LR-4870
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RESEARCH ARTICLE Legume Research- An International Journal, Volume Issue : ()

Estimating Narrow Sense Heritability from Parent Progeny Regression and Inter-generation Correlation Coefficient Analysis for Yield and Component Characters in Segregating Lines of Urdbean [*Vigna mungo* (L.) Hepper]

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10.18805/LR-4870

ABSTRACT

Background: Black gram or urdbean is a self-pollinated short duration diploid grain legume packed with abundant nutrients and acts as a N_2 fixer, fertility restorer agent by using as mulch or catch crop. But still the crop's value is limited due to many genetic as well as biotic and abiotic factors. Keeping this in regard, the present research was undertaken by estimating parent-progeny regression and inter-generation correlation coefficient and in turn attain narrow sense heritability values for the traits so as to determine and identify desirable and probable genotypes and their further improvement by selection in consecutive generations.

Methods: The present research was aimed to ascertain the extent of narrow sense heritability through parent-progeny regression and inter-generation relationships between F_2 and F_3 generations for 11 quantitative traits in 14 crosses using randomised complete block design in the Experimental farm of the Department of Genetics and Plant Breeding, College of Agriculture, CSK HPKV, Palampur (H.P.) during *Kharif* 2018 and 2019.

Result: Regression and intergeneration analysis revealed that five crosses showed positive and significant values for days to 75% maturity, thereby meaning that plants selected in the F_2 population had a significant positive association with that of F_3 for this trait. Estimates of narrow sense heritability were recorded highest for biological yield and days to 75% maturity. Keeping the above parameters in consideration, it was concluded that days to 75% maturity and biological yield affirm the presence of additive variance which determined as a good transmission index of genetic potentials from parent of one generation to the progeny of other, while a high regression suggests low influence of environment along with large genetic effects. So, these can be prioritized as the prime traits and used as a reliable predictor for making effective selection and improvement of genotypes for enhancing yield in subsequent generations.

Key words: Black gram, Crosses, Days to 50% flowering (DTF), Days to 75% maturity (DTM), Inter-generation correlation, Narrow sense Heritability, Regression coefficient.

INTRODUCTION

Black gram commonly called as urad bean, mungo bean or black *matpe* bean is a self-pollinated short duration grain legume belonging to the family Fabaceae with diploid chromosome number 2n=22. It is most extensively grown in Asia and some adjacent areas including India, Pakistan, Afghanistan, Bangladesh and Myanmar. It forms significant part of diet as it contains valuable amount of protein (25-28%), carbohydrates (62-65%), fibre (3.5-4.5%), ash (4.5-5.5%), oil (0.5-1.5%) along with some amino acids (methionine, lysine), vitamins (thiamine, niacin, riboflavin) and minerals (iron and phosphorus). Being a leguminous crop, it nourishes the soil by restoring its fertility through symbiotic nitrogen fixation and thus acts as soil ameliorant with low water requirement. It is grown annually in many parts of India and is also suitable as catch crop, mulch crop, inter crop, mixed crop and green crop. Despite of its varied significance, it doesn't hold key position due to vulnerability to several biotic and abiotic factors, poor ideotype, narrow genetic base and their cultivation in marginal and harsh environments which makes the performance of this crop very low in terms of yield and productivity. As yield is a complex trait and is interaction of many component variables, selection cannot

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How to cite this article: Sood, R., Mittal, R.K., Sharma, S. and Chauhan, A. (2022). Estimating Narrow Sense Heritability from Parent Progeny Regression and Inter-generation Correlation Coefficient Analysis for Yield and Component Characters in Segregating Lines of Urdbean [*Vigna mungo* (L.) Hepper]. Legume Research. DOI: 10.18805/LR-4870.

Submitted: 06-01-2022 **Accepted:** 24-05-2022 **Online:** 22-06-2022

be done directly based on this for development of new black gram genotypes. Therefore, yield can be improved only if the breeder has the knowledge about the association among yield and related traits. Keeping in view, the prime objective was to increase efficiency of selection by using method of parent progeny regression and intergeneration correlation analysis between two generations for better crop yield predictability which determines the degree of dependence of one variate on the other for estimating the amount of genetic potential transferred from parent to progeny. These two parameters will be further helpful in working out narrow sense heritability which is a measure of additive variance and this method will directly provide better chances of improving the traits through their effective selection.

