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Generation Mean Analysis for Seed Yield and its Components in Urdbean (*Vigna mungo* [L.] Hepper)

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ABSTRACT: This research used a six-generation mean analysis for seed yield and its components in five urdbean inter-varietal crossings on scope of gene action. The results of additional scaling tests demonstrated the need for an epistatic model, and an analysis of generation mean analysis (GMA) confirmed that no simple additive-dominance model existed. The variety of gene activities influencing seed yield and quality was another discovery from GMA. The most typical types of interactions are dominance × dominance and duplicate dominant, but additive and epistatic interactions are also feasible. Since these traits are difficult to improve using simple selection methods, pedigree breeding procedures wait until later generations to pick elite lines for maximum efficacy. One or two cycles of recurrent selection, in conjunction with pedigree breeding, would be the optimal technique for choosing superior lines with high seed yield and its components, while also managing epistatic interactions.

Keywords: Generation mean analysis, Urdbean Crossings, Pedigree Breeding, Scaling tests, Epistatic interactions.

INTRODUCTION

The unusual chromosomal number 2n=2x=22 makes Urdbean stand out. It has tremendous potential to improve soil fertility, is a remarkable short-duration legume, and is photo-thermo insensitive. You can't go wrong with it if you're planning to increase crop intensity and diversity. It contains easily digestible components such as protein (25-28 percent), oil (1.0-1.5 percent), fibre (3.5-4.5 percent), ash (4.5-5.5 percent), and carbs (4.5-5.5 percent) (62-65 percent). As a crop with few gastrointestinal issues and a high lysine, vitamin, iron, and phosphorus content, urdbean deserves significant consideration for agricultural use.

Understanding the kinds and amounts of genetic impacts on quantitative features is necessary for the discovery of high-yielding urdbean genotypes. Developing reliable breeding techniques requires a thorough understanding of their complex inheritance. On autogamy crops, such as urdbean, a method based on generation mean analysis works well. This approach takes additive and dominance gene effects into consideration, which improves our understanding of the dominant epistasis. Therefore, this study aims to identify the genes that have a substantial impact on seed yield and crop quality. Five urdbean inter-varietal hybrids are examined in this experiment using six different generation procedures.

MATERIAL AND METHODS

The study utilised five urdbean inter-varietal crosses: Co 5 x PU 31 (C1), Co 5 x VBN (Bg) 4 (C2), Co 5 x VBN (Bg) 6 (C3), LBG 623 x VBN (Bg) 4 (C4), and LBG 623 x VBN (Bg) 6 (C5). A total of six generations were produced by these crosses: P1, P2, F1, F2, B1, and B2. A two-step procedure utilising a compact family block design was used to sow the seeds of these hybrids (C1 to C5). Ten centimetres between plants and thirty centimetres between ridges were the recommended spacing due to the two-meter-long ridges on which the planting was conducted. The assessment was place in the fall of 2014 at the National Pulses Research Center in Vamban. In order to guarantee a healthy crop, the cultivation approach adhered to standard agronomic practises. The following table displays the plant data for six generations from each of the five urdbean inter-varietal crosses.

Table 1.

Sr. No.	Generation	Rows / replication	Plants studied / replication	Total plants studied
1	P_1	1	20	40
2	P_2	1	20	40
3	F_1	1	20	40
4	F_2	8	160	320
5	B_1	3	60	120
6	B_2	3	60	120

In each replication, nine metric parameters were measured from individual plants: plant height, branch number, cluster number, pod number, seed per pod, seed weight per hundred, and seed output per plant. The three simple scaling tests developed by Mather (A, B, and C) were used to determine epistasis (1949). In order to estimate the six parameters, we used Hayman's (1958) model. These parameters are m, d, h, I, j and l. The following nine metric parameters were measured

for each plant in each replication: plant height, branch number, cluster number, pod number, seed per pod, weight of 100 seeds, and seed output per plant. The three primary scaling tests (A, B, and C) suggested by Mather (1949) were used to detect epistasis. In order to predict m, d, h, i, j and l, we utilised Hayman's (1958) suggested six-parameter model.

RESULTS AND DISCUSSION

Table 3 summarises the mean estimates for each of the six generations, while Table 2 summarises them collectively (P1, P2, F1, F2, B1, and B2). The results of the A, B, and C scale scaling test are provided along with the gene effects that are associated with them. These effects include additive, dominance, and epistatic interactions. These results are relevant to five inter-varietal urdbean crosses and the components of seed yield.

A. Days to 50 % Flowering

Across all five of the tested crosses, the P1 generation maintained a significant performance advantage over the P2 generation. Regardless of the crossover, the offspring remained behind their parents. The F2 mean was higher than the F1 mean for all five crossings. Notably, crossovers C1, C2 and C4 had a larger B1 mean compared to the F1 mean, whereas crosses C3 and C5 had a lesser discrepancy. Nevertheless, the B2 mean was consistently lower than the F1 mean, with the most noticeable disparity being in cross C2.

