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Study on Heritability and Genetic Gain in Plus Tree Families of *Bauhinia variegata* L. in Western Himalayas

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Abstract

Thirty two different seed sources of *Bauhinia variegata* L. from Himachal Pradesh, Uttanchal, Haryana and Jammu & Kashmir were studied for morphological and biomass traits of one year old seedling on the mid hills of Himalayas (at an altitude of 1,350 m). The study showed that the phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the morphological and biomass traits which revealed that the traits are sensitive to environmental fluctuations. The plus tree variance for replication \times family (σ^2_{RF}) was highest for shoot fresh weight whereas; variance for family (σ^2_F), phenotypic variance among plus tree families (σ^2_P), phenotypic variance among individuals (σ^2_p), additive genetic variance (σ^2_A) were highest for leaf area. However, the heritability on plus tree family basis (h^2_F), within family basis (h^2_w) and individual plant basis (h^2_I) were highest for shoot dry weight. For all the traits, family heritability (h^2_F) was found higher than the individual tree heritability (h^2_I) and within plus tree family heritability (h^2_w). The genetic gain of family selection (GF), total genetic gain (GT) and ratio of genetic gain of family selection and within family selection (GF/GW) were observed maximum for leaf area and seedling height. Therefore, the selection for leaf area and seedling height can give better results than the shoot dry weight for the improvement of these traits through simple selection.

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Introduction

Bauhinia, a genus of 300 species of trees, shrubs and woody climbers, is distributed through out the tropical region. Nearly 30 species occur in India. *Bauhinia variegata* Linn. belongs to family Leguminosae and sub family Caesalpiniodae. It is generally prevalent in sub-Himalaya and outer Himalaya from the Indus river east wards, ascending to an altitude of 1,830 m, Assam, Burma and other parts of the Indian Peninsula (Troup, 1921). It constitutes the forest types viz., moist Shiwalik sal forest, moist peninsular high level sal forest, west Gangetic moist deciduous forest in association with *Shorea robusta*; *Terminalia alata*; *Syzygium cumini*; *Emblca officinalis*; *Albezia procera*; *Adina cordifolia*. It is also found in dry Shiwalik sal forest, dry peninsular sal forest, northern dry mixed deciduous forest in association with *Anogeissus latifolia*; *Shorea robusta*; *Pinus roxburghii*; *Acacia* species; *Boswellia serrata* etc (Champion and Seth, 1968). The species commands a good reputation for coppicing and wide adaptability; resistance to strong winds, frost and drought; and high aesthetic value for its ornamental flowers. It can feasibly planted for afforestation and wasteland development programme (Anonymous, 1983). It is a medium sized

deciduous tree having elongated spreading crown with bluish green foliage, found chiefly on dry rocky soils. Under optimum conditions, it attains a height up to 15 m and girth up to 1.5 m (Troup, 1921).

The wood of the tree is greyish brown, hard and moderately heavy, used for agricultural implements and fuel. Bark is an astringent, tonic to the liver and anti-inflammatory, used for treating skin diseases and ulcer. It is also used to remove intestinal worms and to prevent the decomposition of tumours (Chopra and Nayar, 1956). Dried buds are used as remedy for piles and dysentery. Flowers are used for curing diseases of bile, cough, eye, stytic haematuria and menorrhagia (Kirtikar and Basu, 1933). Flower buds are also consumed in the form of pickles and vegetables. Trees are lopped for cattle's fodder during the winter lean period (Negi et. al., 1979).

Fodder resources in the country are of paramount importance especially during the lean period when green fodder is not available. For meeting this demand, selection of superior and nutritious palatable fodder tree species and their cultivation on common waste and fallow lands integrating with agricultural and fruit crops under agroforestry and other forestry related programmes can be adopted. One of the fodder species for this purpose is *Bauhinia variegata* Linn.

In any tree breeding programme, there are series of activities for genetic improvement. One of the most important activities is choosing individual, which will serve as a parent for next generation. This process is known as selection and it is based upon observed differences or variation among individuals of a population. Three main advantages selection in tree breeding are: selection could increase overall selection intensity or reduce field-testing size; it could shorten generation interval; and genetic information from early testing could be used to enhance selection efficiency at mature age (Wu, 1999). The effectiveness of tree improvement programmes depends upon the nature and magnitude of existing genetic variability and also on the degree of transmission of traits, because genetic variation is the fundamental requirement for maintenance long term forest ecosystem (Zobel and Talbert, 1984). According to Bagchi (1995) the rate of tree improvement can be increased or decreased by influencing the selection differential or increased heritability by reducing the phenotypic variance in relation to the genetic variation. Since, the amount and pattern of genetic variation determine the ability of forest tree species to adapt environmental conditions; the variation for a trait is as important as heritability in determining the gain achieved through selection. A wide range of variability, present in a species, always provides a better chance of selecting desirable type (Allard, 196; Dhillon et. al., 1995). Hence, to make an improvement in any species, the breeder is constantly engaged in an effective choice of desirable parents of high genetic variability. Genetically, diversified parents are likely to produce high heterotic effect and desirable segregants.