MATERIALS AND METHODS

The present study was undertaken at Experimental Farm of the Department of Genetics and Plant Breeding, College of Agriculture, CSK HPKV, Palampur (H.P.) during *Kharif* 2018 and 2019. The experimental material comprising of 14 crosses (Table 1) derived from seven lines and two testerswas evaluated in randomized complete block design over three replications. The main objectives were determined to estimate parent-progeny regression, intergeneration correlation and from them narrow sense heritability between F_2 and F_3 populations for their genetic improvement.The observations were recorded on 20 randomly selected plants from three rows (2 m each) in F_2 and ten plants from ten progeny rows in F_3 with spacing of 30 × 10cm for each cross along with parents and checks.

Data was analysed on the basis of individual plant mean for 11 agro-morphometric traits using parent progeny regression coefficient which is calculated by regressing the mean values of a character in the progeny (F_3) upon the mean values of a character in the parent (F_2) (Rao and Saxena 1999). Intergeneration correlation coefficients (r) were calculated between selected F_2 and F_3 progenies as suggested by Lush (1940). In each case progeny means (y) of F_3 generation were regressed on the individual plants (x) of F_2 generation.

Based on parent progeny regression, narrow sense heritability was calculated as suggested by Smith and Kinmann (1965) *i.e.* $h^2_{ns} = 2 \times b$. But, this method was not proved to be efficient as the heritability estimates from this method was found to be more than 1 (or 100%). This weakness of the method was tackled by using correction formula (Smith and Kinmann 1965). *i.e.* multiplicative factor of 2/3; $h^2_{ns} = 2/3 * b$ (For F_2- F_3) with the help of MS-Excel and OP-STAT software.

RESULTS AND DISCUSSION

The parent progeny regression and correlation between two generations are less prone towards the influence of environment and thus is very helpful for selection of better genotypes in early segregating generationsso as to make improvements in the existing genotypes or the production of new ones and were calculated for all the crosses in selected F_3:F_2 plants for various traits.The regression and intergeneration correlation for yield and its component characters are presentedin Table 2.

Regression coefficient (b) and intergeneration correlation (r) values in cross IC-281980 × HPBU-111 were found to be positive and significant for two traits namely DTM and seeds per pod. positive and non-significant values were found for plant height andbiological yield and 100 seed weight followed by DTF, plant height and pod length respectively. In cross IC-281982 × HPBU-111 b values were positive and non-significant for biological yield per plant and pod length, while exhibited non-significant positive correlation for pod length, DTM and harvest index. Cross IC-281993 × HPBU-111 possess non-significant positive b values for pods per plant, biological yield and harvest index, whereas r values for harvest index, DTM and seeds per pod.Values of b and rin cross IC-436852 × HPBU-111 were found to be non-significant and positive for plant height, DTM and100 seed weight. Cross IC-398973 × HPBU-111 revealed high degree of non-significant positive b and r values for DTM, pod length and DTF. Cross IC-413306 × HPBU-111 showed significant positive b and r values for DTM whereas positively non-significant for seed yield and biological yield. In cross IC-413304 × HPBU-111, high positive non-significant values of b were observed for pods per plant, DTM and biological yield while DTM, pod length and DTF have high non-significant r values. In cross IC-281980 × Him Mash-1, high positive and non-significant values of b and r were observed for pod length. Cross IC-281982 × Him Mash-1 showed high degree of significant positive b and r values for DTM and non-significant for harvest index and pod length. Cross IC-281993 × Him Mash-1 exhibited significant positive b and r values for DTM and non-significant forplant height and biological yield (b) and DTF, pod length and plant height (r). Cross IC-436852 × Him Mash-1 exhibited high degree

Table 1: Source of genotypes and parents used in the study.

Genotypes	Source
Lines	
IC-281980	Indigenous collection from IIPR, Kanpur
IC-281982	Indigenous collection from IIPR, Kanpur
IC-281993	Indigenous collection from IIPR, Kanpur
IC-436852	Indigenous collection from IIPR, Kanpur
IC-398973	Indigenous collection from IIPR, Kanpur
IC-413306	Indigenous collection from IIPR, Kanpur
IC-413304	Indigenous collection from IIPR, Kanpur
Testers	
HPBU-111*	Pure line selection from local material of Himachal Pradesh by CSK HPKV, Palampur
Him Mash-1*	Advanced line selection from DPU-91-5 × Mash-338
Check	
Palampur-93	Pure line selection from local material of Himachal Pradesh by CSK HPKV, Palampur

(*Parents also used as checks).