Scales A, B, and C all got statistically significant in C4 and C5, C2 and C3, and C1 and C3, respectively, according to the scaling test results. This is why none of the studied crosses could be satisfactorily described by a basic additive-dominance model. The findings of the crosses always indicated that the natural origin played a positive and statistically significant influence, regardless of how many different elements were included (m). We found no statistically significant additive influence (d) in any of the crosses with the exception of C3. While crossing C1 had a beneficial influence on dominance, crossings C2, C4, and C5 all had negative impacts. While crossovers C2 and C1 demonstrated positive interactions, crosses C1, C3, and C4 exhibited a negative and statistically significant additive × additive interaction I. A negative and statistically significant additive × dominance interaction was shown by crosses C3, C4 and C5, in contrast to the positively and unrelatedly significant interaction displayed by crossovers C2 and C1 (j). The dominance × dominance (l) interaction had a positive effect in crossings C2, C4, and C5, a positive effect in crossing C3 that was not statistically significant, and a negative effect in crossing C1.

This trait is governed by all three kinds of epistatic interactions: dominance, inverse interactions, and additivity. Jahagiridar (2001) and Rahecha *et al*. (2006) found evidence of additive gene activity associated with these features. Kute and Deshmukh (2002), Vasline *et al*. (2007), Anbu Selvam and Elangaimannan (2010), Supriyo Chakraborty *et al*. (2010), Isha Parveen *et al*. (2012), Selvam (2012), Gill *et al*. (2014), and Vijay Kumar *et al*. (2014) all attest to the high frequency of this trait's dominating effect. This attribute is affected by additive and dominant variance, as pointed out by Murugan (2005) and Ram *et al*. (2005). Prasad and Murugan (2021), Murugan (2005), Kute and Deshmukh (2002), Singh *et al*. (2007), and Ramakant and Srivastava (2005) all provided evidence of the three kinds of epistatic interactions that regulate this characteristic.

B. Plant Height

P1 had a higher mean than P2 in every single cross. The F1 (intermediate) showed consistency across all crosses. There was a difference between the F1 and F2 means in each of the five crossovers. There was a significant difference between the B1 and F1 means in every single cross. C1, C4, and C5 crossovers were lower in the B2 mean compared to the F1 mean, while C2 and C3 crossovers were higher.

Every one of the crosses required to use an epistatic model in order for them to pass the scaling test. Scale A showed an encouraging but not statistically significant trend across all crossovers. Crosses C3 and C5 were statistically significant on Scale B, whereas Cross C4 was not. There was a constant trend of positive and statistically significant results on Scale C. A positive and statistically significant trend was shown by the parameter 'm' in all the crosses, outperforming all other effects. There was an additive effect that was both positive and statistically significant regardless of the cross (d). The C3 and C5 crossovers showed a non-significant dominance influence (h) that was positive, whereas the C1, C2, and C4 crosses were quite negative. Although cross C2 did not experience the negative and statistically significant effects of additive × additive I, crosses C1, C3, C4, and C5 did. In crosses C3 and C5, the additive × dominance influence (j) was negative and statistically significant; in cross C1, it was non-significant; and in cross C2, it was positive but non-significant. The effects of crossing C4 were positively significant due to an interaction between dominance and dominance (l), in contrast to the non-significant impacts of crossings C1 and C2. As for cross C5, the effect was not statistically significant, but for cross C3 it was negative and significant.

Table 2: Estimates of scaling test for seed yield and its attributes in urdbean.

