

Original Research Article

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## Genetic Variability Analysis in Ashwagandha [*Withania somnifera* (L.) Dunal]

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### ABSTRACT

#### Keywords

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The Present investigation was carried out using 75 genotypes along with two standard checks viz; JA-20 (Jawahar Asgandh-20) and JA-134 (Jawahar Asgandh-134). The examination was spread out in Augmented RBD design during *Kharif* 2019 at the Instructional Farm, Rajasthan College of Agriculture, Udaipur. Sufficient variability was present in the genotypes under study for all the characters indicating sufficient genetic variability among the genotypes. Highest GCV was found for secondary branches (33.04), primary branches (26.36) and fresh plant weight (20.26) where as lowest GCV was observed in the character days to 75% maturity (0.45). Highest PCV was found for Secondary branches (34.44), primary branches (29.90), root diameter (21.03) and fresh plant weight (20.28) where as lowest PCV was observed in days to 75% maturity (1.38). The high estimates of heritability values noticed in characters like Fresh plant weight (99.85), plant height (99.35), and days to flowering (97.64). High heritability with high genetic advance was found in fresh plant weight per plant. High heritability together with high genetic advance was observed for fresh plant weight. The genetic advance was found high (>20%) in the character fresh plant weight (41.38%).

### Introduction

Ashwagandha [*Withania somnifera* (L.) Dunal] generally known as Indian ginseng is likewise named poison gooseberry or winter cherry (Deshpande, 2005). Ashwagandha is an angiosperm plant that belongs to the *Solanaceae* family (Mir *et al.*, 2013). It is a self-pollinated plant bearing chromosome no.  $2n=48$  (Nigam *et al.*, 1995; Das *et al.*, 2009),  $2n=24$  (Ram and Kamini, 1964),  $2n=75$  (Bir and Neelam, 1980). It is hardy and drought-tolerant perennial plant (Ali *et al.*, 1997) that develops well in dry and sub-

tropical regions having well-drained, sandy loam or light red soils (Kukreti *et al.*, 2013) having pH of 7.5 to 8.0 with an average rainfall of 600-750 mm. Two species of Ashwagandha are found in India, viz. *Withania somnifera* (L.) Dunal (Ashwagandha) and *Withania coagulans* (L.) Dunal (Panir). A few reports uncovered that alkaloid content found in Indian root ranges between 0.13 to 0.66 which is lower than 4.3 percent found at places other than India. Ashwagandha is native of North-western and Central India as well as the Mediterranean region of North Africa. It tends to be

developed over a wide scope of locales stretching out from 23<sup>0</sup> N to 33<sup>0</sup> N latitude and from 18 - 170 m altitude above sea level, including the states of Maharashtra, Madhya Pradesh, Gujarat, Rajasthan, Uttar Pradesh, Haryana, Punjab, Orissa, Sikkim and Assam (Billore, 1989; Chaudhari and Vacharajani, 1992; Pandey and Dixit, 1980). Root is the most significant part of the entire plant as it possesses a wide scope of therapeutic agents and its therapeutic utility is due to the presence of alkaloids, essentially *Withanolides* (Devi *et al.*, 1993). Assessment of variability in available germplasm is the most important as well as the initial step of any breeding programme. More noteworthy the variability in the genetic material more odds of genetic improvement. Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) helps to choose the potential genotype and heritability along with genetic advance would be more useful tool in predicting the resultant effect for selection of best genotypes for yield. Keeping these things in the view, the present investigation were made to assess genotypes with the objectives, to estimate the variability, coefficients of variability and the genetic parameters, *viz.* heritability, expected genetic advance (standard), and genetic gain along side the mean and range of different characters in the current examination.