Dorman (1976) reported that heritability estimation has an important place in tree breeding, as it provides an index of relative strength of inheritance versus environment. It is useful for ranking traits according to their importance in cross breeding programmes. Gain from tree breeding programme depends on the type and extent of genetic control and variability. The best gains are achieved for characters that are strongly under genetic control and have a wide range of variability (Zobel, 1971).

Variation refers to the observed differences in an individual for a particular trait. These differences may mainly be due to genetic effect and partly owing to environmental trappings. The combined reflection of both is the phenotypic effect. The observed value of a trait, measured on an individual is the phenotypic value of that individual. The relative magnitude of these components determines the genetic properties of any particular species (Jain, 1982). Therefore, the effective tree improvement programme depends upon the nature and magnitude of existing genetic variability and degree of transmission of the traits.

MATERIAL AND METHODS

The present study was carried out in the department of Tree Improvement and Genetic Resources, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni-Solan, Himachal Pradesh, India. The area is situated at 30°50'30" to 30°52'0"N latitude and 77°8'30"E longitude in the mid hills of outer Himalayas with an altitude varying from 950 to 1,350 m. The climate is sub-temperate characterized by mild summers with maximum temperature of 34°C (May to June) and minimum temperature of 0°C (January and February). The rainfall is well spread during June to August (Monsoon period). For the present study, selection of superior trees was made from naturally distributed zones of Western Himalayas viz., Himachal Pradesh, Haryana, Uttaranchal, Jammu and Kashmir, on the basis of different morphological and biomass characters. Five phenotypically superior trees of same size and free from any disease and pest were selected and observations were made. Out of these, the best one was considered as plus tree. Uniform, healthy seeds from well mature pods of plus trees from 32 representing stands (family) were collected to constitute the seed lot for each family during April to May (Fig. I). The details of the plus tree are given in Table 1. For experimental purpose, the seeds were sown in a randomized block design replicating thrice in the second week of

June in polybags of size 10 × 25 cm filled with a mixture of soil, sand and Farm Yard Manure (1:1:1) at a depth of 0.5 cm. The observations were made for 1 year (12 m) old seedlings for different morphological and biomass traits viz., seedling height, seedling diameter, inter-nodal length, number of leaves, leaf area, shoot fresh weight, root fresh weight, shoot dry weight, root dry weight, shoot/root ratio and seedling biomass.

Various components derived from the analysis of variance were used to estimate heritability (narrow sense) as described by Zobel and Talbert (1984).

Variance component

The phenotypic variance among plus tree families, phenotypic variance among individuals and additive genetic variance were determined using formulae,

$$\sigma^2_P = \sigma^2_F + \sigma^2_{RF}/T + \sigma^2_W/RT \dots \dots \dots (1)$$

$$\sigma^2_p = \sigma^2_W + \sigma^2_{RF} + \sigma^2_F \dots \dots \dots (2)$$

$$\sigma^2_A = 4\sigma^2_F \dots \dots \dots (3)$$

where,

σ^2_{RF} is Variance for replications × family

σ^2_F is Variance for plus tree families

σ^2_W is Variance with in plot (error)

σ^2_P is Phenotypic variance among plus tree families

σ^2_p is Phenotypic variance among individuals

σ^2_A is Additive genetic variance

T is Number of seed sources/Plus trees (32)

R is Number of Replication (3)

Heritability (narrow sense)

$$h^2_F = \sigma^2_F / (\sigma^2_W/TR + \sigma^2_{RF}/T + \sigma^2_F) \dots \dots \dots (4)$$

$$h^2_W = 3\sigma^2_F / \sigma^2_W \dots \dots \dots (5)$$

$$h^2_I = 4\sigma^2_F / (\sigma^2_W + \sigma^2_{RF} + \sigma^2_F) \dots \dots \dots (6)$$

