A READY RECKONER OF EXPECTED F_3 BREEDING BEHAVIOUR USEFUL IN LINKAGE STUDIES

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A ready reckoner for F_2 segregation ratios caused by two to four gene interactions and the expected F_3 breeding behaviour corresponding to those ratios is presented.

The primary aim of a plant breeder is to achieve improvement in the quantity of the economic product. Yield as well as characters contributing to it are usually quantitative in nature. Consequently, studies on quantitative gene-. tics have gained more importance in recent years. However. there are cases where in, economically important characters are simply inherited. Such characters have received the attention of geneticists from time to time in crops like maize, rice and sorghum. In some investigations, only the number and nature of genes governing such characters have been worked out (Ramiah, et al., 1931; Houssaye, 1942; Chandraratna, 1955; Dhulappanavar, 1976 and Hadagal et al., 1980) while in others, the existence of pleibtropy and linkage have been exposed (Dhulappanavar and Kolhe, 1972; Dhulappanavar et al., 1974 Dhulappanavar, 1977; Dhulappanavar, 1979 and Kullaiswamy. 1981). But a review of recent literature reveals that studies leading to finalisation of linkage groups have not been extended even to crops subjected to intensive genetic analyses in the earlier years. In crops like oil seeds, pulses etc., such studies have not been properly initiated. One of the probable reasons for this may be the fact that enormous amount of time and patience is involved in the experimentation and analyses of the data. If a ready reckoner giving the needed information is provided for being perused at a glance, the job of geneticists would be simplified. Keeping this in view, genetic explanations for several F_2 segregation ratios involving two to four gene interactions as well as the expected breeding behaviour of corresponding F_3 families are worked out and compiled in this paper. The genetic explanation for different F_2 ratios (Table 1). refers to the number and nature of genes which when exist in dominant condition, express the dominant character. It is to be noted that an inhibitory gene in the dominant state inhibits the expression of the dominant trait. Thus, for obtaining a particular F_2 ratio the genes mentioned against it must be heterozygous in the F_1. The expected F_3 breeding behaviour for different digenic and trigenic segregation F_2 ratios is given in Table 2 while the same

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for tetragenic F_2 ratios is presented in Table 3. The expected F_3 breeding behaviour corresponding to an F_2 ratio refers to the expected frequencies of different types (Breeding true for the dominant and recessive character and segregating in different ratios) of F_3 families obtained from the F_2 furnishing that ratio. Depending upon the results obtained in a genetic study, one has to just select the suitable F_2 ratio (Table 1) and the corresponding F_3 behaviour (Tables 2 and 3) and test the agreement between the observed and expected figures by X^2 test to determine the mode of inheritance of a character.

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Table. 1 Genetic explanations for different digenic, trigenic and tetragenic F_3 segregation ratios.

Ratio	Genetic explanation
3 : 13	One basic gene and one inhibitory gene.
9 : 7	Two complementary genes.
15 : 1	Two duplicate genes
3 : 61	One basic gene and two duplicate-inhibitory genes.
9 : 55	Two complementary genes and one inhibitory genes.
15 : 49	Two duplicate genes and one inhibitory gene
21 : 43	One basic gene and two complimentary-inhibitory genes
27 : 37	Three complementary genes
39 : 25	One basic gene, one inhibitory gene and one anti-inhibitory gene.
45 : 19	One basic gene and two duplicate-complementary gene
54 : 10	Any two of the duplicate-complementary genes.
57 : 7	Any two of the three duplicate complementary genes, one of the three dominant genes being capable of causing dominant character independently
63 : 1	Three duplicate genes
3 : 253	One basic gene and three duplicate - inhibitory genes
15 : 241	Two duplicate genes and two duplicate - inhibitory genes
27 : 229	Three complementary genes aud one inhibitory gene
63 : 193	Three duplicate genes and one inhibitory gene
81 : 175	Four complementary genes
111 : 145	One basic gene and three complementary inhibitory genes
117 : 139	Two complementary genes, one inhibitory gene one anti-inhibitory gene
129 : 127	One basic gene, one inhibitory gene and two complementary anti-inhibitory genes
135 : 121	Two basic complementary genes and-two duplicate - complementary genes
147 : 109	One basic gene, two duplicate - inhibitory genes and one anti-inhibitory gene
162 : 94	One basic gene and any two of the three duplicate - complementary genes
165 : 91	One basic gene, two inhibitory complementary genes and one anti- inhibitory gene
183 : 73	One basic gene, one Inhibitory gene and two duplicate anti-inhibitory genes
188 : 67	One basic gene and any one of the three duplicate complementary genes
195 : 61	Two duplicate genes. one inhibitory gene and one anti-inhibitory gene
207 : 49	Two duplicate sets of complementary genes with two genes in each set
243 : 13	Any two of the four duplicate complementary genes
255 : 1	Four duplicate genes.

