Agric. Sci. Digest 20 (2) 122-123, 2000

MONOSOMIC ANALYSIS OF CULM THICKNESS AND DAYS TO MATURITY IN BREAD WHEAT

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ABSTRACT

Monosomic lines of Kalyansona were crossed with DWR-39 and the F_2 analysis was employed to locate genes governing two quantitative characters to different chromosomes. This analysis led to the location of genes governing days to maturity to chromosomes 3A, 5A, 6A, 3B, 2D, 5D and 7D. Of these, genes present on 6A and 7D chromosomes were responsible for late maturity while those on others for early maturity. For culm thickness, chromosomes 4A, 5B, 6B, 3D and 5D were found to be significant where genes on all these chromosomes have negative effect on culm thickness.

Polygenes governing inheritance of quantitative characters are distributed over the limited number of chromosomes. This makes it difficult for a detailed analysis of gene-character relationship. However, the techniques like monosomic analysis have made it possible to determine the relative contribution of each chromosome to the expression of the character (Dylenok and Yatsevich, 1978; Evdokomov, 1979; Hoogendoorn, 1985; Sadananda, 1977 and Shnaider and Dorokhova, 1979). The paper pertains to two traits representing days to maturity and culm size. Though there are few earlier reports available on culm size, days to maturity character has not been subjected to monosomic analysis. In the present study, attempts were made to locate the genes influencing these traits by involving carefully chosen parents with contrasting features.

The F_2 populations derived from crossing monosomic series of Kalyansona with DWR-39 constituted the material for this analysis. The analysis was carried out by using all twenty one monosomic lines of Kalyansona. Cytologically confirmed monosomic parents were crossed with DWR-39 and F_1 populations were raised in the Botany Garden of College of Agriculture, Dharwad. Cytologically confirmed F_1 monosomic plants were selfed and forwarded to obtain twentyone F_2 populations corresponding to monosomics. The disomic F_2 population derived by crossing the two parental varieties was grown along with monosome derived F_2 populations. The populations were grown in 5' long row spaced 30cm apart by giving a spacing of 5 cm between plants in a row. At maturity observations were recorded on culm thickness and days to maturity. Mean and variances of the different populations were determined and to detect the critical lines, means of the monosomic F_2 populations were compared with disomic F_2 mean using the formula

$$Z = \frac{\bar{X} - \bar{Y}}{\sqrt{\frac{X^2}{n_x} + \frac{Y^2}{n_y}}}$$

Where $(\bar{X}-\bar{Y})$ = difference between the means of monosomic and disomic populations

X^2 = variance of monosomic population
Y^2 = variance of disomic population
n_x = number of observations in monosomic population
n_y = number of observations in disomic population

When the calculated Z value exceeded 1.96 and 2.58, the two means under consideration were concluded to be significantly different at five per cent and one per cent level of probability, respectively.

Means of parental varieties, their F_2 population and monosomic F_2 populations are presented in the Table 1. The mean values for days to maturity indicated significant deviations of F_2 populations derived from mono 3A, 5A, 6A, 3B, 2D, 5D and 7D. Of these, families of 6A and 7D were early maturing while those of remaining lines were late maturing compared to control F_2 population i.e. disomic.

Monosomic analysis of culm thickness revealed that populations monosomic for chromosomes 4A, 5B, 6B, 3D and 5D were found

Table 1 : Means of F_2 monosomic and disomic population with respect to culm thickness and days to maturity.

Mono	No. of plants	Culm thickness(cm)	Days to maturity
1A	140	0.39±0.01	116.46±0.44
2A	132	0.37±0.004	115.47±0.47
3A	191	0.38±0.25	121.50±0.51**
4A	188	0.47±0.01*	115.50±0.72
5A	174	0.39±0.01	124.07±0.40**
6A	140	0.32±0.01	104.00±0.46**
7A	209	0.39±0.01	116.00±0.53
1B	193	0.41±0.01**	115.56±0.36
2B	205	0.39±0.01	116.67±0.41
3B	205	0.36±0.01	117.45±0.50**
4B	82	0.38±0.01	115.00±0.71
5B	131	0.42±0.01**	116.01±0.48
6B	181	0.55±0.01**	115.59±0.49
7B	133	0.32±0.01	116.00±0.48
1D	189	0.36±0.01	115.92±0.36
2D	165	0.39±0.01	119.50±0.48**
3D	185	0.40±0.02**	116.43±0.32
4D	175	0.38±0.01	115.92±0.77
5D	143	0.58±0.01*	114.99±0.73**
6D	175	0.38±0.01	114.14±0.59
7D	212	0.37±0.01	99.08±0.76**
Disomic	490	0.38±0.05	116.23±0.21
Kalyansona	100	0.41±0.02	111.57±0.31
D-39	100	0.37±0.02	121.21±0.21

*, ** Significant at 5% and 1% level respectively.

to be critical. All of them increased the mean indicating the presence of genes imparting negative effect on this character. Genetic studies on this character are very scanty in wheat. Il'ina *et al.*, (1977) reported the genes present on chromosomes 1B and 2B were causing a reduction in diameter of the stem.

It is relevant here to discuss the point that the contributions of chromosomes studied differ depending on the genetic constitution of the variety studied. In a genotype a chromosome may have attained a perfect balance of contribution from genes increasing and decreasing the expression of a character. As a result the presence of such a chromosome in monosomic or disomic condition makes no impact on F_2 mean even though this chromosome has got genes influencing the character.

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