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Elucidation of mean performance and variance components for different quantitative and biochemical traits for different environments in ashwagandha [*Withania somnifera* (L.) Dunal]

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Abstract
Ashwagandha is a well-known medicinal herb with various nutritional and pharmacological importance's in Indian medical system. This experiment was conducted to acquire information on mean performances, genotypic and phenotypic variability, heritability and genetic advance for various quantitative and biochemical traits in ashwagandha. It consisted of 96 genotypes that were raised in a randomized complete block design (RBD) in three replications over two different years *viz*; *rabi* 2020 and *rabi* 2021 with two different dates of sowing. Analysis of variance (ANOVA) of all eleven traits *viz.*, plant height (cm), primary branches per plant, days to 50% flowering, main root length per plant (cm), root girth per plant (cm), fresh root yield per plant (g), dry root yield per plant (g), total soluble sugar (%), starch content (%), total crude fiber (%) and withanolides (%) for each environment were calculated. For all of the traits, phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV), indicating that the environment has a masking impact on the expression of genetic variability. The differences between PCV and GCV were high for some traits and low for other traits which suggested that influence of environment was large for certain characters and small for other. Genotype AGP-22 exhibited the highest fresh root yield per plant in E2, E3 and E4 and second highest in E1. Also, in respect to dry root yield per plant and root girth per plant, AGP-22 manifested highest value in all the environments except for root girth per plant in E2 (AGP-72). High heritability coupled with high genetic advance as per cent mean were noticed for all the characters except for plant height, primary branches per plant, days to 50% flowering and main root length per plant.

Keywords: Variability, heritability, genetic advance, quantitative, biochemical

1. Introduction
Ashwagandha is botanically named as *Withania somnifera* (L.) Dunal is an utmost important medicinal plant. It belongs to family solanaceae and very well-known for its pharmacological properties and its nutritional benefits in Ayurveda. Commonly ashwagandha is known as Indian ginseng, Indian winter cherry (English) and asgandh or asodh (Hindi). Asgandh is derived from Sanskrit word 'ashwa means horse' and 'gandha means smell'. The smell of horse urine comes from damaged part of plants and roots. It is a self-pollinated crop having chromosome no. 2n=48 (Sharma *et al.*, 2014) [18]. It is believed that consuming the powdered root of this plant on a daily basis will delay senescence, revitalize the muscles and reproductive organs, and boost fertility. Alkaloids, amino acids, steroids, volatile oil, starch, and reducing sugars are all present in its roots (Uddin *et al.*, 2012) [24]. The medicines made from its roots are used to treat a variety of conditions, including rheumatoid arthritis, joint inflammation (Al-Hindawi *et al.*, 1992) [1], nervous system problems, female disorders, hiccups, coughs and colds, ulcers, leprosy, and as sedatives.
The lack of information about genetic variation, inter- and intra-specific variability, and genetic relationships among *W. somnifera* is one of the key obstacles preventing the large-scale production and development of improved cultivars (Kujur *et al.*, 2021) [15]. The economic value of root yield in ashwagandha depends on a variety of other factors. Many of these traits are quantitatively inherited and are very sensitive to changes in the environment. As a result, efforts are conducted to examine genetic variation in order to improve the therapeutic plant *W. somnifera* (Bhat *et al.*, 2012) [4]. The goal of the current study was to better understand the mean performance, phenotypic and genotypic coefficient of variation, its heritability and

genetic advance in the quantitative traits, which would enable genetic improvement to create superior cultivars that will benefit both growers and consumers.

2. Materials and Methods

This experiment consists of 96 genotypes of ashwagandha that were raised in a randomized block design (RBD) in three replications. It was done under two different years (*rabi* 2020 and *rabi* 2021) with two different dates of sowing at Medicinal and Aromatic Plants Research Station, Anand Agricultural University, Anand, Gujarat. A total of four different environments were taken for this investigation with seven quantitative and four biochemical traits. Five plants were randomly selected from each experimental unit in all the replications for recording the observations except for days to 50 per cent flowering. The eleven traits were plant height (cm), days to 50% flowering, number of primary branches per plant, main root length per plant (cm), root girth per plant (cm), fresh root yield per plant (g), dry root yield per plant (g), total soluble sugar (%), starch content (%), crude fiber (%) and withanolides (%). Genetic parameters were calculated using variability package in R studio.

3. Results and Discussion

3.1 Analysis of variance (ANOVA)

Ninety-six genotypes of ashwagandha were investigated in *rabi* 2020-21 and *rabi* 2021-22 with two different dates of sowing for its genetic variability parameters study. The results showed that the mean sum of square due to genotypes were highly significant for all the characters in all the individual environments which indicates the presence of high genetic variability in the genetic material used and tested in the experiment (Table1). The absolute variability, which can be evaluated through phenotypic and genotypic variances by getting the coefficients of variability, may not be shown by analysis of variance. Furthermore, the environmental effect must be separated from total variability. The range of variation can be accurately measured in terms of percentage mean with respect to genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance.

Table 1: Analysis of variance showing mean squares for various characters under individual environments

Source of variation	df	Plant height				Primary branches per plant				Days to 50% flowering			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replication	2	7.18	7.90	253.89	0.56	0.48	0.53	0.15	1.87*	54.42	3.61	23.51	51.15
Genotypes	95	178.02**	127.15**	189.76**	194.63**	1.21**	2.45**	1.31**	0.61**	36.94**	55.64**	117.38**	37.68**
Error	190	54.06	51.41	84.45	53.39	0.79	0.40	0.72	0.40	19.61	12.35	15.00	22.41

Source of variation	df	Main root length per plant				Root girth per plant				Fresh root yield per plant			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replication	2	18.79	13.48	24.31	2.77	1.27	1.08	1.21	0.14	4.41	1.57	13.04	6.58
Genotypes	95	17.81**	36.19**	49.22**	25.98**	2.35**	2.87**	2.84**	2.13**	47.24**	50.15**	50.46**	37.55**
Error	190	8.95	6.53	10.53	7.68	0.50	0.51	0.50	0.49	3.76	3.41	5.52	5.02

