GENETIC DIVERGENCE STUDIES FOR FODDER QUALITY ATTRIBUTES IN OPEN POLLINATED FAMILIES OF *BAUHINIA VARIEGATA* LINN.

R. K. Anand[1] & Santosh Kumar A. Huse[2]

[1]Krishi Vigyan Kendra, Sonbhadra, At: CRS, Tissuhi, Marihan, Mirzapur 231310 U.P.
(N.D.University of Agriculture & Technology, Faizabad)
[2]ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujrat
Corresponding author Email: ratananand@rediffmail.com

ABSTRACT
Bauhinia variegata (Kachnar) is an important medium size fodder tree species of hilly region on which farmers depends during the lean period when grasses are dry, less digestible and unpalatable. Its leaves are highly nutritious and palatable. But farmers are lacking with genotypically superior genotypes which can produce nutritious fodder. Therefore, selection and breeding of the species is essential to produce better offspring which can augment the farmers demand. Present study was conducted to assess the magnitude of genetic divergence in *Bauhinia variegata.* Seed was collected from 48 open pollinated (plus trees) families and sown in nursery under randomized complete block design. After 16 month growth, leaves sample were collected and analyzed for proximate composition. On the basis of this data genetic divergence was studied with the help of non hierarchical Euclidean cluster analysis. All the families were grouped in to the eight clusters with the highest number of families falling under cluster II. Maximum and minimum intra cluster distance was observed for cluster IV(1.993) and II (1.474), respectively. Whereas, maximum inter cluster distance was observed between cluster VI and III (5.528). Leaf fresh weight (34.20%) and leaf dry weight (25.69 %) contributed the highest towards total divergence. Among the eight clusters formed, cluster VI and VIII showed maximum cluster mean values for most of proximate principles. Therefore, on the basis of present findings it is suggested that the crossing between families of cluster VI and III will results in wide range of variation in subsequent generation.

KEY WORDS: *Bauhinia variegata*, genetic divergence, plus tree, proximate composition,

INTRODUCTION
The main source of fodder for livestock in India are the residues of agricultural crop, cultivated fodder, weeds, grasses, leaf fodder from trees and shrubs. Leaf fodder available from trees and shrubs roughly constitutes 10 per cent of the total green fodder available in the country (Dwivedi, 1999). The total fodder yield from trees, shrubs, herbs and climbers from forests is of great significance particularly during scarcity and famine period. Tree which can be grown either in combination with agricultural crops or on marginal, waste land offer opportunity of producing green nutritious fodder for the livestock. Fodder tree is a convention in hilly region as there is a limited scope of production of green fodder in the hills due to rainfed conditions *vis-a-vis* small holding which necessitates the farmers to utilize the land for crop production. Therefore, tree fodder production in the hills is not only important for the rural economy but also exceptionally vital for the ecological insurance. In order to meet the exigency of leaf fodders it is imperative to plant multipurpose trees with high nutritive value on the wasteland and fallow land or to integrate with agricultural and fruit crops under agro-forestry systems.

One of the important fodder species on which farmers bank up during the winter lean period when the grasses are dry, less digestible and unpalatable is *Bauhinia variegata* Linn, which is commonly known as Kachnar belongs to family Leguminaceae and sub family Caesalpenaceae. It is a small or medium sized deciduous tree with elongated spreading crown and green foliage. It commonly grows in the sub-Himalayan tract and outer Himalaya from the Indus River eastwards ascending to 1830 m height across Assam and also in dry forests of east central and south India (Anonymous, 1983 and Thakur, 2010). Its leaves are rich in mineral and proximate composition which makes it highly nutritious and palatable. Therefore, selection and breeding of the species is essential to produce better offspring in respect of leaf fodder value. For a successful tree breeding programme, nature and amount of genetic variability and diversity available in the germplasm is the basic requirement. Genetically diverse individuals are likely to produce more heterotic effects during the crossing programme and produce desirable segregants (Ahmed *et al.*, 2011). The nature and degree of divergence in plus tree families/gemrplasm is use full for classifying them into groups on the basis of their diversity, it helps in choosing parents for specific breeding objectives to get desirable transgressive segregates. Therefore, present study was carried out to know the nature and degree of genetic divergence on the basis of proximate composition of leaves among the plus tree families selected form different parts of Himachal Pradesh.