Table 2: Regression (b) and intergeneration (r) correlation coefficient values between F_2- F_3 generations for various traits in all the crosses.

Characters		IC-281980 × HPB U-111	IC-281982 × HPB U-111	IC-281993 × HPB U-111	IC-436852 × HPB U-111	IC-398973 × HPB U-111	IC-413306 × HPB U-111	IC-413304 × HPB U-111	IC-281980 × Him Mash-1	IC-281982 × Him Mash-1	IC-281993 × Him Mash-1	IC-436852 × Him Mash-1	IC-398973 × Him Mash-1	IC-413306 × Him Mash-1	IC-413304 × Him Mash-1
Days to 50% flowering	r	0.34	0.10	0.13	0.06	0.23	-0.39	0.21	0.14	-0.22	0.47	0.36	-0.31	0.72*	-0.38
	b	0.25	0.06	0.13	0.06	0.23	-0.24	0.31	0.15	-0.73	0.58	0.13	-0.15	0.42*	-0.31
Days to 75% maturity	r	0.68*	0.30	0.48	0.45	0.50	0.89**	0.61	-0.15	0.73*	0.93**	0.57	0.67*	0.60	0.63
	b	0.51*	0.15	0.55	0.26	0.31	0.82**	0.81	-0.15	0.49*	0.84**	0.43	0.67*	0.36	0.30
Plant height (cm)	r	0.32	-0.25	-0.15	0.57	-0.15	-0.32	-0.10	-0.23	-0.11	0.14	0.16	-0.19	0.12	0.09
	b	1.49	-0.50	-0.31	1.18	-0.89	-1.44	-0.35	-1.35	-0.28	1.34	0.47	-0.57	0.54	0.48
Branches per plant	r	-0.60	-0.61	-0.26	-0.20	-0.54	-0.39	0.14	0.16	-0.11	-0.06	-0.18	0.13	-0.21	0.71*
	b	-0.61	-1.25	-0.22	-0.13	-0.50	-0.28	0.24	0.12	-0.12	-0.09	-0.17	0.14	-0.35	0.60*
Pods per plant	r	0.07	-0.03	0.29	-0.14	-0.16	-0.01	0.10	0.21	0.06	-0.29	0.07	-0.05	0.07	-0.10
	b	0.13	-0.19	1.31	-0.33	-1.01	-0.05	0.86	0.02	0.22	-1.41	0.16	-0.15	0.15	0.41
Pod length (cm)	r	0.20	0.44	-0.40	-0.32	0.27	-0.09	0.42	0.41	0.18	0.39	0.29	0.23	-0.27	0.23
	b	0.20	0.37	-0.78	-0.30	0.49	-0.13	0.64	0.38	0.28	0.59	0.74	0.24	-0.62	0.25
Seeds per pod	r	0.71*	-0.02	0.40	-0.42	-0.12	-0.13	0.09	-0.51	-0.11	-0.18	-0.47	0.25	0.30	-0.09
	b	0.49*	-0.02	0.39	-0.75	-0.26	-0.13	0.12	-0.33	-0.12	-0.20	-0.53	0.52	0.51	-0.12
Biological yield per plant (g)	r	0.04	0.07	0.09	-0.07	-0.04	0.02	0.04	-0.04	-0.09	0.05	0.14	0.35	0.11	0.21
	b	0.49	1.16	0.99	-0.86	-0.97	0.14	0.71	-0.40	-0.49	1.05	0.70	1.40	1.39	0.79
Seed yield per plant (g)	r	-0.34	0.01	-0.24	-0.13	-0.09	0.21	-0.09	-0.11	0.10	-0.32	-0.23	0.01	-0.12	0.33
	b	-1.39	0.08	-1.36	-0.60	-0.48	0.99	-1.42	-1.14	0.19	-1.36	-0.70	0.04	-0.37	1.24
Harvest index (%)	r	-0.10	0.14	0.48	0.04	0.07	-0.39	0.21	-0.36	0.28	-0.38	0.12	0.13	0.29	0.11
	b	-0.04	0.22	0.82	0.02	0.08	-0.24	0.57	-0.28	0.92	-0.32	0.05	0.05	0.27	0.25
100 -Seed weight (g)	r	0.43	-0.09	0.23	0.57	0.16	-0.55	0.19	-0.45	0.16	-0.39	-0.08	0.65*	-0.22	0.59
	b	0.41	-0.17	0.14	0.26	0.05	-0.26	0.13	-0.59	0.16	-0.29	-0.03	0.78*	-0.16	0.39

