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Research Article

Multi-environment evaluation of combining ability and heterosis for root yield and attributing traits in ashwagandha [*Withania somnifera* (L.) Dunal]

Preeti Basser[1]*, Hemlata Sharma[1], Amit Dadheech[1], Ruchi Bishnoi[2] and Puneet Basser[3]

[1]Department of Genetics and Plant Breeding, Maharana Pratap University of Agriculture and Technology, Udaipur, Rajasthan, India.
[2]Department of Genetics and Plant Breeding, College of Agriculture, Ummedganj-Kota, Rajasthan.
[3]Department of Physiology, Institute of medical sciences, Banaras Hindu University, Varanasi, India.
***E-Mail**: basserpreeti1410@gmail.com

Abstract

Ashwagandha (*Withania somnifera*), a vital medicinal crop, suffers from limited genetic diversity, which constrains its yield potential on a commercial scale. Exploiting combining ability and heterosis can serve as effective breeding strategies to enhance productivity and alkaloid content. A comprehensive study was conducted during *Rabi* 2022-2023, involving 60 hybrids, their parental lines and standard checks (JA-20, JA-134 and RVA-100), evaluated in a randomized block design across three diverse environments. Significant variability was observed for alkaloid content, dry root yield and its contributing traits. To refine parent selection, combining ability analysis was performed, revealing that both general combining ability (GCA) and specific combining ability (SCA) were significantly influenced by environmental interactions. Parents, including UWS-23, UWS-60, UWS-13, UWS-79, UWS-100, UWS-104, UWS-131, UWS-134, GP-49 and GP-51, exhibited significant positive general combining ability (GCA) effects for dry root yield, indicating the predominance of additive gene action. Among these, UWS-100 emerged as a promising general combiner for both dry root yield and total alkaloid content. Furthermore, specific cross combinations such as UWS-104 × UWS-60, UWS-132 × UWS-10, and UWS-92 × UWS-10 demonstrated high standard heterosis for dry root yield over the superior check variety JA-20 in environment E_3. These hybrids also showed significant positive specific combining ability (SCA) effects, highlighting the role of non-additive gene action in trait expression. These findings highlight the potential of identified genotypes for use in hybrid breeding programs aimed 5at improving both yield and phytochemical composition in Ashwagandha. The integration of heterosis exploitation with combining ability analysis provides a strategic approach for developing superior Ashwagandha cultivars, offering significant scope for commercial cultivation and enhanced utility in the medicinal plant industry.

Keywords: Ashwagandha; Alkaloid content; Dry root yield; GCA; SCA; heterosis

INTRODUCTION

Withania somnifera, often referred as Ashwagandha or Indian ginseng, is a highly regarded medicinal herb belonging to the *Solanaceae* family, renowned for its therapeutic properties that are deeply embedded in Ayurvedic tradition. It is an herbaceous perennial plant native to the Indian subcontinent. In India, it is widely cultivated for its medicinal properties, particularly in the northwestern region of Madhya Pradesh, with an area of 5,000 hectares. Other major producing states include Rajasthan, Gujarat, Uttar Pradesh, Punjab, Haryana, Andhra Pradesh and Maharashtra. In total, approximately 10,768 hectares of land across India are cultivating Ashwagandha (Khabiya *et al.,* 2024). It is mainly cultivated for its roots and leaves which are rich in bioactive compounds such as alkaloids, steroidal lactones (withanolides) (Basser *et al*., 2024) and flavonoids known for their pharmacological significance (Mishra *et al*., 2000; Singh *et al*., 2011).The root of the Ashwagandha plant serves as significant economic asset, prized for its therapeutic properties in both Ayurvedic and Unani medicine. It is used to treat various ailments such as rheumatism, pulmonary diseases, hiccups, women health disorders and dermatological problems. Additionally, Ashwagandha root is recognized for its role as an aphrodisiac, liver tonic, anti-inflammatory agent and for venom detoxification and ulcer treatment. Its versatile applications highlighted its importance in traditional medicinal formulations. (Ahmed *et al*., 2023).

Beyond these benefits, hybrids also serve as a rapid conduit for deploying dominant genes that confer resistance to diseases and pests, as highlighted by Riggs in 1988. Ashwagandha exhibits notable heterotic effects, making it a promising candidate for hybrid breeding programs aimed at improving yield and quality traits. Heterosis, or hybrid vigor, is characterized by superior performance observed in the hybrid offspring compared to their parents, a phenomenon that holds great potential for enhancing Ashwagandha productivity and medicinal value (Chandrasekhar *et al*., 2012).This phenomenon holds immense potential for agricultural improvement, offering avenues to enhance productivity, achieve early maturation, ensure uniformity, elevate quality and broaden adaptability. The dynamic interplay of genetics in heterosis provides a valuable toolkit for advancing various aspects of crop development and resilience in agriculture.

Therefore, integrating the assessment of heterosis with combining ability analysis is crucial for effective parent selection and hybrid development in Ashwagandha. This approach not only helps identify superior genotypes for key traits such as dry root yield and alkaloid content but also provides insights into the stability and expression of these traits across environments. The present investigation was undertaken to evaluate heterosis and combining ability in Ashwagandha, aiming to identify promising parental lines and cross combinations for developing high-yielding, alkaloid-rich genotypes suitable for commercial cultivation and medicinal use.

MATERIALS AND METHODS

During the *Rabi* 2021-22, a line x tester mating design was employed at the Instructional Farm of Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur. The objective was to perform controlled crosses between 20 female parental lines and three male testers to get 60 F_1 crosses. During the subsequent *Rabi* 2022-2023, the experimental material comprising of 86 genotypes including 20 lines *viz*.,UWS-13, UWS-18, UWS-79, UWS-89, UWS-92, UWS-98, UWS-106, UWS-104, UWS-100, UWS-120,UWS-122, UWS-129, UWS-131,UWS-134, UWS-132, UWS-135, UWS-140, GP-49, GP-50 and GP-51; three testers *viz*., UWS-10,UWS-23, UWS-60 and their resultant 60 F_1 crosses along with three checks JA-20, JA-134 and RVR-100 was evaluated using a randomized block design with three replications across three distinct locations. The experimental locations included Instructional Farm at Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur (E_1) (24°58'N; 73°68'E; 582.17 m above mean sea level), Agricultural Research Station (ARS) in Banswara (E_2) (23°55'N; 74°43'E; 302.00 m above mean sea level) and the Krishi Vigyan Kendra in Chittorgarh (E_3) (24°88'N; 74°63'E; 394 m above mean sea level). E_1 exhibits a subtropical humid climate with an annual rainfall of 637 mm and features deep, well-drained clay loam soil of alluvial origin with good moisture holding capacity. E_2 is characterized by a subtropical humid climate with higher annual rainfall of 825.90 mm and the soil in E_2 is red, clay loam, medium black in color and medium to heavy in texture. E_3 represents a sub-humid climate in the southern plain and Aravali hill zone, with an average annual rainfall of 852 mm and the soil in E_3 is grey-brown loam, medium black, moderately deep and medium to heavy in texture. A row-to-row spacing of 30 cm and a plant-to-plant distance of 10 cm were maintained to ensure optimal growth conditions and facilitate systematic evaluation. Observation for traits *viz* Root length (cm) (RL), Root diameter (mm) (RD), Dry root yield (g/plant) (DRY) and Alkaloid content (TA) were recorded on ten randomly selected competitive plants from each plot in each replication for all the characters except for days to 50 % flowering and days to maturity where the observation were recorded on plot basis. Standard agricultural practices were followed to ensure optimal crop growth and development, including appropriate irrigation, fertilization and pest management techniques.