MATERIALS AND METHODS

Present study was conducted to find out the magnitude of genetic divergence for fodder quality attributes in 48 plus tree (open pollinated -half sib) families of *Bauhinia variegata* Linn. The seeds of 48 plus trees of *Bauhinia variegata* were collected from different parts of Himachal Pradesh and sown in nursery of Dr. Y.S. Parmar University of Horticulture and Forestry , Solan (H.P.) under Randomized Complete Block Design in three replications. After the 16 months growth five plants per replication were randomly selected and a composite sample of leaves was drawn from these selected plats during November and weighed immediately. All the samples were properly labeled in paper bags and transported to laboratory to estimate proximate composition. Leaf samples were thoroughly washed in tap water, and then with 0.1 N HCl followed by distilled water. The washed samples were air dried for some time and subsequently in an oven at $60^{o}C$ till the sample attained a constant weight. The dried samples were ground thoroughly and stored in butter paper bags treatment and replication wise and used for analysis of proximate principles. The proximate principles viz. crude protein, crude fibre, ether extract, total ash and nitrogen free extract were estimated as per the method given by AOAC (1995) and Sankaram (1966). Data obtained from proximate composition analysis were statistically analyzed to find out the genetic divergence by using non-hierarchical Euclidian cluster analysis (Beale, 1969 and Spark, 1973). Under this analysis, all the families were grouped in to eight clusters and inter and intra cluster distances were obtained to know the level of genetic divergence among the families.

RESULTS

To identify the diverse genotypes, genetic divergence analysis was carried out by using non hierarchical Euclidean cluster analysis. On the basis of proximate composition data, forty eight plus tree families were grouped into eight clusters (Table 1). Cluster II included the highest 11 number of families followed by cluster IV which contained 8 clusters whereas, Cluster VIII comprised of only two families.

TABLE 1. Composition of Euclidean clusters for proximate compositions among *Bauhinia variegata* Linn. open pollinated families

Cluster	Number of families	Families
I	6	4, 7, 9, 19, 28, 40
II	11	10, 11, 21, 22, 23, 29, 35, 36, 41, 42, 43
III	4	25, 26, 31, 38
IV	8	1, 5, 6, 8, 15, 16, 18, 34
V	6	30, 32, 37, 39, 44, 46
VI	7	2, 3, 12, 13, 14, 20, 33
VII	4	17, 27, 45, 48
VIII	2	24, 47

TABLE 2. Estimates of inter and intra cluster distances for proximate compositions in *Bauhinia variegata* Linn. open pollinated families

Cluster	I	II	III	IV	V	VI	VII	VIII
I	1.689							
II	2.050	1.474						
III	4.588	4.680	1.930					
IV	4.198	2.781	5.036	1.993				
V	2.875	3.027	3.052	4.357	1.717			
VI	2.497	2.322	5.528	3.173	3.402	1.605		
VII	3.011	2.531	3.768	2.818	2.403	2.859	1.535	
VIII	4.759	3.414	5.031	2.510	3.953	3.735	3.643	1.502

Underlined figures are intra cluster distances

TABLE 3. Contribution of different proximate compositions to total divergence among *Bauhinia variegata* Linn. open pollinated families

Traits	Per cent contribution
Leaf fresh weight	34.20
Leaf dry weight	25.69
Dry matter content	14.31
Crude protein	10.10
Crude fibre	8.07
Ether extract	7.16
Total ash	0.26
Nitrogen free extract	0.20

TABLE 4. Cluster mean value for proximate compositions among *Bauhinia variegata* Linn. open pollinated   families

