



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; 7(2): 1899-1902
Received: 13-01-2018
Accepted: 14-02-2018

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Genetic parameters for yield contributing characters in *Valeriana jatamansi* Jones: An endangered medicinal plant

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Abstract

Studies on genetic parameters *i.e* genetic variability, heritability and genetic advance as percentage of mean were carried out among 46 morphotypes of *Valeriana jatamansi* differing in at least one distinct morphological character. The experiment was conducted in Randomized Block Design with three replications. The data were recorded for quantitative characters *viz.* plant height, petiole length, petiole diameter, number of flowering spikes, rhizome length, rhizome diameter, fresh and dry biomass of roots, rhizomes and rootstock along with total valepotriates content and yield estimation from the underground portion. The results revealed that the magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters except total valepotriates content in rhizomes, roots and rootstock where smaller difference between GCV and PCV values were observed indicating low influence of environment. Higher heritability estimate (broad sense) coupled with genetic advance as percent of mean were obtained for rhizome dry weight and roots dry weight. The phenotypic expression of these characters may be governed by the genes acting additively and thereby indicating the importance of these characters for selection.

Keywords: *Valeriana jatamansi*, genetic variability, heritability, morphotypes, medicinal plant

Introduction

Valeriana jatamansi syn. *Valeriana wallichii* DC (Bennet, 1987) commonly known as Sugandhbala or Mushkbala is an important medicinal and aromatic plant belonging to family Valerianaceae. The species is localized mainly to temperate Himalayas and grows abundantly from Kashmir to Bhutan at an altitude of 1200 to 4000 m and in Khasi hills at an altitude of 1200 to 2000 m (Kirtikar and Basu, 1975) [14]. Rhizomes and roots of the plant are the economic part and constitute the drug. Traditionally it is used for treating hysterical fits, insomnia, nervous tension, stress, anxiety and high blood pressure because of its sedative and tranquilizing properties (Kirtikar and Basu, 1975; Houghton, 1999) [14, 10]. The sedative and tranquilizing properties of the species is due to group of compounds known as valepotriates present in its rootstock (Wagner *et al.*, 1980; Grusla *et al.*, 1986) [30, 7]. The species is gynodioecious in nature (Raina and Srivastava, 1992) and hence cross-pollinated due to which many of the traits show continuous variation. Further, it has been reported that out-crossing plant species have higher genetic variations within populations, compared to self-pollinating species or species with mixed mating system (Till *et al.*, 2002) [28]. *V. jatamansi* is a natural tetraploid, and polyploidy can play a significant role in maintaining high heterozygosity and genetic diversity on the basis of sexual reproduction (Soltis and Soltis, 2000) [26]. Variation in morphological and genetic diversity have been studied in this species by several workers suggesting that environmental and genetic factors influence the diversity of the plant and its chemical constituents (Sundearesan *et al.*, 2012; Jugran *et al.*, 2013) [13].

The assessment of variability that exists in the available germplasm collections of any crop is of utmost importance as well as first step of any breeding programme. Hence, consideration of quantitative approaches for exploitation of the extensive genetic variability available in the species is of utmost importance, which in turn is dependent on good estimates of the genetic parameters. Estimates of genetic parameters serve as a base for selection and hybridization as the degree of variability for a given character is a basic prerequisite for its improvement. Evaluation and characterization of genotypes is necessary to describe their performance in terms of growth, yield and quality parameters. Yield is a complex character and its direct improvement is difficult (Jindal *et al.*, 2010) [10]. Knowledge of the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its component is essential for effecting genetic improvement. Breeding work for improvement in this species is of great importance as less effort have been made in this direction. Keeping this

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in view present investigation was undertaken with the objective of comparing the growth and yield parameters of selected superior morphotypes in the field condition as well as to estimate their genetic parameters.

