LR-5056
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RESEARCH ARTICLE Legume Research- An International Journal, Volume Issue : ()

Genetic Evaluation of Yield and its Component Traits by using Generation Mean Analysis in Inter-varietal Crosses of Urdbean [*Vigna mungo* (L.) Hepper]

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10.18805/LR-5056

ABSTRACT

Background: Urdbean is a prominent legume crop with excellent nutritive value that is utilized in many ways throughout India. To fulfill the increasing demand, production must be enhanced through the use of breeding procedures which leads to production of high yielding cultivars. This necessitates a thorough examination of the gene action involved in the regulation of yield and its attributing traits, which can be accomplished by generation mean analysis.

Methods: In present investigation, generation mean analysis was employed for 11 characters by using six-parameter model to determine the nature and magnitude of gene action of yield and its component traits in six inter-varietal crosses of urdbean.

Result: Simple scaling test revealed that the digenic model (additive-dominance model) was inadequate for most of the traits, confirming the existence of non-allelic interactions for all of the crosses. Duplicate type of epistasis was reported for three traits in HimMash-1×Sirmour-2 (days to 50% flowering, days to 75% maturity, harvest index), Palampur-93×Kullu-4 (days to 50% flowering, podlength, 100-seed weight) and Palampur-93×Chamba-8 (days to 50% flowering, days to 75% maturity, podlength). Two in HimMash-1×Kullu-4 (days to 50% flowering, days to 75% maturity), HimMash-1×Chamba-8 (days to 50% flowering, 100-seed weight) and Palampur-93×Sirmour-2 (branches/plant, 100-seed weight). Hence, it was evident from the study that the bi-parental mating trailed by selection in advanced generations should be employed for harnessing desirable recombinants.

Key words: Epistasis, Gene action, Generation means analysis, Scaling test, Six-parameter model.

INTRODUCTION

Urdbean(2n=2×=22), popularly known as blackgram, black lentil or mash, is a tropical self-pollinated pulse crop extensively grown in Indian sub-continent and predominantly used for human consumption and fodder. It belongs to the family Papilionaceae, genus *Vigna* and domesticated from *V. mungo* var. *silvestris*. It is considered to have evolved in India, with a secondary centre of origin in Central Asia (Pratap and Kumar 2011). India is the world's largest producer and consumer of urdbean, accounting for over 70% of global production; hold an area about 4.5 Mha with an annual production of 2.08Mtand average yield of 459 kg/ha (Anonymous 2020-2021). It is cultivated in various parts of India during the summer, *Kharif* and *Rabi* seasons (Singh and Ahlawat 2005). It is having symbiotic nitrogen fixation property, thus restores the soil fertility and soil physical properties.

The improvement of yield and its related component characteristics is the primary focus of most breeding strategies. Acknowledging the inheritance mode of sophisticated quantitative traits is critical for developing an efficient breeding programme in any crop for the improvement of a specific trait. While improving any quantitative trait including seed yield, plant breeders must examine three important elements: the number of genes influencing the trait, the kind of gene action and the genotype×environment interaction, as the selection of any breeding programme directly influenced by the nature of gene action involved in the inheritance of the traits (Kumar *et al*. 2010). Generation mean analysis is a clear, conciseand efficient approach for elucidating gene action since it use first degree statistics to determine allelic and non-allelic interactions. It is more suitable for obtaining unbiased estimates of additive and dominance gene effects as well as additional information on epistasis/inter-allelic interaction, cause of gene action and assisting breeders in choosing the appropriate breeding method to improve various quantitative traits along with qualitative traits in the crop through boosting the frequency of favorable genes. As a consequence, the

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How to cite this article: Soharu, A., Sood, V.K. and Mittal, R.K. (2023). Genetic Evaluation of Yield and its Component Traits by using Generation Mean Analysis in Inter-varietal Crosses of Urdbean [*Vigna mungo* (L.) Hepper]. Legume Research. doi:10.18805/LR-5056

Submitted: 08-10-2022 **Accepted:** 10-03-2023 **Online**: 10-05-2023

current study used generation mean techniques to evaluate different components of gene effects in urdbean.

