	6.21	6.06	6.47
Seed width (mm)	4.65	5.00	5.32	5.28
Seedling height (cm)	44.90	64.32	53.71	68.17
Root shoot ratio	0.47	0.44	0.50	0.47
No. of leaves	45.54	65.12	56.03	69.78
Basal diameter (mm)	3.97	5.96	4.62	6.26
Leaf area (cm <sup>2</sup> )	35.01	33.24	37.02	44.40

different geographic regions. It may be suggested that though geographic diversity may not necessarily be an index of genetic diversity, due attention should be paid to geographic diversity if sufficient genetic diversity has to be accumulated in the germplasm [2, 3, 8, 9].

**Table 3.** Average intra and inter cluster distances (D-value) for seed and seedling parameters among thirty five different families of *Grewia optiva*

Cluster	I	II	III	IV
I	<b>2.293</b>			
II	4.486	<b>1.728</b>		
III	3.103	2.941	<b>1.776</b>	
IV	5.665	2.217	3.276	<b>2.032</b>

Figures in bold face indicates intra cluster distances

Hybridization between genetically distant families can generate promising breeding material [4, 10, 11]. Controlled breeding among the families of clusters having the maximum mean values regarding the desired characters can be of immense use to attain better planting stock through selection and breeding and to obtain heterotic vigour through hybridization of the most divergent families in *Grewia optiva*.

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