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STUDIES ON THE MEIOTIC STABILITY AND AGRONOMIC CHARACTERS OF 5D, 5R CHROMOSOMAL ISOGENIC LINES IN SECONDARY Triticale*

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Abstract

Triticale line 6TA-204 (JFR) carrying two rye homologous 5R-chromosomes with hairy-neck gene (Hp) was crossed to Armadillo 1524 (CIMMYT) carrying two wheat homologous 5D-chromosomes. In the F_4 progeny, 20 plants of the heterozygotes DR were selected and selfed until F_7 generation using genetic mark of hairy-neck. Twenty isogenic lines were planted in field and their meiotic and agronomic characters were investigated. The data of meiotic and agronomic characters of 5D, 5R chromosomal isogenic lines were analyzed statistically.

The results were as follows: The 5R-chromosome of rye in triticale increases normal tetrad cells, plant height, spikelets per spike, kernel weight per spike and weight of 100 kernels. Each hairy-neck genotype has its own correlations among some characters in triticale. Results of step-wise regression analysis indicated that the components of grain yield of triticale were dependent upon the genotypes of hairy-neck.

The result also indicated that the participation of 5D or 5R-chromosome will affect a number of agronomic characters and the stability of meiosis in isogenic lines of triticale.

Introduction

Triticale is a synthetic cereal developed by doubling the chromosomes of sterile hybrid between wheat, *Triticum aestivum* L. em. Thell. (2N=42) or *T. turgidum* L. (2N=28) and rye (*Secale cereale* L.) (2N=14) (Briggle, 1969).

"Hairy neck" or "Pubescent peduncle" is a common character in rye (*Secale*), but not in normal wheat (*Triticum*). The trait is easy to be found in these plants. The phenotype of hairy neck is consistent with genotype, and only one of the rye chromosomes carries the genes (O'Mara, 1940, 1951). O'Mara (1951) observed the meiosis of the wheat-rye addition line involving 5R chromosome.

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A distinct secondary constriction in the long arm of 5R chromosome was used as a good cytological marker. He located the gene for hairy peduncle (Hp) in the long arm of 5R chromosome. The measuring distance between Hp and the centromere was first reported at least 50 crossover units by Chang *et al.* (1973). Later, he indicated that Hp is 44.1 to 49.5 crossover units from the centromere (Chang, 1975). Jones and Jensen (1954) and Lin (1979) reported that the hairy peduncle was inherited as a simple Mendelian character since the trait in F_2 segregation fitted 1:2:1 ratio. Riley *et al.* (1973) reported that the dosage of $5R^s$ gene of rye would influence the pairing of wheat chromosomes when added to wheat.

Triticale meiosis becomes unstable by adding rye chromosomes. The consequences of such meiotic instability reduced fertility, and increased aneuploidy in progeny (Tsuchiya and Larter, 1969). Low yield of triticale was due to cytogenetical instability (Sapra *et al.*, 1973; Merker, 1974). In the past, some workers explained that the improving of meiotic stability would raise the fertility of triticale (Müntzing, 1957; Sanchez-Monge, 1959; Rupert *et al.*, 1973a, 1973b). Weimarck (1973) also indicated that in octaploid triticale (2N=56) meiotic stability could be improved by increasing genetic variation. But other workers showed that no correlation could be found between meiotic instability and fertility in advanced lines of hexaploid or octaploid triticale (Riley and Chapman, 1957; Müntzing, 1966; Merker, 1971, 1973, 1974; Kempana and Seetharam, 1972; Hsam and Larter, 1973, 1974). Hsam and Larter (1973) proposed that the pollen viability could be used as a selection index because of the significant positive correlation between fertility and pollen viability. However, Gustafson and Qualset (1975) and Kempana and Seetharma (1972) indicated that the correlation between pollen viability and fertility or yield were non-significant.

Taylor (1934) found that the plant height of genotype RR is lower than that of DR and DD in 5R addition line of wheat. O'Mara (1940) also found that those plants which were monosomic for 5R chromosome were slightly shorter than normal wheat plants and had heads with broader, coarser spikelets. When the 5R chromosome was disomic, these alternations were exaggerated, and the plants were approximately two third the height of normal wheat, and had coarser, broader spikelets than the plants monosomic for 5R chromosome. So he proposed that the rye chromosomes in addition lines of wheat had double dosage effect (O'Mara, 1940, 1951). Taylor (1934) indicated that the number of fertile tillers of DD was more than that of RR. But Jones and Jensen (1954) and Lin (1979) reported that the differences of plant height, number of fertile tillers and fertility were non-significant among various hairy neck genotypes. Chen (1975) also found that the differences of

plant height and number of fertile tillers were non-significant among various hairy neck genotypes, but the spike length and fertility of RR genotype were larger than those of DD and DR genotypes.

