

LINKAGE STUDIES IN SUNFLOWER (*HELLANTHUS ANNUUS* L.)

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INTRODUCTION

Sunflower has gained an important place as an oilseed crop. The genetic studies in this crop have started as early as 1912 by Cockrell but most of the available literature is on the inheritance of flower/floret colour (Leclerc, 1968 ; Skaloud and Kovacik, 1974 ; Fick, 1976 ; Anand and Malik, 1977 ; Machacek, 1980 ; Shanta and Giriraj, 1984) and disc floret colour (Luckiewicz, 1975 ; Mosjidis 1982). However, the information on their inter-relationships is rather scanty and reports on linkage are meagre. Hence the present studies were undertaken.

MATERIAL AND METHODS

The cross was effected between RM-1 and ITP-1 the two genotypes of Sunflower (*Helianthus Annuus* L.) These genotypes were maintained at the sunflower seed production project, University of Agricultural Sciences, Gandhi Krishi Vignana Kendra, Bangalore, India. The F₁, F₂, F₃ generations were studied in the subsequent seasons. The F₂ generation consisted of 1554 plants and F₃ families were studied to confirm the F₂ segregation. Product ratio method of Fisher and Balamkund (1928) was applied to estimate linkage values. Kosambi's (1944) formula applied to correct the map distances.

RESULTS AND DISCUSSION

Behaviour of parents, F1 and F2 segregations for various pigmented plant parts are given in Table I. F1 was always pigmented due to dominant and complementary gene action. The colour on petiole, leaf tip, leaf margin and midrib is controlled by two complementary genes (9purple:7green) whereas the colour on bract tip and disc floret is governed by a single dominant gene (3purple:1green). Chi-square test was applied to the observed frequencies of the F2 segregation on the basis of ratios and it has given a satisfactory fit. F2 results were confirmed by raising 59 F3 families (Table II).

Study of combined segregation (Table III) data revealed the presence of linkage between the colour on bract tip, leaf tip, leaf margin, midrib, disc floret and petiole. The association is between one of the complementary genes and a single dominant gene of the above mentioned characters. In other words, linkage has been detected between the basic gene for bract tip and disc floret with the complementary gene of leaf tip, leaf margin, midrib and petiole. There are six genes involved in the linkage map, four are complementary and two are monogenic dominant. The linked genes were designated as Pbrt, Ptt_b, Plm_b, Pmd_b, Pdf, and Ptl_b in sequence corresponding to their map distances. Fig 1. depicts the genetic map of these linked genes.

The basic gene of bract tip (Pbrt) and the complementary gene of petiole (Ptl_b) were located at the extreme ends with a map distance of 6.61 units. The other four genes were situated in between the two genes. The genes Ptt_b, Plm_b, Pmd_b, and Pdf were located at a distance of 1.66, 1.81, 2.80 and 4.67 map units respectively from the gene Pbrt of bract tip. The genes

Pmd_b, Plm_b, and Plt_b, were located at a distance of 3.07, 3.11 and 3.54 map units respectively from the gene Pdf. The map distance between Pdf and Ptl_b is 2.51 units. The linkage detected between the six genes of these characters forms the first report on this crop, which is one of the 17 linkage groups in sunflower. Though few linkage reports are available between anthocyanin colouration and male sterility by Stoenescu and Vranceanu(1977) and Burlov and Kostyuk(1981) the present work appears to be the first report on linkage studies on qualitative characters in Sunflower in India.

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Table 1. Characters of the parents, F₁ and F₂ segregation.

Characters	Pigment in :		F ₂ segregation				X	P value
	RM-1	ITP-1	F ₁	Ratio	Purple	Green		
Petiole	G	P	P	9:7	Observed	652.00	2.0317	0.2-0.1
					Expected	874.13	679.88	
Leaf Tip	G	P	P	9:7	Observed	876.00		
					Expected	874.13	679.88	0.0097
Leaf Margin	G	P	P	9:7	Observed	879.00		
					Expected	874.13	679.00	0.0620
Mid rib	G	P	P	9:7	Observed	849.00		
					Expected	874.13	679.00	1.65
Bract tip	G	P	P	3:1	Observed	1160.00		
					Expected	1165.50	388.50	0.1040
Disc floret	B	P	P	3:1	Observed	1179.00		
					Expected	1165.50	388.50	0.63

P - Purple ; G-Green ; B-Black.

Table II F₃ breeding behaviour of 59 families for characters petiole leaf tip, leaf margin mid rib showing 9:7 ratio and bract tip and disc floret showing 3:1 ratio in the cross RM-1 X ITP - 1.

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Characters and expected F ₃ ratios	NUMBER OF FAMILIES SEGREGATING FOR				Chi square	P Value
	BT+	3:1	9:7	BT-		
Expected ** (1:4:4:7)	*3.69	14.75	14.75	25.81		
Observed Petiole (9:7)	5.00	16.00	16.00	22.00	1.24	0.75 - 0.70
Mid rib (9:7)	4.00	17.00	16.00	22.00	1.04	0.90 - 0.75
Leaf tip (9:7)	5.00	16.00	16.00	22.00	1.24	0.75 - 0.70
Leaf margin (9:7)	5.00	16.00	16.00	22.00	1.24	0.75 - 0.70
Bract tip (3:1)	14.75	29.50	-	14.75	0.42	0.95 - 0.90
Expected (1:2:1)	16.00	27.00	-	16.00		
Observed						
Disc floret	14.75	29.50	-	14.75	0.42	0.95 - 0.90
Expected (1:2:1)	16.00	27.00	-	16.00		
Observed						

BT+ Number of families breeding true for dominant character
 BT- Number of families breeding true for recessive character.
 * P - phenotypic ratio
 * P - expected values.