Trials	I	II	III	IV	V	VI	VII	VIII
Leaf fresh weight	1.52	1.61	0.73	1.62	1.02	1.75	1.27	1.29
Leaf dry weight	0.74	0.76	0.46	0.80	0.56	0.87	0.65	0.66
Dry matter content	49.08	47.35	62.17	48.95	56.47	50.85	50.56	51.12
Crude protein	9.61	9.68	12.06	12.08	9.40	9.59	12.06	9.42
Crude fibre	21.63	24.04	23.89	24.95	22.59	21.88	22.58	25.89
Ether extract	3.53	3.38	2.96	5.12	3.42	5.14	3.58	6.42
Total ash	5.25	5.79	5.08	6.08	6.28	6.36	6.54	6.42
Nitrogen free extract	59.98	56.98	56.31	51.60	58.20	56.84	55.73	51.86

Tables 2 show the intra and inter cluster distance for proximate composition of leaf fodder. The intra cluster distance rages from 1.474 to 1.993 and inter cluster distance ranges from 2.05 to 5.528. Maximum intra cluster distance was obtained for cluster IV and minimum for cluster II. Inter cluster distance was found maximum between cluster VI and III whereas, it was recorded minimum between cluster II and I followed by VI and II. Contribution of different characters to total divergence as depicted in Table 3 revealed that leaf fresh weight and leaf dry weight contributed the highest followed by dry matter content and crude protein. It reflects that leaf fresh weight and dry weight was major contributor to total genetic diversity. Minimum contribution was observed for nitrogen free extract and total ash content which shows less genetic divergence. It is evident from the table 4 that cluster mean values reflect lesser variation among the cluster. Maximum variation was observed for Leaf fresh and dry weight. Leaf fresh and dry weight was recorded maximum in Cluster VI, crude fibre, ether extract and total ash content was found maximum in cluster VIII and crude protein was highest in cluster IV.

DISCUSSION
The distribution of families in different clusters indicates that, even though the genotypes were selected from different ecogeographic areas, the genetic make-up along with breeding system, heterogeneity, genetic drift, natural and unidirectional selection pressure must be the cause of genetic diversity among different families, besides geographic variation to some extent. The cluster pattern proved that geographical diversity need not necessarily be related to genetic diversity (Anand, *et al.* 2005). The clustering of genotypes from different eco-geographical locations into one cluster indicates the similarity among the germplasm coming from different geographical regions. This was observed by Sehgal *et al.* (2003) in *Grewia optiva* and Srimathi and Dorairaj (1994) in Napier grass. On the other hand, many genotypes originating from one region were found scattered over different clusters. Such genetic diversity among the genotypes of common geographical origin as described by Murthy and Arunanchalam (1966) and Manga and Sen (2000) could be due to factors like heterogeneity, genetic architecture of the population, past history of selection, developmental traits and degree of general combining ability. The grouping of genotypes/accessions in more number of clusters indicates the presence of genetic diversity and can

Anand, R.K., Chauhan, K.C. and Huse, S. A. (2005) Genetic divergence studies in plus tree families of *Bauhinia variegata* Linn. for its growth and biomass traits.

therefore be used to maximize the expression of heterosis among the studied genotypes. Occurrence of high intra cluster distance indicated the high chance of getting good segregates by crossing the genotypes of same cluster. The crossing between families of two different clusters having high inter cluster distance may give maximum hybrid vigour along with desirable segregates for quality leaf fodder. Similar results were also reported by Chauhan *et al.* (1997) and*,* Anand *et al.* (2005) in *Bauhinia variegata* for morphological traits. The least inter cluster distance between two clusters indicated narrow genetic diversity and closer relationship for many traits of the families in these clusters Ahmed *et al.*(2011). By obtaining high inter cluster distance for biochemical attributes, Tessema *et al.* (2011) reported that magnitude of heterosis largely depends upon the degree of genetic diversity among the parental lines. This agrees with Reddy (1988) who found that hybrid between genotypes with maximum genetic divergence generally displays a greater recombination and segregation than those between closely related strains. The attributes with minimum contribution reveled lack of parallelism between genetic divergence and eco geographical distribution of different families (Sehgal *et al.* 2003). The breeding for the characters which has more contribution to total genetic divergence may give better result.

