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EXPLORING GENETIC VARIABILITY FOR ROOT YIELD AND ITS COMPONENT TRAITS IN ASHWAGANDHA (*WITHANIA SOMNIFERA* L. DUNAL)

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ABSTRACT

The study titled "Exploring Genetic Variability for Root Yield and Its Component Traits in Ashwagandha [*Withania somnifera* (L.) Dunal]" evaluated 74 genotypes alongside three standard checks in late *kharif* 2019-20 at the Instructional Farm of Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, Rajasthan. Observations were recorded for eleven characters, including days to 50 percent flowering, plant height, number of primary and secondary branches, leaf area index, root length, root diameter, fresh and dry root yield, fresh and dry plant weight, 100 seed weight, harvest index, and alkaloid content. High genetic variability was observed in secondary branches, harvest index, and dry root yield, while low variability was seen in days to 75% maturity reveals significant potential for crop improvement. Substantial variability among genotypes underscores diverse genetic backgrounds, offering opportunities for selective breeding. High heritability was noted in secondary branches, fresh plant weight, and days to 50% flowering. Fresh plant weight exhibited high heritability and genetic advance, indicating its potential for improvement through selection. Overall, the study highlights significant genetic variability and potential for improvement in Ashwagandha traits, guiding future breeding efforts for enhanced crop performance and quality.

Keywords **:** Ashwagandha, Variability, Heritability, Dry Root Yield, Alkaloid.

Introduction

Ashwagandha, scientifically known as *Withania somnifera* (L.) Dunal, is a significant medicinal plant belonging to the genus *Withania* and the family *Solanaceae*. It holds a prominent place in traditional medicine systems such as Ayurveda and Unani, where its roots, leaves, and seeds are utilized for various therapeutic purposes. The roots, in particular, are rich in alkaloids and are renowned for their medicinal properties. Alkaloids such as *withanolides, somniferine, somniferinine, somnine, withananine*, pseudo *withananinine,* and *asomnine* are among the compounds identified in Ashwagandha, contributing to its medicinal efficacy (Covello and Ciampa, 1960).

Cultivation of Ashwagandha is primarily undertaken in regions with robust and drought-tolerant crop conditions. It thrives in relatively dry climates, making it suitable for cultivation during the late rabi season at altitudes ranging from 600 to 1200 meters. Semi-tropical areas experiencing rainfall between 60-75cm and temperatures ranging from 20 to 35 ºC provide ideal growing conditions for this crop. Originating from north-western and central India, as well as the Mediterranean region of Africa,

Ashwagandha is extensively cultivated in states such as Madhya Pradesh, Gujarat, Rajasthan, Maharashtra, Punjab, and Karnataka (Kumar *et al.,* 2020).

Despite its significant medicinal uses and widespread cultivation, there is a notable absence of improved varieties of Ashwagandha. Limited research has been conducted on varietal evolution and characterization, highlighting the need for further exploration into identifying desirable genotypes with specific traits. Variability in dry root yield and root size has been observed among Ashwagandha genotypes, emphasizing the necessity for comprehensive studies to assess and utilize the available genetic variation for enhancing crop productivity (Das *et al.*, 2011). Therefore, this study aims to investigate the existing variability in Ashwagandha genotypes, with a focus on identifying superior genotypes to address the current challenges in dry root yield production and to unlock the crop's full potential.

Based on the aforementioned details, we propose conducting an experiment titled "Exploring Genetic Variability for Root Yield and Its Component Traits in Ashwagandha [*Withania somnifera* (L.) Dunal]" utilizing an augmented design methodology. The experiment is scheduled to take place during the *Rabi* season of 2019 at the Instructional Farm within the Department of Genetics and Plant Breeding, located at Rajasthan College of Agriculture, MPUAT, Udaipur.

Material and Method

Plant material : A total of 74 genotypes of Ashwagandha [*Withania somnifera* (L.) Dunal] were selected for the study, along with three standard checks: JA-20 (Jawahar Asgandh-20), JA-134 (Jawahar Asgandh-134), and RVA-100.