The main purpose of this study is to apply the cytological techniques and statistical analysis to determine (a) the effect of 5R chromosome of rye on cytological and agronomic characters in triticale, (b) the correlation of cytological and agronomic characters in various genotypes and (c) the variation of yield components in various genotypes.

Materials and Methods

1. *Materials*

The 5D, 5R chromosomal isogenic lines of secondary triticale (2N=42) were originated from 6TA-204 bred by Jenkins Foundation for Research (JFR) and Armadillo 1524 bred by International Maize and Wheat Improvement Center (CIMMYT). The genome of 6TA-204, AABBRR, includes a pair of 5R homologous chromosomes from rye having a hairy-neck gene (Hp). The genome of Armadillo 1524, AABBDR, has a pair of 5D homologous chromosomes from wheat having no Hp gene. These two triticale lines were crossed in 1971, and the F_2, F_3 progenies were selected at the experimental field of University of California, Davis. F_4 progeny was cultivated at the experimental field of National Taiwan University (N.T.U.) in 1974. The 5D, 5R chromosomal isogenic lines were then achieved by using hairy-neck trait as a phenotypic marker to select twenty DR heterozygous plants, and to self-pollinated these selected plants until the F_7 generation. So the available twenty isogenic lines have carried and identical genotypic background except 5D or 5R chromosome.

2. *Cultivation*

Self-pollinated seeds of DR heterozygous F_6 plant were planted at the experimental field of N.T.U. on Nov. 11, 1978. Each line was planted in a row, spacing 50 cm apart and 3 m long. Space between two plants was 15 cm. The level of N–P_2O_5–K_2O fertilizers applied was 84–54–60 Kg per hectare. One half of nitrogen dose and full dose of phosphorus and potassium were applied at planting, and the other one half of N dose was top-dressed at the 20th day after planting.

3. *Character measurements*

Twenty plants of genotypes DD, DR and RR each were randomly selected and labeled from each line during flowering stage. Then, we excised one spike from each labeled plant, and fixed it in Farmer's solution (3 parts of 95% alcohol: 1 part of glacial acetic acid (v/v)) for 24 hrs and subsequently

transferred it into 70% ethanol. Fixed material was kept in refrigerator for cytological observation. Standard acetocarmine squash method was used in chromosomal study (Chen, 1974; Chen *et al.*, 1978). Sixty plants were harvested individually after maturity and several characters were then measured. A total of 12 cytological, vegetative and reproductive characters (X_1, $X_2 \ldots X_{12}$) was measured. The characters are described as follows:

a. cytological characters:

X_1 : normal MI cell proportion; i.e. the proportion of cells in which univalent can't be found at MI stage in 30 PMC's.

X_2 : normal AI and TI cell proportion; i.e. the proportion of cells in which lagging chromosomes can't be found at AI or TI stage in 30 PMC's.

X_3 : normal tetrad cell proportion; i.e. the proportion of cells in which micronuclei can't be found at tetrad stage in 30 PMC's.

X_4 : pollen I_2-KI stainability; 400 pollen grains were stained with I_2-KI and the stained ones were counted.

b. vegetative characters:

X_5 : number of fertile tillers per plant.

X_6 : plant height. (cm)

c. reproductive characters:

X_7 : spike length. (cm)

X_8 : number of spikelets per spike.

X_9 : number of kernels per spike.

X_{10}: fertility; i.e. X_9/X_8.

X_{11}: kernel weight per spike. (g)

X_{12}: weight of 100 kernels. (g)

4. *Data analysis*

a. estimation of mean, coefficient of variation and *t*-value.

b. calculation of correlation coefficient.

c. multiple regression analysis and step-wise regression analysis:

The model for multiple regression analysis is

$$\hat{Y} = b_0 + b_1 X_1 + \ldots + b_i X_i \ldots + b_n X_n$$

Here $\hat{Y}$ is a dependent variable. X_i are independent variables. b_i are partial regression coefficients. The significant test of partial regression coefficent was determined by *t*-test (Draper and Smith, 1967). The result of multiple regression analysis indicates the compound relation among dependent variable and several independent variables. The partial regression analysis shows the simple relation between dependent variable

and individual independent variable. Besides the multiple regression analysis, we also used step-wise regression to select variables closely related to dependent variable.

Results

The measured characters were separately recorded in three genotypes. According to multiple correlation and regression, we analyzed the influence of 5D and 5R chromosomes to cytological and agronomic characters and yield components of triticale. The plants with two 5R chromosomes (RR) showed dense hairy-neck. Those with both 5R and 5D chromosomes (DR) showed thin hairy-neck, while those with two 5D chromosomes (DD) showed smooth neck (Fig. 1). Meiotic abnormalities and pollen stainability in triticale plants are shown in Fig. 2, A-F.