MATERIALS AND METHODS

In the present investigation, generation mean analysis was performed for seed yield and other component traits of urdbean utilizing six generations *viz*., P_1, P_2, F_1, F_2, B_1 and B_2 of six distinct crosses. The plant material comprised of five distinct urdbean genotypes (Table 1), from these six cross combination were developed *viz*., HimMash-1×Sirmour-2, HimMash-1×Kullu-4, HimMash-1×Chamba-8, Palampur-93×Sirmour-2, Palampur-93×Kullu-4 and Palampur-93×Chamba-8. The six generations *i.e.* P_1, P_2, F_1, F_2, B_1 and B_2 developed during the years from 2019-2021, were evaluated in compact family block design (CFBD) in three replications during *Kharif* 2021 at the experimental farm of department of GPB, CSKHPKV Palampur. The observations were recorded on 11 morphological, yield and quality traits; days to 50% flowering, days to 75% maturity, plant height (cm), branches/plant, pods/plant, pod length (cm), seeds/pod, biological yield/plant (g), harvest index (%), seed yield/plant (g) and 100-seed weight (g). Five plants were randomly selected from each parent (P_1 and P_2), F_1 and backcrosses (B_1 and B_2) and 20 from F_2 for recording the observations.To maintain a healthy crop, all necessary agronomical practices were implemented.

Statistical analysis

The simple scaling tests ‘A’, ‘B’, ‘C’ and ‘D’ was estimated as suggested by Mather (1949) and Hayman and Mather (1955). The significant deviation of A and B tests from zero indicate the presence of all three types of epistatic interactions *viz*., additive×additive[i], additive×dominance [j] and dominance × dominance [l] whereas, C scaling test reveals the presence of dominance × dominance [l] type of interaction and D indicates the significance of additive× additive [i] type of interaction. The generation mean analysis was carried out following the six parameter model proposed by Hayman (1958), which are mean effect [m], additive effect [d], dominance effect [h], additive×additive interaction [i], additive×dominance [j] and dominance×dominance interaction [l].

RESULTS AND DISCUSSION

The simple scaling test (Table 2) was found to be significant for all the cross combinations for days to 50% flowering, indicating the presence of non-allelic interaction,C and D scales were significant in HimMash-1×Sirmour-2 and Palampur-93×Kullu-4, while, HimMash-1×Kullu-4 and HimMash-1×Chamba-8 disclosed the significance of B, C and D scale. Palampur-93×Chamba-8 had significance of A, C and D scale, whereas, Palampur-93×Sirmour-2 revealed the significance of C scale. Thus, additive and dominance gene action was present in the crosses investigated. Panigrahi *et al*. (2020) reported the prevalence of dominance and [l] gene effects in urdbean genotypes. Significant and opposite signs of [h] and [l] (Table 3) were present in all the crosses excluding Palampur-93×Sirmour-2. Kant and Srivastava (2012) divulged the presence of both complementary and duplicate epistasis for the trait in blackgram, whereas in current investigation only duplicate type of epistasis was detected, implying biparental mating followed by selection for trait enhancement.

The simple scaling test for days to 75% maturity was observed to be significant for all the crosses except Palampur-93×Sirmour-2. In HimMash-1×Sirmour-2 and Palampur-93×Chamba-8, B type of scale was significant, HimMash-1×Kullu-4 showed the prevalence of C and D scales, while in HimMash-1×Chamba-8 all of the four scales were significant and in Palampur-93×Kullu-4, A and C scales were significant. Thus, indicating the additive and dominance type of non-allelic interactions is involved in the inheritance of the trait. Alam *et al*. (2014) anticipated the occurrence of additive, dominance and epistatic interactions.HimMash-1×Sirmour-2, HimMash-1×Kullu-4 and Palampur-93×Chamba-8, showed the presence of duplicate gene action. Significant and positive [j] type of genic values in HimMash-1×Sirmour-2, recommends the utilization of recurrent selection method for improvement of this trait. Contrarily, significant negative [i] type of genic values was prevalent in HimMash-1×Kullu-4, which indicates allele dispersion in the parent and selection in subsequent generations. Panigrahi *et al*. (2020) also reported the prevalence of duplicate gene action for days to 75% maturity which is parallel to the current investigation.