Statistical analysis followed are missing: Heterobeltiosis and economic heterosis were estimated as the percentage deviation of F_1 hybrids from the better parent and standard check, respectively in the desirable direction. The calculations were carried out following the methods described by Shull (1908), Fonseca and Patterson (1968) and Meredith and Bridge (1972), for both individual and pooled data across environments. The combining ability effects in the line × tester mating design were analyzed according to the procedure outlined by Kempthorne (1957), considering each environment separately as well as across environments.

RESULTS AND DISCUSSION

Understanding the nature of gene action associated with specific varieties and traits is essential for aligning breeding strategies with defined program objectives. Combining ability analysis serves as a valuable tool in this regard, offering insights into the genetic variance attributed to general combining ability (GCA) and specific combining ability (SCA), which correspond to additive and non-additive gene effects, respectively. It is well established that dominance effects contribute to non-additive genetic variance. Similar results were also reported by Senthil *et al.* (2024) in sweet corn. GCA analysis enables the identification of superior lines and testers for traits such as dry root yield, highlighting their potential utility in hybrid breeding programs. Meanwhile, significant SCA effects reveal specific hybrid combinations with high heterotic potential, making them ideal candidates for exploitation in heterosis breeding (Bagher and Jelodar, 2010). Breeders rely on these variance components to understand underlying gene actions and to assess the genetic merit of parental lines in hybrid development (Gramaje *et al*., 2020). The results (**Table 1**) revealed that in individual environments the mean sum of squares due to lines except TA in E_1 and E_2 among lines, DRY in E_1 and E_2 and TA in E_1 and E_2 among testers and TA in E_1 in L x T were found to be significant for all characters in all three environments. Significant mean sum of squares due to lines and testers indicated that lines and testers played a significant role in the overall combining effects. Similar to L x T, significant mean squares indicated a significant contribution of crosses for SCA effects emphasizing the influence of particular cross combinations on trait expression and genetic interactions. Pooled analysis (**Table 2**) revealed that the mean sums of squares due to lines were found to be significant for most of the traits except TA. The mean sum of squares due to tester were found to be significant only for RD and between L x T the mean sum of squares were found to be significant for all the traits. The pooled variance attributed to genotype x environment was highly significant for most of the traits except RD and TA. Additionally, significant interactions between L and E were found to be significant for FRY and TA indicating that environmental variations impacted the

Table 1. Analysis of variance in each individual environment for different characters in Ashwagandha

S.N.	Characters	Env	Rep	Genotype	Lines	Tester	L X T	Error
		[2]	[2]	[85]	[19]	[2]	[38]	[166]
1	RL	1	0.00	28.41**	14.85**	11.09*	25.43**	3.10
		2	0.12	28.34**	13.22**	12.29**	29.88**	2.35
		3	0.00	27.79**	13.05**	6.82*	29.79**	1.55
2	RD	1	0.00	5.78**	4.75**	8.06**	3.45**	0.34
		2	0.03	4.01**	4.28**	3.73**	3.68**	0.37
		3	0.01	5.60**	7.34**	3.84**	4.03**	0.07
3	DRY	1	0.04	1.60**	1.762**	1.31	1.33**	0.71
		2	0.02	1.04**	1.001*	0.43	0.77*	0.50
		3	0.01	1.60**	1.67**	2.45**	1.10**	0.13
4	TA	1	0.00	0.02*	0.018	0.001	0.01	0.01
		2	0.02	0.02*	0.021	0.014	0.02*	0.01
		3	0.01	0.02**	0.027**	0.004	0.02*	00.01

** indicates 1% level of significant and * indicates 5% level of significant.

Table 2. Pooled analysis of variance for different characters in Ashwagandha

S.N.	Source	d.f.	RL	RD	DRY	TA
1.	Replicates	2	0.07	0.03	0.01	0.002
2.	Environments	2	1726.47**	196.97**	14.97**	0.007
3.	Rep. x Env.	4	0.02	0.03	0.03	0.004
4.	Genotypes	82	76.38**	11.57**	3.10**	0.025**
	Line	19	82.34**	12.26**	2.67**	0.020
	Testers	2	3.22	3.36**	0.09	0.025
	L x T	38	64.19**	12.06**	1.94**	0.026**
5.	G x E	164	1.99	0.87**	0.58	0.020**
	L x E	38	1.66	0.31	0.76	0.022*
	T x E	4	0.84	0.20	0.03	0.030
	L x T x E	76	1.69	0.98**	0.59	0.018
	Pooled Error	492	2.29	0.25	0.53	0.014

** indicates 1% level of significant and * indicates 5% level of significant.

lines. The mean sum of squares attributed between T and E were found to be significant for NSTR and mean sum of squares attributed between L x T x E were found to be significant for most of the traits except RD. This finding suggests that environmental factors had a substantial influence on the estimates of GCA and SCA effects across all the traits studied. The high environmental influence implies that trait expression and genetic interactions were significantly impacted by varying environmental conditions during the study. Similar findings were reported by Ahmed *et. al*. (2023), Dhuri (2016) and Sahu (2015).

For RL (**Table 3**), parent UWS-129 demonstrated the highest significant positive GCA effects in E_1, E_2, E_3 and on pooled basis. Meanwhile, maximum significant positive SCA effects was showed by cross UWS-92 x UWS-23 across environments and on pooled basis. For RD (**Table 3**) parent UWS-106 in E_1, UWS-122 in E_2, UWS-106 in E_3 and UWS-106 on pooled basis showed highest significant positive GCA effects. Highest significant positive SCA effects was showed in cross UWS-92 x UWS-23 in E_1, UWS-92 x UWS-60 in E_2, UWS-92 x UWS-23 in E_3 and UWS-92 x UWS-23 on pooled basis. Traits like RL and RD play pivotal roles in nutrient acquisition, water uptake and overall plant vigor. By identifying parental lines and hybrids with superior root traits, breeders can enhance the efficiency of nutrient and water utilization, leading to improved crop performance and resilience to abiotic stresses. Similar findings for RL and RD were also reported by Balakrishnan *et al*. (2021). For DRY (**Table 3)** parental line UWS-104 demonstrated the maximum significant positive GCA effects in E_2 and E_3 and crosses include UWS-134 x UWS-60, UWS-131 x UWS-10, UWS-120 x UWS-60 and UWS-131 x UWS-10 demonstrated the highest significant positive SCA effects across environments. Traits such as FRY and DRY directly influence crop productivity and economic returns for farmers. Similar findings were reported by Ahmed *et al.* (2023), Balakrishnan *et al*. (2021) and Sahu (2015). For TA **(Table 3)** parent UWS-122 in E_1, UWS-140 in E_2, UWS-100 in E_3 and UWS-100 on pooled basis showed highest significant positive GCA effects. Among crosses UWS-79 x UWS-10 in E_2, UWS-106 x UWS-10 in E_3 and UWS-79 x UWS-10 on pooled basis showed maximum significant positive SCA effects for TA. Similar results were also reported by Ahmed *et al.* (2023). Developing cultivars with enhanced root yield potential can contribute to food security and livelihood improvement for agricultural communities. Thus, the insights gleaned from this research not only advance our understanding of genetic mechanisms governing agronomic traits but also provide valuable guidance for breeders striving to develop high-yielding and resilient crop varieties tailored to diverse agro ecological contexts. These findings align with prior research conducted by Sahu (2015) and Tirkey (2016).

The findings from combining ability analysis form the genetic basis for exploiting hybrid vigor in crop improvement. The practical application of these genetic insights is exemplified by the commercial use of heterosis, which relies heavily on the selection of parents with high GCA and cross combinations with significant SCA. The strategic use of hybrid vigor remains a pivotal approach to enhancing crop performance and yield potential, underlining the importance of understanding gene interactions. Heterosis, a genetic manifestation of heterozygosity achieved through hybridization, was further quantified in terms of heterobeltiosis and economic heterosis to reveal the influence of dominance and overdominance in trait expression.