Details of Ashwagandha genotypes used for the present investigation:

S.No.	Genotype	S.No.	Genotype
1	UWS-7	40	UWS-79
2	UWS-11	41	UWS-80
3	UWS-13	42	UWS-83
4	UWS-14	43	UWS-84
5	UWS-15	44	UWS-85
6	UWS-16	45	UWS-89
7	UWS-18	46	UWS-90
8	UWS-20	47	UWS-91
9	UWS-21	48	UWS-92
10	UWS-22	49	UWS-93
11	UWS-27	50	UWS-95
12	UWS-28	51	UWS-96
13	UWS-32	52	UWS-97
14	UWS-35	53	UWS-98
15	UWS-37	54	UWS-99
16	UWS-38	55	UWS-100
17	UWS-40	56	UWS-104
18	UWS-41	57	UWS-106
19	UWS-44	58	UWS-110
20	UWS-46	59	UWS-111
21	UWS-47	60	UWS-120
22	UWS-48	61	UWS-122
23	UWS-56	62	UWS-125
24	UWS-57	63	UWS-127
25	UWS-58	64	UWS-129
26	UWS-59	65	UWS-131
27	UWS-60	66	UWS-132
28	UWS-61	67	UWS-134
29	UWS-62	68	UWS-135
30	UWS-63	69	UWS-136
31	UWS-65	70	UWS-139
32	UWS-66	71	UWS-140
33	UWS-67	72	UWS-144
34	UWS-71	73	UWS-148
35	UWS-72	74	UWS-153
36	UWS-75	75	CHECK,JA-20
37	UWS-76	76	CHECK, JA-134
38	UWS-77	77	CHECK, RVA-100
39	UWS-78		

Experimental Design: The experiment was conducted using an augmented randomized complete block design (ARCBD) during the late *kharif* season of 2019-20.

Experimental Site: Topographically, Udaipur is situated at 240 -350 N scope and 730 -420 E longitude and at a rise of 582.17 meters above mean sea level. The climatic states of the zone speak to subtropical condition with damp atmosphere. The study was carried out at the Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, Rajasthan

Crop Management: The sound yield seeds of each genotype were individually planted in single plots measuring 3 meters in length, maintaining crop geometry of 30 x 5 cm row-to-row and plant-to-plant spacing. Recommended agronomic practices were followed to ensure the healthy growth of the crop.

Observations: Observations were recorded on ten randomly selected competitive plants for fifteen characters, including: days to 50% flowering, days to 75% maturity, plant height, number of primary branches per plant, number of secondary branches per plant, leaf area index, root length, root diameter in the collar region, fresh root yield per plant, dry root yield

per plant, fresh plant weight per plant, dry plant weight per plant, 100-seed weight, Harvest index and total alkaloid content.

Statistical Analysis: Analysis of variance for quantitative characters was conducted following the standard procedure for Augmented Randomized Complete Block Design (ARCBD) as outlined by Federer (1956).

Analysis of Variance

Analysis of variance for quantitative character was held out as per standard statistical procedure for Augmented Randomized Complete Block Design (ARCBD) as given by Federer (1956).

ANOVA for Augmented Randomized Complete Block Design

Source of variation	Degree of freedom	SS (Sum of square)	MSS (Mean sum of square)	F Ratio
Block	(b-1)	SS(B)	MSS(B)	MSS(B)/MSSE
Check varieties	(v-1)	SS(V)	MSS(V)	MSS(V)/MSSE
Genotypes	(g-1)	SS(G)	MSS(G)	MSS(G)/MSSE
Genotypes /Check	[g+(v-1)]	SS(GV)	MSS(GV)	MSS(GV)/MSSE
Error	(v-1)(b-1)	SS(E)	MSS(E)	
Total	N-1	TSS		

Where,
b = No. of Block
v = No. of Check Varieties
g = No. of germplasm accession tested

The significance test was carried out by referring "F" table value given by Fisher and Yates 1936.