of non-significant positive r values for DTM, DTF and pod length, whereas b values for pod length, biological yield and plant height. For cross IC-398973 × Him Mash-1, band r values were significant for 100 seed weight andDTM whereas positively non-significant for biological yield. In cross IC-413306 × Him Mash-1, significant b and r values were observed for DTF and high positive non-significant for biological yield and plant height (b) and DTM, seeds per pod andharvest index (r) between parent and progeny. Cross IC-413304 × Him Mash-1exhibited high significant positive b and r values for branches per plant and non-significant for seed yield and biological yield and days to 75% maturity and 100-seed weight respectively.

Similar results were supported by (Muralidhara *et al*. 2015) for branches per plant and seeds per pod in green gram, Kumar et al. (2011) and Singh et al. (2017) for 100-grain weight in rice and wheat respectively and (Kavithamani *et al*. 2013; Lalitha *et al*. 2018) for days to 50% flowering in rice.

However, plant height, pods per plant, pod length, biological yield per plant, seed yield and harvest index had not shown any significant regression and intergeneration correlation values in any of the crosses between F_2 and F_3 generations indicating that direct selection for yield on the basis of phenotypic performance may not be effective during early generation or otherwise selection must be delayed in later succeeding generations. Result is in line with the findings of Barman and Borah (2012) and Manohara and Shashidhar (2018) for yield in rice and Gandi and Shunmughavalli 2017 in blackgram.

In terms of regression (b) and intergeneration correlation analysis(r), five crosses *viz*., IC-281980 × HPBU-111, IC-413306 × HPBU-111, IC-281982 × Him Mash-1, IC-281993 × Him Mash-1and IC-398973 × Him Mash-1 showed positive and significant values for days to 75% maturity, whereas IC-281980 × HPBU-111, IC-413306 × Him Mash-1, IC-413304 × Him Mash-1and IC-398973 × Him Mash-1for seeds per pod, days to 50% flowering, branches per plant and 100-seed weight in F_2-F_3 generations respectively.

Narrow sense heritability (NSH)

Narrow sense heritability for F_3 over F_2 generation by regression coefficient in all crosses for 11 traits is given in Table 3. Narrow sense heritability is measured as the ratio of additive variance to the total phenotypic variance, involving additive and additive × additive type of fixable variance. So, higher values of narrow sense heritability provide more possibility for improving the characters through selection in F_2 or later generations.

For cross IC-281980 × HPBU-111, NSH was highest for the plant height followed by DTM and biological yield. For cross IC-281982 × HPBU-111, NSH was found highest for biological yield and pod length. For cross IC-281993 × HPBU-111 pods per plant has highest NSH followed biological yield and harvest index. For cross IC-436852 × HPBU-111 plant height has highest NSH, following 100-seed weight and DTM. NSH for cross IC-398973 × HPBU-111 was maximum for pod length and DTM. Cross IC-413306 ×

Table 3: Narrow sense heritability based on parent-progeny regression between F_2- F_3 generations for various traits in all the crosses.