Root characteristics are vital in Ashwagandha since the economic value of the plant is determined by its root yield. To improve root biomass yield, longer RL and RD are necessary. For RL (**Table 4**) significant positive heterobeltiosis on pooled basis was observed in UWS-18 x UWS-60, UWS-79 x UWS-60 and UWS-18 x UWS-23. For RD (**Table 4**) on pooled basis crosses, UWS-132 x UWS-10, UWS-134 x UWS-60 and UWS-131 x UWS-60 showed significant positive heterobeltiosis and significant standard heterosis showed by cross UWS-106 x UWS-10 in E_1 and E_3 over the best check (JA-134).Ahmed *et al*. (2022) presented comparable results regarding heterosis in RL and RD.

For DRY (**Table 5**) out of sixty crosses, sixteen exhibited significant positive heterobeltiosis across environments on pooled basis. The cross UWS-140 x UWS-23 demonstrated the highest significant positive heterobeltiosis for DRY. Economic heterosis in Ashwagandha is vital for plant breeding as it can lead to crosses with improved growth rates, higher root yield and better stress tolerance. These advancements can enhance the economic viability of Ashwagandha cultivation, meeting the rising demand for its medicinal uses. Among crosses evaluated for dry root yield, three crosses *viz*., UWS-104 x UWS-60 and UWS-132 x UWS-10 and UWS- 92 x UWS-10 exhibited significant positive heterosis over the best check (JA-20) in the E_3 environment highlights their potential as superior combinations for the enhancement of this critical trait in Ashwagandha cultivation. Plants and their various parts exhibit significant variability in secondary metabolism, with alkaloids being one of the most extensively studied groups of these compounds (Chauhan *et al.,* 2019). On pooled basis, four crosses UWS-13 x UWS-60, UWS-140 x UWS-10, UWS-135 x UWS-10 and UWS-98 x UWS-10 demonstrated significant positive heterobeltiosis for TA (**Table 5**). Similar results were reported by Ahmed *et al*. (2023).

In conclusion, the assessment of GCA effects on pooled basis identified ten parental lines, including UWS-23, UWS-60, UWS-13, UWS-79, UWS-100, UWS-104, UWS-131, UWS-134, GP-49 and GP-51, as promising general combiners for enhancing DRY and UWS-100 for TA across different locations in Ashwagandha crop. Among crosses

Table 3. GCA and SCA effects for RL, RD, DRY and TA

S.N.	Genotypes	RL				RD				DRY				TA			
		E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool
1	UWS-10	0.34	-0.03	0.12	0.14	0.29**	0.25**	0.15**	0.23**	0.02	0.01	0.06	0.03	-0.004	-0.01	0.009	-0.004
2	UWS-23	-0.48*	-0.43*	-0.38*	-0.43**	-0.41**	-0.23**	-0.29**	-0.31**	0.13	0.08	0.16**	0.12*	0.005	0.01	-0.002	0.005
3	UWS-60	0.13	0.46*	0.25	0.28**	0.12	-0.02	0.13**	0.07	-0.16	-0.08	-0.22**	-0.15**	-0.001	0.007	-0.007	0.001
4	UWS-13	0.23	0.44	0.30	0.33	-1.01**	-0.76**	-1.03**	-0.93**	0.57*	0.44	0.21	0.41**	-0.006	0.003	0.075	0.024
5	UWS-18	0.54	0.98	1.46**	1.00**	1.00**	-0.12	0.40**	0.42*	0.35	0.17	0.23	0.25	0.011	-0.016	0.013	0.003
6	UWS-79	-1.35*	-0.96	-2.16**	-1.49**	-0.58**	-1.40**	-1.29**	-1.09**	-0.29	-0.09	-0.60**	-0.33*	0.00	-0.013	-0.001	-0.005
7	UWS-89	-0.36	-0.55	-0.59	-0.50	-0.76**	0.16	-0.20*	-0.26	0.34	0.09	0.06	0.16	0.05	0.046	0.01	0.035
8	UWS-92	-0.34	1.51**	0.27	0.48	-1.33**	-1.02**	-1.55**	-1.30**	0.27	0.05	0.36**	0.23	0.069	0.062	-0.007	0.041*
9	UWS-98	-1.41*	-0.39	-0.78	-0.86**	0.81**	0.34	0.82**	0.66**	-0.45	-0.07	0.30*	-0.07	0.023	0.048	0.025	0.032
10	UWS-100	-0.44	-1.15*	-0.2	-0.61*	0.71**	0.53**	1.29**	0.84**	0.40	0.29	0.36**	0.35*	0.044	0.078	0.084*	0.069**
11	UWS-104	0.59	-0.01	1.75**	0.78**	-0.49*	0.01	-0.30**	-0.25	0.71*	0.61*	0.58**	0.63**	0.027	-0.029	0.016	0.005
12	UWS-106	-0.57	-1.13*	0.37	-0.43	1.05**	0.70**	1.52**	1.09**	-0.07	-0.07	0.22	0.02	-0.046	-0.049	0.002	-0.031
13	UWS-120	-0.52	-0.82	-0.30	-0.55*	0.31	0.48*	0.71**	0.50*	0.24	0.21	0.21	0.22	-0.047	-0.037	-0.031	-0.038*
14	UWS-122	0.33	0.03	0.16	0.17	0.51*	1.00**	0.57**	0.69**	0.12	0.12	0.27*	0.17	0.092*	0.053	0.051	0.065**
15	UWS-129	3.67**	3.37**	2.59**	3.21**	-0.40*	-0.61**	-0.57**	-0.52**	0.17	0.20	-0.20	0.05	-0.055	-0.04	-0.105**	-0.067**
16	UWS-131	-0.88	-0.65	-1.50**	-1.01**	0.38	-0.37	0.16	0.05	-0.60*	-0.61*	-0.26*	-0.49**	0.027	0.032	0.045	0.035
17	UWS-132	0.59	0.88	0.08	0.52	0.69**	0.57*	0.57**	0.59**	-0.56*	-0.52*	0.28*	-0.27	-0.069	-0.088*	-0.128**	-0.095**
18	UWS-134	-2.76**	-2.59**	-2.47**	-2.61**	0.19	0.65**	0.58**	0.47*	-0.80**	-0.34	-0.91**	-0.69**	-0.014	-0.008	-0.057	-0.026
19	UWS-135	-0.05	-0.12	-0.13	-0.10	0.69**	0.84**	1.00**	0.85**	0.09	0.03	-0.50**	-0.12	-0.031	0.001	-0.046	-0.025
20	UWS-140	1.68**	0.39	0.44	0.84**	-0.17	-0.42*	-0.46**	-0.35	-0.33	-0.15	-0.10	-0.19	0.021	0.084*	-0.037	0.023
21	UWS-93	0.22	-0.01	-0.37	-0.05	-0.26	0.30	-0.15	-0.03	-0.64*	-0.62*	-0.63**	-0.63**	0.003	-0.03	0.023	-0.001
22	UWS-95	0.66	0.36	0.69	0.57*	-0.89**	-1.00**	-0.79**	-0.89**	0.17	-0.03	-0.44**	-0.10	-0.04	-0.042	0.019	-0.021
23	UWS-96 -	0.17	0.38	0.42	0.32	-0.47*	0.17	-1.27**	-0.52**	0.31	0.30	0.54**	0.38**	-0.059	-0.056	0.05	-0.022
24	UWS-13 x UWS-10	-0.73	-0.86	-0.31	-0.63	-0.45	-0.81*	-0.84**	-0.70*	-0.94	-0.79	-0.35	-0.69**	-0.02	-0.09	-0.02	-0.04
25	UWS-13 x UWS-23	4.30**	4.52**	4.31**	4.38**	0.75*	0.63	1.10**	0.83*	-0.03	0.15	0.29	0.13	-0.11	-0.10	-0.15*	-0.12**
26	UWS-13 x UWS-60	-3.57**	-3.66**	-4.00**	-3.75**	-0.29	0.18	-0.26	-0.12	0.96	0.65	0.07	0.56*	0.13	0.18**	0.16*	0.16**
27	UWS-18 x UWS-10	-4.67**	-5.03**	-5.34**	-5.02**	-1.23**	-0.50	-0.54**	-0.76*	0.21	0.41	-0.30	0.11	-0.11	-0.11	-0.07	-0.09**
28	UWS-18 x UWS-23	2.99**	2.20*	2.50**	2.56**	-0.63	0.10	0.05	-0.16	0.45	0.16	-0.27	0.11	0.09	0.07	0.05	0.07*
29	UWS-18 x UWS-60	1.69	2.83**	2.84**	2.45**	1.86**	0.39	0.49**	0.91**	-0.66	-0.57	0.57**	-0.22	0.02	0.03	0.01	0.02
30	UWS-79 x UWS-10	0.89	0.58	1.83*	1.10*	0.53	-0.42	-0.24	-0.05	0.45	0.49	-0.53*	0.14	0.03	0.00	-0.06	-0.01
31	UWS-79 x UWS-23	-3.34**	-4.08**	-3.76**	-3.73**	-0.21	0.23	0.58**	0.20	0.01	-0.15	0.03	-0.04	-0.02	-0.01	-0.13	-0.05
32	UWS-79 x UWS-60	2.45*	3.50**	1.93**	2.63**	-0.32	0.19	-0.33*	-0.15	-0.45	-0.34	0.50*	-0.10	-0.02	0.01	0.18**	0.06
33	UWS-89 x UWS-10	2.94**	3.21**	2.22**	2.79**	0.42	-0.62	0.61**	0.14	-0.61	-0.34	0.48*	-0.15	0.01	-0.01	-0.09	-0.03
34	UWS-89 x UWS-23	-1.73	-1.89*	-1.07	-1.56**	-1.26**	-1.08**	-1.73**	-1.35**	0.01	0.31	-0.20	0.04	0.01	0.01	0.03	0.02
35	UWS-89 x UWS-60	-1.21	-1.32	-1.15	-1.23*	0.83*	1.71**	1.11**	1.22**	0.59	0.02	-0.28	0.11	-0.02	0.00	0.06	0.02