Source of variation	df	Dry root yield per plant				Total soluble sugar				Starch content			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replication	2	0.51	0.14	0.84	3.36*	0.0008	0.0019	0.0013	0.0027	0.48	1.50	0.77	0.77
Genotypes	95	6.13**	5.64**	5.02**	4.65**	0.2129**	0.2038**	0.2068**	0.1986**	133.57**	143.06**	148.39**	141.02**
Error	190	0.53	0.48	0.78	0.74	0.0011	0.0010	0.0010	0.0009	0.70	0.94	0.74	0.96

Source of variation	df	Crude fiber				Withanolides			
		E1	E2	E3	E4	E1	E2	E3	E4
Replication	2	0.13	0.12	2.25	1.98	0.0002	0.0003	0.0001	0.0002
Genotypes	95	33.67**	28.04**	26.37**	30.28**	0.0371**	0.0374**	0.0390**	0.0385**
Error	190	1.18	1.11	0.93	1.07	0.0002	0.0002	0.0002	0.0002

*, ** Significant at 5% and 1% level of significance, respectively
(E1: 09/10/2020, E2: 09/11/2020, E3: 09/10/2021, E4: 09/11/2021)

3.2 Range values (Table 2) of genotypes in different environments with its mean performance

a) Quantitative Traits

For plant height (cm) data showed significant differences among genotypes for this character and it varied from 101.90 to 62.92 cm (E1), 98.02 to 59.83 cm (E2), 103.85 to 51.67 cm (E3) and 105.68 to 51.75 cm (E4) with general mean 81.15 cm (E1), 71.53 cm (E2), 69.58 cm (E3) and 71.53 cm (E4). Among all the genotypes, AGP-57 (101.90 cm) was tallest in E1 and AGP-79 (98.02 cm) was tallest in E2 but AGP-22 was tallest in both E3 (103.85 cm) and E4 (105.68 cm). In case of primary branches higher values are preferred for number of branches per plant. Data varied from 6.90 to 3.40 branches (E1), 8.07 to 2.87 branches (E2), 6.47 to 3.33 (E3) and 5.47 to 3.13 branches (E4) with general mean of 4.79 branches (E1), 5.25 branches (E2), 4.78 branches (E3) and 4.09 branches (E4). It was observed from the data that genotype AGP-14 (6.90) had the highest number of branches per plant in E1, AGP-79 (8.07) in E2, AGP-88 (6.47) in E3 and AGP-81 (5.47) in E4.

Mean values for days to 50% flowering ranged from 65.33 to 81.33 days (E1), 62.33 to 78.33 days (E2), 57.33 to 78.33 days (E3) and 61.67 to 77.0 days (E4) with a general mean of 71.51 days (E1), 69.87 (E2) days, 67.42 days (E3) and 68.63 days (E4). The genotype AGP-4 (65.33 days) was the earliest to flower in E1, AGP-82 (62.33 days) in E2, AGP-46 (57.33 days) in E3 and AGP-47 (61.67 days) in E4. Main root length (cm) per plant showed high range of variability in different environment *viz.*, E1 (17.54 to 29.15 cm), E2 (14.87 to 31.37 cm), E3 (15.41 to 33.33 cm) and E4 (16.88 to 30.99 cm) with

general mean of 21.23 cm (E1), 21.05 cm (E2), 21.41 (E3) and 22.92 cm (E4). From the data, it was analyzed that genotype AGP-22 manifested highest main root length per plant in E2 (31.37 cm), E3 (33.33 cm) and E4 (30.99 cm) while AGP-81 had highest main root length per plant in E1 (29.15 cm). Root is the most economical part of ashwagandha plant as it has wide range of pharmaceutical properties, data also showed significant differences among genotypes for this trait.

For the trait root girth range varied from E1(3.93 to 7.94 cm), E2 (3.62 to 8.28 cm), E3 (4.56 to 10.79 cm) and E4 (4.08 to 8.29 cm) with general mean of E1 (5.54 cm), E2 (5.70 cm), E3 (6.36 cm) and E4 (5.66 cm). Among all the genotypes, it was observed that AGP-22 had the highest root girth per plant in all the three environments viz., E1 (7.94 cm), E3 (10.79 cm), E4 (8.29 cm) except in E2 having AGP-79 (8.28 cm) as highest. Fresh root yield (g) is an important trait and it showed significant differences among genotypes which ranged from 6.60 to 21.07 g (E1), 5.37 to 23.75 g (E2), 7.47 to 26.80 g (E3) and 6.87 to 26.53 g (E4) with general mean of 12.88 (E1), 13.92 (E2), 15.23 (E3) and 13.47 (E4). From the perusal of data, it was observed that the highest fresh root yield per plant was recorded for AGP-22 in all the three environments viz., E2 (23.75 g), E3(26.80 g) and E4 (26.53 g) except for E1 (21.07 g) which had AGP-70 as the highest fresh root yield per plant.

Dry root yield per plant (g**)** showed significant differences among the genotypes for this trait, and it varied from E1 (2.60 to 8.0 g), E2 (2.33 to 8.17 g), E3 (2.90 to 9.53 g) and E4 (2.67 to 9.43 g) with general mean of E1 (4.74 g), E2 (5.05 g), E3 (5.48 g) and E4 (4.92 g). Among all the genotypes, genotypes AGP-70 (8.0 g) had the highest dry root yield per plant in E1, AGP-22 (8.17 g) in E2, AGP-22 (9.53 g) in E3 and AGP-22 (9.43) in E4.

b) Biochemical Traits

The genotypic difference was found significant for total soluble sugar, which ranged from 0.32 to 1.46% in E1, 0.31 to 1.45% in E2, 0.33 to 1.44% in E3 and 0.34 to 1.41% in E4, with the average performance of 0.79% (E1), 0.79% (E2), 0.79% (E3) and 0.80% (E4). Among all the genotypes AGP-50 produced highest total soluble sugar content in all the four environments *viz*., E1(1.46), E2 (1.45%), E3 (1.44%) and E4 (1.41%). For starch content (%) significant differences was observed among genotypes and showed wide range of variability from 10.06 to 34.21% (E1), 9.95 to 34.36% (E2), 9.75 to 33.67% (E3) and 9.68 to 33.37% (E4) with general mean of 20.26% (E1), 20.06% (E2), 20.0% (E3) and 19.95% (E4). From the perusal of data, it was observed that genotype AGP-3 performed highest starch content in both environment E1 (34.21%) and E2 (34.36%) while genotype AGP-26 and AGP-50 showed highest starch content in E3 (33.67%) and E4 (33.37%) respectively.

