

STUDIES ON TRANSGRESSIVE SEGREGATION IN F₂ GENERATION IN MAIZE (*ZEA MAYS* L.)

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ABSTRACT

The present study was conducted at research farm of Seed Technology Research Unit, Rahuri. The experimental material for present study comprised of eight parental lines collected from Maize Improvement Project, Kolhapur. Diverse maize parental lines were effected in full diallel fashion. Eight parents with fifty six F₁s (direct and reciprocal) and two standard checks were evaluated and data of results recorded on yield and yield contributing characters. The best performing single cross were selected on the basis of yield and yield contributing characters and conducted transgressive segregation field trial. Transgressive segregants were reported for five characters viz., kernel yield, protein, starch, tryptophan and lysine content in F₂ generation. The highest transgression was recorded for kernel yield (9.20 %), followed by starch (1.80 %), protein (1.60 %), tryptophan (1.20 %) and lysine content (1.00 %). The simultaneous transgression of kernel yield occurs with starch and tryptophan content. It was concluded that either kernel yield is dependent on these characters or there is a linkage drag so that genes responsible for these traits move together. The plant number 428 of GPM-456 x HYD-09R-1204-1 in F₂ generation reported to be the most promising transgressive segregant. It produced 7.07 percent more kernel yield than better increasing parent and transgressed for two quality characters i.e. starch and tryptophan content.

KEYWORDS: Diverse maize line, F₂ generation, kernel yield, protein, starch, tryptophan and lysine.

INTRODUCTION

Maize (*Zea mays* L.) is a new world coarse cereal belonging to Poaceae family and tribe Maydeae, which includes eight genera. Maize is a crop with a versatile nature. It is grown in more than 166 countries across the globe. In India, it is cultivated throughout the year in most of its states for various purposes that include grain, feed, fodder, green cobs, sweet corn, baby corn, popcorn, starch and industrial products.

The embryo and endosperm contain proteins but the germ proteins are superior in both quality as well as quantity. Major proportion of the kernel protein is located in endosperm (80-85 %). Maize is deficient in certain essential amino acids, such as lysine and tryptophan. Lysine is critical in protein synthesis for the growth of tissues and found to be important in the absorption of calcium from the intestinal mucosa. On the other hand, tryptophan being an essential amino acid is the biological precursor of the B vitamin, niacin (Bressani, 1991).

Appearance of individuals in segregating populations that fall beyond their one or both parents termed as transgressive segregation. Hybrid individuals inherit both parents' "plus" alleles of extreme phenotype. Researchers reported transgressive segregation is effective tool. Genetic analysis of segregation pattern and transgressive segregation in F₂ is helpful for determining prepotency of different crosses, achieving efficiency in early generation selection. Maize crop has great commercial value, but the information on transgressive segregation is limited (Shivani *et al.*, 2011).

MATERIAL AND METHODS

Present investigation was conducted at research farm of Seed Technology Research Unit, Rahuri. Experimental material for investigation comprised of eight parental lines viz., Hyd-09R-2168-1, Hyd-09R-2178-2, Hyd-08R-656-1, Hyd-08R-2570-2, Hyd-09R-1204-1, Hyd-08R-2453-2, GPM-456 and GPM-342 collected from Maize Improvement Project, Kolhapur. The Fifty six crosses in full diallel were effected using eight parents at research farm of STRU, MPKV, Rahuri. F₁ evaluation trial: The 56 F₁s (direct and reciprocal crosses) along with 8 parents and 2 checks was evaluated in RBD design with three replications. Transgressive segregation trial: The best performing single cross (GPM-456 x HYD-09R-1204-1) was selected and evaluated with 500 populations. The spacing between plants was 20 cm and between row was 75 cm. Population of parent and F₁ was 30, while F₂ was 500 plants. Transgressive segregants were reported for five characters viz., kernel yield, protein, starch, tryptophan and lysine content. Crude protein content of grain was estimated by determining total nitrogen content using standard Micro-kjeldahl method. Starch content in seed was estimated by usual chemical analysis using Anthrone Reagent method as per procedure given by the Protocols for Biochemical Analysis of Maize-A laboratory Handbook, DMR, New Delhi. The absorbance or optical density recorded on Spectronic-20 Spectrophotometer at 620 nm was scored against the concentration of stock solution on a standard curve. Tryptophan present in the seed sample was determined by the colorimetric method as described by Mertz (1975). For estimation of lysine content, 100 mg finely ground defatted sample was taken and analysed as per the method suggested by A.O.A.C. (1970). The model proposed by Panse and Sukhatme determined the percentage of transgression segregation by classifying

extreme progeny as significantly transgressive segregates by calculating the lines that surpassed their better parent mean and L.S.D. at 0.05 probability.

