

Study of Skewness and Kurtosis for Spikelet Sterility and Yield Related Traits in Segregating Generations of a Rice (*Oryza sativa* L.) Cross to Identify Gene Action

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Abstract

An investigation was performed in the F_6 and F_7 generation of the cross Pusa-1176 x BPT-5204. The phenotypic screening was done intensely for spikelet sterility in F_6 generation (Kharif, 2021) based on which some families were selected and grown as F_7 generation (Kharif, 2022) that were sown as panicle to progeny rows at two different dates as set I and set II with the interval of 15 days in order to study the influence of environment on the traits under study. The segregates were studied for skewness and kurtosis to identify the presence of gene interactions in 13 quantitative traits including grain yield per plant (Fisher *et al.*, 1932). The results displayed that various traits exhibited positive skewness along with platykurtic and leptokurtic frequency distribution in set I and set II. Similarly, a combination of negative skewness with platykurtic and leptokurtic frequency distribution was observed for diverse traits in set I and set II. Normal curve without skewness indicating symmetry of the trait and platykurtic frequency distribution was observed for L/B ratio in set I and for 100 seed weight in set II.

Keywords: Kurtosis, Gene Action, Skewness, Spikelet, Sterility

Introduction

Rice (*Oryza sativa* L.) belongs to Poaceae family and is one of the major staple foods for more than half of the world's population. It is also an essential commodity for food and nutritional security since it provides 20% of the regular calorie intake (Ricepedia, 2020). It is cultivated nearly on 162 million hectares of land in a wide range of environments with an annual production of about 756 million tonnes globally (FAO, 2022) that mostly does not reach its potentiality in terms of production and productivity due to various

factors affecting the yield of the crop such as biotic and abiotic stresses that are unpredictable in nature. Thus, a breeder should be capable of selecting the better-performing genotypes from a large population which requires intensive studies on various yield and yield-attributing traits. The extent of selection pressure given to the population depends on the study of a frequency distribution that is analyzed via skewness and kurtosis estimation (Choo and Reinbergs, 1932). The nature of gene action is

revealed by the estimates of skewness whereas the number of genes controlling the trait is determined by kurtosis (Savitha *et al.*, (2015) and accordingly choice is made whether selection should be mild or intensive. Thus, to enhance the selection efficiency and breeding strategy, appropriate information on the gene interactions is essential which may lead to progressive research work thereby improving the performance of the population. The present investigation was thereby undertaken in the F_7 generation of the cross Pusa-1176 x BPT-5204. The main objective of the experiment was to assess the existence of variability among the characters under study, nature of gene action, number of genes controlling the trait and statistical analysis through frequency distribution patterns based on skewness and kurtosis (Roy, 2000, Robson, 1956).

Materials and Methods

The present investigation was carried out at the experimental plot of Birsa Agricultural University, Kanke under the rainfed conditions of Jharkhand, India during *Kharif* 2021. The phenotypic screening was done intensely for spikelet sterility in 23,083 F_6 plants (from 482 families) of the cross Pusa-1176 x BPT-5204 as large number of plants in a family showed sterile panicles as well as segregation among the traits under study. The parents of Pusa-1176 and BPT-5204 are [Bindli mutant 34 (BM34) x ARC line] and [GEB-24 x T(N)1 x Mahsuri], respectively. The parent, Pusa-1176 is an aromatic rice and the other parent BPT-5204 is resistant to blast. Also, both the parents were well suited to rainfed and shallow land. As the families of F_6 generation showed segregation among the traits under study, 15 families comprising of 158 sterile F_6 plants were selected based on the maximum number of sterile progeny plant with sterility % above 55% within the family. In the next generation (F_7 generation), it was sown as panicle to progeny rows

on the seed bed nursery and thereafter transplanted into the field. Sowing was done at different dates designated as set I and set II with the interval of 15 days in order to study the influence of the environment on the traits under study. The method of sowing adopted was panicle to progeny row. The transplanting was done by maintaining row-to-row distance as well as plant-to-plant distance of 20 cm. Other recommended agronomic practices were followed throughout the crop growth period. The data was recorded on individual plants representing each of the segregants due to segregation pattern observed among the traits under study. The traits for which observations were taken are days to flowering, number of tillers, plant height, panicle length, panicle number, number of filled spikelets, number of unfilled spikelets, spikelet fertility, grain length, grain width, L/B ratio, 100 seed weight and grain yield per plant. After that statistical analysis was done based on the estimation of skewness and kurtosis which was calculated using the frequency distribution of the characters under study (Kapur, 1981; Savitha *et al.*, 2015).

Results and Discussions

The study of frequency distribution via skewness and kurtosis provides information about the nature of gene action and the number of genes controlling the traits respectively. The genes controlling the character with skewed frequency distribution tend to be predominantly dominant regardless of whether the effect on the trait has been enhanced or reduced. The results obtained have been presented in **Table 1**. The frequency distribution was found to be positively skewed and platykurtic for the number of panicles, number of unfilled spikelets, 100 seed weight and seed yield per plant in set I and for days to flowering, number of tillers, number of panicles and spikelet fertility in set II. Positive skewness in the segregants indicates its association



with complementary gene actions and platykurtic distribution shows that it is controlled by a large number of genes (**Figure 1**). Similar results were reported by Kiran *et al.*, (2012) for number of tillers panicle length and grain yield per plant, Harshiya and Jagadeesh (2014) for plant height and test weight, Raghavendra and Hittalmani (2015) for number of filled grains and grain length, Savitha *et al.*, (2015) for 1000-grain weight and single plant yield and Rani *et al.*, (2016) for number of tillers per plant, panicle length and also for grain yield per plant. It is also supported by Sheshaiah *et al.*, (2018) for panicle length and grain yield per plant. Sushma Lilly *et al.*, (2018) reported for the number of filled grains and grain length whereas Prisca Seeli *et al.*, (2021) reported for number of unfilled grains.