Table—2. Expected F₃ breeding behaviour for different digenic and trigenic F₂ segregation ratios.

Frequencies of families under each class of F₃ for different digenic and trigenic F₂ ratios

In F₃	Digenic			Trigenic									
	3:13	9:7	15:1	3:61	9:55	15:49	21:43	27:37	39:25	45:19	54:10	57:7	63:1
0:1 (BIR)*	7	7	1	37	37	19	19	37	19	19	10	7	1
1:3	2	—	—	4	2	14	4	—	2	—	—	—	—
1:15	—	—	—	4	—	—	—	—	—	—	—	—	—
3:1	2	4	4	2	4	4	14	6	16	8	12	18	6
3:13	4	—	—	—	8	8	8	—	4	—	—	—	—
7:9	—	4	—	8	4	—	4	—	4	8	12	4	—
9:7	—	4	—	8	—	—	—	12	4	8	12	8	12
13:3	—	—	—	—	—	—	—	—	—	—	—	—	—
15:1	—	4	—	8	—	4	8	8	—	4	12	8	—
3:61	—	—	—	—	—	—	—	—	—	—	—	—	—
9:55	—	—	—	—	—	—	—	—	—	—	—	—	—
15:49	—	—	—	—	—	—	—	8	—	8	—	—	—
21:43	—	—	—	—	—	—	—	—	—	—	—	—	—
27:37	—	—	—	—	—	—	—	—	8	—	8	—	—
39:25	—	—	—	—	—	—	—	—	—	—	—	—	—
45:19	—	—	—	—	—	—	—	—	—	—	—	—	—
54:10	—	—	—	—	—	—	—	—	—	—	8	8	—
57:7	1	1	—	1	1	7	7	—	7	7	—	—	8
63:1	—	—	7	—	—	—	—	—	—	—	—	19	37
1:0 (BTD)*	1	1	7	1	1	7	7	1	7	10	10	19	37

*BTD : Breeding true for dominant character

*BTR : Breeding true for recessive character

Table : 3 Expected F₃ breeding behaviour for different *tetragenic* F₃ segregation ratios

Frequencies of families under each class of F₃ for different F₃ ratios

Expected ratios in F₃	3:352	15:251	27:229	63:163	81:175	111:145	117:139	129:127	135:121	147:109	162:94	165:91	183:73	189:67	195:61	207:49	243:13	255:1
0:1 (BTR)*	175	121	135	67	175	67	121	85	121	85	94	67	67	67	31	49	13	1
1:3	6	28	2	74	—	6	2	10	—	4	30	2	2	—	14	—	—	—
1:15	12	28	—	—	—	—	—	—	—	4	—	—	—	—	—	55	24	8
3:1	2	4	6	6	6	74	26	42	32	52	—	70	78	80	40	—	—	8
3:13	12	16	12	12	—	12	12	28	—	8	—	8	4	—	8	—	—	—
7:9	—	—	—	—	24	—	—	—	44	—	36	4	—	—	—	56	—	—
9:7	—	—	12	12	—	—	36	12	—	28	—	8	8	12	8	16	24	8
13:3	—	4	—	—	—	—	4	12	4	8	12	8	8	13	28	—	48	—
15:1	8	—	—	—	—	—	—	—	—	—	—	—	4	—	28	—	—	24
1:63	—	16	24	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
3:61	24	—	8	—	32	24	8	8	—	8	24	8	—	—	—	—	—	—
9:55	—	16	—	—	—	—	—	16	16	—	—	4	—	—	—	—	—	—
15:49	—	—	8	12	—	8	8	8	—	16	—	16	16	—	16	—	—	—
21:43	—	—	4	—	—	—	16	16	—	—	—	22	16	—	—	—	—	—
27:37	—	—	—	—	—	—	—	8	—	—	—	—	—	—	—	—	—	—
37:27	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
39:25	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
42:22	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
43:21	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—

Table 3 Contd.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
45 : 19				24					16		24		8	24	8			
49 : 15									8						8		32	
54 : 10																		32
55 : 9	16	16	16	8							8	8	8	8			32	32
57 : 7																		
61 : 3		16																
63 : 1																		
3 : 253																		
15 : 241																		
27 : 229																		
63 : 193																		
81 : 175																		
111 : 145					16													
117 : 139						16	16											
129 : 127								16	16									
135 : 121										16	16							
147 : 109												16	16					
162 : 94														16				
165 : 91															16			
183 : 73																16		
89 : 67																	16	16
195 : 61																		
207 : 49																		
243 : 13																		16
255 : 1																		
1 : 0 (BTD)*	1	7	1	37	3	37	7	19	7	19	12	37	37	37	51	31	67	175

*BTD : Breeding true for dominant character.
*BTR : Breeding true for recessive character.