The character showed wide range of variability for crude fiber (%) from 15.06% to 27.06% (E1), 15.54 to 27.26% (E2), 15.41 to 27.11% (E3) and 15.43 to 27.16% (E4) with general mean of 21.83% (E1), 21.98% (E2), 21.97% (E3) and 21.73% (E4). From the data, it was observed that genotype AGP-47 (27.11%) showed highest crude fiber content in both E2 and E3 while genotype AGP-14 (27.06) showed highest in E1 and AGP-66 (27.16%) showed highest in E4. Withanolides content is one of the most important alkaloids present in ashwagandha genotypes used as therapeutic agents for treatment of various diseases and disorders. Genotypic differences were found significant for withanolides content (%), which ranged from 0.14 to 0.62% (E1), 0.14 to 0.60% (E2), 0.13 to 0.61% (E3) and 0.14 to 0.62% (E4) with the general mean of 0.30% in all the four environments. AGP-42 had highest withanolides content of 0.62% in E1, 0.62% in E2, 0.61% in E3 and 0.62% in E4.

3.3 Phenotypic and genotypic coefficient of variation (Table 2)

The absolute variability, which can be evaluated through phenotypic and genotypic variances by getting the relevant coefficients of variability, may not be shown by analysis of variance (ANOVA). Furthermore, the environmental effect must be separated from total variability. This reflects how far a genotype can be identified by its phenotypic performance. The relative proportion of heritable and inheritable variation can be determined by evaluating the genotypic and phenotypic coefficient of variation. For initiating any breeding programme, it is extremely important to understand the kind and amount of genetic diversity present in the population. The phenotypic coefficient of variation (PCV) estimates in the present investigation was higher than the genotypic coefficient of variation (GCV) estimates for all of the traits. But the difference was relatively small for some traits and high for other traits. It shows that some traits were less influenced by the environment for small differences and other traits were highly influenced by the environment for large differences.

Table 2: Estimates of variance components and other genetic parameters for different characters of ashwagandha genotypes in four environments

CHR	ENV	Mean	Range		σ^2g	σ^2p	GCV (%)	PCV (%)	h^2_b(%)	GA% Mean
			MIN	MAX						
PH	E1	81.15	62.92	101.9	41.32	95.38	7.92	12.04	0.4332	10.74
	E2	71.53	59.83	98.02	25.25	76.65	7.02	12.24	0.3294	8.31
	E3	69.58	51.67	103.85	35.10	119.55	8.52	15.71	0.2936	9.51
	E4	71.53	51.75	105.68	47.08	100.47	9.59	14.01	0.4686	13.53
PBP	E1	4.79	3.40	6.90	0.14	0.93	7.84	20.15	0.1515	6.29
	E2	5.25	2.87	8.07	0.68	1.08	15.75	19.82	0.6313	25.77
	E3	4.78	3.33	6.47	0.20	0.92	9.32	20.03	0.2166	8.94
	E4	4.09	3.13	5.47	0.07	0.47	6.47	16.80	0.1483	5.13
DFL	E1	71.51	65.33	81.33	5.78	25.39	3.36	7.05	0.2276	3.30
	E2	69.87	62.33	78.33	14.43	26.78	5.44	7.41	0.5388	8.22
	E3	67.42	57.33	78.33	34.13	49.13	8.66	10.4	0.6946	14.88

	E4	68.63	61.67	77.00	5.09	27.50	3.29	7.64	0.1852	2.91
MRLP	E1	21.23	17.54	29.15	2.95	11.91	8.09	16.25	0.2481	8.31
	E2	21.23	14.87	31.37	9.89	16.41	14.94	19.24	0.6023	23.88
	E3	21.41	15.41	33.33	12.90	23.42	16.77	22.60	0.5507	25.64
	E4	22.93	16.88	30.99	6.10	13.78	10.77	16.19	0.4427	14.76
RGP	E1	5.55	3.93	7.94	0.61	1.12	14.13	19.07	0.549	21.56
	E2	5.71	3.62	8.28	0.79	1.30	15.54	19.98	0.6055	24.92
	E3	6.36	4.56	10.79	0.78	1.28	13.88	17.77	0.6102	22.33
	E4	5.67	4.08	8.29	0.55	1.03	13.03	17.94	0.5277	19.50
FRYP	E1	12.88	6.60	21.07	14.49	18.25	29.55	33.16	0.7939	54.23
	E2	13.92	5.37	23.75	15.58	18.99	28.35	31.30	0.8204	52.89
	E3	15.23	7.47	26.80	14.98	20.50	25.40	29.72	0.7306	44.73
	E4	13.47	6.87	26.53	10.84	15.86	24.44	29.56	0.6834	41.62
DRYP	E1	4.74	2.60	8.00	1.87	2.40	28.82	32.66	0.7787	52.39
	E2	5.05	2.33	8.17	1.72	2.20	26.00	29.37	0.7838	47.41
	E3	5.48	2.90	9.53	1.41	2.19	21.69	27.04	0.6434	35.84
	E4	4.92	2.67	9.43	1.30	2.04	23.21	29.02	0.6394	38.23
TSS	E1	0.79	0.32	1.46	0.07	0.07	33.58	33.84	0.9847	68.64
	E2	0.79	0.31	1.45	0.07	0.07	32.8	33.04	0.9854	67.07
	E3	0.79	0.33	1.44	0.07	0.07	32.97	33.21	0.9856	67.44
	E4	0.80	0.34	1.41	0.07	0.07	32.14	32.36	0.9865	65.76
SC	E1	20.26	10.06	34.21	44.29	44.99	32.85	33.10	0.9844	67.13
	E2	20.06	9.95	34.36	47.37	48.31	34.31	34.64	0.9806	69.98
	E3	20.00	9.75	33.67	49.22	49.96	35.07	35.33	0.9851	71.70
	E4	19.95	9.68	33.37	46.69	47.65	34.26	34.61	0.9799	69.86
CF	E1	21.83	15.06	27.06	10.83	12.01	15.08	15.88	0.9021	29.50
	E2	21.98	15.54	27.26	8.98	10.08	13.63	14.45	0.8903	26.50
	E3	21.97	15.41	27.11	8.48	9.41	13.26	13.96	0.9015	25.93
	E4	21.73	15.43	27.16	9.74	10.80	14.36	15.13	0.9012	28.08
WTH	E1	0.30	0.14	0.62	0.01	0.01	36.92	37.22	0.9840	75.43
	E2	0.30	0.14	0.60	0.01	0.01	36.72	37.01	0.9841	75.05
	E3	0.30	0.13	0.61	0.01	0.01	37.78	38.07	0.9847	77.24
	E4	0.30	0.14	0.62	0.01	0.01	37.86	38.15	0.9846	77.40