Material and Methods

The experimental material for the present investigation comprised of 46 morphotypes of *Valeriana jatamansi* isolated from inbred population of UHFVAL (INGR 11036), UHFVAL A type chemotype and general population. The study was conducted at Medicinal and Aromatic Plants Research Farm, Shilly, Distt. Solan (Altitude 1550m amsl, latitude-N 30° 54' 30" and longitude E 77° 07' 30") Himachal Pradesh. The experiment was laid out in randomized block design at 30×45 cm spacing. The morphotypes were selected based on their morphological parameters *i.e.* growth, form and habit. The plants were uprooted after one year of transplanting and quantitative parameters *viz.* plant height, petiole length, petiole diameter, number of flowering spikes, rhizome length, rhizome diameter, fresh and dry biomass of roots, rhizomes and rootstock were recorded. Observations were recorded on an individual plant basis from three randomly selected plants per morphotypes in a replicate. The total valepotriates content were estimated utilizing the underground portion *i.e.* rhizomes and roots through High Pressure Liquid Chromatography technique as described by Bos *et al.*, (1996) [3] with slight modifications.

The variability was estimated as per procedure for analysis of variance suggested by Panse and sukhatme (1985) [16]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per formula suggested by Burton (1952) and Johanson *et al.* (1955). Heritability in broad sense and expected genetic advance as per cent of mean were calculated according to method suggested by Burton and De Vane (1953) [4] and Johanson *et al.* (1955), respectively.

Results and Discussions

The analysis of variance revealed significant variations among the morphotypes for all the characters studied. The amount of genotypic and phenotypic variability that exists in a species is essential in developing better varieties and in initiating a breeding program. During the present investigation, the estimates of GCV, PCV, h² and GA as % of mean for characters have been studied and presented in Tables 1 to 3. The phenotypic variance was partitioned into genotypic and environmental variances for clear understanding of the pattern of variations. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the quantitative growth parameters, indicating the presence of environmental influence to some degrees in the phenotypic expression of characters (Tables 1-2). The results are in line with Rajagopal and Kandhasamy (2009) [20] in *Gloriosa superba*; Alam *et al.*, (2014) [1] in *Dioscorea alata*. The smaller the difference in values between PCV and GCV, the lesser will be the environmental effect on the character. The characters that had close GCV and PCV values indicating low contribution of environmental variances for the characters were plant height, petiole length, leaf length, leaf width, ratio between leaf length and leaf width. The results were similar to earlier findings of Rajagopal and Kandhasamy (2009) [20] in *Gloriosa superba*, Mathur (2003) [15] in *Centella asiatica* and Sethi (1991) [21] in palmarosa. The active constituents responsible