The results of three genotypes mean, CV and *t*-test of investigated characters were shown in Table 1. It indicated that the variation of CV values among different characters was larger than that among different genotypes. The CV values of cytological characters were found to be the largest of all characters. The CV values of X_1 were the largest of all characters no matter of genotypes. The CV values of X_1 in DD, DR and RR genotypes were 86.03, 69.3 and 59.87%, and those of X_2 were 44.79, 40.92 and 28.77%, respectively. The high CV values of X_1 and X_2 in three genotypes indicated that these two characters were unstable. The CV value 2.76% of X_6 in RR genotype was the smallest of all. This data indicated that the plant height was the stablest in 12 characters.

According to the *t*-test, the value of DR genotype in X_2 was significantly smaller than that of RR. The same result was also found in X_3. In X_6, the value of DD genotype was significantly smaller than that of DR and RR. The X_8 and X_{12} values of DD genotype were also significantly smaller than those of RR. But the X_{11} value of RR genotype was significantly larger than that of DD and DR. The *t*-values among the three genotypes in the other characters were non-significant, however.

The rank of association among measured characters was described by simple correlation. The significance of correlation coefficient between any two measured characters in three genotypes is shown in Table 2. From Table 2, the correlations between cytological characters were as follows: There was a significant positive correlation in DD and DR genotypes between X_2 and X_3, but not in RR genotypes.

The correlations between cytological and vegetative characters were as follows: Significant positive correlations between X_4 and X_5 in DD genotype, and between X_2 and X_5 in DD genotype were found.

Table 1. *Means, coefficients of variation and t-test of the mean among the measurement characters in various hairy-neck genotypes*

Statistics	Genotype	Measurement characters											
		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
Mean	DD	0.21	0.43	0.64	0.89	14.85	83.20	10.20	23.75	54.83	2.27	2.05	3.70
	DR	0.19	0.35	0.63	0.90	16.10	87.35	10.65	24.25	53.75	2.31	2.13	3.95
	RR	0.22	0.52	0.71	0.92	14.50	90.95	10.71	25.20	58.64	2.34	2.40	4.09
Coefficients of variation	DD	86.03	44.79	19.27	12.24	21.55	5.63	10.11	8.41	21.36	20.69	25.31	13.47
	DR	69.30	40.92	20.32	7.25	26.95	7.21	8.07	7.31	17.73	14.38	19.50	7.31
	RR	59.87	28.77	15.93	5.08	21.98	2.76	10.46	8.00	11.33	11.61	12.83	5.70
t-value	DD-DR	0.30	1.50	0.22	−0.54	−1.04	−2.36*	−1.50	−0.84	0.32	0.50	−0.50	−1.91
	DD-RR	−0.25	−1.55	−1.87	−1.05	0.35	−4.32**	−1.50	−2.29*	−1.27	−0.51	−2.60*	−3.22**
	DR-RR	−0.65	−3.58**	−2.06*	−0.68	1.33	−1.78	−0.19	−1.58	−1.88	−1.34	−2.41*	−1.81

*, ** Significant at 5% and 1% level of *t*-test respectively.

Table 2. *Significant tests of correlation coefficients among 12 measurement characters in various hairy-neck genotypes*

Character	Genotype	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_2	DD											
	DR											
	RR											
X_3	DD		**									
	DR		**									
	RR											
X_4	DD											
	DR											
	RR											
X_5	DD		**		*							
	DR											
	RR											
X_6	DD											
	DR					*						
	RR											
X_7	DD											
	DR											
	RR		—*									
X_8	DD			—*				**				
	DR			*				**				
	RR		—*		—**			**				
X_9	DD							*				
	DR			*		*			**			
	RR							*				
X_{10}	DD		*	*			—*			**		
	DR			*						**		
	RR									**		
X_{11}	DD		*			*				**	**	
	DR			**		*			**	**	**	
	RR							*		**	**	
X_{12}	DD		*			*					**	**
	DR											*
	RR											*

$r\left(18\ \begin{matrix}0.05\\0.01\end{matrix}\right)=\begin{matrix}0.444\\0.561\end{matrix}$

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

The correlations between cytological and reproductive characters were as follows: There were significant negative correlations between X_2 and X_7 or X_8 in RR genotype and between X_3 and X_8 in DD genotype. Significant positive correlations were found in DD genotype between X_2 and X_{10}, X_{11}, X_{12}. The significant positive correlations were also found in DR genotype between X_3 and X_8, X_9, X_{10}, X_{11}. Correlation between X_3 and X_{10} in DD genotype was positive, and the negative correlation between X_4 and X_8 in RR genotype was also significant.