Table 3. Continued...

S.N.	Genotypes	RL				RD				DRY				TA			
		E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool
36	UWS-92 x UWS-10	-4.10**	-6.86**	-5.35**	-5.44**	0.35	0.14	0.91**	0.47	1.10*	0.95*	1.00**	1.02**	-0.01	0.01	0.00	0.00
37	UWS-92 x UWS-23	2.74**	4.06**	3.56**	3.45**	-0.89**	0.00	-0.59**	-0.49	1.40**	1.13**	0.55*	1.03**	-0.06	-0.05	-0.01	-0.04
38	UWS-92 x UWS-60	1.36	2.80**	1.79*	1.98**	0.54	-0.14	-0.33*	0.02	0.30	0.18	-0.45*	0.01	0.07	0.04	0.01	0.04
39	UWS-98 x UWS-10	3.06**	2.12*	3.62**	2.93**	-0.80*	-0.24	-0.48**	-0.51	0.05	-0.32	-0.02	-0.10	0.10	0.05	0.03	0.06
40	UWS-98 x UWS-23	-3.88**	-3.63**	-4.50**	-4.00**	1.68**	0.76*	1.19**	1.21**	0.26	0.27	0.17	0.23	-0.04	-0.06	-0.03	-0.04
41	UWS-98 x UWS-60	0.82	1.51	0.87	1.07*	-0.88*	-0.52	-0.71**	-0.70*	-0.31	0.05	-0.15	-0.13	-0.07	0.00	-0.01	-0.02
42	UWS-100 x UWS-10	0.53	0.88	1.02	0.81	0.99**	0.89*	0.37*	0.75*	-0.12	0.00	0.61**	0.17	-0.04	-0.07	0.03	-0.03
43	UWS-100 x UWS-23	-0.78	-0.42	-1.01	-0.74	-0.58	-0.86*	-1.08**	-0.84*	-0.48	-0.33	-0.68**	-0.50*	-0.07	-0.10	0.02	-0.05
44	UWS-100 x UWS-60	0.25	-0.46	-0.01	-0.07	-0.41	-0.03	0.70**	0.09	0.60	0.32	0.07	0.33	0.11	0.16*	-0.05	0.07*
45	UWS-104 x UWS-10	-1.11	-0.77	-3.15**	-1.68**	-0.27	-1.20**	-0.12	-0.53	-0.46	-0.35	-0.31	-0.38	-0.07	-0.03	0.15*	0.02
46	UWS-104 x UWS-23	1.07	1.33	4.52**	2.31**	0.88*	2.04**	1.17**	1.36**	-0.20	-0.06	-0.82**	-0.36	-0.01	0.04	-0.03	0.00
47	UWS-104 x UWS-60	0.04	-0.57	-1.36	-0.63	-0.62	-0.83*	-1.05**	-0.83*	0.66	0.41	1.13**	0.73**	0.08	-0.02	-0.13	-0.02
48	UWS-106 x UWS-10	5.29**	5.20**	4.63**	5.04**	2.14**	0.54	2.01**	1.56**	-0.28	-0.26	0.48*	-0.02	-0.05	-0.03	-0.02	-0.03
49	UWS-106 x UWS-23	-0.62	-0.43	-1.80*	-0.95*	-0.39	0.76*	0.13	0.17	0.18	0.23	-0.24	0.05	0.04	0.05	0.08	0.06
50	UWS-106 x UWS-60	-4.67**	-4.77**	-2.83**	-4.09**	-1.75**	-1.30**	-2.14**	-1.73**	0.11	0.04	-0.24	-0.03	0.01	-0.02	-0.06	-0.02
51	UWS-120 x UWS-10	1.56	1.95*	2.17**	1.89**	0.58	0.51	0.36*	0.49	0.52	0.56	-0.09	0.33	-0.02	-0.02	0.00	-0.01
52	UWS-120 x UWS-23	-0.11	-0.15	-0.38	-0.22	-0.16	-0.16	-0.19	-0.17	-1.00*	-0.94*	0.09	-0.62*	0.01	0.02	0.00	0.01
53	UWS-120 x UWS-60	-1.46	-1.79*	-1.79*	-1.68**	-0.42	-0.35	-0.17	-0.31	0.48	0.38	0.01	0.29	0.00	0.00	0.00	0.00
54	UWS-122 x UWS-10	-1.82	-1.44	-0.63	-1.30**	-0.68*	1.42**	-0.83**	-0.03	-0.21	-0.19	-0.24	-0.21	0.08	0.10	-0.02	0.05
55	UWS-122 x UWS-23	2.27*	2.22*	1.98**	2.16**	-0.64	-1.66**	-0.61**	-0.97**	0.26	0.31	0.06	0.21	0.04	0.03	0.02	0.03
56	UWS-122 x UWS-60	-0.45	-0.78	-1.35	-0.86	1.31**	0.24	1.44**	1.00**	-0.05	-0.12	0.18	0.00	-0.12	-0.13	0.00	-0.08*
57	UWS-129 x UWS-10	-0.60	-0.22	-0.03	-0.28	0.86*	1.17**	1.37**	1.13**	0.47	0.18	0.41	0.35	0.05	0.06	0.00	0.04
58	UWS-129 x UWS-23	0.52	0.48	0.65	0.55	0.00	0.09	0.25	0.11	0.66	0.31	-0.15	0.27	0.00	-0.01	0.01	0.00
59	UWS-129 x UWS-60	0.08	-0.26	-0.62	-0.27	-0.86*	-1.26**	-1.62**	-1.24**	-1.12*	-0.49	-0.26	-0.62*	-0.05	-0.05	0.00	-0.04
60	UWS-131 x UWS-10	-4.28**	-4.43**	-5.06**	-4.59**	-1.77**	-0.92**	-1.22**	-1.30**	-0.18	-0.16	-0.72**	-0.35	-0.02	-0.04	-0.02	-0.03
61	UWS-131 x UWS-23	1.64	1.97*	2.48**	2.03**	-0.08	0.57	0.23	0.24	0.35	0.40	0.79**	0.52*	0.01	0.02	0.00	0.01
62	UWS-131 x UWS-60	2.63*	2.45**	2.58**	2.56**	1.85**	0.36	0.99**	1.06**	-0.17	-0.25	-0.08	-0.16	0.01	0.02	0.02	0.02
63	UWS-132 x UWS-10	0.70	1.33	1.19	1.08*	0.96**	1.23**	1.42**	1.20**	-0.02	-0.05	1.15**	0.36	0.00	-0.03	-0.08	-0.04
64	UWS-132 x UWS-23	-1.09	-1.73	-1.14	-1.32**	-0.33	-0.77*	-0.62**	-0.57	-0.12	-0.12	-0.42*	-0.22	0.03	0.04	0.07	0.05
65	UWS-132 x UWS-60	0.39	0.40	-0.05	0.24	-0.63	-0.46	-0.80**	-0.63	0.15	0.17	-0.73**	-0.14	-0.03	0.00	0.01	-0.01
66	UWS-134 x UWS-10	2.30*	2.22*	0.74	1.75**	-0.40	-1.15**	-0.84**	-0.80*	-0.13	-0.13	-0.41	-0.23	-0.09	-0.08	-0.07	-0.08*
67	UWS-134 x UWS-23	1.11	-0.28	-0.45	0.13	-0.32	-0.67	-0.41*	-0.46	0.34	0.44	0.09	0.29	0.06	0.07	0.05	0.06
68	UWS-134 x UWS-60	-3.42**	-1.94*	-0.29	-1.88**	0.72*	1.82**	1.24**	1.26**	-0.21	-0.30	0.31	-0.07	0.02	0.01	0.02	0.02
69	UWS-135 x UWS-10	1.10	1.25	1.43*	1.26**	0.25	0.57	0.27	0.36	0.01	0.09	0.23	0.11	0.07	0.16*	-0.01	0.07*