HimMash-1×Sirmour-2 and Palampur-93×Chamba-8 exhibited the predominance of A, B and C scales, indicating the prevalence of [i], [j] and [l] type of epistasis. HimMash-1×Chamba-8 and Palampur-93×Sirmour-2 demonstrated significant C scale, suggesting the preponderance of [l] type of epistasis. The assessments of gene effects in a six-parameter model demonstrated the existence of [d] and [h] genic effect; therefore selection should be delayed to later generation to obtained plants with desirable height. Similar but negative [i] and [l] gene interaction for the trait was observed by Lenka *et al*. (2020), Panigrahi *et al*. (2020),

Table 1: Parentage/source of genotypes used for inter-varietal hybridization.

Genotype	Source
Palampur-93 (Parent/check)	Pure line selection from local material of H.P.
Him Mash-1 (Parent/check)	Advanced line selection from DPU-91-5×Mash-338
Sirmour-2	Landrace collected from Shillai, Sirmour of H.P.
Kullu-4	Landrace collected from Haripur, Kullu of H.P.
Chamba-8	Landrace collected from Bharmour, Chamba of H.P.

Table 2: Simple scaling test for the adequacy of additive-dominance model for yield and component traits.

Traits	Scales	Crosses					
		I	II	III	IV	V	VI
		Him Mash -1×Sirmour-2	Him Mash -1×Kullu-4	Him Mash -1×Chamba-8	Palampur-93×Sirmour-2	Palampur-93×Kullu-4	Palampur-93×Chamba-8
Days to 50% flowering	A	2.67±1.27	2.33±1.33	0.67±1.33	-1.33±0.94	-1.67±1.45	6.67*±1.33
	B	-1.17±1.28	4.00*±0.94	3.33*±0.82	-1.33±0.82	-1.00±1.60	1.00±0.94
	C	-5.17*±1.19	-9.67*±1.83	-9.33*±2.49	-6.67*±2.49	-19.33*±2.31	-0.33±1.83
	D	-3.33*±0.88	-8.00*±0.94	-6.67*±1.33	-2.00±1.25	-8.33*±1.05	-4.00*±0.94
Days to 75% maturity	A	-0.67±0.94	-1.33±0.82	-4.33*±2.00	-2.00±1.11	-5.00*±2.16	-2.00±1.41
	B	-6.33*±1.33	1.33±1.33	-6.67*±2.36	-1.00±2.05	-3.33±1.94	-6.67*±1.56
	C	-3.00±1.70	6.67*±1.63	-18.33*±1.76	-4.33±3.87	-7.00*±2.71	-2.00±3.86
	D	2.00±0.94	3.33*±0.94	-3.67*±1.60	-0.67±2.00	0.67±1.76	3.33±1.94
Plant height (cm)	A	-11.13*±2.93	-5.80±3.32	3.00±3.32	-3.27±2.93	2.68±2.94	-9.93*±3.24
	B	-8.33*±3.46	-3.80±2.95	0.43±2.78	-1.47±2.93	-0.70±4.25	-11.80*±2.95
	C	-23.87*±4.17	-3.00±6.18	13.97*±5.55	-9.65*±4.40	-2.87±5.33	-19.91*±5.59
	D	-2.20±2.58	3.30±2.05	5.27±2.87	-2.45±2.48	-2.42±2.96	0.91±3.05
Branches/plant	A	-0.93±0.72	0.80±0.67	0.83±0.61	-0.63±0.71	-0.25±0.88	-2.07*±0.83
	B	-0.13±0.99	-1.20*±0.56	-0.21±0.62	-0.45±0.60	-1.17*±0.67	-2.27*±0.86
	C	-0.67±1.40	-1.80*±0.97	-1.29±0.91	-4.06*±1.01	-2.89*±1.13	-7.00*±1.52
	D	0.20±0.65	-0.70±0.52	-0.96*±0.51	-1.49*±0.54	-0.73±0.66	-1.33*±0.63
Pod length (cm)	A	-0.74±0.36	-1.06*±0.34	0.07±0.42	0.24±0.33	-0.55±0.37	-0.69*±0.32
	B	-0.19±0.38	-0.36*±0.39	0.09±0.34	0.19±0.37	-0.18±0.45	0.08±0.30
	C	-0.70±0.45	-2.79*±0.42	-0.97±0.46	0.48±0.44	-1.85±0.63	-1.11*±0.40
	D	0.12±0.27	-0.68±0.28	-0.57*±0.27	0.03±0.26	-0.56±0.27	-0.25±0.22
Pods/plant	A	-7.33*±1.85	-6.40*±2.00	6.93*±2.68	-1.88±2.33	1.20±1.95	-1.60±2.67
	B	-2.00±2.09	-4.00*±1.44	2.47±3.18	-1.20±2.99	8.00*±2.38	-3.13*±1.76
	C	-5.93*±2.66	-13.93*±2.67	11.53*±3.93	-7.87*±3.45	-0.47±3.62	-17.07*±3.71
	D	1.70±1.56	-1.77±1.59	1.07±2.46	-2.39±2.06	-4.83*±1.82	-6.17*±1.79
Seeds/pod	A	-1.93*±0.47	-2.33*±0.47	-0.33±0.65	0.13±0.62	-0.47±0.51	-1.00±0.58
	B	-1.40*±0.71	-2.13*±0.48	0.27±0.56	-1.27*±0.64	-0.33±0.57	-1.40±0.75
	C	-2.53*±0.69	-3.27*±0.66	-1.40±0.81	-1.33±0.87	-2.07*±0.88	-2.73*±0.92
	D	0.40±0.48	0.60±0.36	-0.67±0.44	-0.10±0.49	-0.63±0.42	-0.17±0.46
Biological yield/plant (g)	A	-3.07*±1.16	-0.21±1.14	0.90±1.20	-1.73±1.19	-0.67±1.35	0.20±1.29
	B	-2.53±1.83	-0.87±1.27	2.37±1.50	-1.87±1.06	-1.93±1.36	-0.33±1.24
	C	-7.81*±2.49	-5.73*±1.81	0.98±2.11	-6.33*±1.94	-1.47±1.61	-4.73*±1.58
	D	-1.11±1.08	-2.33*±0.98	-1.14±1.15	-1.37±0.91	0.57±1.04	-2.30*±0.95