The correlation between vegetative and reproductive characters was shown in Table 2. The significant positive correlations exist between X_5 and X_9 or X_{11} in DR, between X_5 and X_{11} or X_{12}, and between X_6 and X_{10} in DD.

The correlations among reproductive characters were as followers: The significant positive correlations existed between X_7 and X_8, between X_9 and X_{10} or X_{11} and between X_{10} and X_{11} in the three genotypes. The positive correlations between X_7 and X_9 or X_{11} and between X_{11} and X_{12} were significant in RR. But in DD genotype, positive correlations existed between X_7 and X_9 and between X_{12} and X_{10} or X_{11}; in DR genotype, they existed between X_{11} and X_{12} and between X_8 and X_9 or X_{11}. The other correlations among the characters were non-significant.

If correlations among each independent variables were significant, the multiple regression analysis would be interfered. Therefore, according to the results of Table 2, we only selected X_1, X_2, ...X_7 as independent variables and used X_9, X_{10}, X_{11} and X_{12} as dependent variables. The multiple regression analysis were processed in three genotypes. The results of multiple regression analysis and significant test of partial regressions coefficients were shown in Table 3. Every partial regression coefficient of the same dependent variable in three genotypes had different expression. Regressions with X_9 as the dependent variable gave the results that the partial regression coefficients of X_1, X_2, X_4, X_6 and X_7 were significant in DD genotype. The regression coefficients of all seven independent variables were non-significant in DR and RR. Regressions with X_{10}, as the dependent variable gave the results that the partial regression coefficients of X_2 and X_6 were significant in DD genotype. All seven independent variables were non-significant in DR and RR. Using X_{11} as dependent variable, the partial regression coefficients of X_2, X_4, X_6 and X_7 were significant in DD but in DR and RR genotypes all seven independent variables were non-significant. Using X_{12} as dependent variable, only the partial regression coefficient of X_6 was significant in DD genotype and X_2 was also the only significant character in DR genotype. None of the seven partial regression coefficients was significant in RR genotype.

For R^2 values (Table 3), DD genotype was greater than those of RR and

Table 3. *Multiple regression analyses and significant tests of partial regression coefficients of the measurement characters in various hairy-neck genotypes*

Dependent variables	Genotype	Intercept	Measurement characters							R^2
			X_1	X_2	X_3	X_4	X_5	X_6	X_7	
X_9	DD	60.55	21.72*	25.95*	-5.71	35.73*	-0.12	-1.29*	5.83**	0.86
	DR	-0.07	-1.65	-9.13	47.43	13.85	0.62	-0.03	0.69	0.52
	RR	12.37	-2.09	4.96	22.10	-31.46	0.32	0.27	2.64	0.52
X_{10}	DD	4.78	0.53	1.31*	0.24	1.39	-0.01	-0.06**	0.07	0.77
	DR	0.84	-0.14	-0.31	1.32	0.69	0.02	0.01	-0.06	0.37
	RR	-0.76	0.02	0.57	1.06	0.92	0.02	0.00	0.05	0.41
X_{11}	DD	3.42	0.49	1.41**	-0.40	1.33*	0.03	-0.06**	0.19*	0.88
	DR	-0.31	-0.33	0.49	1.37	-0.09	0.03	-0.00	0.10	0.56
	RR	-0.72	0.30	0.38	1.04	-0.48	0.00	0.01	0.13	0.49
X_{12}	DD	7.72	-0.55	1.09	-0.55	0.47	0.08	-0.06*	-0.03	0.66
	DR	3.10	-0.39	1.72*	-1.22	-1.04	0.03	0.00	0.15	0.43
	RR	1.98	0.72	0.32	0.37	1.20	-0.02	0.00	0.04	0.24

*, ** significant at 5% and 1% level of *t*-test respectively.

Table 4. *Step-wise multiple regression analyses of the measurement characters in various hairy-neck genotypes*

Dependent variables	Genotype	Intercept	Measurement characters							R^2
			X_1	X_2	X_3	X_4	X_5	X_6	X_7	
X_9	DD	52.92	21.49**	22.76**	—	35.16**	—	-1.25**	5.95**	0.86
	DR	3.10	—	—	37.94*	16.82	0.72	—	—	0.50
	RR	8.91	—	8.28	19.24	-27.15	—	0.27	2.98*	0.51
X_{10}	DD	6.16	0.58	1.25**	—	1.28*	—	-0.07**	—	0.76
	DR	1.07	—	—	1.02	0.78	0.02	—	-0.05	0.36
	RR	-0.39	—	0.63	0.95	0.88	0.02	—	0.06	0.40
X_{11}	DD	2.74	0.50	1.25**	—	1.35*	0.03	-0.06**	0.20**	0.88
	DR	-0.29	—	—	1.70**	—	0.03	—	0.08	0.54
	RR	-1.20	0.32	0.41	1.04	—	—	0.01	0.13	0.48
X_{12}	DD	6.86	-0.58	0.92	—	—	0.08*	-0.06**	—	0.64
	DR	3.14	-0.39	1.72*	-1.22	-1.04	0.03	—	0.15	0.43
	RR	2.22	0.68	—	0.56	1.11	-0.01	0.01	—	0.21

*, ** Significant at 5% and 1% level of *t*-test respectively.