σ^2g – Genotypic variance
σ^2p – Phenotypic variance
GCV – Genotypic coefficient of variation
PCV – Phenotypic coefficient of variation
h^2_b – Broad sense heritability
GA% Mean – Genetic advance as per cent of mean
CHR – Characters
ENV – Environment
PH- Plant height
PBP- Primary branches per plant
DFL- Days to 50% flowering
MRLP- Main root length per plant
RGP- Root girth per plant
FRYP- Fresh root yield per plant
DRYP- Dry root yield per plant
TSS- Total soluble sugar
SC- Starch content
CF- Crude fiber
WTH- Withanolides

a) Quantitative Traits

The results revealed that for plant height estimates of GCV in E1 (7.92%), E2 (7.02%), E3 (8.51%) and E4 (9.59%) were low while value of PCV in E1 (12.03%), E2 (12.23%), E3 (15.71%) and E4 (14.01%) were moderate which indicates more influence of environment on expression of trait. Similar results for moderate GCV and PCV were also reported by Das *et al.* (2011) [7], Bharathi *et al.* (2013) [3], Bhosale and More (2013) [5] and Joshi *et al.* (2014), Kujur *et al.* (2021) [15]. For primary branches per plant estimates of GCV (15.74%) and PCV (19.81%) was moderate for E2 indicated the presence of insufficient variability in the genotypes for this environment. In E1 (7.84%), E3 (9.32%) and E4 (6.46%) estimates of GCV were low while moderate values of PCV was observed for E1 (20.14%), E2 (19.81%), E3 (20.03%) and E4 (16.79%) which suggests more contribution of environment for expression of trait. Singh *et al.* (2014) [19], Sundesha and Tank (2013) [22] and Joshi *et al.* (2014) reported GCV and PCV in lower magnitude for number of primary branches per plant in ashwagandha.

For days to 50% flowering estimates of GCV in E1 (3.36%), E2 (5.43%), E3 (8.66%) and E4 (3.28%) were low, while value of PCV in E1 (7.04%), E2 (7.40%), E3 (10.39%) and E4 (7.64%) were also low that revealed low variability in the genotypes under study. Low GCV and PCV values were also reported by Sangwan *et al.* (2013) [17], Sundesha and Tank (2013) [22], Gami *et al.* (2016) [10] and Kujur *et al.* (2021) [15] in this crop. For main root length per plant estimates of GCV in E1 (8.09%), E2 (14.93%), E3 (16.77%) and E4 (10.77%) were low to moderate while values of PCV in E1 (16.24%), E2 (19.24%), E3 (22.60%), and E4 (16.18%) were moderate indicating insufficient variability for this trait. The close estimates of GCV and PCV values suggested genetic constitution of character play important role in expression of character than environment. Tiwari *et al.* (2002) [23], Dubey (2010) [8], Kumar *et al.* (2007) [16], Kakaraparthi *et al.* (2013) [13], Sundesha and Tank (2013) [22], Joshi *et al.* (2014) and Singh *et al.* (2014) [19] reported moderate GCV and PCV for this trait under their respective studies.

For root girth per plant high estimates of GCV in E1 (14.12%), E2 (15.54%), E3 (13.88%) and E4 (13.03%) while, values of PCV in E1 (19.06%), E2 (19.97%), E3 (17.76%)

and E4 (17.94%) for this trait indicated the presence of appreciable variability in the genotypes. The small differences between GCV and PCV also confirmed the environment had little role in the expression of this trait. Moderate GCV and PCV were reported by Sangwan *et al*. (2013) [17], Dubey (2010) [8] and Kujur *et al*. (2021) [15]. From the perusal of data, it was observed that for fresh root yield per plant estimates of GCV in E1 (29.54%), E2 (28.34%), E3 (25.40%) and E4 (24.43%), while value of PCV in E1 (33.15%), E2 (31.29%), E3 (29.72%) and E4 (29.56%) were high, indicating fair amount of variability was present in the population. A small difference between GCV and PCV indicated a little role of environment in the expression of the trait. Bharathi *et al.* (2013) [3], Sangwan *et al.* (2013) [17], Srivastava *et al*. (2018) [21] and Kujur *et al*. (2021) [15] reported moderate values for GCV and PCV for this character.

For dry root yield per plant (g) estimates of GCV in E1 (28.82%), E2 (26.0%), E3 (21.69%) and E4 (23.21%), while value of PCV in E1 (32.66%), E2 (29.37%), E3 (27.04%) and E4 (29.02%) were high, indicating fair amount of variability was present for dry root yield per plant in the population. Tiwari *et al.* (2002) [23], Dubey (2010) [8], Kumar *et al.* (2007) [16], Kakaraparthi *et al.* (2013) [13], Joshi *et al.* (2014) and Singh *et al.* (2014) [19] reported moderate to high values among genotypes and less differences between two coefficients of variation. These all results are summarized in table 2 and depicted in Fig. 1.