Character	Scaling test	Cross				
		C_1	C_2	C_3	C_4	C_5
Days to 50% flowering	A	1.23+ 0.45	-0.47+ 0.44	-0.43 + 0.38	-2.60** + 0.45	-3.17** + 0.46
	B	1.03+ 0.41	-2.47**+ 0.45	1.10** + 0.43	0.37 + 0.48	-0.13 + 0.43
	C	-7.40*+ 0.65	1.12+ 0.70	-2.24** + 0.74	-1.06 + 0.83	-1.46 + 0.77
Plant height	A	0.37+ 2.28	2.33+ 1.98	1.87 + 1.92	-0.07 + 1.97	0.60 + 2.04
	B	1.13 + 1.70	0.97 + 1.49	19.00**+ 1.30	-3.43* + 1.44	17.40**+ 1.38
	C	12.50**+ 3.81	13.10**+ 3.01	31.68**+ 3.00	6.58* + 3.32	27.44**+ 3.27
Branches plant^{-1}	A	-0.30 ± 0.34	-0.30 ± 0.31	-0.33 ± 0.28	-0.53 ± 0.30	-0.57* ± 0.23
	B	0.17 ± 0.30	-0.07 ± 0.30	0.07 ± 0.28	-0.63* ± 0.28	-0.43 ± 0.25
	C	-0.56* ± 0.45	-0.82* ± 0.45	-1.16**± 0.44	-1.50**± 0.43	-1.28** ± 0.38
Clusters plant^{-1}	A	-1.00 ± 0.90	-1.50 ± 0.81	-1.97 ± 0.77	-1.73* ± 0.83	-1.73* ± 0.81
	B	-2.70**± 0.90	-2.27**± 0.86	-2.27**± 0.80	-3.00** ± 0.85	-3.17** ± 0.75
	C	-6.42**± 1.43	-5.78**± 1.33	-6.46**± 1.28	-6.16** ± 1.36	-5.90** ± 1.24
Pods plant^{-1}	A	-1.37 ± 1.09	-1.77 ± 1.06	-1.60 ± 0.99	2.43* ± 1.05	2.63** ± 0.98
	B	0.37 ± 1.04	-0.03 ± 1.03	0.97 ± 0.87	1.10 ± 1.04	1.43 ± 0.96
	C	-11.60**± 1.79	-11.32**± 3.09	-10.82**± 1.66	-5.00** ± 1.78	-4.00* ± 1.64
Pod length	A	-0.23**± 0.09	-0.14 ± 0.08	-0.27** ± 0.10	-0.18* ± 0.08	-0.13 ± 0.07
	B	0.05 ± 0.08	0.07 ± 0.07	-0.16 ± 0.09	-0.10 ± 0.07	-0.05 ± 0.06
	C	-0.35* ± 0.14	-0.22* ± 0.11	-0.57** ± 0.15	-0.53** ± 0.13	-0.44** ± 0.10
Seeds pod^{-1}	A	-0.63* ± 0.31	-0.73**± 0.26	-0.20 ± 0.27	-0.43 ± 0.23	-0.20 ± 0.21
	B	-0.60* ± 0.30	-0.50 ± 0.27	-0.23 ± 0.25	-0.77** ± 0.30	-0.33 ± 0.20
	C	-0.98* ± 0.49	-0.90* ± 0.39	-0.50 ± 0.40	-1.36** ± 0.34	-0.80** ± 0.31
Hundred seed weight	A	-0.20**± 0.06	-0.16** ± 0.06	-0.17** ± 0.06	0.68** ± 0.08	0.62** ± 0.07
	B	-0.65**± 0.07	-0.57** ± 0.07	-0.54** ± 0.07	-0.06 ± 0.06	-0.03 ± 0.06
	C	-0.64**± 0.11	-0.53** ± 0.11	-0.51** ± 0.11	0.38** ± 0.15	0.38** ± 0.14
Seed yield plant^{-1}	A	-1.27**± 0.33	-1.40** ± 0.40	-0.96* ± 0.41	1.46** ± 0.34	1.52** ± 0.33
	B	-1.88**± 0.37	-1.75** ± 0.29	-1.13**± 0.38	-0.43 ± 0.25	-0.13 ± 0.28
	C	-4.82**± 0.59	-4.55** ± 0.49	-4.57**± 0.61	-1.95** ± 0.47	-1.40** ± 0.47

*Significance at 5% level of probability **Significance at 1% level of probability

Table 3: Estimates of gene action for seed yield and its attributes in urdbean.