for the therapeutic properties of the species are valepotriates and valerenic acids (Singh *et al.*, 2006; Singh *et al.*, 2010). Valepotriates (Val+epo+triatres) are group of natural products belonging to the iridoid group having epoxy group and are triesters. The total valepotriates content were estimated from the rhizomes, roots and rootstock portion of the species. The data revealed that, in all the three parts smaller difference between GCV and PCV values were observed indicating low influence of environment. But in terms of total valepotriates yield (mg/plant) phenotypic coefficient of variation was observed to be greater than genotypic coefficient of variation (Table 3). Genotypic coefficients of variation give indication of the amount of genetic variation for a particular character. However, it does not indicate the proportion of the total variation that is heritable. Heritability estimates in broad sense (h²) were used to estimate the heritable portion of variation. Estimates of heritability serves as a useful guide to the breeder. Broad sense individual heritabilities of the traits ranged from (52.75%) in rhizome diameter to (92.54%) in petiole length (Tables 1-2). The values were relatively higher for all the traits studied. Maximum heritability was recorded for petiole length (92.540%), plant height (84.347%) leaf length (79.125%), petiole diameter (80.696%), rhizome dry weight (79.233%), roots dry weight (79.927%) and rootstock dry weight (79.143%). Similarly higher broad sense heritability was observed for root yield in *Chlorophytum borivillianum* by Singh *et al.*, (2008). In case of total valepotriates percentage in official part *i.e.* rootstock containing rhizomes and roots, heritability estimates were also recorded higher *i.e.* (96.964%), (97.399%) and (95.322%). For valepotriates yield (mg/plant) in rhizomes, roots and rootstock, moderate heritability were recorded (Table 3). Even though heritability estimates represent the heritable portion of variation, they do not indicate the effectiveness with which selection of best individual could be made based on the phenotypic performance (Burton and De Vane, 1953; Johnson, 1955) [4] and thus high heritability could not be considered as an indication of higher genetic gain. Heritability estimates along with genetic advance is a useful criteria in selecting an individual. Panse (1957) [17] reported that high heritability associated with high genetic advance is mainly attributed to the action of additive gene. Genetic advance as percent of mean is expressed as genetic gain. Genetic advance as percentage of mean was recorded highest (104.003%) for rhizome dry weight and lowest (22.155 %) for ratio between leaf length and leaf width. Similarly Gupta *et al.*, (2016) observed maximum genetic advance as percentage of mean (110.19%) for rhizome dry weight in *Curcuma longa*. High magnitude of genetic advance was also observed for plant height by Haritwal *et al.*, (2017); Singh *et al.*, (2000) in *Papaver somniferum*. High heritability (h²) estimates (> 60%) coupled with high genetic advance as per cent of mean was observed highest in rhizome dry weight (104.003%) followed by roots dry weight (100.685%) and rootstock dry weight (85.232%) suggesting the role of additive gene action in the expression of these characters and as such could be considered as reliable indices for selection. In terms of total valepotriates content in rhizomes, roots and rootstock, similar results were obtained showing high heritability coupled with high genetic advance as percentage of mean. High magnitude of genetic advance as percentage of mean was observed for total valepotriates yield (mg/plant) in roots (124.276%). High heritability (h²) estimates along with high genetic advance as per cent of mean was observed highest for total valepotriates yield (mg/plant) in roots, followed by rootstock (Table 3). The

results suggested that further improvement through individual plant selection would be effective. Similar results were obtained by Dubey (2010) in *Withania somnifera* for dry root yield per plant, Praveen *et al.*, (2011) in *Asparagus racemosus*

for root related characters and Yadav *et al.*, (2007) in *Chlorophytum borivilianum*. Tuppad *et al.*, (2017) observed high heritability estimates for yield contributing characters in *Holostemma ada-kodien*.

Table 1: Estimates of variability and genetic parameters in 46 morphotypes of *V. jatamansi*

	PH	PL	PD	NL	LL	LW	RLL & LW	NFS	FAB	DAB
Mean	43.370	18.754	3.338	40.783	10.460	10.277	1.030	14.783	31.197	5.199
Range	15.03-75.13	8.33-29.43	2.34-4.92	8.00-109.00	6.8-14.3	7.1-15.4	0.72-1.36	6.33-33.67	5.56-74.65	0.96-11.81
CV	12.625	5.775	7.882	35.207	8.288	7.973	9.074	29.280	32.961	32.243
VG	161.548	14.553	0.289	322.437	2.849	2.915	0.018	29.637	193.972	4.804
VE	29.979	1.173	0.069	206.158	0.752	0.672	0.009	18.738	105.736	2.810
VP	191.527	15.726	0.359	528.595	3.601	3.586	0.027	48.375	299.708	7.615
GCV	29.307	20.341	16.114	44.030	16.136	16.612	13.070	36.827	44.643	42.158
PCV	31.910	21.145	17.938	56.375	18.140	18.427	15.884	47.050	55.492	53.075
ECV	12.625	5.775	7.881	35.207	8.288	7.974	9.027	29.283	32.961	32.243
Heritability	84.347	92.540	80.696	60.999	79.125	81.275	67.707	61.265	64.720	63.094
GA	24.047	7.560	0.995	28.890	3.093	3.171	0.228	8.778	23.081	3.587
GA%	55.446	40.310	29.819	70.840	29.568	30.851	22.155	59.379	73.985	68.983