Estimation of mean, range, standard error, coefficient of variation and critical differences according to following formula:

i) Mean (X)

The mean value of each character was worked by dividing the total sum of values with corresponding number of observations.

$$\overline{X} = \frac{\sum X}{N}$$

Where,

$\sum X$ = summation of total observation

N = Total number of genotypes under study

ii) Range

The differences between highest and lowest values of each character were recorded.

iii) Standard error of difference

Standard error of difference between two treatment means was formulated by using the given equation:

$$SEm\pm = \sqrt{\frac{2EMS}{r}}$$

Where,

EMS = Error mean sum of square

r = number of replications in the experiment

iv) Coefficient of variation (CV)

CV is the ratio of standard deviation to the arithmetic mean. It is expressed as percentage.

$$CV = \frac{SD}{\overline{X}} \times 100$$

v) Critical difference (CD)

For every character, the critical difference as the difference of any two mean values in order to compare the treatment means was calculated using the following formula and tabulated 't' value at error degree of freedom and at 5 or 1% level of significance.

Critical difference was estimated by the formula:

$$CD = \sqrt{\frac{2EMS}{r}} \times t - value$$

Where,

t - value = tabulated value at error degree of freedom at 5 per cent or 1

per cent level of significance

Estimation of variability parameters

The following genetic parameters were estimated for the character having significant mean square due to the genotypes.

(a) Genotypic variance:

It was calculated using following formula

$$\text{Genotypic variance } VG = \frac{(MSg - MSe)}{r}$$

Where,

VG = Genotypic variance,

MSg = Mean square due to germplasm

MSe = Error mean square

r = Number of blocks

(b) Phenotypic variance:

It was calculated as follows:

$$Vp = Vg + Ve$$

Where,

Vp = Phenotypic variance,

Vg = Genotypic variance

Ve = Error variance i.e. MSE

(c) Genotypic coefficient of variation (GCV):

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

$$GCV = \frac{\sqrt{Vg}}{\overline{X}} \times 100$$

Where,

Vg = Genotypic variance

$\overline{X}$ = Population mean

(d) Phenotypic coefficient of variation (PCV):

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

$$PCV = \frac{\sqrt{Vp}}{\overline{X}} \times 100$$

Where,

Vp = phenotypic variance

$\overline{X}$ = Population mean

The genotypic and phenotypic coefficients of variation were categorized as per the classification given by Shivasubramaniam and Madhavamenon (1973):

0-10% = Low

10-20% = Medium

>20 = High

(e) Heritability in Broad sense (h2BS):

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

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

Where,

Vg = genotypic variance

Vp = phenotypic variance

h^2_{bs} = broad sense heritability

The calculated heritability was classified into three groups as suggested by Johnson et al. (1955).

0-30% = Low

30-60% = Medium

>60 = High

(f) (GA) = Genetic advance

$$GA = \frac{K.Vg}{\sqrt{Vp}}$$

Where,

Vg = Genotypic variance

Vp = Phenotypic variance

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

(g) 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).

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

Where,

$\overline{X}$ = Population mean

Classification of genetic advance was categorized as per the formula by Johansson et al. (1955)

0-10% = Low

10-20% = Medium

>20 = High

Results and Discussion

The mean sum of squares character of genotypes demonstrated significant differences for a majority of the evaluated traits, including days to 50 percent flowering, plant height (cm), number of secondary branches per plant, root length (cm), fresh root yield per plant, and fresh plant weight per plant (Table 1). These findings underscore the substantial variability present among the genotypes for these key characteristics, suggesting diverse genetic backgrounds and potential for selective breeding to enhance desired traits.

Table 1 : ANOVA for augmented RBD design

SN	Character	Block	Treatment	Check	Germplasm	C v/s G	Error
		[2]	[76]	[2]	[74]	[1]	[4]
1.	Days to 50% Flowering	0.11	12.95*	3.44	13.21*	12.21	1.94
2.	Days to 75% maturity	0.11	12.62	5.78	12.97	0.01	6.11
3.	Plant Height (cm)	9.56	11.46**	0.94	11.90	0.07	3.54
4.	Number of Primary Branches per plant	2.25*	0.91	0.02	0.94	0.47	0.19
5.	Number of Secondary Branches per plant	0.34	4.94**	0.27	5.08**	3.98*	0.20
6.	Leaf area Index	0.01	0.01	0.00	0.01	0.00	0.00
7.	Root Length(cm)	5.87	7.86**	4.32	8.04	1.33	7.72
8.	Root Diameter at Collar region(mm)	0.13	2.32	1.23	2.07	22.97*	2.62
9.	Fresh root Yield per plant (g)	6.38	8.71**	0.95	8.69*	25.72	5.84
10.	Dry plant weight per plant (g/plant)	13.53	87.53	3.72	89.27	126.47	22.22
11.	Fresh plant weight per plant (g/plant)	217.11	411.93*	62.67	394.98	2365.16**	68.17
12.	100 Seed weight (g)	0.00	0.00	0.00	0.00	0.00	0.00
13.	Harvest Index (%)	1.73	11.19	0.09	11.64	0.23	2.83
14.	Total Alkaloid content (%)	0.01	0.02	0.00	0.02	0.05	0.01
15.	Dry root Yield per plant (g)	0.09	0.66	0.03	0.67	1.33*	0.14