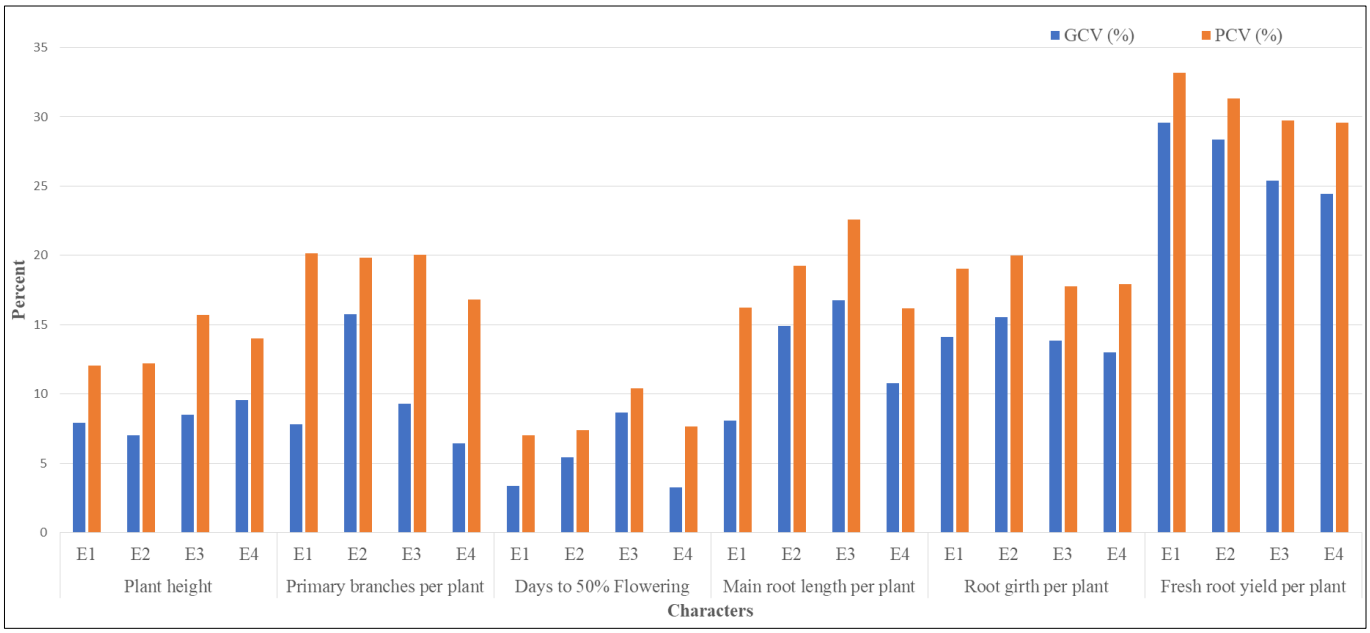

Fig 1: Graphical representation of GCV and PCV for qualitative traits in ashwagandha (E1: 09/10/2020, E2: 09/11/2020, E3: 09/10/2021, E4: 09/11/2021)

b) Biochemical Traits

Estimates of both GCV and PCV value were high (33.58%, 32.80%, 32.97% and 32.14%) and (33.84%, 33.04%, 33.21% and 32.36%) in E1, E2, E3 and E4 respectively for total soluble sugar. The small differences between GCV and PCV confirmed the environment had little role on the expression of this trait. Khanna *et al.* (2006) [14] and Gulati *et al.* (2017) [11] reported similar results for the character under study. For the trait starch content values of both GCV and PCV were high 32.85, 34.31, 35.07 and 34.26% and 33.10, 34.64, 35.33 and 34.61% in E1, E2, E3 and E4, respectively, indicating sufficient variability in studied population for starch content. The close estimates of GCV and PCV values suggested genetic constitution of character play important role in expression of character than environment**.** Joshi *et al.* (2014) and Chauhan *et al.* (2018) [6] reported similar results. Values of GCV and PCV for total crude fiber were moderate (15.08%, 13.63%, 13.26% and 14.36%) and (15.88%, 14.45%, 13.96% and 15.13%) in E1, E2, E3 and E4 respectively, indicating sufficient variability for crude fiber contents. Gulati *et al.* (2017) [11] and Chauhan *et al.* (2018) [6] reported the similar results. The most important trait Withanolides content have value high of estimates of GCV and PCV (36.91%, 36.71%, 37.78% and 37.85%) and (37.21%, 37.01%, 38.07% and 38.15%) in E1, E2, E3 and E4 respectively, indicating ample variability in studied population for withanolides content. Kumar *et al.* (2007) [16], Sangwan *et al*. (2013) [17] and Chauhan *et al*. (2018) [6] also found the similar results. These all results are summarized in table 2 and depicted in Fig. 2.