## Materials and Methods

The diverse genotypes were collected from Herbal Park, RCA (UDAIPUR). Topographically, Udaipur is situated at 24<sup>0</sup>-35<sup>0</sup> N scope and 73<sup>0</sup>-42<sup>0</sup> E longitude and at a rise of 582.17 meters above mean sea level. Field explore was led to get the genetic variability among 75 genotypes with two standard checks *viz.*; JA-20 and JA-134 were evaluated in Augmented RBD design. The sound yield seeds of every genotype were planted in single plot of 3 meter length

keeping up crop geometry 30 x 5 cm row to row and plant to plant spacing respectively at Instructional Farm, Rajasthan College of Agriculture, MPUAT, Udaipur, during *Kharif* 2019. The recommended package of practices was adopted for raising the healthy crop. Observations were recorded for eleven characters on ten randomly selected competitive plants for each genotype except some of the characters which were recorded on whole plot basis.

## Statistical analysis

To test the difference among the genotypes, the analysis of variance was worked out separately for each character as per method suggested by fisher (1954) and using standard statistical procedure given by Panse and Sukhatme (1954). Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were calculated as per the standard formula suggested by Burton (1952).

## Genotypic coefficient of variation (GCV)

It was calculated using the following formula as suggested by the Burton (1952).

$$GCV = \frac{\sqrt{V_g}}{\bar{X}} \times 100$$

Where,

$V_g$  = Genotypic variance

$\bar{X}$  = Population mean

## Phenotypic coefficient of variation (PCV)

It was calculated using the following formula as suggested by Burton (1952).

$$PCV = \frac{\sqrt{V_p}}{\bar{X}} \times 100$$

Where,

$V_p$  = phenotypic variance

$\bar{X}$  = Population mean

### Heritability in Broad sense ( $h^2_{BS}$ )

It was computed using the following formula stated by Burton and De vane (1953) and Hanson *et al.*, (1956).

$$h^2_{bs} (\%) = \frac{V_g}{V_p} \times 100$$

Where,

$V_g$  = genotypic variance

$V_p$  = phenotypic variance

$h^2_{bs}$  = broad sense heritability.

$$GA = \text{Genetic advance} = \frac{K \cdot v_g}{\sqrt{v_p}}$$

Where,

$V_g$  = Genotypic variance

$V_p$  = Phenotypic variance

$K$  = Selection differential at 5 per cent selection pressure *i.e.* 2.06

### Genetic gain

It is percent expected genetic advance over the population mean. It was computed as follows using the formula of Johnson *et al.*, (1955)

$$GG = \frac{GA}{\bar{X}} \times 100$$

Where,

$\bar{X}$  = Population mean

## Results and Discussion

The maximum dry root yield exhibited by the PWS-6 (3.20 g) followed by UWS-89 (3.10), PWS-27 (2.90) and UWS-83 (2.86). The magnitude of GCV varied from 0.45 percent in days to 75 percent maturity to 33.04 percent in secondary branches. It was found that GCV was found low (<10%) for the characters days to flowering (2.24%), days to maturity (0.45%), dry root yield (7.14%). The GCV was moderate (10-20%) for plant height (13.33%), root length (14.71%) root diameter (19.68%), fresh root yield (17.73%), alkaloid content (10.97%) and for primary branches (26.36%), secondary branches (33.04%), fresh plant weight (20.26%), the GCV was found high (>20 %). The present findings are In accordance with the findings of Kumar *et al.*, (2007), Yadav *et al.*, (2008), Sangwan *et al.*, (2013), Sundesha and Tank (2013), Joshi *et al.*, (2014), Singh *et al.*, (2014) and Dev *et al.*, (2015). It was found that PCV was found low (<10%) for the characters days to flowering (2.27%), days to maturity (1.38%). The PCV was moderate (10-20%) for Plant height (13.37%), root length (15.02%), Fresh root yield (18.35%), dry root yield (18.73%) and alkaloid content (11.65%). The PCV was found high (>20 %) for primary branches (29.90%), secondary branches (34.44%), fresh plant weight (20.28%) and root diameter (21.03%). The present findings are In accordance with the findings of Kumar *et al.*, (2007), Yadav *et al.*, (2008), Sangwan *et al.*, (2013), Sundesha and Tank (2013), Joshi *et al.*, (2014), Singh *et al.*, (2014) and Dev *et al.*, (2015). The high estimates of heritability values noticed in characters like Fresh plant weight (99.85), plant height (99.35), days to flowering (97.64). High heritability with high genetic advance was found in fresh plant weight per plant. High heritability together with high genetic advance was observed for fresh plant weight (Table 1 and 2).