Table 2: Continue...

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Yield/plant (g)	A	-1.55±0.94	-0.65±0.53	0.23±0.76	-3.05*±0.71	-0.86±0.63	-0.73±0.60
	B	-0.83±0.83	-0.09±0.65	0.41±0.74	-1.32±0.73	0.04±0.65	-0.93±0.69
	C	-0.83±1.19	-0.01±0.88	0.59±0.99	-3.65*±0.90	-1.29±0.89	-2.23*±0.70
	D	0.78±0.59	0.36±0.50	-0.03±0.57	0.36±0.52	-0.21±0.49	-0.28±0.49
Harvest index (%)	A	2.09±2.16	-3.39±2.02	-3.20±2.76	-7.16*±2.80	-2.63±1.72	-3.86*±2.06
	B	3.04±1.72	-3.78±2.52	-1.75±2.88	-7.09*±2.13	1.25±1.98	-6.27*±2.10
	C	-22.40*±2.91	-4.98*±2.81	-3.12±3.93	-9.14*±3.01	-9.51*±2.96	-7.81*±2.44
	D	-13.76*±1.25	1.10±1.86	0.92±2.30	2.55±1.98	-4.07*±1.65	1.16±1.62
100-seed weight	A	0.07±0.24	-0.73*±0.22	-0.83*±0.24	-0.90*±0.21	-0.83*±0.31	0.01±0.26
	B	-0.23±0.15	-0.30±0.15	-0.30±0.14	-1.23*±0.22	-0.33±0.16	-0.70*±0.24
	C	1.10*±0.38	-1.90*±0.31	-0.27±0.30	-0.27±0.41	-0.30±0.23	-0.90*±0.38
	D	0.63*±0.22	-0.43*±0.16	0.43*±0.12	0.93*±0.22	0.43*±0.17	-0.10±0.19

*Significance at 5% level of probability, Scale 'A' and 'B' indicates [i], [j] [l] epistasis 'C' indicates [l] and Scale 'D' indicates [i] epistasis.

while Parsad *et al*. (2021) obtained positive [i] and [l] for plant height. This attribute was therefore regulated by additive and dominance gene effects.