The progeny produced by crossing between clusters with proportionally higher mean values may give better performance. Thus it may be suggested that crosses between families with higher mean values may result in substantial transgressive segregates and further selection under these clusters may be given preference for the overall fodder quality improvement of the species. Present study supports the findings of Arunprasad *et al.* (2003) in *Tectona grandis*

CONCLUSION
On the basis of present findings it can be concluded that the crossing between families of cluster VI and III may give maximum hybrid vigour along with desirable segregates for quality leaf fodder. Selection and breeding of families grouped into same cluster must be avoided to get better performance and adoptability.

REFERENCES
A.O.A.C. (1995) Official methods of analysis of AOAC international. Vol. 1, 26th edn. Washington   D. C. : Association of Official Analytical Chemists. pp. 4.1-4.20.

In: Multipurpose trees in the Tropics: Management & improvement Strategies. Tewari, V.P and Srivastava, R.L. (eds). AFRI, Jodhpur. Pp.744-748.

Anonymous (1983) Troup's the silviculture of Indian Trees. Vol. IV, Delhi: controller of Publication. pp. 184-187.

Ahmed, S., Roy, A. K. and Majumdar, A.B. (2011) Genetic diversity and variability analysis in oat (Avena sativaL.). *Range Management and Agroforestry*. 32(2): 96-99.

Arunprasad, K.C.A., Surendran, C., Partibhan, K.T. and Saudagar, R.J. (2003) Genetic divergence studies in Teak (*Tectona grandis*). *Indian Journal of Forestry*. 26(4): 438-441.

Beale, E.M.L. (1969) Euclidean cluster analysis contributed paper to the 37th session of the International Statistical Institute.

Chauhan, K.C., Srivastava, A. and Thakur, R.C. (1997) Analysis of genetic divergence in seed stands of *Bauhinia variegata* Linn. *Indian. J. of Plant Genetic Resources*. 10(1): 115-121.

Dwivedi, A.P. (1999) Forests: non wood resources. Deharadun: International Book Distributors. pp. 86-87.

Manga, V.K. and Sen, David N. (2000) Genetic diversity among different genotypes of *Prosopis cineraria* Druce. *Indian Jouranl of Forestry*. 33(3):291-295.

Murthy, B. R. and Arunanchalam, V. (1966) The nature of divergence in relation to breeding system in some crop plants. *Indian Journal of Genetics*. 26: 188-198.

Reddy, P.S. (1988) Genetics, breeding and varieties. *In:* Groundnut. Reddy, P.S., (ed.). ICAR, New Delhi. Pp. 200-317.

Sankaram, A. (1966) A laboratory mannual for agricultural chemistry. Asia Pub. House, Madras. pp. 252-263.

Sehgal, R.N., Rathore, A. and Chauhan, S.K. (2003) Divergence studies in selected genotypes of *Grewia optiva. Indian Journal of Agroforestry*. 5(1&2): 99-102.

Spark, D.N. (1973) Euclidean cluster analysis Algorithm. As 58 *Appl. Stats*. 22: 126-130.

Srimati, P. and Dorairaj, M.S. (1994) D^2 analysis for fodder yield in Napier grass (*Pennisetum perpurreum*). *Indian Journal of Genetics*. 54: 225-228.

Tessema, A., Alamerew, S., Kufa,T. and Garedew, W. (2011) Genetic diversity analysis for quality attributes of some promising *Coffea Arabica* germplasm collection in southwestern Ethiopia. *Journal of Biological Science.*11 (3): 236-244.

Thakur, I. K. (2010) Seed source evaluation for growth and nutrient parameters of *Buhinia variegata* Linn. *Indian Journal of Agroforestry*. 12(2): 96-101.