DR. Especially in X_{12}, the R^2 value was only 24% in RR genotype, so the use of the seven independent variables to explain X_{12} was not sufficient.

The results of step-wise regression analysis are shown in Table 4. Regressions with X_9 as the dependent variable revealed that the selected characters in DD genotype were X_1, X_2, X_4, X_6 and X_7. All of them were significant. The characters in DR genotype were X_3, X_4 and X_5. Only X_3 was significant. As to RR, the selected characters were X_2, X_3, X_4, X_6 and X_7. However, only X_7 was significant. Using X_{10} as the dependent variable, the selected characters in DD genotype were X_1, X_2, X_4 and X_6. All were significant except for X_1. The characters in DR genotype were X_3, X_4, X_5 and X_7 but all were non-significant. As to RR, the important characters were X_2, X_3, X_4, X_5 and X_7. All were non-significant too. Using X_{11} as the dependent variable, the selected characters in DD genotype were X_1, X_2, X_4, X_5, X_6 and X_7, and all were significant except X_1, and the characters in DR genotype were X_3, X_5 and X_8, and only X_3 was significant. As to RR, the selected characters were X_1, X_2, X_3, X_6 and X_7, and all were non-significant. Regressions with X_{12} as the dependent variable revealed that the selected characters in DD genotype were X_1, X_2, X_5 and X_6, and the partial regression coefficient of X_5 and X_6 were significant, and in DR genotype they were X_1, X_2, X_3, X_4, X_5 and X_7 but only X_2 was significant. In RR genotype they were X_1, X_3, X_4, X_5 and X_6, and all were non-significant. Since the slight or no differences of R^2 values between Table 4 and 3 were found, indicating that using the step-wise regression which only selects partial characters does not reduce the explaining extent of yield components.

Discussion

According to the CV values, character variations are larger than genotypic variations. The cytological characters have the largest CV in these characters. Owing to this instability, we can not predict any preferences of agronomic characters by using cytological characters as index. In the four cytological characters, DD has the largest (except in X_3) variation in three genotypes, DR the next and RR is the most stable one. Müntzing (1939) and Larter *et al.* (1968) reported that the univalent was caused by rye chromosomes. Riley *et al.* (1973) also pointed out that the addition of rye 5R chromosome to wheat did influence the pairing of chromosomes. However, the results of this study seem to indicate that the 5R chromosome of rye can promote the pairing of other chromosomes in secondary triticale.

Mean of four cytological character, increase from X_1 to X_4. It denotes that though pollen mother cells may be abnormal at MI (forming univalent), some of them restore to normal in AI and TI (without forming lagging

chromosomes). In tetrad stage another parts of them restore to normal again (without forming micronucleus). Then at pollen maturation, only 10% pollen grains are abnormal. Univalent chromosomes at MI became laggards during AI. They were excluded from the nucleus at TI, forming micronucleus at dyad. Chromatid laggards at TII became micronucleus at tetrad (Scoles and Kaltsikes, 1974). However, not all univalents, laggards or chromatid laggards became micronucleus. Some will reinclude into nucleus, again. Müntzing (1939) called it "reinclusion".

The performances of characters have some extent of differences among various genotypes. In Table 1, the differences of X_1, X_4, X_5, X_7, X_9 and X_{10} characters within various genotypes are non-significant. It indicated that 5D, 5R chromosomes do not carry the genes which may affect the performances of these characters; or they may carry the genes of same effect so that characters perform the same extent. Taylor (1934), and Jones and Jensen (1954) showed that the fertility of hairy-neck genotypes were similar. Chen (1975) indicated that spike length and fertility had promotive effect in RR genotype. The difference may be caused by different materials. Jones and Jensen (1954), Chen (1975) and Lin (1979) reported no difference among various genotypes in fertile tillers. Their finding seems to agree with the results of this study. However Taylor (1934) did indicate that DD genotype had more fertile tillers than RR genotype.