None of the scale was observed to be significant for branches/plant in HimMash-1×Sirmour-2 which showed the adequacy of additive-dominance model. Significance of scales B and C were observed for HimMash-1×Kullu-4 and Palampur-93×Kullu-4, while, A, B, C and D in Palampur-93×Chamba-8, whereas, in HimMash-1×Chamba-8 scale D was found to be significant. In Palampur-93×Sirmour-2 scales C and D were significant. Therefore, above results implicated the prevalence of [i], [j] and [l] type of gene interaction for the transmission of the trait. Six-parameter model disclosed the prevalence of positive [h] gene effect in HimMash-1×Kullu-4 and Palampur-93×Kullu-4. In Palampur-93×Sirmour-2 and Palampur-93×Chamba-8 the preponderance of [h] gene effect and [i] inter-allelic interaction was observed, recommending hybridization and selection in later generations.The occurrence of duplicate gene action and positive [i] type interactions in Palampur-93×Sirmour-2, thus, biparental mating proceeded by selection is recommended to increase the number of pods per plant. Singh *et al*. (2007) and Pathak *et al*. (2015)had also observed the prevalence of duplicate type epistasis and inter-allelic interactionsfor the trait.

For pod length A, B and C scales were significant in HimMash-1×Kullu-4 and in Palampur-93×Chamba-8 A and C, while, in HimMash-1×Chamba-8 [i] type gene interaction was prevalent as represented by significant D scale, confirmed the preponderance of [i], [j] and [l] type of non-allelic interactions. Murugan (2005) also observed all three types of epistatic interaction. Parsad *et al*. (2021) showed the involvement of [i] non-allelic interaction. Estimates of [d] and [i] genic effects demonstrated significant and positive values in HimMash-1×Kullu-4, HimMash-1×Chamba-8 and Palampur-93×Kullu-4. This shows the complex nature of inheritance of this trait. Therefore, hybridization and selection in advanced generations is recommended when desirable recombinants become available.Vaithiyalingam *et al*. (2002) found additive and dominant effects for this characteristic.

Number of pods/plant is one of the most prominent morphological traits that make a significant contribution to seed yield/plant. In HimMash-1×Sirmour-2 and HimMash-1×Chamba-8 A and C scales, in HimMash-1×Kullu-4 scales A, B and C, in Palampur-93×Kullu-4 scales B and D and in Palampur-93×Sirmour-2 scales B, C and D were significant, thus revealing [i], [j] and [l]non-allelic interactions were controlling the inheritance of the character. Palampur-93×Sirmour-2 showed the preponderance of [l] type of gene interaction, since scale C was significant. Six-parameter estimates disclosed the presence of significant positive values of [h] and significant negative values of [l] along with significant and positive [i] type of interaction incross combinations Palampur-93×Kullu-4 and Palampur-93×Chamba-8, indicating the presence of duplicate gene

Table 3: Estimates of scaling tests and genic effects.