Where,

h^2_F is Heritability on a plus tree family basis

h^2_W is Heritability with in family basis

h^2_I is Heritability on an individual plant basis

Genetic gain

$$\text{Genetic gain of family selection } (G_F) = 4 i_F h^2_F \sigma^2_F \dots \dots \dots (7)$$

Where,

$i_F = 0.19$ (Zobel and Talbert 1984, 90 per cent selection intensity)

$$\text{Genetic gain of within family selection } (G_W) = 4/3 i_W h^2_W \sigma^2_W \dots \dots \dots (8)$$

Where,

$i_W = 1.12$ (Zobel and Talbert 1984, 30 per cent selection intensity)

$$\text{Total genetic gain } (G_T) = G_F + G_W \dots \dots \dots (9)$$

$$\text{Ratio of family and within family genetic gains } (G_F/G_W) \dots \dots \dots (10)$$

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) showed significant difference at 1 percent level of significance for all the morphological and biomass traits, which indicated a large amount of phenotypic variation among the 32 plus tree families, selected. The observation on various morphological and biomass traits along with their range, mean, genetic coefficient of variance (GCV) and phenotypic coefficient of the variance (PCV) of 32 plus tree progeny are presented in Table 2. It is apparent from Table 2 that the higher phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) was found in all the traits except number of leaves. It reveals that there is ample scope of improvement through simple selection of desirable traits (Zobel and Talbert, 1984; Cotterill and Dean 1988). The highest PCV and GCV was found in root dry weight followed by root fresh weight, shoot/root ratio, leaf area, seedling biomass, shoot dry weight and shoot fresh weight, which indicated higher variation for these traits. The difference of the values between PCV and GCV for seedling height, internodal length, number of leaves, leaf area, shoot fresh weight, shoot dry weight and seedling biomass were smaller than seedling diameter, root fresh weight, root dry weight, and shoot/root ratio, which indicated less influence of environment on seedling

height, internodal length, number of leaves, leaf area, shoot fresh weight, shoot dry weight and seedling biomass. The efficiency of selection on the magnitude of variability, present in the material depends on the extent to which the desirable characters are inherited. Higher PCV than the corresponding GCV for all the characters studied indicated that the environment interacts with these characters. Therefore, there is ample scope of improvement for these desirable traits through simple selection. Burton and De Vane (1953) suggested that the study of GCV together with heritability gives the best picture of progress to be achieved through selection (Burton and DeVane 1953). Again, the lower differences between PCV and GCV for seedling height, seedling diameter, internodal length, number of leaves, shoot fresh weight and shoot dry weight indicated that these traits might not be influenced exactly by the same genes under field condition (Zobel and Talbert, 1984).

The various components like replication \times family (σ^2_{RF}), family (σ^2_F), replication (σ^2_R) and within plots (σ^2_w) used to calculate heritability and genetic gain subsequently are presented in Table 3. The plus tree variance for replication \times family (σ^2_{RF}) was highest (178.11) for shoot fresh weight and lowest (0.01) for seedling diameter, whereas variance for family (σ^2_F) was highest (473.32) for leaf area and lowest (0.02) for seedling diameter. The maximum variance among replication (41.30) was observed for seedling biomass and minimum (0.01) for seedling diameter. The highest phenotypic variance among plus tree families (σ^2_P), phenotypic variance among individuals (σ^2_p) and additive genetic variance (σ^2_A) were observed for leaf area and the lowest for seedling diameter. It is evident from the Table 3 that maximum variation was recorded for leaf area and minimum for seedling diameter. On the other hand, all morphological and biomass traits variance for plus tree family were more compared to replication (σ^2_R) and replication \times family (σ^2_{RF}) variance. The highest phenotypic variance amongst plus tree families (σ^2_P), phenotypic variance amongst individuals (σ^2_p) and additive genetic variance (σ^2_A) was observed for leaf area. The higher variation between families in comparison to within family variation might be due to different inherent genetic traits amongst plus tree families (Matheson and Raymond, 1984; Gautam, 2001).