*, ** Significant at 5 % and 1 % level of significance, respectively

Understanding the genetic control of yield components is crucial for plant breeders striving to develop improved crop varieties. The success of breeding programs largely hinges upon the extent of genetic variability present within breeding materials, as greater diversity increases the likelihood of identifying promising and desired traits. However, the influence of the environment on quantitative and qualitative traits complicates the assessment of genetic variability. Therefore, parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), and genetic gain play vital roles in estimating the heritable and non-heritable components of observed variability. (Johanson *et al.,* 1955) emphasized the utility of heritability and genetic gain in predicting the effects of selection, highlighting their importance in breeding programs.

Table 2 : Genetic variability parameters of different characters in Ashwagandha

SN	Character	GCV	PCV	h^2	GA	GG
1	Days to 50% Flowering	4.04	4.37	85.29	6.39	7.68
2	Days to 75% maturity	1.85	2.55	52.89	3.92	2.77
3	Plant Height (cm)	7.76	9.25	70.23	4.99	13.39
4	Primary Branches per plant	26.13	29.22	79.97	1.60	48.15
5	Secondary Branches per plant	39.16	39.98	95.98	4.46	79.04
6	Leaf area Index	9.32	10.43	79.82	0.16	17.15
7	Root Length(cm)	3.49	17.56	3.94	0.23	1.43
8	Root Diameter at Collar region(mm)	10.51	20.89	75.29	0.75	10.89
9	Fresh root Yield per plant (g)	12.28	21.44	32.82	1.99	14.49
10	Dry plant weight per plant (g/plant)	24.52	28.29	75.11	14.62	43.78
11	Fresh plant weight per plant (g/plant)	18.21	20.01	82.74	33.87	34.11
12	100 Seed weight (g)	7.15	9.22	60.19	0.03	0.24
13	Harvest Index (%)	34.76	39.96	75.68	5.32	62.30
14	Total Alkaloid content (%)	18.56	31.87	33.89	0.10	22.25
15	Dry root Yield per plant (g)	27.14	30.58	78.73	1.33	49.60

Genotypic coefficient of variation

The magnitude of genotypic coefficient of variation (GCV) varied significantly across the studied traits, ranging from 1.85 percent in days to 75 percent maturity to 39.16 percent in secondary branches (Table 2). Specifically, GCV values were low (<10%) for traits such as days to 75% maturity (1.85%), root length (3.49%), days to 50% flowering (4.04%), 100 seed weight (7.15%), plant height (7.76%), and leaf area index (9.32%). Moderate levels of GCV (10-20%) were observed for root diameter in collar region (10.51%), fresh root yield (12.28%), fresh plant weight (18.21%) and alkaloid content (18.56%). Traits exhibiting high GCV (>20%) included dry plant weight (24.54%), primary branches per plant (26.13%), dry root yield (27.14%), harvest index (34.76%) and secondary branches (39.16%).

The observed variation in GCV among the studied traits reflects the underlying genetic diversity and potential for selection and improvement within the Ashwagandha (*Withania somnifera*) population. Traits with low GCV values (<10%), such as days to maturity, root length, days to flowering, and plant height, suggest limited genetic variability for these traits within the studied germplasm. This finding indicates that selection for these traits may yield minimal improvements in subsequent generations due to the low genetic diversity present.