Traits	Cross no.	Gene effects						Types of epistasis
		Main effect±SE			Interaction effect±SE			
		m	d	h	i	j	l	
Days to 50% flowering	I	40.75*±1.78	-0.92±0.22	16.25*±5.14	6.67*±1.76	1.92*±0.85	-8.17*±3.48	Duplicate
	II	31.50*±1.90	0.17±0.24	36.83*±4.89	16.00*±1.89	-0.83±0.71	-22.33*±3.23	Duplicate
	III	32.00*±2.69	0.67±0.33	32.67*±6.20	13.33*±2.67	-1.33±0.75	-17.33*±3.65	Duplicate
	IV	42.67*±2.52	-0.67±0.33	5.33±5.52	4.00±2.49	0.01±0.58	-1.33±3.13	-
	V	29.00*±2.13	-0.67±0.33	33.67*±5.73	16.67*±2.11	-0.33±0.88	-14.00*±4.00	Duplicate
	VI	37.50*±1.90	-0.17±0.24	26.17*±4.89	8.00*±1.89	2.83*±0.71	-15.67*±3.23	Duplicate
Days to 75% maturity	I	85.50*±1.93	-1.50±0.41	-11.17*±4.97	-4.00±1.89	2.83*±0.78	11.00*±3.16	Duplicate
	II	86.33*±1.91	0.67±0.33	-11.33*±4.92	-6.67*±1.89	-1.33±0.75	6.67±3.13	Duplicate
	III	74.17*±3.23	-0.83±0.47	6.50±9.23	7.33*±3.20	1.17±1.53	3.67±6.07	-
	IV	-	-	-	-	-	-	-
	V	83.83*±3.55	-0.50±0.41	-8.50±9.34	-1.33±3.53	-0.83±1.39	9.67±5.98	-
	VI	87.00*±3.92	-0.33±0.53	-18.33*±8.75	-6.67±3.89	2.33*±0.97	15.33*±5.06	Duplicate
Plant height (cm)	I	22.53*±0.81	-5.93*±2.01	11.40*±5.33	4.40±5.16	-1.40±2.12	15.07±9.07	-
	II	-	-	-	-	-	-	-
	III	25.30*±1.12	1.47±1.78	-6.42±5.96	-10.53±5.74	1.28±1.88	7.10±9.03	-
	IV	22.54*±0.88	-1.80±1.73	6.87±5.12	4.90±4.95	-0.90±1.97	-0.15±8.20	-
	V	-	-	-	-	-	-	-
	VI	27.06*±1.21	2.27±1.85	2.11±6.25	-1.82±6.09	0.93±2.05	23.55*±9.28	-
Branches/plant	I	-	-	-	-	-	-	-
	II	3.73*±0.19	0.63±0.36	3.70*±1.08	1.40±1.03	1.00±0.39	-1.00±1.73	-
	III	4.11*±0.17	0.03±0.37	2.94*±1.05	1.91*±1.01	0.52±0.40	-2.53±1.72	-
	IV	4.09*±0.19	-0.61±0.38	3.64*±1.13	2.99*±1.08	-0.09±0.42	-1.91*±0.84	Duplicate
	V	4.03*±0.23	0.01±0.47	2.62*±1.35	1.47±1.31	0.46±0.52	-0.04±2.21	-
	VI	4.57*±0.24	0.07±0.40	2.97*±1.39	2.67*±1.26	0.10±0.45	1.67±2.20	-
Pod length (cm)	I	-	-	-	-	-	-	-
	II	4.14*±0.08	-0.35±0.23	1.94*±0.58	1.37*±0.56	-0.35±0.24	0.05±1.02	-
	III	4.41*±0.07	0.02±0.23	1.67*±0.56	1.14*±0.54	-0.01±0.24	-1.31±1.02	-
	IV	-	-	-	-	-	-	-
	V	-	-	-	-	-	-	-
	VI	4.54*±0.06	-0.46±0.18	0.90±0.47	0.50±0.45	-0.38±0.20	0.11±0.83	-
Pods/plant	I	18.22*±0.50	-3.80±1.20	0.67±3.25	-3.40±3.13	-2.67±1.30	12.73*±5.49	-
	II	13.92*±0.57	-1.07±1.11	5.53±3.26	3.53±3.19	-1.20±1.16	6.87±5.18	-
	III	18.43*±0.81	0.33±1.85	2.90±5.04	-2.13±4.92	2.23±2.01	-7.27±8.36	-

Table 3: Continue....

Table 3: Continue....