Table III Combined segregation of bract tip (3:1) with other characters in the cross RM₁ X ITP-1

Characters with ratio	Joint Ratio	Remarks	Pp	Fg	Gp	Gg	X	F Value
Disc floret (3:1)	9:3:3:1	Observed:	1133.00	27.00	46.00	348.00		
		Exp Ind. basis	874.13	291.37	291.37	97.13	1171.12	
	C.O.V. 4.67%	Exp. Linkage	1130.03	35.47	35.47	353.03	5.23	0.20 - 0.10
Midrib (9:7)	27:21:9:7	OBS.	834.00	326.00	15.00	379.00		
		Exp. Ind.	655.59	509.94	218.53	169.99	561.42	
	C.O.V. 2.80%	Exp. Linkage	859.21	306.29	14.92	373.58	2.09	0.70 - 0.50
Leaf Margin (9:7)	27:21:9:7	OBS.	868.00	292.00	11.00	303.00		
		Exp. Ind.	655.50	509.94	218.53	169.99	625.94	
	C.O.V. 1.81%	Exp. Linkage	863.66	301.83	10.46	378.04	0.43	0.95 - 0.90
Leaf Tip (9:7)	27:21:9:7	OBS.	866.00	294.00	10.00	384.00		
		Exp. Ind.	655.59	509.91	218.53	169.99	592.38	
	C.O.V. 1.66%	Exp. Linkage	864.51	301.00	9.61	378.83	0.26	> 0.95
Petiole tip (9:7)	27:21:9:7	OBS.	860.00	300.00	42.00	352.00		
		Exp. Ind.	655.59	509.91	218.53	169.99	487.63	
	C.O.V. 6.61%	Exp. Linkage	836.89	328.61	37.24	351.26	3.74	0.50 - 0.30

OBS - Observed values

Exp. Ind - Expected values on independent basis

C.O.V. - Cross over values in percentage

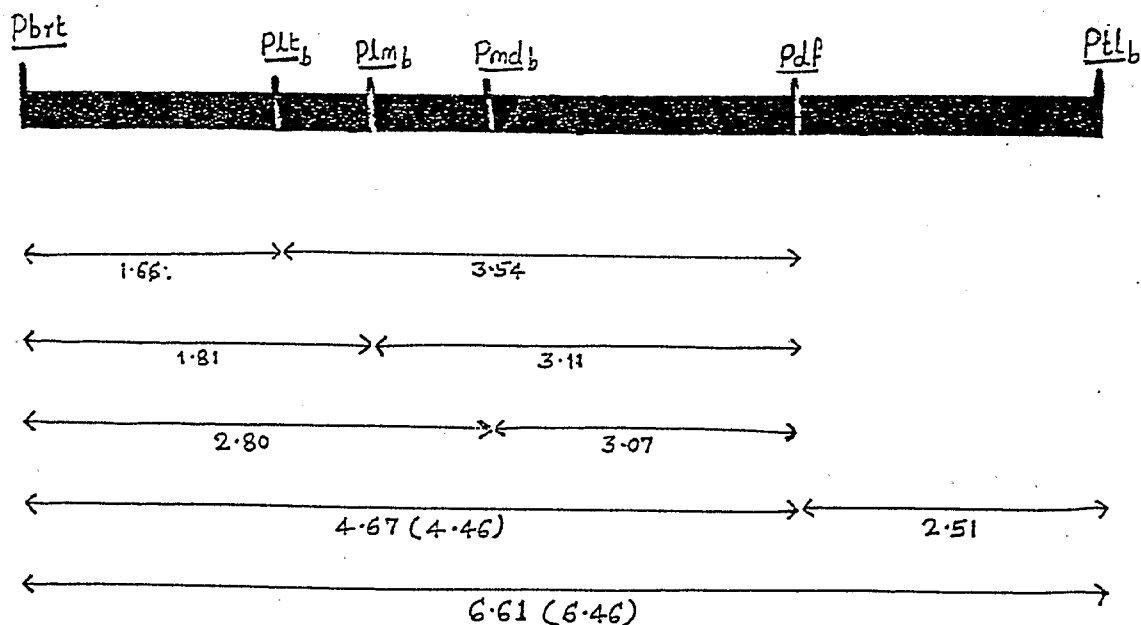


Fig.1 Linkage map showing the relative positions of the genes Pbrt, Plt_b, Plm_b, Pmd_b, Pdf and Ptl_b (Bract tip, leaf tip, leaf margin, midrib disc floret and petiole) in the cross $RM_1 \times ITP-1$. Cross over values given in the parenthesis indicate corrected map distance applying Kosambi's Formula.

Breeding

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BasavalingappaLINKAGE STUDIES IN SUNFLOWER (HELIANTHUS ANNUUS L.)

Inheritance studies undertaken at the University of Agricultural Sciences, Gandhi Krishi Vignana Kendra, Bangalore, India, on Sunflower revealed a case of linkage in the cross RM₁ X ITP-1. Analysis of F₂ generation showed that pigmentation on petiole, leaf tip, leaf-margin and midrib is controlled by two complementary genes and segregated in the ratio of 9 Purple : 7 green respectively. Colour on bract tip and disc floret is monogenic in inheritance. Combined segregation of F₂ data exhibited the linkage between these characters involving the complementary gene and the basic gene. Linkage map was drawn and the sequence of genes were located as per the cross over values. Gene symbols were designated for the above mentioned six qualitative characters as Pt₁, Plt, Plm, Pnd, Pbrt and Pdf respectively. The linkage detected between the genes of these characters forms the first report on Sunflower in India.

Key words: sunflower, linkage, qualitative characters.