On the other hand, traits with moderate GCV values (10-20%), including root diameter, fresh root yield, fresh plant weight, alkaloid content, and, exhibit a more promising degree of genetic variability. Moderate levels of GCV suggest that these traits are influenced by both genetic and environmental factors, providing opportunities for selection and improvement through breeding programs and agronomic interventions.

Furthermore, traits with high GCV values (>20%), such as dry plant weight, primary branches per plant, dry root yield, harvest index and secondary branches, demonstrate substantial genetic diversity within the population. High levels of GCV indicate a greater potential for selection and improvement, as these traits are primarily under genetic control with minimal influence from environmental factors. Selection for traits with high GCV can lead to significant gains in desired characteristics, such as increased yield, biomass, and adaptability to varying environmental conditions.

The consistency of the present findings with previous studies by Kumar *et al.* (2007), Yadav *et al.* (2008), Sangwan *et al.* (2013), Sundesha and Tank (2013), Joshi *et al.* (2014), Singh *et al.* (2014), Dev *et al.* (2015), and Deeksha (2020) reinforces the robustness and reliability of the observed genetic variability in Ashwagandha. These findings collectively underscore the importance of genetic diversity assessment in breeding programs, guiding breeders in selecting appropriate traits for improvement and developing superior cultivars with enhanced agronomic performance and yield potential.

Phenotypic coefficient of variation

The magnitude of phenotypic coefficient of variation (PCV) varied significantly across the studied traits, ranging from 2.55 percent in days to 75 percent maturity to 39.98 percent in secondary branches (Table 2). Specifically, PCV values were low (<10%) for traits such as days to maturity (2.55%), days to 50% flowering (4.37%), 100 seed weight (9.22%), and plant height (9.25%). Moderate levels of PCV (10-20%) were observed for leaf area index (10.43%), root length (17.56%), and fresh plant weight (20.01%). Traits exhibiting high PCV values (>20%) included root diameter (20.89%), fresh root yield (21.44%), dry plant weight (28.29%), primary branches (29.22%), dry root yield (30.58%), alkaloid content (31.87%), harvest index (39.96%), and secondary branches (39.98%).

The observed variation in PCV among the studied traits reflects the phenotypic diversity and potential for selection and improvement within the Ashwagandha (*Withania somnifera*) population. Traits with low PCV values (<10%), such as days to maturity, days to flowering, 100 seed weight, and plant height, suggest limited phenotypic variability for these traits within the studied germplasm. This finding indicates that phenotypic selection for these traits may result in minimal improvements due to the low diversity present in the phenotypic expression of these traits.

On the other hand, traits with moderate PCV values (10-20%), including leaf area index, root length, and fresh plant weight, exhibit a more promising degree of phenotypic variability. Moderate levels of PCV suggest that these traits are influenced by both genetic and environmental factors, providing opportunities for selection and improvement through breeding programs and agronomic practices aimed at optimizing environmental conditions.

Furthermore, traits with high PCV values (>20%), such as root diameter, fresh root yield, dry plant weight, primary branches, dry root yield, alkaloid content, harvest index, and secondary branches, demonstrate substantial phenotypic diversity within the population. High levels of PCV indicate a greater potential for phenotypic selection and improvement, as

these traits exhibit significant variability in their phenotypic expression across genotypes. Selection for traits with high PCV can lead to substantial improvements in desired characteristics, such as increased yield, biomass, and alkaloid content.

The consistency of the present findings with previous studies by Kumar *et al.* (2007), Yadav *et al.* (2008), Sangwan *et al.* (2013), Sundesha and Tank (2013), Joshi *et al.* (2014), Singh *et al.* (2014), Dev *et al.* (2015), and Deeksha (2020) validates the robustness and reliability of the observed phenotypic variability in Ashwagandha. These findings collectively highlight the importance of assessing phenotypic diversity in breeding programs, guiding breeders in selecting appropriate traits for improvement and developing superior cultivars with enhanced agronomic performance and yield potential.