The positively skewed and leptokurtic frequency distribution was observed for days to flowering, number of tillers, plant height and number of filled spikelets in set I and for plant height, number of filled spikelets, number of unfilled spikelets and seed yield per plant in set II that exhibited the presence of complementary gene action by the estimation of skewness and the leptokurtic nature indicated that it is controlled by a few genes. The results were appropriately supported by Kiran *et al.*, (2013) for panicle length, Harshiya and Jagadeesh (2014) for spikelet fertility, Manjappa *et al.*, (2014) found positively skewed distribution for grain yield plant per plant and tiller number, Lestari *et al.*, (2015) for panicle weight, Savitha *et al.*, (2015) and Nikhitha *et al.*, (2020) for the number of productive tillers per plant, panicle length and Govintharaj *et al.*, (2017) for number of grains.

The presence of gene interactions is represented by a positive value of kurtosis while it is negative or close to zero in the absence of gene interaction (Kotch *et al.*, 1992). Negatively skewed and platykurtic frequency

distribution was observed for spikelet fertility and grain width in the set I and for panicle length, grain width and L/B ratio in set II. It is also supported by Kiran *et al.*, (2013) who noticed duplicate interaction for panicle length, Harshiya and Jagadeesh (2014) for panicle length, grain yield per plant, grain length, grain breadth, length to breadth ratio, Manjappa *et al.*, (2014) found negatively skewed distribution for plant height, days to flowering, days to maturity, panicle length, panicle exertion, test weight and spikelet fertility, Lestari *et al.*, (2015) reported that the panicle length and weight. Savitha *et al.*, (2015) found platykurtic with left-skewed distribution for days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, hundred-grain weight and single plant yield. Vijaya and Shailaja (2016) reported platykurtic and negatively skewed distribution for plant height, Rani *et al.*, (2016) recorded for test weight, grain length and grain breadth.

Negative skewness and leptokurtic frequency distribution were found for panicle length and grain length in set I and for grain length in set II. Similar results were supported by Kiran *et al.*, (2013) for plant height, Savitha *et al.*, (2015) for the number of productive tillers per plant, panicle length and Sushma Lilly *et al.*, (2018) for L/B ratio. The frequency curve depicting negative skewness is associated with duplicate (additive x additive) gene interactions and it is controlled by many genes or by few genes indicating platykurtic or leptokurtic nature respectively. Normal curve without skewness indicating symmetry of the trait and platykurtic frequency distribution was observed for L/B ratio in set I and for 100 seed weight in set II. A similar result was reported by Kiran *et al.*, (2013) for test weight indicating complete ambi-directional epistasis.

Table 1: Estimates of skewness and kurtosis for different characters under study in F₇ generation of the cross Pusa-1176 and BPT-5204 for both sets

Sl. No.	Characters	Mean		Skewness		Kurtosis	
		Set I	Set II	Set I	Set II	Set I	Set II
1	Days to Flowering	89.40	87.77	0.69	0.75	1.40	0.18
2	Number of Tillers	11.02	21.59	0.87	0.67	1.02	0.49
3	Plant Height	93.78	77.76	1.09	0.68	4.86	1.36
4	Panicle Length	23.66	22.01	-0.13	-0.20	1.18	0.54
5	Panicle Number	9.76	18.4	0.82	0.90	0.92	0.95
6	Number of Filled Spikelets	69.72	36.27	0.84	1.19	1.12	1.28
7	Number of Unfilled Spikelets	58.63	80.86	0.77	0.76	0.23	1.31
8	Spikelet Fertility	54.77	30.89	-0.13	0.56	-1.12	-0.92
9	Grain Length	0.90	0.89	-0.25	-0.92	1.19	3.11
10	Grain Width	0.28	0.28	-0.01	-0.12	-0.49	-0.14
11	L/B Ratio	3.23	3.14	0.00	-0.11	0.06	0.47
12	100 Seed Weight	1.74	1.82	0.24	0.02	0.66	-0.27
13	Grain Yield per plant	12.83	10.37	0.24	3.40	0.66	16.88

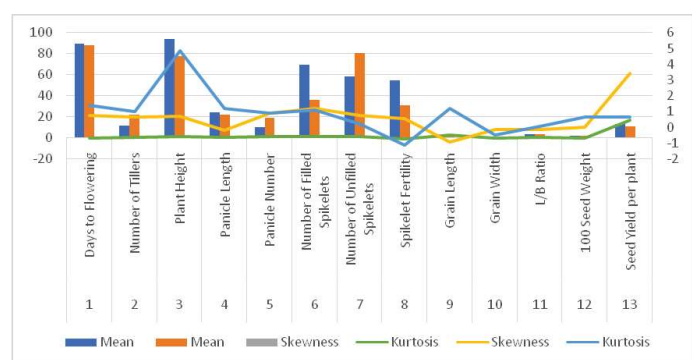


Figure 1: Graphical representation of the estimates of skewness and kurtosis

Conclusion

To increase the efficiency of selection in breeding programs among large populations, breeders should have adequate knowledge of the prevailing amount of gene interaction and the number of genes governing the trait. The results indicated that mild selection would be sufficient for improvement in the characters number of panicles, number of unfilled spikelets, 100 seed weight and seed yield per plant in the set I and for days to flowering, number of tillers, number of panicles and spikelet fertility in set II whereas stringent selection might be deployed for trait improvement in panicle length and grain length in set I and only for grain length in set II. Therefore, it is concluded from the study that progress in improving the performance of genotypes would be higher under complementary

gene interaction as compared to duplicate gene interaction.

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