It is apparent from Table 4 that the maximum heritability on plus tree family basis (h^2_F), was observed for shoot dry weight (0.963) followed by leaf area (0.956) and seedling height (0.954). Heritability within family basis (h^2_w) was found to be maximum for shoot dry weight (0.814) followed by seedling height (0.713) and leaf area (0.706). However, maximum heritability on individual plant basis (h^2_I) was recorded for shoot dry weight (0.852) followed by leaf area (0.752) and seedling height (0.750). Therefore, from Table 4 it can be inferred that these traits (shoot dry weight, leaf area and seedling height) were under the strong genetic control (Dean and Burdon, 1991). In all the traits, family heritability (h^2_F) was higher than the individual tree heritability (h^2_I) and within family heritability (h^2_w). The higher family heritability than individual tree heritability might be due to average estimates within a sample of many progenies for family heritability (Zobel and Talbert, 1984). On the other hand, higher plus tree family heritability than within family heritability might be due to phenotypic variance and environmental predominance among plus tree families (Mebrahtu and Hanover, 1989; Chaudhary, 2000).

The genetic gain of family selection (GF), total genetic gain (GT) and ratio of family and within family genetic gain (GF/GW) was observed maximum for leaf area and seedling height, whereas, all the genetic gains were found minimum for internodal length (Table 5). Johnson et al., (1955) pointed out that heritability estimates along with genetic gain is more useful than heritability alone, because the heritability estimates indicates only the effectiveness of selection of genotype based on phenotypic performance, but fails to indicate real genetic progress (Johnson et al., 1955; Seghal, et. al., 1995). The traits with low genetic gain and high heritability indicate that the expression is possibly controlled by intra and inter allelic interactions. The genetic gain of family selection (GF), total genetic gain (GT) and ratio of family and within family genetic gain (GF/GW) was observed maximum for leaf area and seedling height (Table 5). From our present study it was observed that shoot dry weight recorded high heritability estimates but showed less genetic gain in comparison to leaf area and seedling height (Table 4 and Table 5). Therefore, the selection for leaf area and seedling height can give better results than the shoot dry weight. These two traits with high heritability and genetic gain indicated the additive gene action on these two traits for their expression. Therefore, it can be concluded that the simple selection is quite desirable for the improvement of these traits.

Table 1. Details of 32 plus tree of *Bauhinia variegata* Linn

S. No. of sites	Name of seed sources	Code	Altitude (m)	Latitude*	Longitude*	Annual rainfall (mm)
1.	Nalagarh	T ₁	500	31° 02'N	76° 42'E	1,352
2.	Paonta Sahib	T ₂	320	30°26'N	77° 36'E	1,936
3.	Pinjore	T ₃	540	30° 47'N	76° 54'E	580
4.	Subathu	T ₄	1,380	30° 59'N	76° 58'E	1,435
5.	Solan	T ₅	1,300	31° 55'N	77° 06'E	1,372
6.	Kunihar	T ₆	960	31° 03'N	77° 55'E	1,354
7.	Nahan	T ₇	760	30° 35'N	77° 18'E	1,428
8.	Mandi	T ₈	800	31° 44'N	76° 56'E	1,938
9.	Sundernagar	T ₉	740	31° 35'N	76° 53'E	1,115
10.	Kandaghat	T ₁₀	1,180	30° 59'N	77° 06'E	1,412
11.	Rajgarh	T ₁₁	1,760	30° 51'N	77° 18'E	1,021
12.	Giripul	T ₁₂	1,120	30° 50'N	77° 12'E	939
13.	Nauni	T ₁₃	1,200	30° 54'N	76° 10'E	934
14.	Una	T ₁₄	740	31° 28'N	76° 16'E	2,300
15.	Jabli	T ₁₅	620	30° 51'N	76° 59'E	1,926
16.	Kalka	T ₁₆	470	30° 50'N	76° 56'E	1,897
17.	Arki	T ₁₇	1,280	31° 09'N	76° 57'E	1,527
18.	Bilaspur	T ₁₈	660	31° 19'N	76° 46'E	1,032
19.	Hamirpur	T ₁₉	780	31° 40'N	76° 31'E	1,173
20.	Jawalajee	T ₂₀	520	31° 88'N	76° 00'E	2,532
21.	Palampur	T ₂₁	1,280	32° 07'N	76° 31'E	3,148
22.	Narag	T ₂₂	1,060	31° 15'N	77° 28'E	1,972
23.	Sarahan	T ₂₃	1,480	31° 33'N	77° 47'E	1,358
24.	Renuka	T ₂₄	1,060	30° 37'N	77° 25'E	1,620
25.	Dhaulakuan	T ₂₅	380	30° 29'N	77° 31'E	756
26.	Dehradun	T ₂₆	620	30° 20'N	78° 02'E	1,500
27.	Chandrabani	T ₂₇	660	30° 19'N	77° 59'E	1,381
28.	Sahastradhara	T ₂₈	740	30° 22'N	78° 05'E	2,073
29.	Jammu	T ₂₉	440	32° 42'N	74° 51'E	1,115
30.	Kathua	T ₃₀	380	32° 22'N	75° 31'E	1,678
31.	Udhampur	T ₃₁	680	32° 55'N	75° 07'E	1,129
32.	Jhajjer Kotti	T ₃₂	540	32° 53'N	74° 57'E	1,121