Character	Cross	Gene action					
		m	d	h	i	j	l
Days to 50% flowering	C_1	23.13**+ 0.54	3.00**+ 0.16	21.70**+ 1.44	9.67**+ 0.52	0.10 + 0.26	-11.93**+ 1.03
	C_2	39.75**+ 0.66	0.30*+ 0.15	-12.14**+ 1.70	-4.05**+0.64	1.00**+ 0.27	6.99**+ 1.15
	C_3	37.07**+ 0.68	0.100 + 0.14	-2.68 + 1.65	-1.57* + 0.66	-0.77**+ 0.24	0.91 + 1.08
	C_4	36.92** + 0.66	0.65** + 0.14	-3.93* + 1.63	-1.17 + 0.64	-1.48** + 0.25	3.41** + 1.17
	C_5	37.79** + 0.63	0.65** + 0.15	-6.43** + 1.57	-1.84** + 0.61	-1.52** + 0.25	5.14** + 1.10
Plant height	C_1	57.15**+ 3.19	9.95**+ 0.94	-28.65**+ 7.57	-11.00**+ 3.05	-0.38 + 1.22	9.50 + 4.94
	C_2	56.15**+ 3.25	7.25**+ 0.65	-25.65**+ 7.99	-9.80 + 3.18	0.68 + 1.18	6.50 + 4.97
	C_3	46.91**+ 2.94	17.40**+ 0.66	0.44 + 7.11	-10.81**+ 2.87	-8.57**+ 1.06	-10.05* + 4.47
	C_4	55.63**+ 3.06	7.45** + 0.66	-28.21**+ 7.28	-10.08**+ 2.99	1.68 + 1.05	13.58** + 4.66
	C_5	44.84**+ 2.98	17.00** + 0.72	4.12 + 7.14	-9.44** + 2.89	-8.40** + 1.08	-8.56 +-3.97
Branches plant^{-1}	C_1	2.27**± 0.39	0.20 ± 0.14	1.22 ± 1.07	0.43 ± 0.37	-0.23 ± 0.21	-0.29 ± 0.74
	C_2	2.40**± 0.35	0.15 ± 0.13	0.99 ± 0.96	0.45 ± 0.33	-0.12 ± 0.19	-0.09 ± 0.69
	C_3	2.01**± 0.34	0.20 ± 0.12	1.92* ± 0.90	0.90**± 0.32	-0.20 ± 0.17	-0.63 ± 0.65
	C_4	2.82** ± 0.35	-0.05 ± 0.11	-0.35 ± 0.96	0.33 ± 0.34	0.05 ± 0.18	0.83 ± 0.69
	C_5	2.92** ± 0.31	-0.10 ± 0.09	-0.44 ± 0.81	0.28 ± 0.29	-0.07 ± 0.14	0.72 ± 0.58
Clusters plant^{-1}	C_1	16.13**± 1.10	-0.85**± 0.33	1.69 ± 2.92	2.72**± 1.05	0.85 ± 0.51	0.98 ± 2.14
	C_2	16.84**± 1.06	-0.55 ± 0.32	0.41 ± 2.77	2.01* ± 1.01	0.38 ± 0.49	1.75 ± 1.98
	C_3	16.42**± 1.01	-0.25 ± 0.30	1.27 ± 2.62	2.23* ± 0.96	0.15 ± 0.46	2.01 ± 1.87
	C_4	17.77** ± 1.03	-0.60* ± 0.30	-2.28 ± 2.72	1.43 ± 0.99	0.63 ± 0.47	3.31 ± 2.00
	C_5	17.85** ± 1.00	-0.55 ± 0.30	-2.65 ± 2.61	1.00 ± 0.95	0.72 ± 0.46	3.90* ± 1.85
Pods plant^{-1}	C_1	19.40**± 1.50	-3.50**± 0.46	26.20**± 3.76	10.60**± 1.42	-0.87 ± 0.65	-9.60**± 2.55
	C_2	20.88**± 1.48	-3.40**± 0.38	22.74**± 3.73	9.52**± 1.43	-0.87 ±0.61	-7.72** ±2.58
	C_3	19.96**± 1.46	-2.75**± 0.38	25.19**± 3.57	10.19**± 1.41	-1.28* ± 0.57	-9.55**± 2.36
	C_4	22.47**± 1.40	-3.90** ± 0.36	20.80** ± 3.56	8.53** ± 1.35	0.67 ± 0.58	-12.07**± 2.56
	C_5	22.83** ± 1.31	-3.80** ± 0.37	19.90** ± 3.33	8.07** ± 1.26	0.60 ± 0.56	-12.13** ± 2.35
Pod length	C_1	4.70**± 0.11	0.34**± 0.03	0.10 ± 0.28	0.17 ± 0.10	-0.14**± 0.05	0.01 ± 0.21
	C_2	4.73**± 0.11	0.29**± 0.03	0.11 ± 0.28	0.15 ± 0.10	-0.11* ± 0.05	-0.08 ± 0.19
	C_3	4.77** ± 0.11	0.23**± 0.03	-0.13 ± 0.28	0.14 ± 0.10	-0.05 ± 0.05	0.29 ± 0.21
	C_4	4.68** ± 0.10	0.24** ± 0.02	0.15 ± 0.27	0.26** ± 0.10	-0.04 ± 0.04	0.02 ± 0.19
	C_5	4.68** ± 0.10	0.21** ± 0.02	0.22 ± 0.25	0.26** ± 0.09	-0.04 ± 0.04	-0.08 ± 0.17
Seeds pod^{-1}	C_1	6.00**± 0.34	-0.05 ± 0.10	-1.29 ± 0.90	-0.25 ± 0.32	-0.02 ± 0.16	1.49* ± 0.70
	C_2	6.08**± 0.33	0.05 ± 0.10	-1.45 ± 0.90	-0.33 ± 0.32	-0.12 ± 0.16	1.57* ± 0.63
	C_3	5.48**± 0.32	-0.15 ± 0.11	0.35 ± 0.84	0.07 ± 0.30	0.02 ± 0.16	0.37 ± 0.60
	C_4	5.84** ± 0.31	-0.20* ± 0.09	-0.78 ± 0.83	0.16 ± 0.30	0.17 ± 0.15	1.04 ± 0.56
	C_5	5.73** ± 0.28	-0.10 ± 0.07	-0.10 ± 0.74	0.27 ± 0.27	0.07 ± 0.12	0.27 ± 0.51
Hundred seed weight	C_1	4.59**± 0.09	-0.17**± 0.03	-0.88**± 0.23	-0.21* ± 0.09	0.23**± 0.04	1.06**± 0.15
	C_2	4.57**± 0.09	-0.15**± 0.03	-0.78**± 0.22	-0.20* ± 0.08	0.21**± 0.04	0.94**± 0.15
	C_3	4.58**± 0.09	-0.15**± 0.03	-0.76**± 0.21	-0.21* ± 0.08	0.18**± 0.04	0.91**± 0.15
	C_4	4.13** ± 0.12	-0.29** ± 0.03	0.80** ± 0.27	0.24* ± 0.11	0.37** ± 0.04	-0.86** ± 0.18
	C_5	4.14** ± 0.12	-0.27** ± 0.03	0.73** ± 0.27	0.21* ± 0.11	0.33** ± 0.04	-0.80** ± 0.17
Seed yield plant^{-1}	C_1	4.77**± 0.51	-1.44**± 0.11	2.77* ± 1.29	1.67**± 0.50	0.30 ± 0.20	1.49 ± 0.90
	C_2	5.32**± 0.56	-1.16**± 0.10	1.95 ± 1.47	1.40* ± 0.55	0.18 ± 0.23	1.74 ± 0.96
	C_3	3.90**± 0.59	-1.05**± 0.14	5.78**± 1.52	2.48**± 0.57	0.08 ± 0.25	-0.40 ± 1.02
	C_4	3.79** ± 0.51	-1.68** ± 0.06	6.91**± 1.30	2.97** ± 0.51	0.95** ± 0.19	-4.00** ± 0.85
	C_5	4.15** ± 0.50	-1.53** ± 0.10	6.33**± 1.29	2.79** ± 0.50	0.83** ± 0.20	-4.18** ± 0.84