According to Lin (1979), the pollen grain I_2-KI stainability in DD genotype was the largest while in RR genotype was the smallest and their difference is highly significant. But Chen (1975) reported that the differences among various genotypes were non-significant in pollen grain I_2-KI stainability. Chen (1975) and Lin (1979) also indicated that the differences among various genotypes were non-significant in number of kernels per spike. These results meet ours. From *t*-test of normal AI and TI cells, it denotes that two rye 5R chromosomes existed the laggards of triticale reduce. With the same reason, we can deduce that the formation of micronucleus will be reduced in RR genotype. The deduction meets that the proportion of normal tetrad cell of RR is larger than that of DR genotype.

Jones and Jensen (1954), Chen (1975) and Lin (1979) reported that the differences among various genotypes in plant height were non-significant. But, 5R addition lines of wheat, all plants were rather short. However, Taylor (1934) and O'Mara (1940, 1951) reported that in the aneuploid of rye addition line of wheat, plants with two 5R chromosomes were the shortest, with one 5R chromosome next without rye 5R chromosome the tallest. Our results do not meet their findings. They also proposed that rye 5R chromosomes in addition lines of wheat had double dosage effect.

The *t*-test of spikelets per spike indicated that a pair of 5R chromosomes had increasing effect. This result did not match that of Chen (1975) by using F_2 generation. As to the kernel weight per spike, it also indicates that 5R chromosomes have double dosage effect in euploid level.

The weight of 100 kernels of RR was larger than that of DD; their difference was significant. But the difference between DD and DR orDR and RR was non-significant. It also means that only double 5R chromosomes can promote the weight of 100 kernels. Lin (1979) also reported that the weight of 100 kernels of RR was larger than that of DD. Its tendency was RR the heaviest, DR the next, and DD the lightest. Chen (1975) pointed out that 5R chromosome did not have effect on increasing kernel weight in F_2 generation however.

Different compositions of 5D, 5R chromosomes not only affect a single character's performance but also affect correlations between characters. The correlations between normal MI cell proportion and any other characters in three genotypes were non-significant. It meets the proposition that the selection of breeding on the basis of univalent number does not have effect (Gustafson and Qualset, 1975).

The correlations between any two characters of normal MI cell proportion, normal AI and TI cell proportion, normal tetrad cell proportion and pollen grain I_2-KI stainability are non-significant except that the one between normal AI and TI cell proportion and normal tetrad cell proportion is highly positive significant in DD or DR genotype. However, Hsam and Larter (1973) reported that correlations between any two characters of univalent proportion, laggard proportion and micronucleus proportion were significant. And the correlations between normal pollen proportion and any one of univalent proportion, laggard proportion and micronucleus proportion were non-significant. It was not consistent with this study; it might be caused by different material or sampling. The correlation between pollen I_2-KI stainability and number of spikelets per spike is highly negative significant in RR genotype. It revealed that a pair of 5R chromosomes had more influence on correlation between these two characters than 5D chromosomes. It was consistent with Lin's result (Lin 1979).

Among all correlations between cytological characters and fertility, only the correlations of fertility and normal AI and TI cell proportion or normal tetrad cell proportion are significant and only exist in DD and DR genotypes. Thus it is concluded that 5D chromosome has more effect on the correlations between cytological characters and fertility than 5R chromosome. Some worker reported that meiotic stability and fertility were correlated positively. If meiotic stability is improved, the plant fertility will also be improved.

(Müntzing, 1957; Sanchez-Monge, 1959; Boyd *et al.*, 1970; Rupert *et al.*, 1973a, 1973b). But several workers opposed. (Riley and Chapman, 1957; Müntzing, 1966; Merker, 1971, 1973, 1974; Kempana and Seetharam, 1972; Hsam and Larter, 1973, 1974; Gustafson and Qualset, 1975). According to this study, meiotic stability correlated with fertility in DD and DR genotypes but not in RR. So if we want to improve fertility by improving meiotic stability, it only succeeds in DD and DR genotypes.

Correlations between vegetative characters and reproductive characters performed differently in various genotypes. The DR and DD genotypes would have similar performance, if the effect of 5D chromosome was larger than that of 5R chromosome. For instances, the correlations between fertile tillers and kernel weight per spike or weight of 100 seeds, between plant height and fertility and between fertility and kernel weight per spike in DR and DD are of the same performances. Interaction between 5D and 5R chromosomes would cause the correlations of DR to be inconsistent with that of DD and RR. For instance, the correlations between fertile tillers and plant height or number of kernels per spike, between spike length and number of kernels per spike, and between number of spikelets per spike and number of kernels per spike or kernel weight per spike.