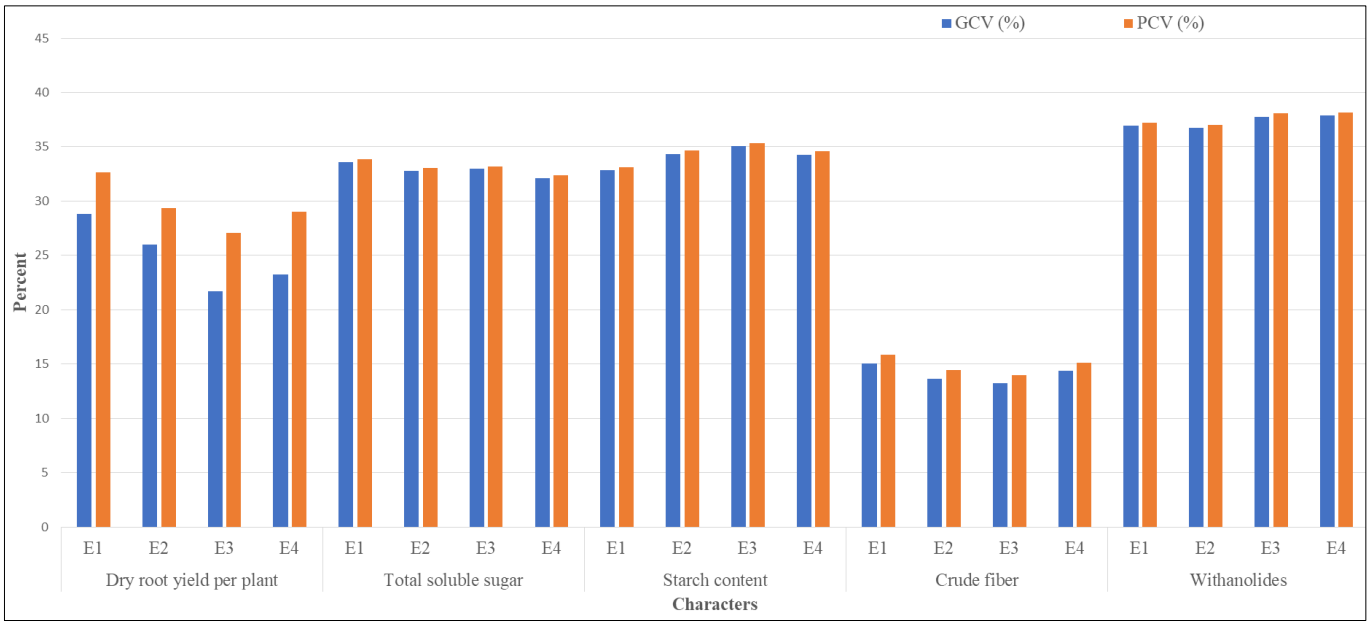

Fig 2: Graphical representation of GCV and PCV for biochemical traits in ashwagandha (E1: 09/10/2020, E2: 09/11/2020, E3: 09/10/2021, E4: 09/11/2021)

3.2 Broad sense heritability and genetic advance as per cent of mean (Table 2)

Heritability refers to the heritable component of phenotypic variation. It shows how traits are passed from parents to their offspring's (Falconer, 1989) [9]. Broad sense heritability is defined as the proportion of genotypic variance to phenotypic variance. It is measured in terms of percentages. Heritability estimates alone are insufficient to predict the response to selection. As a result, estimating heritability in relation with genetic advance appeared to be more useful. Genetic advance is defined as an improvement in the mean genotypic value of selected plants over the parental population. It is a measurement for how much genetic progress has been made as a result of selection. The success of genetic progress under selection is determined by three key factors: genetic variability, heritability and selection intensity (Allard, 1960) [2].

a) Quantitative Traits

For the trait plant height (cm) moderate genetic advance as per cent of mean (10.74%) accompanied with moderate broad sense heritability (43.32%) was observed in E1, low genetic advance as per cent of mean (8.31%) with moderate heritability (32.92%) in E2, low genetic advance as per cent of mean (9.51%) with moderate heritability (29.36%) in E3, moderate genetic advance as per cent of mean (13.53%) with moderate heritability (46.86%) in E4 which suggested the presence of non-additive gene effects in the expression of this trait. The low and moderate heritability exhibited due to favorable influence of environment rather than genotype and selection for such trait may not be rewarding. Low heritability with low genetic advance was reported by Singh *et al*. (2014) [19]. High heritability with high genetic advance was also observed by Bharathi *et al.* (2013) [3], Bhosale and More (2013) [5], Sundesha and Tank (2013) [22], Kakaraparthi *et al.* (2013) [13], Joshi *et al.* (2014) and Srivastava *et al*. (2018) [21]. For the trait primary branches per planthigh heritability in E2 (63.13%) along with high genetic advance (25.77%) indicated this trait for this environment was under the predominance of additive gene action. Low heritability in E1 (15.15%), E3 (21.66%) and E4 (14.83%) along with low genetic advance as per cent of mean in E1 (6.28%), E3 (8.93) and E4 (5.12%) which suggests presence of non-additive gene effects in the expression of this trait. The low heritability exhibited due to favourable influence of environment rather than genotype and selection for such trait may not be rewarding. Bharathi *et al.* (2013) [3], Bhosale and More (2013) [5], Sundesha and Tank (2013) [22], Joshi *et al.* (2014) and Srivastava *et al.* (2018) [21] reported high heritability coupled with high genetic advance.

In case of 50 per cent flowering heritability was found to be high for E3 (69.46%) coupled with moderate genetic advance as per cent of mean (14.87%) which indicates the presence of non-additive gene effects in the expression of this trait. The high heritability exhibited due to favorable influence of environment rather than genotype and selection for such trait may not be rewarding. Moderate heritability (53.88%) in E2 along with low genetic advance as per cent of mean (8.22%) and in E1 (22.76%) and E4 (18.52%) low heritability was observed with low genetic advance as per cent of mean that all suggests involvement of non-additive gene effect for expression of this trait and hence population improvement approach would be most effective for improvement of this character. Low heritability with low genetic advance was reported by Singh *et al*. (2014) [19], Sangwan *et al*. (2013) [17] and Gami *et al*. (2016) [10] reported high heritability for this trait in ashwagandha. For main root length, estimates of GCV in E1 (8.09%), E2 (14.93%), E3 (16.77%) and E4 (10.77%) were low to moderate while values of PCV in E1 (16.24%), E2 (19.24%), E3 (22.60%), and E4 (16.18%) were moderate indicating insufficient variability for main root length per plant. The close estimates of GCV and PCV values suggested genetic constitution of character play important role in expression of character than environment. Tiwari *et al.* (2002) [23], Dubey (2010) [8], Kumar *et al.* (2007) [16], Kakaraparthi *et al.* (2013) [13], Sundesha and Tank (2013) [22], Joshi *et al.* (2014) and Singh *et al*. (2014) [19] reported moderate GCV and PCV for this trait under their respective studies.

High genetic advance as per cent of mean for root girth per plant was observed in E2 (24.91%) and E3 (22.33%) coupled with high heritability in E2 (60.55%) and E3 (61.02%)

suggesting that there is ample scope for improvement of this trait through simple selection. In E1 (54.9%) and E4 (52.77%) moderate heritability was observed along with high genetic advance per cent of mean in E1 (21.56%) to moderate genetic advance as per cent of mean in E4 (19.50%). suggesting that genes with additive effect were largely responsible for variation among genotypes for this trait. Hence, there would be a good response to the selection for improvement of the character. Moderate heritability with moderate genetic advance was also reported by Dubey (2010) [8], Sangwan *et al.* (2013) [17] and Kujur *et al*. (2021) [15]. For trait fresh root yield per plant heritability was found to be high in E1 (79.39%), E2 (82.04%), E3 (73.06%) and E4 (68.34%) coupled with high genetic advance as per cent of mean (54.23%, 52.88%, 44.73% and 41.61%) in E1, E2, E3 and E4 respectively, which indicated the predominance of additive gene action in the expression of the character and independence of phenotypic expression reflect the genotypic ability to transmit the genes to their offspring. Hence, selection may be made in the desired direction based on phenotypic performance. High heritability with high genetic advance as per cent of mean was reported by Kujur *et al*. (2021) [15]. Moderate genetic advance with moderate heritability was observed by Bharathi *et al.* (2013) [3], Sangwan *et al.* (2013) [17] and Srivastava *et al.* (2018) [21].