Table 3. Continued...

S.N.	Genotypes	RL				RD				DRY				TA			
		E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool	E_1	E_2	E_3	Pool
70	UWS-135 x UWS-23	-2.11*	-1.69	-2.16**	-1.99**	0.81*	0.45	0.48**	0.58	0.77	0.33	0.25	0.45	-0.06	-0.07	-0.03	-0.05
71	UWS-135 x UWS-60	1.01	0.44	0.74	0.73	-1.06**	-1.01**	-0.75**	-0.94**	-0.79	-0.42	-0.48*	0.56*	-0.01	-0.09	0.04	-0.02
72	UWS-140 x UWS-10	1.29	2.67**	1.72*	1.89**	-0.82*	-0.73*	-1.19**	-0.92**	-0.55	-0.51	-0.88**	-0.65**	0.12	0.13	0.07	0.11**
73	UWS-140 x UWS-23	-4.63**	-5.13**	-5.57**	-5.11**	1.19**	1.49**	1.71**	1.46**	0.49	0.27	1.16**	0.64*	0.00	0.02	0.00	0.01
74	UWS-140 x UWS-60	3.34**	2.47**	3.86**	3.22**	-0.37	-0.76*	-0.51**	-0.55	0.06	0.24	-0.29	0.01	-0.13	-0.15*	-0.07	-0.11**
75	UWS-93 x UWS-10	-0.02	0.30	1.21	0.50	-0.08	-0.91*	0.15	-0.28	-0.47	-0.48	0.14	-0.27	0.01	0.02	0.12	0.05
76	UWS-93 x UWS-23	0.49	0.57	-0.22	0.28	-0.20	-0.79*	-1.25**	-0.75*	-0.05	0.05	-0.48*	-0.16	-0.01	0.01	-0.02	-0.01
77	UWS-93 x UWS-60	-0.47	-0.87	-0.99	-0.78	0.27	1.70**	1.10**	1.02**	0.53	0.43	0.35	0.43	0.00	-0.03	-0.10	-0.04
78	UWS-95 x UWS-10	-2.62*	-2.24*	-0.99	-1.95**	0.12	-0.10	-0.07	-0.01	1.11*	0.82*	-0.48*	0.48	-0.04	-0.02	0.07	0.00
79	UWS-95 x UWS-23	2.64*	2.59**	2.28**	2.50**	0.24	0.15	-0.20	0.06	-0.22	-0.26	0.75**	0.09	0.10	0.07	0.08	0.08*
80	UWS-95 x UWS-60	-0.01	-0.35	-1.29	-0.55	-0.36	-0.06	0.27	-0.05	-0.89	-0.56	-0.28	-0.58*	-0.07	-0.05	-0.14*	-0.09**
81	UWS-96 x UWS-10	0.27	0.13	-0.92	-0.17	-0.71*	1.14**	-1.12**	-0.23	0.05	0.07	-0.16	-0.01	-0.02	-0.01	0.00	-0.01
82	UWS-96 x UWS-23	-1.49	-0.50	-0.22	-0.74	0.12	-1.28**	-0.19	-0.45	-0.28	-0.23	0.13	-0.13	-0.04	-0.07	-0.03	-0.05
83	UWS-96 x UWS-60	1.22	0.36	1.14	0.91	0.59	0.14	1.31**	0.68	0.23	0.16	0.03	0.14	0.06	0.07	0.02	0.05
*	S.E. (gca for line)	0.57	0.51	0.42	0.27	0.19	0.20	0.10	0.18	0.30	0.26	0.14	0.15	0.039	0.040	0.038	0.019
*	S.E. (gca for tester)	0.22	0.20	0.16	0.10	0.07	0.08	0.04	0.07	0.12	0.10	0.05	0.06	0.015	0.015	0.015	0.007
*	S.E. (SCA effects)	0.99	0.87	0.72	0.47	0.32	0.34	0.17	0.31	0.52	0.45	0.24	0.25	0.068	0.069	0.066	0.033
*	S.E. (gi - gj)line	0.81	0.71	0.59	0.38	0.26	0.28	0.14	0.25	0.43	0.37	0.19	0.21	0.055	0.056	0.054	0.027
*	S.E. (gi - gj)tester	0.31	0.28	0.23	0.15	0.10	0.11	0.05	0.10	0.16	0.14	0.07	0.08	0.021	0.022	0.021	0.010
*	S.E. (sij - skl)tester	1.40	1.24	1.02	0.66	0.46	0.49	0.24	0.44	0.74	0.64	0.34	0.36	0.096	0.097	0.093	0.047