*Significance at 5% level of probability **Significance at 1% level of p

Evidently, additive, dominant, and all three forms of epistasis impacted this attribute. Multiple studies have linked this characteristic to a higher dominance variance. Some of these publications are: Jiji Joseph and Santhosh Kumar (2000), Manivannan (2002), Vaithiyalingam *et al*. (2002), Singh and Dikshit (2003), Anbumalarmathi *et al*. (2004), Murugan (2005), Vasline *et al*. (2007), Anbu Selvam and Elangaimannan (2010), Supriyo Chakraborty *et al*. (2010), Selvam (2012), Gill *et al*. (2014), Vijay Kumar *et al* (2014), Prasad and Murugan (2021). On the flip side, studies have demonstrated additive gene action; for example, Rahecha *et al*. (2006) and Isha Parveen *et al.* (2012). All three kinds of epistasis have been recorded by Ramakant and Srivastava (2005), Bhattak *et al*. (2002), Murugan (2005) and Singh *et al*. (2007).

P1 had a higher mean than P2 in every single cross. The F1 (intermediate) showed consistency across all crosses. There was a difference between the F1 and F2 means in each of the five crossovers. There was a significant difference between the B1 and F1 means in every single cross. C1, C4, and C5 crossovers were lower in the B2 mean compared to the F1 mean, while C2 and C3 crossovers were higher.

Every one of the crosses required to use an epistatic model in order for them to pass the scaling test. Scale A showed an encouraging but not statistically significant trend across all crossovers. Crosses C3 and C5 were statistically significant on Scale B, whereas Cross C4 was not. There was a constant trend of positive and statistically significant results on Scale C. A positive and statistically significant trend was shown by the parameter'm' in all the crosses, outperforming all other effects. There was an additive effect that was both positive and statistically significant regardless of the cross (d). The C3 and C5 crossovers showed a non-significant dominance influence (h) that was positive, whereas the C1, C2, and C4 crosses were quite negative. Although cross C2 did not experience the negative and statistically significant effects of additive × additive I, crosses C1, C3, C4, and C5 did. In crosses C3 and C5, the additive × dominance influence (j) was negative and statistically significant; in cross C1, it was non-significant; and in cross C2, it was positive but non-significant. The effects of crossing C4 were positively significant due to an interaction between dominance and dominance (l), in contrast to the non-significant impacts of crossings C1 and C2. As for cross C5, the effect was not statistically significant, but for cross C3 it was negative and significant.

The three forms of epistasis—additivity, dominance, and convergent—appear to have had an impact on this attribute. This attribute has a higher dominance variance, according to several research. Here are some of the studies that fall under this category: Jiji Joseph, Santhosh Kumar *et al*. (2000), Manivannan (2002), Vaithiyalingam *et al*. (2002), Singh and Dikshit (2003), Anbumalarmathi *et al*. (2004), Murugan (2005), Vasline *et al*. (2007), Anbu Selvam and Elangaimannan (2010), Supriyo Chakraborty *et al*. (2010), Selvam (2012), Gill *et al*. (2014), Vijay Kumar *et al.* (2014), Prasad and Murugan (2021). A number of studies, including one by Rahecha *et al*. (2006), have demonstrated additive gene activity. Many researchers have documented the three distinct kinds of epistasis: Ramakant and Srivastava (2005), Singh *et al*. (2007), Khattak *et al*. (2002), Murugan (2005), Prasad and Murugan (2021).