For dry rot yield per plant heritability was found to be high 77.87%, 78.38%, 64.34% and E4 63.94 coupled with high genetic advance as per cent of mean 52.39, 47.41, 35.83 and 38.22% in E1, E2, E3 and E4, respectively, which indicated the predominance of additive gene action in the expression of the character and independence of phenotypic expression reflect the genotypic ability to transmit the genes to their offspring. Hence, selection may be made in the desired direction based on phenotypic performance. Tiwari *et al.* (2002) [23], Dubey (2010) [8] and Joshi *et al.* (2014) stated high heritability with high genetic advance. While Kakaraparthi *et al.* (2013) [13], Singh *et al.* (2014) [19] and Kujur *et al*. (2021) [15] reported moderate heritability coupled with moderate genetic advance for this trait. These all results are summarized in table 2 and depicted in Fig. 3.

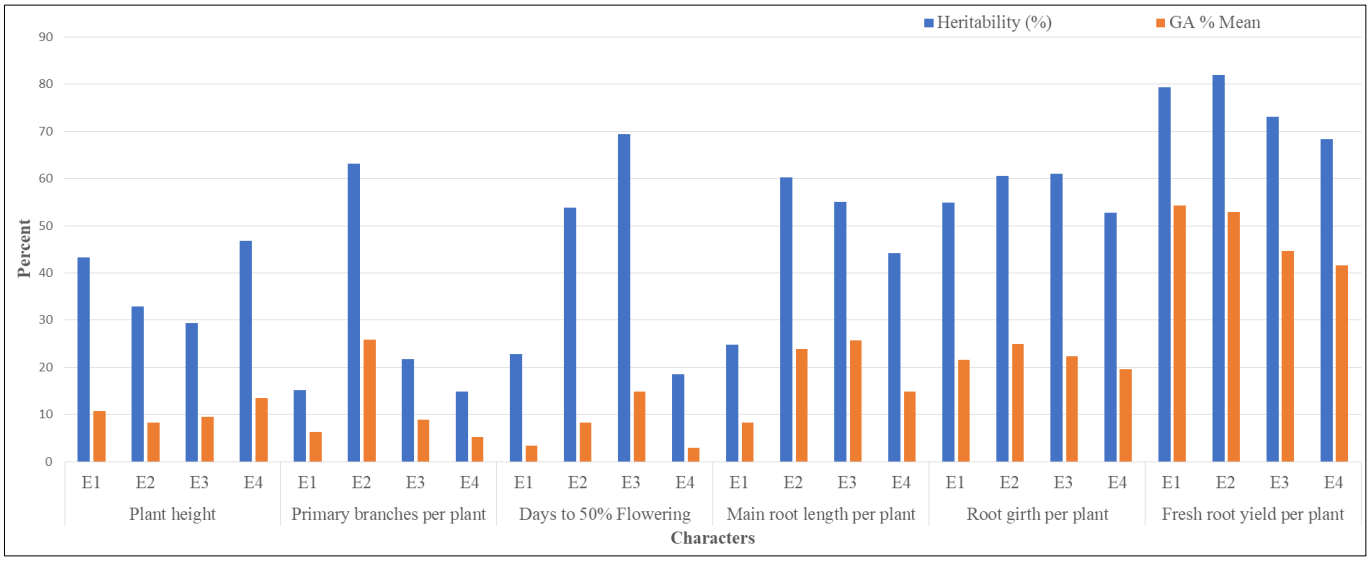

Fig 3: Graphical representation of broad sense heritability and genetic advance as per cent of mean for quantitative traits in ashwagandha (E1: 09/10/2020, E2: 09/11/2020, E3: 09/10/2021, E4: 09/11/2021)

b) Biochemical traits

For total soluble sugar heritability was found to be high in 98.47, 98.54, 98.56 and in 98.65% for total soluble sugar, which was accompanied with high genetic advance 68.64, 67.07, 67.44 and 65.76% in E1, E2, E3 and E4, respectively, suggesting that there is scope for improvement of total soluble sugar through selection. The results are in accordance with Khanna *et al.* (2006) [14] and Gulati *et al.* (2017) [11]. The per cent genetic advance was high in E1 (98.44%), E2 (98.06%), E3 (98.51%) and E4 (97.99%), which were accompanied by high heritability in E1 (67.13%), E2 (69.98%), E3 (71.70%) and E4 (69.86%) indicates that most likely the heritability is due to additive gene effects and selection may be effective. The results are in accordance with Joshi *et al.* (2014) and Chauhan *et al.* (2018) [6].

In case of crude fiber estimates of heritability was found to be high 90.21, 89.03, 90.15 and in 90.12% for crude fiber content, which was accompanied by high genetic advance 29.50, 26.50, 25.93 and 28.08% in E1, E2, E3 and E4, respectively, suggesting that genes with additive effect were largely responsible for variation among genotypes for this trait. Hence, improvement in total crude fiber content is possible through simple selection. The results are in accordance with Gulati *et al.* (2017) [11], Singh *et al*. (2017) [20] and Chauhan *et al.* (2018) [6]. Also, Kujur *et al*. (2021) [15] reported high heritability with high genetic advance as per cent of mean for this trait in ashwagandha. High genetic advance as per cent of mean was observed in 75.42, 75.04, 77.23 and in 77.40% coupled with high heritability 98.40, 98.41, 98.47 and 98.46% in E1, E2 E3 and E4, respectively, suggesting that there is scope for improvement of withanolides content through selection. The results are in accordance with Kumar *et al.* (2007) [16], Sangwan *et al.* (2013) [17] and Chauhan *et al.* (2018) [6]. These all above mentioned results of heritability and genetic advance as per cent of mean for biochemical traits are summarized in table 2 and depicted in Fig. 4.