In DD genotype, considering the regression with number of kernels per spike as dependent variable, the partial regression coefficients of normal MI cell proportion, normal AI and TI cell proportion, pollen grain I_2-KI stainability, plant height and spike length are significant. But in DR and RR genotypes, they are non-significant. Lin (1979) indicated that the partial regression coefficients of spike length are significant in three genotypes and those of pollen grain I_2-KI stainability, plant height and fertile tillers are all non-significant in three genotypes. But Chen (1975) pointed out that the partial regression coefficients of pollen grain I_2-KI stainability, plant height, fertile tillers and spike length were non-significant among three genotypes in F_2 population. Using fertility as dependent variable, only the partial regression coefficients of normal AI cell proportion and plant height were significant in DD genotype and they are non-significant in DR and RR genotypes. But Lin (1979) reported that the partial regression coefficients of spike length were significant in all three genotypes. However Chen (1975) indicated that the partial regression coefficients of these characters were non-significant in three genotypes. When the kernel weight per spike was used as dependent variable, the partial regression coefficients of normal AI and TI cell proportion, pollen grain I_2-KI stainability, plant height and spike length were significant in DD genotype and in DR and RR genotypes they were all non-significant. When the weight of 100 kernels was used as dependent variable,

only the partial regression coefficient of plant height was significant in DD genotype, but in DR genotype it was normal AI and TI cell proportion and none was significant in RR genotype. According to Lin (1979), using weight of 100 kernels as dependent variable, the partial regression coefficient of plant height was significant in DD genotype and the coefficients of plant height and spike length were significant in DR genotype. The difference may be caused by various independent variables and materials.

In Table 3, the R^2 value of DD is greater than that of DR and RR, indicating that the explaining extent of seven characters to four reproductive characters in DD is larger than DR and RR. But by using the weight of 100 kernels as dependent variable, the R^2 value of RR is only 0.24, indicating that some other factors influencing weight of 100 kernels are not involved.

In view of the R^2 values of Table 4, they are almost equal to those of Table 3. But in significant tests of partial regression coefficients, some characters were changed from non-significance to significance because some characters were deleted in step-wise regression analysis.

According to the results and discussion described above, various hairy-neck genotypes would cause the agronomic characters to have different performance; in the meantime, they also affected the correlations between characters. The compound relation between reproductive characters and other agronomic characters are influenced by various genotypes too. Generally speaking, if any hairy-neck genotypes is involved in triticale breeding programs, we must select different characters in order to extend the best of selection efficiency. In addition to this, how 5D or 5R chromosome affects meiotic instability, plant height, number of spikelets per spike or kernel weight is remained to be studied.

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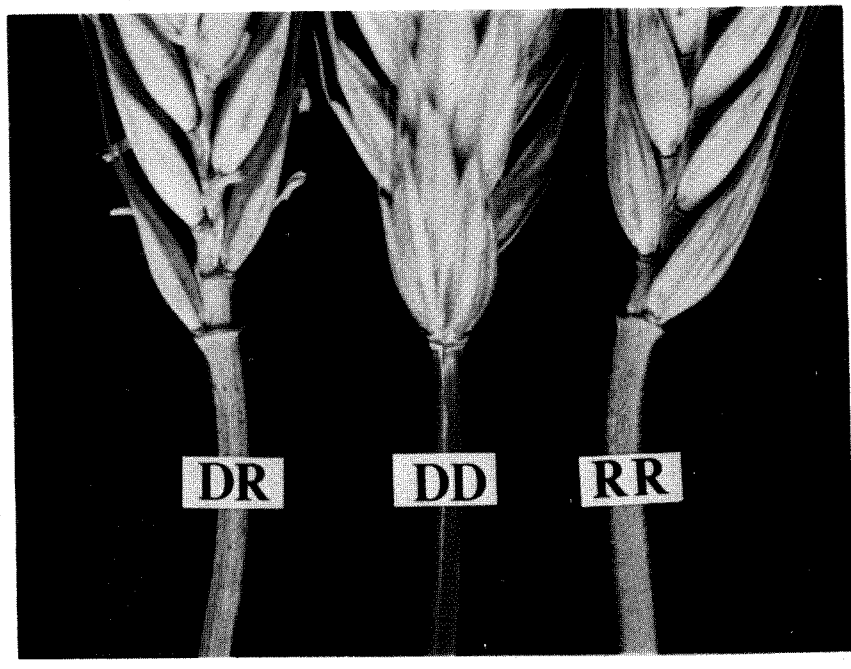

Fig. 1. Expression of hairy-neck genotypes in triticale.
DR thin, DD smooth, RR dense.