C. Branches Plant^{-1}

The only crossovers where P1 had a higher mean than P2 were C4 and C5. Except for cross C5, which had a value in the middle, the F1 mean was always greater than the parental means. The F2 mean was much lower than the F1 mean in every single cross. In every single cross, the B1 mean was either lower than or equal to the recurrent parent mean. Importantly, with the exception of crossovers C4 and C5, the mean in B2 was higher than the value of the repeating parent in every single cross. There was a non-significant negative trend for scale A in all crosses except C5. On the other hand, scale B demonstrated a tendency toward the negative in cross C4, a trend toward the positive in crosses C2 and C5, and a trend toward the positive in crosses C1 and C3, but this trend did not reach statistical significance. In the meantime, Scale C showed a statistically significant downward trend in all crosses. The flaws of an elementary additive-dominance model were exposed by the five crossings. Among all the effects tested, the m effect proved to be the most beneficial. Outside of crossing C5, where it displayed non-significant negativity, additive impact (d) was non-significantly positive in all other crossings. There was a positive trending but non-significant dominance impact (h) for crosses C1, C2, and C3, and a negative trending but non-significant trend for crosses C4 and C5. Only in Cross C3 was the additive x additive I effect statistically significant; in all the others, it was not. All crossings except C4 had non-significantly negative interaction effects, meaning that neither the additive nor the dominance x dominance combination effects nor the dominance x dominance impact (j) were negative.

This feature appeared to be under the control of additive and dominant gene activity, as well as the three kinds of interactions (including the duplicate dominant interaction). Earlier studies on this characteristic were validated by these findings. Numerous studies have confirmed the rise of dominant gene activity, including those by Murugan, Vaithiyalingam *et al*. (2002), Manivannan (2002), Anbumalarmathi *et al*. (2004), Jiji Joseph and Santhosh Kumar (2000), and Vaithiyalingam *et al*. (2002). In addition, as Murugan (2005), Prasad and Murugan (2021) pointed out, this feature is linked to all three kinds of epistasis.

D. Clusters Plant^{-1}

The P2 means were higher than the P1 ones in every single cross. Cross C3 had the most extreme F1 means relative to the parents' means, while the remaining crosses had intermediate F1 values. In every single cross, the F1 and F2 means were less apart. When compared to the repeating parents in any particular cross, B1 indicates a total and utter failure. When B2 was considered, the pattern still remained. While scales A were only significant in crosses C4 and C5, scales B

and C were significant in all crosses according to the scaling test. This meant that a basic additive model failed miserably every time. Of all the factors that were considered, the natural origin (m) was the most crucial and consistently significant in all of the crosses. Crossovers C1, C4, and C5 showed statistical significance and negativity for the additive impact (d), however crosses C2, C3, and C5 did not. The dominance influence (h) was positive but not statistically significant for crosses C1, C2, and C3, and negative for crosses C4 and C5. In crosses C1, C2, and C3, the additive × additive I impact was positive and statistically significant, but in crosses C4 and C5, it was not present. The additive × dominance impact (j) was also positive across the board, though it was not statistically significant. The influence of the dominance × dominance (l) interaction was positively significant in cross C5, which was different from the other crossings.

Ultimately, the additive effect took a back seat to the established dominant effect. The main areas where epistatic interactions were significant were the additive × additive (i) and dominance x dominance (l) components that impacted this specific feature. Results from studies by Singh and Dikshit (2003), Jiji Joseph and Santhosh Kumar (2000), and Murugan (2005) all pointed to dominant genes as the controllers of this feature. The existence of additive and dominating variables was recognised by Murugan (2005) and Jahagiridar (2001) as well. The existence of epistatic interactions has been verified by other scholars as well, including Murugan (2005), Prasad and Murugan (2021). The additive × additive interaction effect was emphasised by Kute and Desmukh (2002) for this specific characteristic.

E. Pods Plant^{-1}

No matter the genetic cross, P2 always performed better than P1. When compared to the parental means, the F1 means in crosses C4 and C5 were intermediate, while in crossings C1, C2, and C3 they were significantly higher. In every single genetic cross, the F2 mean was far lower than the F1 mean. B1 consistently outperformed its like repeating parent in all crosses. As opposed to the P2 mean, the B2 mean showed an increase in crosses C1, C2, and C3, whereas crosses C4 and C5 showed a reduction. Although scale C was consistently significant across all crossings, scale A was only significantly different in cross C4. But in none of the five comparisons did scale B demonstrate statistical significance. As a result, none of the hybrids under consideration could be well described by a basic additive-dominance model. The magnitude of the dominant impact (h) was determined to be greater than the natural origin, with the exception of crossings C1, C2, and C3, all of which demonstrated positive significance (m). In every cross, the dominance impact (h) and the additive × additive I effect were positive, whereas the additive effect (d) was consistently negative. Crosses C1 and C2 had a negative, but not statistically significant, additive × dominance effect (j). Results showed that cross C3 was statistically significantly positive, but crosses C4 and C5 were positive but did not reach statistical significance. It was clear in every single crossing that interactions between dominance and dominance (l) had a negative impact.

The results suggest that additive, dominant, and epistatic interactions all play a role in controlling this feature. There is evidence of dominant gene duplication, with interactions mostly being additive × additive or dominance × dominance. Singh and Dikshit (2003), Anbumalarmathi *et al*. (2004), Jiji Joseph and Santhosh Kumar (2000), Manivannan (2002), Murugan (2005), Prasad and Murugan (2021) are among the many researchers who have discovered evidence indicating the role of dominant genes is involved in the control of this feature. Epistatic interactions involving this specific feature have been demonstrated by studies carried out by Murugan (2005), Ganesamurthy and Seshadri (2002).