* Encarta U.S. Geological Survey

Table 2. Progeny variability parameters for morphological and biomass traits for 32 plus tree families of *Bauhinia variegata* Linn

Traits	Range	Mean	PCV	GCV
Seeding height (cm)	30.92- 61.04	50.09	13.68	11.90
Seedling diameter (mm)	2.48 - 4.08	3.34	17.59	11.92
Internodal length (cm)	3.14 - 6.31	4.99	16.53	12.97
Number of leaves	7.73 - 10.37	8.92	9.51	6.45
Leaf area (cm ²)	30.10 - 76.63	46.64	30.19	27.63
Shoot fresh weight (g)	3.28 - 7.37	4.97	21.38	18.87
Root fresh weight (g)	1.52 - 4.38	2.48	40.40	28.08
Shoot dry weight (g)	1.46 - 3.61	2.49	23.87	20.70
Root dry weight (g)	0.42 - 2.39	1.15	53.67	44.94
Shoot/root ratio	1.39 - 4.27	2.74	36.81	26.16
Seedling biomass (g)	4.96 - 11.65	7.46	25.21	21.11

Table 3. Variances of different morphological and biomass traits for 32 plus tree families of *Bauhinia variegata* Linn

Traits	σ^2_{RF}	σ^2_F	σ^2_R	σ^2_w	σ^2_P	σ^2_p	σ^2_A
Seeding height (cm)	40.23	312.40	0.30	1,314.2	327.35	1,666.83	1,249.60
Seedling diameter (mm)	0.01	0.02	0.01	0.12	0.02	0.15	0.08
Internodal length (cm)	0.17	0.80	0.04	7.86	0.89	8.83	3.20
Number of leaves	4.57	6.16	0.09	26.23	6.58	36.96	24.64
Leaf area (cm ²)	33.81	473.32	2.65	2,011.52	495.33	2,518.65	1,893.28
Shoot fresh weight (g)	178.11	209.13	0.43	1,072.50	225.87	1,459.74	836.52
Root fresh weight (g)	25.13	75.36	5.92	1,851.62	95.43	1,952.11	301.44
Shoot dry weight (g)	0.25	23.92	0.05	88.12	24.85	112.29	95.68
Root dry weight (g)	6.92	20.16	0.32	111.81	21.54	138.89	80.64
Shoot/root ratio	5.65	14.13	1.92	341.16	17.86	360.94	56.52
Seedling biomass (g)	0.23	1.32	41.3	12.12	1.45	13.67	5.28

Table 4. Estimates of heritability of different morphological and biomass characters for 32 plus tree families of *Bauhinia variegata* Linn.

Traits	h^2_F	h^2_w	h^2_I
Seeding height (cm)	0.954	0.713	0.750
Seedling diameter (mm)	0.928	0.500	0.533
Internodal length (cm)	0.902	0.305	0.362
Number of leaves	0.937	0.705	0.667
Leaf area (cm ²)	0.956	0.706	0.752
Shoot fresh weight (g)	0.926	0.585	0.573
Root fresh weight (g)	0.790	0.122	0.154
Shoot dry weight (g)	0.963	0.814	0.852
Root dry weight (g)	0.936	0.541	0.581
Shoot/root ratio	0.791	0.124	0.157
Seedling biomass (g)	0.908	0.327	0.386

Table 5. Estimates of genetic gain for different morphological and biomass characters for 32 plus tree families of *Bauhinia variegata* Linn.

