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GENETIC ARCHITECTURE OF NARCOTINE IN OPIUM POPPY (*PAPAVER SOMNIFERUM* L.)

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Genetic studies of narcotine based on additive-dominance model was carried out in opium poppy. A partial dominance to dominance was noticed. Partial dominance was coupled with duplicate epistasis with negative (j) and (i) while dominance was coupled with complementry epistasis and positive (j) and (i). Additive as well as dominance gene effect were both prevalent in the inheritance of narcotine. High heritability coupled with high genetic advance was noticed in both the crosses. Considering gene effects, the intermating among the segregants followed by the recurrent selection is recommended to isolate high narcotine genotypes.

Key words : Opium poppy, narcotine, heritability, genetic advance

Narcotine is one of the major alkaloid of opium poppy (*Papaver somniferum* L.), which is beneficial in allaying cough and headache. It may be useful in asthama, whooping cough and spasms of intestine, bile duct and urethera. For the improvement of narcotine, the knowledge of different gene actions is essential to formulate a proper breeding system. The genetics of narcotine is rarely known. However, Khanna and Shukla (1986) observed that the absence of narcotine was generally governed by dominant gene over its presence. Absence of narcotine (noscapsine) resulted in enhanced content of morphinane alkaloids and that can be ascribed to a block in biosynthetic steps (Nyman and Hansoon, 1978). Considering the importance of narcotine, the present investigation was undertaken following additive-dominance model.

MATERIALS AND METHODS

Six generations, P_1, P_2, F_1, F_2, B_1 and B_2 of two crosses, viz., NBRI-1 x BR-222 (a) and NBRI-2 x BR-222 (b) were grown in RBD with three replications at NBRI, Lucknow during 1990-91. The row length was 3 meter with crop geometry 30 x 10 cm^2. The data on 5 plants for each parent and F_1 and 10 plants for each backcrosses and F_2 were recorded. The analysis of narcotine was done by HPLC (Khanna and Shukla, 1986). The weighted least square using the reciprocals of the squared errors of each mean as weight were used

for estimating 3 parameter $\hat{m}, \hat{d}$ and $\hat{h}$ from the generation means based on F_α matrix. An additive-dominance model ($\hat{m}, \hat{d}, \hat{h}$) non-epistatic and a model including epistatic interactions were applied to data (Hayman, 1958) and tested for goodness of fit using joint scaling test (Cavalli, 1952 Mather and Jinks, 1982). The joint scaling test uses chi-square test for adequacy of the model, by comparing observed and expected mean for adequacy of model at three degrees of freedom.

RESULTS AND DISCUSSION

The analysis of variance for narcotine was significant in both the crosses. The generation means and the estimates of genetic components based on the best fit model are given in Table 1. The mean value of narcotine in F_1 was observed tending towards the mid parental vlue in both the crosses. In F_2 mean values were lower than in F_1 though it was variable from 5.87 to 9.53, which showed high magnitude of F_2 variances. Similar trend was also noticed in B_1 population (Table 1). The low heterosis observed may have been caused by the absence of genes with dominance effect at most of the loci. Similarly, a low degree of inbreeding depression from F_1 to F_2 was also indicative of absence of *loci* with dominance effect. A partial dominance coupled with duplicate type of epistasis in cross NBRI-1 x BR-222 (a) and dominance coupled with complementary epistasis in cross NBRI-2 x BR-222 (b) were noticed. Duplicate epistasis in addition of negative ($\hat{j}$) and ($\hat{l}$) components make it difficult to select suitable genotypes in cross NBRI-1 x BR-222 (a) while complementry epistasis in addition of positive ($\hat{j}$) and ($\hat{l}$) indicates the possibility of transgressive segregants andthus makes it possible to select genotypes with high narcotine content in cross NBRI-2 x BR-222 (b).

Simple scaling test was not significant in both the crosses showing absence of epistatic interaction. This was further confirmed through χ^2 test. Additive gene effect was positively non-significant in both the crosses while dominance effect was negatively significant in NBRI-1 x BR-222(a) and positively significant in NBRI-1 x BR-222 (b) in 3 parameter model. Considering digenic interaction additive x additive ($\hat{i}$) was more prevalent in NBRI-1 x BR-222 (a) and additive x additive ($\hat{l}$) followed by dominance x dominance ($\hat{j}$) in NBRI12 x BR-222 (b). The positive dominance effect of six parameter model in NBRI-1 x BR-222 (a) was, however, nullified by negative additive x dominance ($\hat{j}$) and dominance x dominance ($\hat{l}$) digenic interaction and duplicate type of epistasis. While the complementry epistasis with positive dominance ($\hat{l}$) followed by additive x additive ($\hat{i}$) and dominance x dominance ($\hat{l}$) interactions showed possibility of better segregants for high narcotine content. From overall genetic studies it was concluded that the narcotine is controlled by additive and dominance effect. Under the situation inter-mating among the segregants,

followed by recurrent selection is recommended to isolate suitable genotypes for high narcotine content. Further high heritability coupled with high genetic advance in both crosses emphasized that by sorting out 5 per cent of top population from segregating generations, desired selection response in desired direction can be obtained.

Table 1 : The generation means, variance and estimates of genetic components of opium poppy (*P. somniferum* L.)

Parameters	NBRI-1 x BR-222 (a)		NBRI-2 x BR-222 (b)	
	Mean ± S.E.	Variance	Mean ± S.E.	Variance
P_1	8.99 ± 0.19	0.33	8.08 ± 0.09	0.08
P_2	8.35 ± 0.27	0.65	8.87 ± 0.25	0.59
F_1	7.60 ± 0.14	0.19	8.16 ±0.14	0.18
F_2	7.34 ± 0.34	1.05	7.21 ± 0.32	0.90
B_1	7.74 ± 0.31	0.85	7.47 ± 0.27	0.68
B_2	7.77 ± 0.27	0.67	7.72 ± 0.20	0.36
	Simple Scaling Test			
$\overline{A}$	–1.11 ± 0.75		–1.30 ± 1.26	
$\overline{B}$	–0.41 ± 1.90		–1.59 ± 1.79	
$\overline{C}$	–3.18 ± 1.27		–4.43 ± 2.14	
	Six parameter model (Hayman 1958)			
$\hat{m}$	7.34^{**} ± 0.34		7.21^{**} ± 0.32	
$\hat{d}$	–0.03 ± 0.84		– 0.25 ± 0.66	
$\hat{h}$	0.59 ± 2.15		1.22 ± 2.17	
$\hat{i}$	1.66^{*} ± 0.84		1.54^{*} ± 0.76	
$\hat{j}$	–0.70 ± 1.99		0.29 ± 1.56	
$\hat{l}$	–0.14 ± 3.82		1.35 ± 3.75	
Type of epistasis	Duplicate		Complementry	
	Three parameter model (Mather & Jinks 1982)			
$\hat{m}$	10.35 ± 0.37		8.29 ± 0.36	
$\hat{d}$	0.18 ± 0.30		0.26 ± 0.33	
$\hat{h}$	-5.47^{*} ± 0.65		1.53^{*} ± 0/71	
X^2 (6–3)	4.69		4.82	
Δh	78.89		80.00	
GA	1.65		1.56	
GA%	20.70		19.70	

*Significance at 5% level; **Significance at 1% level

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