PH-plant height, PL-petiole length, PD-petiole diameter, NL-number of leaves, LL-leaf length, LW-leaf width, RLL& LW-

ratio of leaf length and leaf width, NFS-number of flowering spikes, FAB-fresh aerial biomass, DAB-dry aerial biomass

Table 2: Estimates of variability and genetic parameters in 46 morphotypes of *V. jatamansi*

	RD	RL	RHFW	RHDW	RFW	RDW	RSTKFW	RSTKDW
Mean	8.916	8.507	10.048	2.437	8.632	2.271	18.680	4.708
Range	4.67-12.97	3.00-17.73	1.78-28.33	0.46-9.48	2.13-21.90	0.48-6.66	3.91-34.99	1.02-12.01
CV	18.936	21.146	30.597	29.037	35.522	27.398	29.421	23.878
VG	3.183	6.163	16.563	1.910	17.839	1.542	41.407	4.795
VE	2.850	3.236	9.452	0.501	9.402	0.387	30.204	1.263
VP	6.033	9.399	26.015	2.411	27.241	1.929	71.611	6.058
GCV	20.011	29.182	40.504	56.719	48.931	54.670	34.448	46.508
PCV	27.550	36.038	50.762	63.720	60.465	61.151	45.303	52.278
ECV	18.936	21.146	30.598	29.038	35.522	27.398	29.422	23.875
Heritability	52.757	65.570	63.668	79.233	65.486	79.927	57.822	79.143
GA	2.670	4.141	6.690	2.534	7.041	2.287	10.080	4.013
GA%	29.941	48.678	66.578	104.003	81.569	100.685	53.961	85.232

RD-rhizome diameter, RL-rhizome length, RHFW-rhizome fresh weight, RHDW-rhizome dry weight, RFW-roots fresh

weight, RDW-roots dry weight, RSTKFW-rootstock fresh weight, RSTKDW-rootstock dry weight

Table 3: Estimates of variability and genetic parameters in 46 morphotypes of *V. jatamansi*

	Total valepotriates content (%) in rhizome	Total valepotriates yield (mg/plant) in rhizome	Total valepotriates content % in roots	Total valepotriates yield (mg/plant) in roots	Total valepotriates content (%) in rootstock	Total valepotriates yield (mg/plant) in rootstock
Mean	1.662	102.160	1.760	96.287	1.714	198.447
Range	1.329-2.201	12.777-308.928	1.264-2.534	11.932-317.157	1.359-2.208	24.708- 587.303
CV	1.901	44.480	3.758	38.933	2.228	37.392
VG	0.037	2571.270	0.089	4441.815	0.047	10498.570
VE	0.001	2064.834	0.004	1405.295	0.001	5506.113
VP	0.038	4636.104	0.094	5847.111	0.048	16004.683
GCV	11.600	49.636	16.973	69.217	12.585	51.632
PCV	11.755	66.649	17.385	79.415	12.781	63.750
ECV	1.903	44.480	3.760	38.933	2.227	37.392
Heritability	97.379	55.462	95.322	75.966	96.964	65.597
GA	0.392	77.79	0.601	119.66	0.438	170.95
GA%	23.581	76.148	34.138	124.276	25.529	86.145

Conclusion

Genetic improvement of any crop is largely depending on the magnitude of genetic variability and the extent to which desirable traits are heritable. In the present investigation significant differences among different morphotypes of *V. jatamansi* for rootstock parameters were observed. High heritability (h^2) estimates coupled with high genetic advance as per cent of mean was observed highest in rhizome dry

weight (104.003%) followed by roots dry weight (100.685%) and rootstock dry weight (85.232%) accompanied with total valepotriates yield in roots (124.276%) suggesting good scope of improvement for these characters. As rhizome and roots are the official parts of the species, obtaining heritability in their dry weights is favorable which can be primarily taken into further breeding programme.

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