Characters	IC-281980 × HPBU-111	IC-281982 × HPBU-111	IC-281993 × HPBU-111	IC-436852 × HPBU-111	IC-398973 × HPBU-111	IC-413306 × HPBU-111	IC-413304 × HPBU-111	IC-281980 × Him Mash-1	IC-281982 × Him Mash-1	IC-281993 × Him Mash-1	IC-436852 × Him Mash-1	IC-398973 × Him Mash-1	IC-413306 × Him Mash-1	IC-413304 × Him Mash-1
Days to 50% flowering	16.67	3.67	8.73	4.07	15.40	-16.27	20.87	9.80	-48.93	38.60	8.67	-10.00	27.73	-20.87
Days to 75% maturity	34.20	10.13	36.67	17.13	20.40	54.47	53.93	-10.20	32.87	55.93	28.47	44.53	23.87	19.67
Plant height (cm)	99.27	-33.53	-20.73	78.60	-59.20	-96.00	-23.33	-89.93	-18.40	89.47	31.53	-38.13	35.73	31.93
Branches per plant	-40.87	-83.00	-14.73	-8.60	-33.53	-18.87	15.87	8.20	-8.13	-6.07	-11.20	9.33	-23.33	39.80
Pods per plant	8.40	-12.73	87.07	-22.00	-67.47	-3.27	57.60	1.53	14.47	-93.67	10.67	-10.20	10.07	-27.53
Pod length (cm)	13.60	24.40	-51.73	-19.87	32.67	-8.40	42.60	25.60	18.33	39.00	49.20	15.87	-41.07	16.67
Seeds per pod	32.33	-1.60	25.67	-49.93	-17.60	-8.67	8.00	-22.27	-8.00	-13.27	-35.00	34.93	34.13	-7.73
Biological yield per plant (g)	32.80	77.00	65.80	-57.27	-64.53	9.00	47.13	-26.40	-32.33	69.93	46.80	93.40	92.93	52.33
Seed yield per plant (g)	-92.60	5.53	-90.47	-40.07	-31.93	65.87	-94.40	-75.93	12.73	-90.87	-46.80	2.67	-24.80	82.47
Harvest index (%)	-2.60	14.73	54.33	1.47	5.13	-15.67	37.67	-18.80	61.60	-21.07	3.00	3.60	18.00	16.67
100-seed weight (g)	27.40	-11.07	9.20	17.13	3.33	-17.27	8.73	-39.27	10.40	-19.27	-2.20	51.93	-10.87	25.87

HPBU-111 has highest NSH for seed yield followed by DTM. For cross IC-413304 × HPBU-111, pods per plant has highest NSH followed by DTM and biological yield. For cross IC-281980 × Him Mash-1, NSH was found to be highest for pod length followed by days to 50% flowering. For cross IC-281982 × Him Mash-1, harvest index has highest NSH followed by DTM. NSH for cross IC-281993 × Him Mash-1 was maximum for plant height followed by biological yield and DTM. Cross IC-436852 × Him Mash-1, has highest NSH for pod length followed by biological yield per plant and plant height. NSH for cross IC-398973 × Him Mash-1 was maximum for biological yield per plant, 100-seed weight, DTM and seeds per pod. For cross IC-413306 × Him Mash-1, biological yield per plant has highest NSH followed by plant height and seeds per pod. NSH for cross IC-413304 × Him Mash-1 was found to be highest for seed yield followed by biological yield, branches per plant and plant height.

The estimates of NSH were noticed higher for biological yield and days to 75% maturity while lower heritability was recorded for seeds per pod, branches per plant and seed yield in most of the crosses. Higher values of narrow sense heritability indicates effect of additive variance and provides better chances of improving the traits through their effective selection, whereas low heritable traits can be improved only through hybridization as dominance or epistatic effects may be present. Hence, in the present study, biological yield has the better chances of improvement through selection.

CONCLUSION

In any crop development effort, the ultimate goal of a plant breeder is to boost production. Because yield is a complicated feature and straightforward choices based on yield components may not always provide acceptable results, the pattern of association takes note on further importance. The data estimation for regression and intergeneration correlation for F_2-F_3 progenies revealed positive significance fordays to 75% maturity meaning that effective selection can be done during this stage based on phenotypic observations while four crosses showed the significant positive relationship for seeds per pod, days to 50% flowering, branches per plant and 100-seed weight respectively indicating to be cautious while going for direct selection on the basis of these traits or selection may be done in later generations. As narrow sense heritability is the ratio of additive variance to the total phenotypic variance, it includes additive and additive × additive component of variance, which are fixable. Higher the narrow sense heritability, higher is the chances of improving the characters through selection.The amplitude of NSH values based on the parent-offspring regression coefficient was maximum for biological yield and days to 75% maturity implying to be the reliable indicator of the performance of their progeny in subsequent generations and thus provides usefulness of selection in early generation with greater impact on blackgram breeding program.

Conflicts of interest

The authors would hereby like to declare that there is no conflict of interests that could possibly arise.

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