** indicates 1% level of significant and * indicates 5% level of significant.

Table 4. Extent of heterosis for RL and RD

S.N.	Genotypes	RL					RD				
		HB	SH				HB	SH			
		Pool	E_1	E_2	E_3	Pool	Pool	E_1	E_2	E_3	Pool
1	UWS-13 x UWS-10	3.80	-16.15**	-20.03**	-20.63**	-17.57**	-26.57**	-33.44**	-37.40**	-48.78**	-39.60**
2	UWS-13 x UWS-23	24.30**	-2.21	-1.87	-4.42	-1.30	-15.03**	-28.95**	-27.89**	-33.67**	-30.11**
3	UWS-13 x UWS-60	-9.96**	-26.31**	-28.42**	-34.69**	-28.50**	-21.61**	-33.53**	-30.23**	-43.14**	-35.52**
4	UWS-18 x UWS-10	4.49	-28.21**	-33.28*	-35.87**	-31.20**	-10.45*	-22.40**	-27.83**	-31.14**	-26.93**
5	UWS-18 x UWS-23	43.53**	-5.53	-8.36	-6.96	-5.49*	-9.87	-23.26**	-26.79**	-29.72**	-26.46**
6	UWS-18 x UWS-60	46.91**	-7.80	-2.77	-3.15	-3.27	7.50	3.83	-21.72**	-20.89**	-12.28**
7	UWS-79 x UWS-10	27.09**	-16.04**	-19.91**	-21.94**	-17.90**	-22.13**	-20.87**	-39.91**	-45.33**	-34.79**
8	UWS-79 x UWS-23	-3.37	-32.85**	-38.38**	-45.99**	-37.77**	-25.66**	-33.77**	-38.41**	-41.58**	-37.75**
9	UWS-79 x UWS-60	45.32**	-11.58*	-7.45	-21.05**	-11.79**	-25.18**	-29.97**	-36.54**	-46.52**	-37.35**
10	UWS-89 x UWS-10	7.63**	-5.97	-8.85	-14.19**	-8.06**	-18.21**	-23.35**	-26.26**	-25.66**	-25.02**
11	UWS-89 x UWS-23	-13.58**	-24.23**	-28.90**	-29.17**	-26.18**	-39.78**	-44.73**	-35.84**	-53.96**	-44.80**
12	UWS-89 x UWS-60	-9.06**	-20.46**	-23.55**	-26.98**	-22.32**	-8.47	-21.17**	-5.74	-20.86**	-16.09**
13	UWS-92 x UWS-10	-12.01**	-29.27**	-38.02**	-40.60**	-34.65**	-29.60**	-29.10**	-30.50**	-36.31**	-31.85**
14	UWS-92 x UWS-23	29.08**	-9.29*	0.32	-7.50	-4.13	-44.74**	-46.62**	-36.90**	-56.09**	-46.50**
15	UWS-92 x UWS-60	25.35**	-11.85*	-0.98	-11.98**	-6.90**	-35.66**	-28.95**	-36.17**	-49.15**	-37.71**
16	UWS-98 x UWS-10	-2.70	-9.07	-12.25**	-9.41*	-8.86**	-5.42	-20.21**	-20.59**	-26.27**	-22.26**
17	UWS-98 x UWS-23	-32.17**	-34.85**	-34.67**	-43.43**	-36.46**	8.31	-4.25	-15.58**	-13.89**	-10.97**
18	UWS-98 x UWS-60	-9.48**	-17.22**	-12.62**	-19.76**	-15.21**	-9.59	-22.46**	-26.23**	-28.80**	-25.69**
19	UWS-100 x UWS-10	28.74**	-14.23**	-19.54**	-17.56**	-15.74**	24.82**	-5.03	-7.37	-12.88**	-8.28
20	UWS-100 x UWS-23	16.78**	-21.35**	-25.74**	-27.60**	-23.57**	-3.40	-25.42**	-29.93**	-32.15**	-29.02**
21	UWS-100 x UWS-60	24.56**	-15.87**	-22.58**	-21.12**	-18.48**	13.98*	-19.13**	-19.39**	-9.80**	-16.25**
22	UWS-104 x UWS-10	1.70	-16.21**	-21.37**	-26.11**	-19.74**	5.61	-27.13**	-33.50**	-34.08**	-31.39**
23	UWS-104 x UWS-23	17.53**	-11.73*	-15.17**	2.10	-7.25**	25.65**	-23.08**	-6.04	-25.56**	-18.38**
24	UWS-104 x UWS-60	7.20*	-13.11**	-18.81**	-18.57**	-15.40**	-1.21	-31.77**	-32.57**	-43.71**	-35.83**
25	UWS-106 x UWS-10	40.60**	1.11	-3.63	-0.87	0.44	7.74	8.44*	-9.24	6.09*	1.99
26	UWS-106 x UWS-23	6.82*	-21.24**	-25.62**	-28.25**	-23.69**	-12.17**	-20.63**	-11.98*	-17.55**	-16.86**
27	UWS-106 x UWS-60	-5.63	-32.63**	-38.14**	-29.82**	-32.58**	-27.55**	-28.08**	-30.40**	-36.21**	-31.41**
28	UWS-120 x UWS-10	26.89**	-11.06*	-14.44**	-13.27**	-11.53**	10.70	-12.22**	-11.68*	-18.86**	-14.16**
29	UWS-120 x UWS-23	12.73**	-19.36**	-23.55**	-25.36**	-21.41**	-4.41	-25.24**	-23.39**	-29.11**	-25.87**
30	UWS-120 x UWS-60	8.81*	-21.79**	-26.23**	-28.38**	-24.14**	-1.28	-22.78**	-23.09**	-24.54**	-23.44**

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Table 4. Continued..