F. Pod Length

In every cross between the two lines of parents, the pod length was consistently longer in the P1 generation compared to the P2 generation. Much like in other crosses, the F1 mean mediates between the parental means. With the exception of cross C2, where the two crossings were identical, the F2 mean was consistently lower than the F1 mean. In spite of this, B1 proved in every cross that its mean was less than P1. B2, on the other hand, showed a contrasting pattern with a mean greater than the corresponding recurrent parent. In the scaling study, all crossings showed a negative trend on scale C, and all four crosses showed a matching pattern on scale A. In crosses C1 and C2, scale B yielded positive results; in crosses C3, C4, and C5, the results were non-significantly negative. There was a strong increasing trend in the residual effect (m), which outperformed all other effects across all crosses. It was clear from every crossing that there was a powerful positive cumulative effect (d). The dominance influence (h) was helpful in most cases, but it wasn't significant enough to warrant further investigation. With the exception of crossovers C4 and C5, all other positive additive × additive I effects were either nonexistent or very small. Only crossings C1 and C2 showed a statistically significant additive × dominance impact (j), but none of the others did. Except for crossings C1, C3, and C4, the interaction impact of dominance V dominance (l) was negative. The lone crossing C4 had a non-significant positive sign.

This attribute is mostly governed by interactions like additive × additive interactions, dominance and epistatic interactions, and others. Vaithiyalingam *et al*. (2002) state that this characteristic is associated with dominating and additive effects. All three types of epistatic interaction are associated with this trait, as Murugan noted (2005), Prasad and Murugan (2021).

G. Seeds Pod^{-1}

P2 has maintained a higher mean than P1 unless cross C2 is taken into account. The F1 mean values were higher than the parents' in crossings C1, C2, and C3, intermediate in C4, and perfect in C5. The F2 mean decreased significantly relative to the comparable F1 in every single crossover. B1 had a lower mean than the repeating parent in a single cross (C3). While taking the

P2 mean into account, the B2 mean performed better in cross C3, was on par with cross C2, and performed worse in every other cross except one. The results of the scaling tests showed that the only crossovers with a considerably negative scale A were C1 and C2. On scale B, we also noticed a similar pattern, with the exception of crosses C1 and C4, which were not statistically significant. Scale C always showed a negative significance, with the exception of cross C3. Aside from all other consequences, the natural origin (represented by "m") in all crossings established a positive importance. The other crossings did not show a substantial additive effect (d), only C1 and C4 did. The dominance impact (h) was negative and non-significant in all crosses except for C2, when it became positive. The additive × additive impact I was positive for all crossings except C1 and C2, which were non-significant and had a negative sign. Though all the other crossovers were successful, the dominance × dominance interaction effect (l) and the additive × dominance impact (j) were both negatively affected by crossing C1.

Dominance × dominance and duplicate dominant interactions, as well as additive and epistatic interactions, govern this feature. In this setting, Aher *et al*. found that additive effects predominated. According to multiple researchers, including Prasad and Murugan (2021), Murugan (2005), Anbumalarmathi *et al*. (2004), Singh and Dikshit (2003), and others, there is evidence that this feature is influenced by non-additive gene activity. Murugan (2005) began by explaining the impact of dominance x dominance on this aspect.

H. Hundred Seed Weight

In each of the crosses, P_2 exhibited a higher mean than P_1. Contrarily, in the F_1 generation, the mean surpassed the corresponding parental means, with the exception of crosses C_4 and C_5, where it dipped below their respective parental means. Across all crosses, the F_2 mean generally fell short of the respective F_1 mean, except in crosses C_4 and C_5, where it exceeded. Upon comparing the B_1 mean with their respective recurrent parent, all crosses manifested higher mean values. In contrast, B_2 in each cross displayed a mean lower than its corresponding recurrent parent.

The examination using scaling tests indicated that the negative significance was observed in all three scales across the crosses C_1, C_2 and C_3. Conversely, both scale A and scale C demonstrated positive significance in the context of crosses C_4 and C_5. In contrast, the negative non-significance of scale B was evident in crosses C_4 and C_5. Across all the crosses, the natural origin m exhibited positive significance, surpassing other effects. The additive effect (d) consistently showed negative significance in every cross. Meanwhile, the dominance effect (h) and the additive × additive effect (i) displayed consistent negative significance in crosses C_1, C_2 and C_3, while demonstrating positive significance in crosses C_4 and C_5. The additive × dominance effect (j) maintained a significantly positive status across all crosses. Regarding the dominance x dominance (l) interaction effect, it exhibited positive significance in crosses C_1, C_2 and C_3, except in crosses C_4 and C_5, where it showed significant negativity. The opposing signs of effects (h) and (l) were consistent across all five crosses.