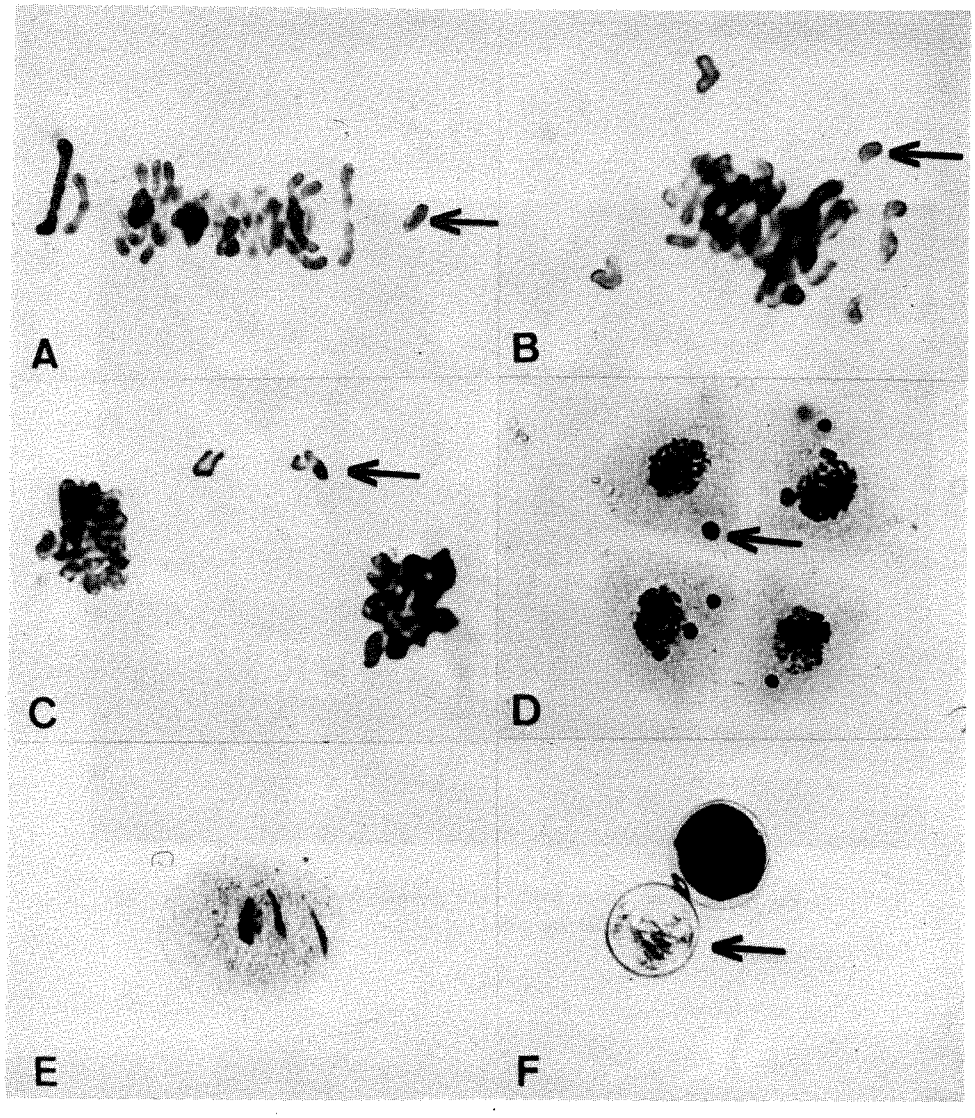

Fig. 2. Meiotic abnormalities and pollen stainability in secondary hexaploid triticale. (A) and (B) Univalents at MI (arrows). (C) Lagging chromosomes at TI (arrow). (D) Micronuclei (arrow) in a tetrad. (E) A young normal with 3 nuclei pollen. (F) Aborted (arrow) and normal mature pollen grains (I_2-KI).

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次級型黑小麥5D，5R染色體同源系之減數分裂穩定性及農藝性狀之研究*

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"6TA-204" 是由 JFR 所育成之初級型黑小麥，具有一對黑麥之 5R 同源染色體，在此染色體上携帶有穗頸毛基因 (Hp)。"Armadillo 1524" 則是由 CIMMYT 所育成之次級型黑小麥，具有一對小麥之 5D 同源染色體，而不具有 5R 染色體。利用穗頸毛之有無做爲遺傳標識性狀，從雜交後裔世代育成了20套之 5D，5R 染色體同源遺傳背景系。利用此20套同源系做爲材料，種植田間，分別調查其細胞減數分裂及農藝性狀。

試驗結果摘要如下：黑小麥同源系中之具有黑麥 5R 染色體對於正常 AI 細胞之比例，正常四分子細胞之比例，株高，一穗小花穗數，一穗子實重及百粒重均有顯著增加之效果。不同之穗頸毛基因型會影響到某些性狀間之相關性，此外不同基因型之產量決定性狀也不同。由本試驗之結果可知，在黑小麥中 5D 或 5R 染色體之不同組成會影響到某些重要之農藝性狀及減數分裂之穩定性。

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