**Table.1** ANOVA for augmented RBD design

SN	Character	Block	Treatment	Check	Germplasm	C v/s G	Error
		[4]	[76]	[1]	[74]	[1]	[4]
1.	Days to flowering	1.20*	5.38**	8.06**	5.41**	0.01	0.13
2.	Days to 75% maturity	4.00	5.65	4.90	5.48	18.47	4.90
3.	Plant height(cm)	1.33**	9.68**	6.96**	8.48**	101.29**	0.06
4.	Primary branches	0.24	1.20	1.10	1.13	6.31**	0.25
5.	Secondary branches	0.43	4.37*	0.00	4.48*	0.00	0.36
6.	Root length(cm)	0.78	7.13**	33.60**	6.79**	5.82*	0.28
7.	Root diameter(mm)	0.68	1.81*	0.71	1.85*	0.15	0.23
8.	Fresh root yield (g)	2.16	6.63*	15.20**	6.52*	6.40*	0.43
9.	Dry root yield (g)	0.04	0.18	0.01	0.18	0.02	0.16
10.	Fresh plant weight (g)	6.74*	462.97**	43.43**	404.76**	5190.61**	0.59
11.	Alkaloid content (%)	0.00	0.00*	0.00*	0.00*	0.00	0.00

\* and \*\* indicates significant level at 5% and 1% respectively. [ ] Degrees of freedom.

**Table.2** Genetic variability parameters of different characters in ashwagandha

SN	Character	GCV	PCV	H <sup>2</sup>	GA	GG
1	Days to flowering	2.24	2.27	97.64	4.68	4.57
2	Days to 75% maturity	0.45	1.38	10.64	0.51	0.30
3	Plant height(cm)	13.33	13.37	99.35	5.96	27.37
4	Primary branches	26.36	29.90	77.75	1.70	47.88
5	Secondary branches	33.04	34.44	92.01	4.01	65.28
6	Root length(cm)	14.71	15.02	95.89	5.15	29.67
7	Root diameter(mm)	19.68	21.03	87.60	2.45	37.94
8	Fresh root yield (g)	17.73	18.35	93.34	4.91	35.28
9	Dry root yield(g)	7.14	18.73	14.53	0.13	5.61
10	Fresh plant weight(g)	20.26	20.28	99.85	41.38	41.71
11	Alkaloid content (%)	10.97	11.65	88.67	0.07	21.27

GCV-Genotypic coefficient of variation, PCV-Phenotypic coefficient of variation, h<sup>2</sup> -Heritability, GG-Genetic Gain

Similar findings have also been reported by Mohsina and Dutta (2007), Dubey (2010), Sangwan *et al.*, (2013), Joshi *et al.*, (2014), Singh *et al.*, (2014), Dev *et al.*, (2015), Gami *et al.*, (2015). The genetic advance was found high (>20%) in the character fresh plant weight (41.38%). Similar findings have also been reported by Mohsina and Dutta (2007), Sangwan *et al.*, (2013), Nagar (2018).

The phenotypic coefficient of variation was higher in magnitude than the respective genotypic coefficient of variation for all the characters. The phenotypic coefficient of variation estimate was generally higher than genotypic coefficient of variation estimates indicating positive effect of environment on character expression. High heritability together with high genetic advance was observed for fresh plant weight. Panse (1957) reported that high heritability together with high genetic advance was indicative of additive gene effects and high heritability associated with low genetic advance was indication of dominance and epistatic effects.

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