Traits	G_F	G_w	G_T	G_F/G_w
Seeding height (cm)	11.56	0.06	11.62	192.67
Seedling diameter (mm)	0.42	1.23	1.65	0.34
Internodal length (cm)	0.15	0.43	0.58	0.35
Number of leaves	0.43	1.21	1.64	0.36
Leaf area (cm ²)	15.07	0.07	15.14	215.28
Shoot fresh weight (g)	8.43	0.06	8.49	140.50
Root fresh weight (g)	1.42	0.21	1.63	6.76
Shoot dry weight (g)	2.91	0.15	3.06	19.40
Root dry weight (g)	2.28	0.20	2.48	11.40
Shoot/root ratio	5.40	1.25	6.65	4.32
Seedling biomass (g)	5.09	1.26	6.35	4.04

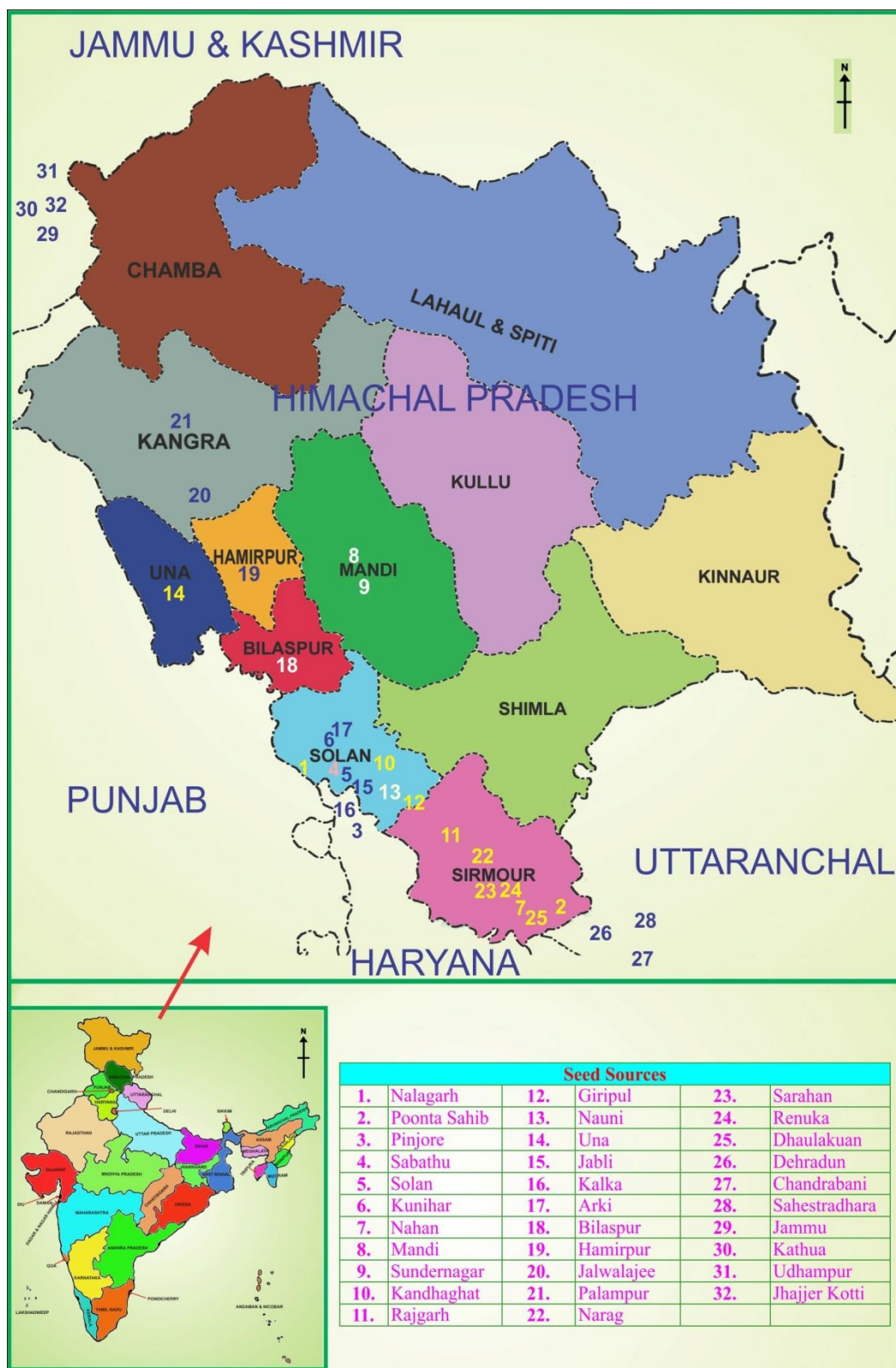


Fig 1: Map showing the location of seed sources

CONCLUSIONS

Considering the heritability estimates and genetic gain from our present study, it can be concluded that leaf area and seedling height showed better results, which indicated additive gene action on these two traits. Therefore these two traits would give better results for improvement of *Bauhinia variegata* by simple selection.

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