In summary, the control of this characteristic seems to be influenced by a combination of additive, dominance, epistatic interactions, and duplicate dominant effects. Previous studies have provided insights into the genetic mechanisms governing the weight of a hundred seeds. Researchers such as Indrani Dana and Das Gupta (2001) and Aher *et al.* (2001) documented instances of additive gene action. Conversely, non-additive gene actions were identified by Jehagiridar (2001), Vaithiyalingam *et al.* (2002), Singh and Dikshit (2003), and Anbumalarmathi *et al.* (2004). In contrast, the occurrence of duplicate dominant epistasis was documented by Murugan (2005), Prasad and Murugan (2021).

I. Seed Yield Plant^{-1}

In every crossing, P2 outperformed P1. F1 means exceeded parent line means in all five crosses. The F2 means were much lower than the comparable F1 ones in every single cross. No matter the cross, B1 always performed much better than its recurring parent. The B2 mean performed worse than the corresponding recurrent parent in most cases, except in cross C3, where it showed signs of superiority. According to the results of the scaling test, there was a negative statistical significance for all three scales in the C1, C2, and C3 crossings. The results showed that scale A was significantly positive in crosses C4, whereas scale C was significantly negative in crosses C5. It was determined that scale B was negatively non-significant only in crossings C4 and C5. In every crossing, the natural origin, represented by "m," was the most important impact and showed positive significance continuously. The cumulative impact (d) was always statistically significant in the negative in all crossovers. Aside from C2, every single cross had a positive and statistically significant impact on dominance (h). No matter how many times the variables were switched, the additive × additive effect was still there. I Crosses C4 and C5 had a highly favourable additive × dominance influence (j), but all other crosses were found to be non-significant. The dominance × dominance (l) interaction effect was negatively affected by crossovers C4 and C5, but positively affected by crosses C1, C2, and C3.

Epistasis dominant, dominance x dominance, and additive interactions tend to predominate in this feature as a whole. Aher *et al*. (2001) demonstrated the presence of additive gene action, while prior researchers such as Jiji Joseph and Santhosh Kumar (2000), Pooran Chand and Raghunadha Rao (2002), Manivannan (2002), Vaithiyalingam *et al*. (2002), Anbumalarmathi *et al*. (2004), Murugan (2005), Prasad and Murugan (2021) had insisted on the dominance effect. Indrani Dana and Das Gupta found examples of dominant and additive gene action in a study that was conducted in 2001. It has been demonstrated by Kute and Desmukh (2002) and Ganesamurthy and Seshadri (2002) that this attribute is affected by an additive × additive interaction effect (i). For this feature, Prasad and Murugan (2021), Murugan (2005) found several

dominance × dominance interaction effects (l) and also provided detailed descriptions of the three kinds of epistatic interaction that can affect this feature.

CONCLUSIONS

Upon a thorough exploration of generation strategies in the context of this study, it is evident that the intricate dynamics of gene activities significantly influence all nine parameters related to yield. These interactions encompass a spectrum of possibilities, ranging from additive and dominance to complex epistatic relationships, exemplified by types such as dominance x dominance and duplicate dominant. The nuanced understanding of gene activities uncovered in our analysis, particularly the prevalence of various interaction types, underscores the complexity inherent in the genetic regulation of seed yield and its components in urdbean inter-varietal crossings. Conventional selection methods, geared towards enhancing these crucial yield-related traits, prove to be inherently challenging and insufficient for creating superior progeny. Recognizing this challenge, an alternative approach to bolster the effectiveness of pedigree breeding involves deferring the selection of elite lines to subsequent generations. This strategic delay allows for the identification of superior lines with optimal genetic combinations, ultimately maximizing efficacy in achieving desired yield outcomes. On a contrasting note, the pedigree breeding method emerges as a potent strategy in unearthing improved lines with robust yield components. Employing one or two cycles of recurrent selection within the pedigree breeding framework proves to be an optimal technique. This approach not only facilitates the selection of superior lines with high seed yield and its associated components but also adeptly manages the intricate web of epistatic interactions that play a pivotal role in shaping the genetic landscape.

FUTURE SCOPE

The study titled offers a comprehensive exploration of the gene action influencing seed yield in urdbean. The future scope of this research lies in its potential application to enhance breeding strategies for improving urdbean varieties. The identification of the need for an epistatic model, as revealed by additional scaling tests, suggests that the genetic architecture of urdbean traits is more complex than a simple additive-dominance model. The study's confirmation of various gene activities influencing seed yield and quality provides a foundation for future investigations into the specific genes and pathways involved. The prevalent types of gene interactions, such as dominance x dominance and duplicate dominant, pose challenges for traditional selection methods. Therefore, the study recommends the use of advanced breeding techniques like pedigree breeding with recurrent selection. This approach, applied over one or two cycles, is proposed as an optimal strategy for selecting superior urdbean lines with high seed yield and its components while effectively managing epistatic interactions. In essence, this research opens avenues for targeted and efficient breeding practices to contribute to the improvement of urdbean varieties and their agricultural productivity.

Conflict of Interest. None

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