Heritability

High estimates of heritability (>60%) were observed for several traits in the Ashwagandha (*Withania somnifera*) population, indicating a strong genetic control over these characteristics. Specifically, traits with high heritability values included secondary branches (95.98%), days to flowering (85.29%), fresh plant weight (82.74%), primary branches (79.97%), leaf area index (79.82%), dry root yield (78.73%), harvest index (75.68%), root diameter (75.29%), dry plant weight (75.11%), plant height (70.23%), 100 seed weight and days to 75% maturity (52.89%), (60.19%). Conversely, low estimates of heritability (0-50%) were observed for traits such as alkaloid content (33.89%), fresh root yield (32.82%), and root length (3.94%).

The high estimates of heritability (>60%) for several traits indicate that these characteristics are primarily governed by genetic factors rather than environmental influences. Traits with high heritability values, such as secondary branches, days to flowering, and fresh plant weight, demonstrate strong genetic control and are likely to respond favourably to selection in breeding programs. The high heritability observed for these traits suggests that genetic improvement efforts targeting these characteristics are likely to result in predictable and substantial improvements in subsequent generations.

Conversely, traits with low estimates of heritability (0-50%) exhibit greater susceptibility to environmental influences and may show less predictable responses to selection. For example, days to 75% maturity, alkaloid content, fresh root yield, and root length exhibit lower heritability values, indicating that environmental factors play a significant role in shaping these traits. While genetic improvement efforts targeting these traits may still be feasible, breeders may need to consider additional factors such as environmental conditions and management practices when selecting for desired characteristics.

The consistency of the present findings with previous studies 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), Nagar (2018), and Deeksha (2020) underscores the reliability and robustness of the observed heritability estimates in Ashwagandha. These findings provide valuable insights into the genetic control of key traits in Ashwagandha and can inform breeding strategies aimed at improving crop performance, yield potential, and quality attributes.

Genetic advance

The genetic advance, an indicator of the potential gain from selection, varied among the studied traits in the Ashwagandha (*Withania somnifera*) population. High estimates of genetic advance (>20%) were observed for fresh plant weight (33.87%) and dry plant weight (14.62%). Conversely, low estimates of genetic advance (<10%) were found for traits such as days to flowering (6.39%), harvest index (5.32%), plant height (4.99%), secondary branches (4.66%), days to 75% maturity (3.92%), fresh root yield (1.99%), primary branches (1.60%), dry root yield (1.33%), root diameter (0.75%), root length (0.23%), leaf area index (0.16%), alkaloid content (0.10), and 100 seed weight (0.03%).

The observed variation in genetic advance among the studied traits reflects the potential for improvement through selection within the Ashwagandha population. Traits with high genetic advance values (>20%), such as fresh plant weight and dry plant weight, demonstrate substantial potential for genetic improvement. These traits are likely influenced by a strong genetic component, allowing breeders to make significant gains in yield and biomass through targeted selection.

Conversely, traits with low genetic advance values (<10%) exhibit limited potential for improvement through selection. These traits may be influenced by a combination of genetic and environmental factors, resulting in smaller gains from selection efforts. While genetic improvement may still be possible for these traits, breeders may need to consider additional factors such as environmental management practices and trait interactions when selecting for desired characteristics.

The consistency of the present findings with previous studies by Mohsina and Dutta (2007), Sangwan *et al.* (2013), Nagar (2018), and Deeksha

(2020) reinforces the reliability and robustness of the observed genetic advance estimates in Ashwagandha. These findings provide valuable insights into the potential for genetic improvement and guide breeders in prioritizing traits for selection and breeding programs aimed at enhancing crop performance, yield potential, and quality attributes in Ashwagandha.

Conclusion

In conclusion, the assessment of genetic variability, heritability, and genetic advance in the Ashwagandha (*Withania somnifera*) population underscores the significant potential for crop improvement and breeding advancement. The substantial variability among genotypes for key agronomic traits highlights the diverse genetic backgrounds present within the population, offering ample opportunities for selective breeding to enhance desired characteristics. The variability in genotypic and phenotypic coefficients of variation reflects the extent of genetic and phenotypic diversity, guiding breeders in prioritizing traits for improvement. High heritability estimates for several traits indicate strong genetic control, facilitating predictable improvements through targeted selection. Additionally, the identification of traits with high genetic advance values highlights promising avenues for genetic enhancement. These findings, supported by previous research, provide valuable insights for breeders, informing strategic selection and breeding efforts aimed at improving crop performance, yield potential, and quality attributes in Ashwagandha, thereby contributing to its sustainable cultivation and utilization

References

Biennial progress report of AICRP on Medicinal & Aromatic Plant 2006-08.