	IV	16.20**±0.64	-0.27±1.62	5.79±4.28	4.79±4.11	-0.34±1.78	-1.71±7.33	-
	V	15.52*±0.69	-2.53*±1.19	12.13*±3.82	9.67*±3.64	-3.40*±1.39	-18.87*±5.98	Duplicate
	VI	18.22*±0.68	-0.07±1.17	15.37*±3.80	12.33*±3.59	0.77±1.47	-7.60*±5.98	Duplicate
Seeds/pod	I	5.63*±0.14	-0.47±0.39	0.00±0.98	-0.80±0.95	-0.27±0.41	4.13*±1.70	-
	II	5.73*±0.12	0.07±0.27	-0.43±0.75	-1.20±0.71	-0.10±0.32	5.67*±1.26	-
	III	-	-	-	-	-	-	-
	IV	5.68*±0.15	0.27±0.37	0.57±1.02	0.20±0.97	0.70±0.41	0.93±1.73	-
	V	5.55*±0.15	-0.13±0.29	1.53±0.90	1.27±0.84	-0.07±0.33	-0.47±1.45	-
	VI	5.88*±0.14	0.33±0.37	0.27±0.99	0.33±0.92	0.20±0.43	2.07±1.73	-
Biological yield/plant(g)	I	21.81*±0.38	-1.00±0.75	6.81*±2.37	2.21±2.16	-0.27±0.91	3.39±3.91	-
	II	19.62*±0.35	0.36±0.67	5.22*±2.03	4.65*±1.95	0.33±0.83	-3.57±3.24	-
	III	-	-	-	-	-	-	-
	IV	18.85*±0.35	0.40±0.59	3.73±1.94	2.73±1.82	0.07±0.69	0.87±3.05	-
	V	-	-	-	-	-	-	-
	VI	19.45*±0.28	0.00±0.76	4.53*±1.97	4.60*±1.89	0.27±0.85	-4.47±3.43	-
Yield/plant(g)	I	-	-	-	-	-	-	-
	II	-	-	-	-	-	-	-
	III	-	-	-	-	-	-	-
	IV	5.27*±0.15	-0.63±0.42	-0.31±1.10	-0.72±1.05	-0.87±0.48	5.09*±1.92	-
	V	-	-	-	-	-	-	-
	VI	5.91*±0.13	0.05±0.41	1.01±1.01	0.57±0.99	0.10±0.44	1.10±1.80	-
Harvest index(%)	I	25.60*±0.40	-2.54*±0.97	30.64*±2.78	27.52*±2.50	-0.48±1.18	-32.65*±4.84	Duplicate
	II	30.68*±0.57	-0.25±1.47	-0.95±3.81	-2.19±3.73	0.19±1.55	9.36*±6.51	-
	III	-	-	-	-	-	-	-
	IV	28.87*±0.60	0.43±1.57	-3.66±4.05	-5.10±3.95	-0.04±1.71	19.35*±6.95	-
	V	28.92*±0.62	-1.75±1.10	9.06*±3.41	8.14*±3.31	-1.94±1.25	-6.76±5.30	-
	VI	29.98*±0.48	0.96±1.30	0.70±3.33	-2.32±3.24	1.20±1.44	12.45*±5.75	-
100-seed weight	I	4.38*±0.44	-0.25*±0.04	-1.75±1.06	-1.27*±0.44	0.15±0.13	1.43*±0.64	-
	II	2.25*±0.32	-0.15±0.05	1.62±0.80	0.87±0.31	-0.22±0.12	0.17±0.52	-
	III	4.40*±0.24	0.30±0.06	-2.27*±0.66	-0.87*±0.23	-0.27*±0.11	2.00*±0.48	Duplicate
	IV	5.93*±0.44	0.03±0.05	-5.40*±1.04	-1.87*±0.43	0.17±0.14	4.00*±0.64	Duplicate
	V	4.75*±0.35	0.15±0.02	-2.45*±1.00	-0.87*±0.35	-0.25±0.16	2.03*±0.68	Duplicate
	VI	3.45*±0.39	-0.18±0.10	0.58±1.01	0.20±0.38	0.35*±0.17	0.50±0.65	-

* Significance at 5% level of probability.

action. Thus, the investigation recommending the biparental mating followed by selection to effect the enhancement of the attribute. Results were in accordance with findings of Pathak *et al*. (2015) for duplicate type of epistasis and Ragul *et al*. (2021) for [i] gene action, supporting the above finding.

The number of seeds/pod is a major yield contributing attribute andits enhancement, together with the number of pods/plant, is the primary goal of plant breeding. The simple scaling test revealed the significant A, B and C scales in HimMash-1×Sirmour-2 and HimMash-1×Kullu-4 and significant B scale in Palampur-93×Sirmour-2, representing the presence of [i], [j] and [l] gene interaction. While, Palampur-93×Kullu-4 and Palampur-93×Chamba-8 possessed the [l] type of interaction as revealed by C scale. Significant [l] genic interaction was present in HimMash-1×Sirmour-2 and HimMash-1×Kullu-4. Significant and positive [h] gene effect was observed in cross HimMash-1×Chamba-8. The preponderance of non-additive gene action as well as [l] effect were also previously recorded by Murugan (2005) and Parsad and Murugan (2021). As a result, selection for the character may be extended to advanced generations, when desirable recombinants become attainable, (Inderjit *et al*., 2006; Patel *et al*., 2012).

The biological yield refers to the total dry matter accumulation of a plant system. It is a significant component and contributor to the harvest index. Increased harvest index indicates increased physiological potential to absorb photosynthates and transmit them towards organs with economic yield. The scaling tests revealed the significance of C and D scales in HimMash-1×Kullu-4 and Palampur-93×Chamba-8. In HimMash-1×Sirmour-2, scales A and D were significant. Palampur-93×Sirmour-2 showed significant C scale. Thus, confirmed the presence of [i], [j] and [l] type gene interaction. Six-parameter model for digenic control disclosed the presence of significant and positive [h] and [i] inter-allelic interaction in HimMash-1×Kullu-4 and in Palampur-93×Chamba-8. HimMash-1×Sirmour-2 pertained significant positive [h] gene effect, implicating the biparental mating accompanied by selection. Bindra (2017) also reported [h] and [i] genic interaction for the character.