RESULTS AND DISCUSSION

The cross GPM-456 x HYD-09R-1204-1 expressed desirable transgressive segregants along with their frequency distribution for five characters. It expressed individually and in combination of characters with the kernel yield.

Protein content (%): showed that two parental lines GPM-456 and HYD-09R-1204-1 had 9.64 and 6.48 per cent protein, respectively. In the F₂ segregating generation the average protein content was 8.75 per cent. The percentage of transgressive segregation for protein content was 1.60 per cent with a range of 9.72 to 10.85 (Table 2). The threshold value for protein content was 10.27.

Starch content (%): as evident from the Table 1 both parental lines viz., GPM-456 and HYD-09R-1204-1 had 71.11 and 70.80 per cent starch, respectively. In F₂ average percentage transgressive segregants for starch content were 69.00 per cent. The transgressive segregants in F₂ in terms of more starch content than higher parent was 1.80 per cent. The range in starch content in F₂ segregants was 71.23 to 74.59 (Table 2). The threshold value for this trait was 73.15.

Tryptophan content (%): tryptophan content in parental lines GPM-456 was 0.35 per cent while HYD-09R-1204-1 contains 0.38 per cent (Table 1). The average transgressive segregation in F₂ generation for tryptophan content was 0.35 per cent. Transgressive segregants in F₂ in terms of more tryptophan content than higher parent was 1.20 per cent with a range of 0.38 to 0.42 (Table 2). Threshold value for tryptophan content was 0.40.

Lysine content (%): parents GPM-456 and HYD-09R-1204-1 had 2.06 and 2.01 per cent lysine, respectively. In F₂ average percentage of transgressive segregants for lysine content was 1.80 per cent. The transgressive segregants in F₂ in terms of more lysine content than higher parent was 1.00 per cent. The range in lysine content in F₂ segregants was 2.06 to 2.41 (Table 2). Threshold value for this trait was 2.23.

Kernel yield (g): The grain kernel yield (g) in parental line GPM-456 was 107.25 g while HYD-09R-1204-1 yielded 115.31 g (Table 1). In F₂ average percentage transgressive segregants for this trait was 110.17 g. Transgressive segregants in F₂ in terms of higher kernel yield than higher parent was 9.20 per cent with a range of 115.4 to 163.57 (Table 2). Threshold value for kernel yield was 124.96.

Table 1. Mean, Standard deviation, frequency distribution and per centage of desirable transgressive segregants (T.S.) in F₂ generations of the cross GPM-456 x HYD-09R-1204-1

Name of the character		Mean ± S.E.	S.D.	Frequency distribution in standard deviation											Frequency total	N.D. value	% T.S.
				-5	-4	-3	-2	-1	0	1	2	3	4	5			
Protein content (%)	GPM-456	9.64±0.06	0.32	-	-	-	-	1	12	17	-	-	-	-	30	-	-
	HYD-09R-1204-1	6.48±0.04	0.24	15	15	-	-	-	-	-	-	-	-	30	-	-	
	F ₂	8.74± 0.03	0.73	-	9	48	88	111	236	5	3	-	-	-	500	2.08	1.60
Starch content (%)	GPM-456	71.11± 0.19	1.04	-	-	-	-	-	12	18	-	-	-	-	30	-	-
	HYD-09R-1204-1	70.80± 0.18	0.99	-	-	-	-	1	17	12	-	-	-	-	30	-	-
	F ₂	68.95± 0.10	2.16	-	5	26	62	108	290	7	2	-	-	-	500	1.94	1.80
Trypto phan content (%)	GPM-456	0.35± 0	0.01	-	-	-	-	2	21	7	-	-	-	-	30	-	-
	HYD-09R-1204-1	0.38± 0	0.01	-	-	-	-	1	12	17	-	-	-	-	30	-	-
	F ₂	0.35± 0	0.02	-	8	14	72	124	276	4	1	1	-	-	500	2.26	1.20
Lysine content (%)	GPM-456	2.06± 0.02	0.09	-	-	-	-	2	5	23	-	-	-	-	30	-	-
	HYD-09R-1204-1	2.01± 0.01	0.06	-	-	-	-	2	21	7	-	-	-	-	30	-	-
	F ₂	1.80 ± 0.01	0.23	-	13	79	91	104	208	2	2	1	-	-	500	1.89	1.00
Kernel yield (g)	GPM-456	107.25± 0.85	4.63	-	-	-	-	1	13	15	1	-	-	-	30	-	-
	HYD-09R-1204-1	115.31± 0.90	4.92	-	-	-	-	10	19	1	-	-	-	-	30	-	-
	F ₂	110.17± 0.48	10.64	-	5	11	18	56	364	17	12	9	5	3	500	1.39	9.20