Covello, M. and Ciampa, G. (1960). Paper chromotatography of *Withania somnifera*. Alkaloid *J. Chromatography*, **3**, 591-92.

Das, A., Datta, A.K., Ghose, S. and Bhattacharyya, A. (2011). Genetic analysis in Poshita and Jawahar 22 varieties of *Withania somnifera* (L.) Dunal (Solanaceae). *Plant Archives*, **1**(11), 59-62.

Das, A., Datta, A.K., Ghose, S. and Bhattacharyya, A. (2011). Genetic analysis in Poshita and Jawahar 22 varieties of Withania somnifera (L.) Dunal (Solanaceae). *Plant Archives*, **1(11)**, 59-62.

Deeksh (2020). Genetic Variability and Path Analysis for Dry Root Yield in Ashwagandha [*Withania somnifera* (L.) Dunal]. M.Sc. thesis submitted to Rajasthan College of Agriculture, MPUAT, Udaipur.

Deshpande, D.J. (2005). Commercial cultivation of medicinal and aromatic plants. *Himalaya Publishing house,* 203-206.

Dev, S., Dubey, R.B. and Ameta, K.D. (2015). Studies on variability and character association in Ashwagandha [*Withania somnifera* (L.) Dunal]. *Progressive Horticulture*, **47(1)**,154-157.

Dubey, R. B. (2010). Genetic variability, correlation and path analysis in Ashwagandha [*Withania somnifera* (L.) Dunal]. *Journal of Medicinal and Aromatic Plant Sciences,* **32(3)**, 202-205.

Gami, R.A., Solanki, S.D., Patel, M.P., Tiwari, K., Bhadauria, H.S. and Kumar, M. (2015). *International Journal of Agricultural Science and Research*, **5(5)**, 271-276.

Joshi, N.R., Patel, M.A., Prajapati, K.N. and Patel, A.D. (2014). Genetic variability, correlation and path analysis in ashwagandha *[Withania somnifera* (L.) Dunal]. *Electronic Journal of Plant Breeding*, **5(4)**, 875-880.

Mohsina, I. and Dutta, A.K. (2007). Genetic variability, correlation and path analysis in ashwagandha [*Withania somnifera* (L.) Dunal]. *Journal of Phytological Research*, **20(1)**,119-122.

Nagar, K. (2018). Studies on genetic divergence in ashwagandha [*Withania somnifera* (L.) Dunal]. M.Sc. thesis submitted to Rajasthan College of Agriculture, MPUAT, Udaipur.

Nigam, K.B. and Kandalkar, V.S. (2006). Ashwagandha – *Advances in Horticulture, Medicinal and Aromatic plants. Malhorta Publishing House*, New Delhi, India, **11**, 337-344.

Sangwan, O., Avtar, R. and Singh, A. (2013). Genetic variability, character association and path analysis in ashwagandha [*Withania somnifera* (L.) Dunal] under rainfed conditions. *Research in Plant Biology*, **3(2)**, 32-36.

Senthil, K. (2010). Medicinal plant research in India with special reference to Indian ginseng-Ashwagandha. In "*National Conference on Biotechnology*". North Maharashtra University, Jalgaon, 27.

Singh, A.K., Tirkey, A. and Nagvanshi, D. (2014). Study of genetic divergence in ashwagandha [*Withania somnifera* (L.) Dunal]. *International Journal of Basic and Applied Biology* (IJBAB), **2(1)**, 5-11.

Sundesha, D. L. and Tank, C. J. (2013). Genetic variability, heritability, expected genetic gain for dry root yield *in Ashwagandha* [Withania somnifera (L.) Dunal]. *Asian Journal of Horticulture,* **(8)2**, 475-477.

Yadav, O. P.; Kumar, Y. and Verma, P. K. (2008). Genetic variability, association among metric traits and path coefficient analysis in Ashwagandha (*Withania somnifera*). *Haryana Agriculture University Journal of Research*, **38(1/2)**, 23- 26.