The estimates of scaling tests disclosed the adequacy of additive-dominance model for the yield/plant in HimMash-1×Sirmour-2, HimMash-1×Kullu-4, HimMash-1×Chamba-8 and Palampur-93×Kullu-4 as these cross combinations had all the four scales non-significant. Palampur-93×Sirmour-2 possessed all three types of interactions, since scales A and C were significant. Palampur-93×Chamba-8 had significant C scale, demonstrating the [l] type of interaction. Murugan *et al.* (2005) also reported the similar results as there were preponderance all the three types of epistatic interaction and [l] genic effect. Palampur-93×Sirmour-2 had [l] type of inter-allelic interaction, so the breeding objective should be towards development of hybrids for commercial purpose.

Harvest index has the ability to dramatically enhance breeding for improved grain yield in any crop improvement strategy. The true objective of any breeding program is to improve yield, especially seed yield, where the crop's economic product is seed. Thereby, in order to be designated as a commercial variety, a novel genotype/line must outperform the yield levels of a popularly established commercial variety while also containing useful genes for number of important traits. In current investigation, significance of scales A, B and C in Palampur-93×Sirmour-2 and Palampur-93×Chamba-8 revealed [i], [j] and [l] type of inter-allelic gene control was associated in the inheritance of the trait. Whereas, in HimMash-1×Sirmour-2 and Palampur-93×Kullu-4, scales C and D were significant, indicating the preponderance of [i] and [l] type of interaction. In Palampur-93×Kullu-4 [l] type of gene interaction was present, since scale C was significant. Six-parameter model revealed the prevalence of duplicate epistasis, along with [i] type of interaction in HimMash-1×Sirmour-2, thus recommending the hybridization and selection in advanced generations would be beneficial for the improvement of the trait. Pathak (2015) and Bindra (2017) also obtained the alike outcomes illustrating existence of duplicate epistasis for the trait.

HimMash-1×Kullu-4, HimMash-1×Chamba-8, Palampur-93×Sirmour-2, Palampur-93×Kullu-4 and Palampur-93×Chamba-8 exhibited [i], [j] and [l] gene interactions for 100-seed weight. Whereas, HimMash-1×Sirmour-2, demonstrating the preponderance of [i] and [l] type of interaction. Duplicate type of epistasis in HimMash-1×Chamba-8, Palampur-93×Sirmour-2 and Palampur-93×Kullu-4 revealed that bi-parental mating accompanied by selection in later segregants could lead to improvements. Bindra *et al*., (2017), Singh *et al*., (2016),Sinha *et al*., (2020) also found duplicate epistasis; Parsad and Murugan (2021) got additive, dominance, epistatic interactions and duplicate dominant interaction for the trait; Ragul *et al*. (2021) reported [d], [i] gene action and duplicate type of epistasis.

CONCLUSION

In current study, the nature and magnitude of gene effects on seed yield and its component traits in urdbean were investigated. The results demonstrated the importance of additive, dominant and epistatic interaction in the transmission of morphological, yield and quality characteristics in urdbean. The greater intensity of dominance gene action for most variables indicated that heterosis breeding would be successful in boosting yield traits such as days to 50% flowering, days to 75% maturity, branches/plant, biological yield/plant, harvest index and 100-seed weight.The results showed that genic interactions varied cross-wise and trait-wise. Hence, specific breeding strategy has to be adopted for a particular cross to effect improvement in seed yield along with desirable yield contributing traits. Whereas, duplicate type of epistasis, suggested biparental mating followed by selection in advanced generations would also be beneficial for yield improvement. Outstanding segregants from particular crosses can be recognized and intermated, then succeeded by reciprocal recurrent selection. Thus, will leads in the formation of desirable high yielding urdbean genotypes. Furthermore, the gene action must be confirmed further by utilizing a large number of genotypes and subsequent generations because the detected gene action is particular to the collection of experimental genotypes employed in the study.

ACKNOWLEDGEMENT

Authors are thankful to Department of GPB, CSKHPKV, Palampur for providing necessary facilities and there is no conflict of interest among authors.

Conflict of interest: None.

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