Table 2. Threshold value, frequency and range in values of transgressive segregants for five characters of the cross GPM-456 x HYD-09R-1204-1

Characters	Transgressive segregants		
	Threshold value	Frequency	Range
Protein content (%)	10.27	8 (1.60)	9.72 - 10.85
Starch content (%)	73.15	9 (1.80)	71.23 - 74.59
Tryptophan content (%)	0.40	6 (1.20)	0.38 - 0.42
Lysine content (%)	2.23	5 (1.00)	2.06 - 2.41
Kernel yield (g)	124.96	46 (9.20)	115.4 - 163.57

The data showing frequency distribution and percentage of desirable transgressive segregants for kernel yield and for combination of four characters with kernel yield are mentioned in Table 3.

Table 3. Frequency and percentage of simultaneous transgressive segregation (T.S) for grain yield and qualitative characters in F₂ generation.

Sr. No.	Character combinations	Transgressive segregation	
	Kernel yield with	Frequency	Per cent
1	Starch content + Tryptophan content	1	0.2
2	Tryptophan content	1	0.2
3	Lysine content	1	0.2
4	Kernel Yield alone	43	8.6
	Total	46	9.2

Only one character combination in which the transgression of kernel yield was found to be associated with transgression of two other *i.e.* kernel yield along with starch content and tryptophan content was 0.2 %. The two characters combination in which, the kernel yields were found associated with one other character *viz.*, Kernel yield with tryptophan content and lysine content was also 0.2 %. The kernel yields alone expressed 8.6 per cent desirable transgressive segregants. F₂ generation showed a total 9.20 per cent transgressive segregants for kernel yield alone and for other characters along with yield.

Earlier researchers Cox and Frey (1985), Dhole and Reddy (2011), Kamble (2012), Shreya and Vasanthi (2017), Deokar *et al.* (2019), Reddyamini *et al.* (2019) and Pawar *et al.* (2020) reported frequency of transgressive segregation.

The promising transgressive segregants

The plant number 428 in F₂ generation was reported to be the most promising transgressive segregant. It had yielded more than the increasing parent by 7.07 per cent, and transgressed two other quality characters *i.e.* starch content and tryptophan content. Besides this, the transgressant had higher intensity of expression than the increasing parent for protein content. However, transgressants have lower than the decreasing parent for lysine content reported in Table 4. Earlier de Vicente and Tanksley (1993), Rieseberg *et al.* (1999) observed that combination of alleles from both the parents occurs in hybrid and hybrid was having extreme genotype than the both parents. Similar findings were reported by Kamble (2012) in maize, Deokar *et al.* (2019), Reddyamini *et al.* (2019) and Pawar *et al.* (2020).

Table 4. Promising transgressive segregants having combination of desirable attributes in F₂ generation.

Generation	Plant No.	Protein content (%)	Starch content (%)	Tryptophan content (%)	Lysine content (%)	Kernel yield (g)	Per cent yield increased over increasing parent
F ₂	428	7.16	73.59*	0.40*	1.72	123.46	7.07
GPM-456		9.64	71.11	0.35	2.06	107.25	
HYD-09R-1204-1		6.48	70.80	0.38	2.01	115.31	

*Intensity of expression of character higher than the increasing parent starch content and tryptophan content

CONCLUSION

The plant number 428 of GPM-456 x HYD-09R-1204-1 in F₂ generation reported to be the most promising transgressive segregant. It produced 7.07 percent more kernel yield than better increasing parent and transgressed for two quality characters *i.e.* starch and tryptophan content. These transgressants need to be evaluated in further generations for consistency in their performance.

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