S.N.	Genotypes	RL					RD				
		HB	SH				HB	SH			
		Pool	E_1	E_2	E_3	Pool	Pool	E_1	E_2	E_3	Pool
31	UWS-122 x UWS-10	-18.98**	-19.47**	-23.68**	-22.47**	-20.59**	3.99	-21.80**	2.74	-32.35**	-17.25**
32	UWS-122 x UWS-23	-8.19**	-8.63	-11.76**	-14.19**	-10.02**	-14.21**	-27.75**	-33.13**	-34.79**	-31.73**
33	UWS-122 x UWS-60	-16.80**	-15.60**	-19.42**	-24.80**	-18.46**	14.49**	-5.48	-11.95*	-9.63**	-8.89*
34	UWS-129 x UWS-10	14.63**	-4.31	-7.02	-10.51**	-5.70*	16.88**	-16.17**	-16.08**	-21.70**	-17.90**
35	UWS-129 x UWS-23	15.77**	-3.33	-5.93	-9.84*	-4.76	-4.76	-30.27**	-31.80**	-37.63**	-33.10**
36	UWS-129 x UWS-60	15.32**	-2.77	-5.32	-12.37**	-5.13*	-18.07**	-33.14**	-43.18**	-52.23**	-42.45**
37	UWS-131 x UWS-10	-13.36**	-31.64**	-37.04**	-46.52**	-37.04**	1.57	-32.78**	-34.60**	-40.47**	-35.81**
38	UWS-131 x UWS-23	17.17**	-14.73**	-15.17**	-18.79**	-14.85**	16.73*	-23.89**	-24.69**	-30.43**	-26.23**
39	UWS-131 x UWS-60	23.44**	-9.40*	-10.12*	-15.90**	-10.29**	35.41**	-1.83	-24.59**	-18.36**	-14.43**
40	UWS-132 x UWS-10	24.38**	-10.22*	-10.43*	-15.60**	-10.60**	41.05**	-5.39	-4.07	-9.53**	-6.28
41	UWS-132 x UWS-23	9.17**	-18.92**	-23.07**	-26.81**	-21.53**	7.14	-23.35**	-29.00**	-34.79**	-28.81**
42	UWS-132 x UWS-60	20.84**	-11.98*	-12.01**	-20.01**	-13.15**	11.98	-21.26**	-23.76**	-32.35**	-25.59**
43	UWS-134 x UWS-10	-13.29**	-16.04**	-19.91**	-27.46**	-19.61**	10.78	-22.16**	-26.59**	-32.35**	-26.83**
44	UWS-134 x UWS-23	-22.03**	-22.73**	-30.48**	-34.17**	-27.71**	7.57	-27.69**	-26.79**	-32.56**	-28.95**
45	UWS-134 x UWS-60	-27.14**	-35.73**	-33.22**	-31.04**	-32.45**	38.62**	-13.56**	0.27	-11.49**	-8.45*
46	UWS-135 x UWS-10	-2.43	-11.06*	-14.44**	-15.51**	-12.23**	23.77**	-11.86**	-7.51	-16.84**	-12.04**
47	UWS-135 x UWS-23	-18.04**	-24.45**	-26.59**	-31.67**	-26.26**	19.26**	-13.08**	-13.68**	-19.27**	-15.24**
48	UWS-135 x UWS-60	-4.02	-12.06**	-15.53**	-17.74**	-13.65**	3.89	-25.15**	-26.09**	-27.38**	-26.16**
49	UWS-140 x UWS-10	13.31**	-4.65	-7.39	-12.09**	-6.43**	-22.37**	-29.22**	-33.40**	-46.55**	-36.08**
50	UWS-140 x UWS-23	-20.42**	-27.06**	-37.29**	-42.84**	-34.29**	-0.86	-17.49**	-16.08**	-21.70**	-18.38**
51	UWS-140 x UWS-60	19.84**	1.44	-6.27	-3.15	-1.04	-19.90**	-26.74**	-36.44**	-39.89**	-34.05**
52	UWS-93 x UWS-10	24.45**	-13.83**	-17.48**	-17.29**	-14.82**	13.12*	-23.35**	-27.69**	-29.82**	-26.81**
53	UWS-93 x UWS-23	20.15**	-14.91**	-17.96**	-24.97**	-17.77**	-2.13	-30.75**	-31.50**	-48.61**	-36.68**
54	UWS-93 x UWS-60	18.34**	-16.04**	-19.91**	-25.49**	-19.00**	30.25**	-21.74**	-4.37	-20.45**	-15.73**
55	UWS-95 x UWS-10	-2.91	-21.02**	-25.38**	-21.76**	-21.51**	8.63	-27.28**	-32.60**	-38.44**	-32.54**
56	UWS-95 x UWS-23	14.69**	-6.31	-9.21*	-10.91**	-7.29**	2.72	-32.49**	-35.10**	-44.42**	-37.13**
57	UWS-95 x UWS-60	4.09	-13.05**	-16.63**	-22.47**	-15.86**	4.24	-33.14**	-35.00**	-35.29**	-34.43**
58	UWS-96 x UWS-10	-9.99**	-13.05**	-16.63**	-22.56**	-15.89**	11.05	-30.93**	-8.44	-54.06**	-31.04**
59	UWS-96 x UWS-23	-14.48**	-21.64**	-20.39**	-21.81**	-20.08**	4.31	-29.79**	-37.64**	-49.26**	-38.52**
60	UWS-96 x UWS-60	-5.20*	-10.62*	-13.95**	-13.93**	-11.41**	21.16**	-20.81**	-21.25**	-29.72**	-23.79**

** indicates 1% level of significant and * indicates 5% level of significant.

Table 5. Extent of heterosis for DRY and TA

S.N.	Genotypes	DRY					TA				
		HB	SH				HB	SH			
		Pool	E_1	E_2	E_3	Pool	Pool	E_1	E_2	E_3	Pool
1	UWS-13 x UWS-10	-10.23	-31.54	-26.31	-23.80*	-26.58**	12.30	-37.02*	-51.05**	-19.08	-36.21**
2	UWS-13 x UWS-23	20.88	-6.37	2.15	-2.15	-1.13	-18.93	-49.72**	-48.42**	-43.35**	-47.24**
3	UWS-13 x UWS-60	25.60*	11.01	11.42	-20.00*	2.73	52.74**	-12.15	-4.74	9.83	-2.57
4	UWS-18 x UWS-10	59.27**	-8.53	-0.28	-21.76*	-8.89	-33.81**	-49.17**	-57.37**	-38.15*	-48.53**
5	UWS-18 x UWS-23	64.20**	-0.17	-5.06	-17.66	-6.07	3.55	-13.81	-24.74	-19.65	-19.49*
6	UWS-18 x UWS-60	34.46*	-35.02	-30.24	-4.49	-23.08*	-8.27	-27.62	-31.05*	-27.17	-28.68**
7	UWS-79 x UWS-10	13.56	-18.79	-5.43	-53.17**	-24.25*	-14.36	-27.07	-39.47*	-39.31*	-35.29**
8	UWS-79 x UWS-23	10.34	-27.15	-21.35	-33.56**	-26.39**	-22.38*	-34.25*	-37.37*	-53.18**	-41.36**
9	UWS-79 x UWS-60	-4.04	-45.86*	-31.55	-31.41**	-35.99**	0.73	-34.81*	-35.26*	0.00	-23.90**
10	UWS-89 x UWS-10	32.17*	-28.97	-23.41	-3.80	-18.39	-29.62*	-22.65	-32.63*	-43.35**	-32.72**
11	UWS-89 x UWS-23	45.03**	-11.01	-3.09	-20.88*	-10.45	-20.00*	-20.99	-25.26	-24.28	-23.53**
12	UWS-89 x UWS-60	35.55*	-3.89	-16.01	-34.44**	-16.31	-20.96*	-27.62	-26.32	-19.08	-24.45**
13	UWS-92 x UWS-10	27.06*	11.75	11.80	20.10*	15.73	-2.20	-22.65	-26.32	-30.64	-26.47**
14	UWS-92 x UWS-23	-32.11**	-47.85**	-44.76*	-22.24*	-38.17**	-9.29	-30.39	-31.58*	-33.53*	-31.80**
15	UWS-92 x UWS-60	-9.36	-13.00	-12.64	-30.83**	-17.44	7.33	-8.84	-18.42	-31.21	-19.30*
16	UWS-98 x UWS-10	5.01	-32.70	-27.62	-11.51	-23.57*	27.35*	-12.15	-22.11	-19.08	-17.83*
17	UWS-98 x UWS-23	20.94	-25.00	-9.08	-3.02	-11.99	2.82	-33.15*	-34.74*	-31.21	-33.09**
18	UWS-98 x UWS-60	-3.62	-46.27*	-19.76	-23.71*	-29.86**	6.55	-39.23*	-26.32	-28.32	-31.25**
19	UWS-100 x UWS-10	25.67*	-15.56	-8.24	8.68	-4.54	-3.37	-31.49*	-36.84*	-9.25	-26.29**
20	UWS-100 x UWS-23	5.04	-21.94	-15.45	-26.15**	-20.20*	-6.51	-35.91*	-36.32*	-12.72	-28.68**
21	UWS-100 x UWS-60	24.74	-2.48	-1.87	-15.61	-5.24	19.28	-6.63	4.21	-26.01	-9.01
22	UWS-104 x UWS-10	-4.98	-16.39	-9.18	-11.80	-11.59	21.20	-39.78*	-46.84**	0.00	-29.60**
23	UWS-104 x UWS-23	-1.65	-7.20	1.22	-23.61*	-8.49	6.50	-28.73	-31.05*	-32.37*	-30.70**
24	UWS-104 x UWS-60	22.31*	6.79	9.55	22.15*	13.80	1.44	-13.81	-41.58**	-50.87**	-35.29**
25	UWS-106 x UWS-10	36.09*	-31.37	-26.12	0.78	-18.73	-34.56**	-48.62**	-50.53**	-32.95*	-44.30**
26	UWS-106 x UWS-23	44.05**	-17.38	-10.30	-17.07	-13.98	-14.90	-32.04*	-33.68*	-16.18	-27.57**
27	UWS-106 x UWS-60	26.95	-26.32	-20.41	-28.49**	-24.19*	-31.32**	-38.12*	-44.74**	-41.62*	-41.54**
28	UWS-120 x UWS-10	2.57	-3.56	5.34	-16.20	-3.46	-25.82**	-43.09**	-47.37**	-34.68*	-41.91**
29	UWS-120 x UWS-23	-22.51*	-38.99*	-34.74	-7.80	-27.07**	-19.01	-37.02*	-35.79*	-36.99*	-36.58**
30	UWS-120 x UWS-60	-4.27	-9.35	-2.53	-21.66*	-9.90	-21.60*	-39.23*	-40.00**	-36.42*	-38.60**

Table 5. Continued..