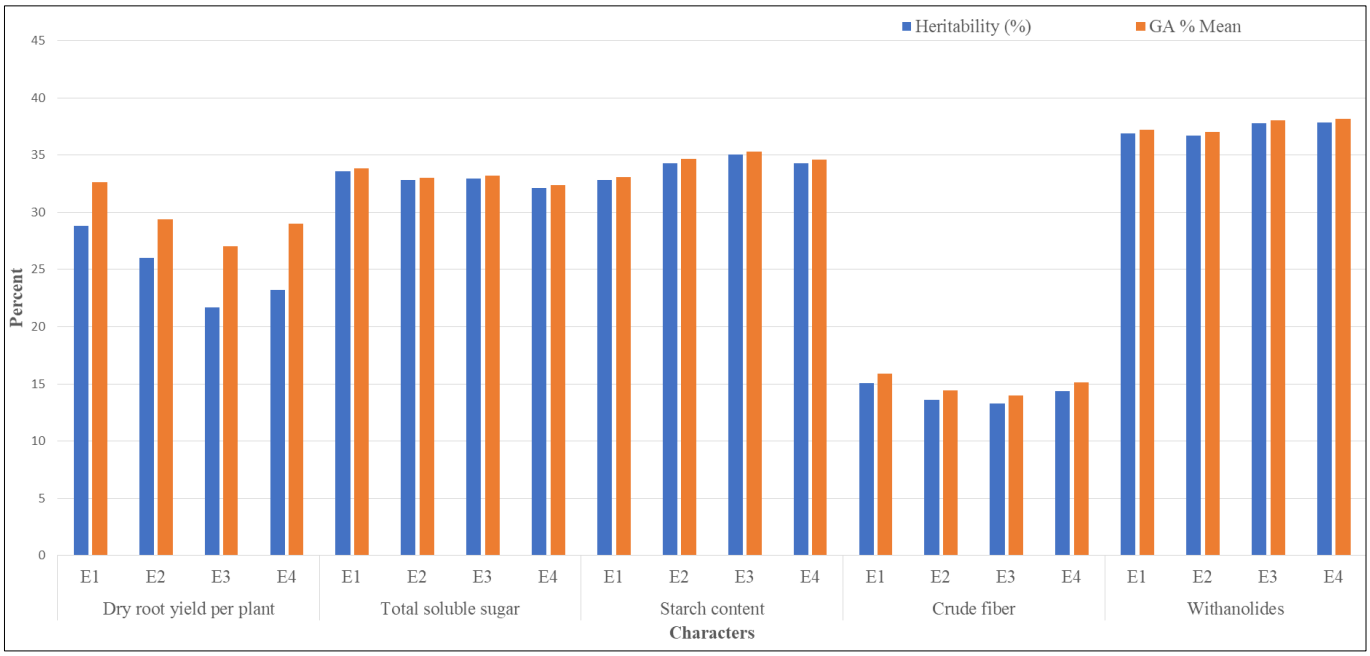

Fig 4: Graphical representation of broad sense heritability and genetic advance as per cent of mean for biochemical traits in ashwagandha (E1: 09/10/2020, E2: 09/11/2020, E3: 09/10/2021, E4: 09/11/2021)

In respect to fresh root yield per plant, genotype AGP-22 exhibited the highest fresh root yield per plant in E2, E3 and E4 and second highest in E1. Also, in respect to dry root yield per plant and root girth per plant, AGP-22 manifested highest value in all the environments except for root girth per plant in E2 (AGP-72). This genotype AGP-22 showed highest main root length per plant in E2, E3 and E4, while AGP-81 showed highest main root length per plant in E1. AGP-22 was found elite genotypes in all the environments for important morphological root traits as it shows promising results based on *per se* performance. In all the environments, AGP-50 had the highest total soluble sugar content, while genotype AGP-42 had the highest withanolides content and thereby were promising for quality traits. Wide genetic variability can be exploited through selection and breeding for improved varieties and parents for hybrids. Genetic variability is the raw material of crop breeding on which selection acts to evolve superior genotypes. The higher amount of variation presents for a character in the breeding materials, the greater the scope for its improvement through selection.

Low difference between phenotypic and genotypic variance was observed in all the characters except plant height, primary branches per plant, days to 50% flowering and main root length per plant indicating less influence of environment on the expression of characters in all environments under study. It suggested that selection could be possible based on the phenotypic expression of characters.GCV and PCV were high for fresh weight per plant, dry weight per plant, total soluble sugar content, starch content and withanolides content offering better scope for selection due to less influence of environment and suggesting potential variability available in germplasm for these traits. While GCV and PCV were low to moderate for plant height, primary branches per plant, days to 50% flowering and main root length per plant in all environments which indicated low to moderate variability was available in studied genotypes for these traits.

High heritability coupled with high genetic advance as per cent mean were noticed for all the characters except for plant height, primary branches per plant, days to 50% flowering and main root length per plant which suggested additive gene action and hence, these traits may be improved through hybridization followed by selection. Root girth per plant, on the other hand, exhibited moderate heritability with moderate genetic advance which suggest that character could be controlled by additive and non-additive gene action, whereas plant height and days to 50% flowering had moderate heritability coupled with low genetic advance, suggesting preponderance of non-additive gene action for this action.

4. Conclusion

Identification of genotypes with higher dry root yield per plant along was possible amongst the genotypes studied. In the present study, AGP-22 was found promising in the three environments *viz.*, E2, E3, E4 and genotype AGP-70 had highest dry root yield per plant in E1. Characters viz., main root length per plant, fresh root yield per plant, dry root yield per plant, total soluble sugars, starch content, crude fiber and withanolides had moderate to higher genotypic and phenotypic coefficient of variation which indicated moderate to higher amount of variability present among ashwagandha genotypes for these traits in E1, E2, E3 and E4. Most of the characters had high heritability coupled with high genetic advance indicating predominance of additive gene action in all environments.

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7. Conflict of interest statement

The authors declare that they have no conflict of interest in the publication. All the information related to this article is well-known by all the authors.

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