S.N.	Genotypes	DRY					TA				
		HB	SH				HB	SH			
		Pool	E_1	E_2	E_3	Pool	Pool	E_1	E_2	E_3	Pool
31	UWS-122 x UWS-10	0.77	-24.59	-18.45	-18.93	-19.90*	3.33	-4.97	-14.21	-24.28	-14.34
32	UWS-122 x UWS-23	18.67	-10.43	-2.43	-7.02	-5.67	1.33	-8.84	-20.53	-18.50	-15.99*
33	UWS-122 x UWS-60	1.54	-25.41	-19.38	-15.02	-19.28	-21.95*	-36.46*	-45.79**	-22.54	-35.29**
34	UWS-129 x UWS-10	3.54	-6.71	-5.99	-13.85	-7.60	-17.94	-33.15*	-35.26*	-47.98**	-38.60**
35	UWS-129 x UWS-23	4.02	0.58	-0.09	-27.22**	-7.17	-23.59*	-39.78*	-41.05**	-47.98**	-42.83**
36	UWS-129 x UWS-60	-32.46**	-50.91**	-27.34	-41.76**	-39.73**	-32.68**	-50.28**	-48.42**	-50.29**	-49.63**
37	UWS-131 x UWS-10	7.46	-42.05*	-38.20*	-48.68**	-42.18**	-25.60**	-32.04*	-39.47*	-24.28	-32.17**
38	UWS-131 x UWS-23	56.75**	-26.32	-20.41	-1.37	-15.67	-16.73	-24.31	-24.74	-23.12	-24.08**
39	UWS-131 x UWS-60	7.29	-46.61*	-43.35*	-38.24**	-42.27**	-17.14*	-25.97	-26.32	-20.81	-24.45**
40	UWS-132 x UWS-10	15.09**	-37.25*	-32.77	22.15*	-16.37	-31.64**	-44.20**	-57.37**	-65.32**	-55.51**
41	UWS-132 x UWS-23	-28.79**	-37.25*	-32.77	-20.78*	-29.86**	-7.34	-37.02*	-41.58**	-40.46*	-39.71**
42	UWS-132 x UWS-60	-34.33**	-37.75*	-29.40	-41.07**	-35.32**	-23.16	-49.17**	-48.42**	-52.60**	-50.00**
43	UWS-134 x UWS-10	-30.96*	-45.86*	-30.15	-58.63**	-44.08**	-38.14**	-49.17**	-52.63**	-51.45**	-51.10**
44	UWS-134 x UWS-23	-10.18	-31.46	-12.08	-40.88**	-27.25**	-6.28	-23.20	-23.16	-31.79*	-25.92**
45	UWS-134 x UWS-60	-31.98**	-52.40**	-37.55*	-45.85**	-44.91**	-16.51	-30.39	-33.68*	-38.15*	-34.01**
46	UWS-135 x UWS-10	40.98*	-19.95	-13.20	-27.71**	-19.22	31.07*	-25.97	-13.16	-38.73*	-25.55**
47	UWS-135 x UWS-23	61.80**	1.49	-4.40	-24.20*	-7.30	-14.69	-45.86**	-44.21**	-43.35**	-44.49**
48	UWS-135 x UWS-60	-0.59	-44.54*	-30.06	-56.98**	-43.04**	-6.92	-39.78*	-47.89**	-33.53*	-40.63**
49	UWS-140 x UWS-10	8.07	-44.37*	-35.39	-48.68**	-42.12**	52.06**	-8.84	-4.21	-23.70	-11.95
50	UWS-140 x UWS-23	79.11**	-16.14	-11.42	14.15*	-4.08	12.43	-27.07	-17.37	-36.99*	-26.84**
51	UWS-140 x UWS-60	31.83	-33.94	-16.95	-39.71**	-29.40**	-18.44	-49.72**	-44.21**	-50.29**	-47.98**
52	UWS-93 x UWS-10	-12.58	-50.25**	-47.47**	-34.44**	-43.78**	2.26	-30.39	-38.95*	-4.62	-25.18**
53	UWS-93 x UWS-23	-3.91	-37.33*	-30.52	-49.56**	-38.20**	-8.79	-32.04*	-37.37*	-30.06	-33.27**
54	UWS-93 x UWS-60	9.49	-30.13	-24.72	-36.68**	-29.58**	-18.34	-32.04*	-43.68**	-45.09**	-40.26**
55	UWS-95 x UWS-10	2.82	9.11	5.43	-46.73**	-8.34	-10.85	-45.30**	-48.42**	-14.45	-36.58**
56	UWS-95 x UWS-23	-6.40	-21.19	-22.85	-7.71	-16.55	10.34	-20.44	-28.95	-14.45	-21.51**
57	UWS-95 x UWS-60	-35.87**	-45.12*	-36.05*	-49.37**	-42.83**	-30.49**	-50.28**	-48.42**	-53.18**	-50.55**
58	UWS-96 x UWS-10	4.63	-13.66	-6.09	-8.59	-8.55	-13.85	-45.86**	-47.89**	-19.65	-38.24**
59	UWS-96 x UWS-23	4.03	-19.21	-12.36	2.83	-9.07	-20.51	-47.51**	-53.16**	-27.17	-43.01**
60	UWS-96 x UWS-60	3.44	-13.82	-6.27	-11.51	-9.60	1.03	-32.04*	-31.05*	-19.08	-27.57**

** indicates 1% level of significant and * indicates 5% level of significant.

Table 6 Promising crosses on the basis of *per se* performance, economic heterosis and specific combining ability effects for dry root yield

S.N.	Crosses /Parents	Dry root yield (g) (E_3)	Heterosis over better parent (%) (E_3)	Economic heterosis % (E_3)	SCA /GCA effects (E_3)
1.	UWS-92 x UWS-10	4.10 g	13.88 %	20.10%	1.00**
2.	UWS-104 x UWS-60	4.17 g	48.34 %	22.15 %	1.13**
3.	UWS-132 x UWS-10	4.17 g	31.93 %	22.15%	1.15**
4.	UWS-92	3.60 g	-	-	Good
5.	UWS-10	1.18 g	-	-	Average
6.	UWS-104	2.81 g	-	-	Good
7.	UWS-60	1.35 g	-	-	Poor
8.	UWS-132	3.16 g	-	-	Good

13 x UWS-60,UWS-140 x UWS-10, UWS-135 x UWS-10 and UWS-98 x UWS-10 demonstrated significant positive heterobeltiosis and for dry root yield, three crosses *viz*., UWS-104 x UWS-60, UWS-132 x UWS-10 and UWS-92 x UWS-10 exhibited significant positive heterosis over the best check (JA-20) in the E_3 environment with significant positive SCA effects. The superior cross combinations identified in this study especially those showing significant positive heterobeltiosis, economic heterosis and specific combining ability (SCA) effects appear to be promising candidates for future heterosis breeding programs. Crosses involving parents with high general combining ability (GCA) can be further advanced to select transgressive segregants, which may be used in subsequent hybridization efforts to improve yield and quality traits. These improved lines could play a vital role in meeting the growing demand for Ashwagandha in medicinal applications.

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