

パン小麦のクロロシス遺伝子Ch1のモノソミック分析

誌名	The Japanese journal of genetics
ISSN	0021504X
著者	常脇, 恒一郎
巻/号	50巻2号
掲載ページ	p. 151-154
発行年月	1975年4月

農林水産省 農林水産技術会議事務局筑波産学連携支援センター
Tsukuba Business-Academia Cooperation Support Center, Agriculture, Forestry and Fisheries Research Council
Secretariat



MONOSOMIC ANALYSIS OF A CHLOROSIS GENE Ch_1 IN COMMON WHEAT¹⁾

KOICHIRO TSUNEWAKI

Laboratory of Genetics, Faculty of Agriculture, Kyoto University, Kyoto 606

Received December 18, 1974

Two types of hybrid chlorosis, 1 and 2, are known in wheat. The factorial basis of type 1 chlorosis was established by Hermesen (1966) and Tsunewaki (1966). It is caused by two complementary genes, Ch_1 and Ch_2 . Ch_2 was located by Tsunewaki and Kihara (1961) on chromosome 3D. For the Ch_1 gene, Nishikawa (1964) reported a location in the A or B genome but not in D. Recently, Hermesen and Waninge (1972) have suggested that this gene is carried by chromosome 2A. However, some ambiguities exist in their results. The present experiment was done to confirm their results, using a more critical monosomic analysis procedure.

MATERIALS AND METHODS

Three strains of common wheat, *Triticum aestivum* L. were used in this experiment; a cultivar Chinese Spring, and two experimentally produced strains NIG 4 and NIG 7. Their genotypes for chlorosis type 1 are as follows:

Chinese Spring	$ch_1 ch_1 Ch_2 Ch_2$
NIG 4	$ch_1 ch_1 ch_2 ch_2$
NIG 7	$Ch_1 Ch_1 ch_2 ch_2$

Fourteen monosomic lines of Chinese Spring, which correspond to 14 chromosomes of the A and B genomes of common wheat, were first crossed to NIG 4 in 1971. The next year, three monosomic plants were selected in the F_1 generation for each chromosome by cytological observation of their PMC's, and were crossed as the female parent to NIG 7, producing three progenies in each chromosome. In the spring of 1973 normal and chlorotic plants were segregated in a 1:1 ratio. Of these only normal plants were cytologically examined, and a single monosomic plant was selected from each progeny, thus there were three monosomics for each chromosome. Their pollen grains were used in the test-cross to Chinese Spring, and segregation of the normal and chlorotic plants in each monosomic line was tested in the spring of 1974.

The entire scheme of the crossing program, and the expected segregation ratio in the final test-cross are shown in Fig. 1.

1) Contribution from the Laboratory of Genetics, Faculty of Agriculture, Kyoto University, Japan, No. 373.

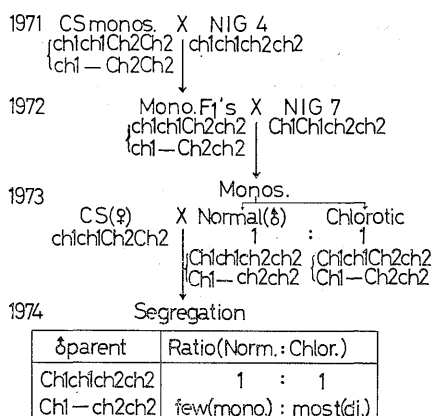


Fig. 1. Experimental design of the monosomic analysis of the Ch_1 gene.

(14 monosomic lines corresponding to 1A-7B chromosomes were used)

RESULTS AND DISCUSSION

In 1973, segregation of normal and chlorotic plants was expected, because the female parents were heterozygous for the Ch_2 and ch_2 genes. The ratios actually ob-

Table 1. Segregation of normal and chlorotic plants in 14 monosomic lines of the crosses, (Chinese Spring monosomics × NIG 4) mono-F₁s × NIG 7

Line	No. of progenies	No. of plants		χ^2 -value (1:1)
		Normal	Chlorotic	
Mono-1A	3	33	33	0.00
" 2A	3	25	24	0.02
" 3A	3	30	31	0.02
" 4A	3	29	40	1.75
" 5A	3	23	26	0.18
" 6A	3	40	34	0.49
" 7A	3	36	31	0.37
" 1B	2	16	20	0.44
" 2B	3	25	38	2.68
" 3B	3	18	39	7.74**
" 4B	3	30	37	0.73
" 5B	3	40	25	3.46
" 6B	3	44	34	1.28
" 7B	3	31	31	0.00
Total	41	420	443	0.61
χ^2 for heterogeneity ($df=13$)				18.56

** : Significant at the 1% level.

tained are shown in Table 1.

All monosomic lines, except Mono-3B, showed the expected 1:1 ratio. Mono-3B produced chlorotic plants in excess. However, a test of the heterogeneity among the 14 monosomic lines indicated no heterogeneity. Therefore, we believe that the deviation of the segregation ratio observed in Mono-3B is due to a sampling error.

From the final test-cross, the results summarized in Table 2 were obtained. As the control, eight progenies of the disomic line were tested and showed the expected 1:1 ratio of normal and chlorotic plants. Eleven monosomic lines also fitted this ratio while Mono-2A, -3A and -4B showed significant deviations. The deviation found in Mono-2A was extreme, the chlorotic plants occupying 86% of the total. A test of heterogeneity among all the lines examined revealed a highly significant heterogeneity of the segregation ratio. On the other hand, the heterogeneity became negligible when Mono-2A was excluded from the test. From factorial analysis, it is known that a single gene (Ch_1) in the A or B genome complements the Ch_2 gene in the D genome. From this information, we draw the definite conclusion that the Ch_1 gene is located on chromosome 2A.

In the experiment of Hermsen and Waninge (1972), a similar monosomic analysis design was used to locate this gene. However, in the final test-cross, they used pheno-

Table 2. Segregation of normal and chlorotic plants in 14 monosomic lines and in the disomic line after the final test-cross shown in Fig. 1

Line	No. of progenies	No. of plants			χ^2 -value (1:1)
		Total	Normal	Chlorotic	
Disomic	8	201	100	101	0.01
Mono-1A	3	65	29	36	0.75
" 2A	3	103	16	87	48.94**
" 3A	2	45	15	30	5.00*
" 4A	3	75	33	42	1.08
" 5A	3	95	43	52	0.85
" 6A	3	92	52	40	1.57
" 7A	3	92	48	44	0.17
" 1B	3	83	50	33	3.48
" 2B	3	70	35	35	0.00
" 3B	3	82	46	36	1.22
" 4B	3	92	57	35	5.26*
" 5B	3	93	53	40	1.82
" 6B	3	73	35	38	0.12
" 7B	3	60	27	33	0.60
Total	49	1,321	639	682	1.40
Total except Mono-2A	46	1,218	623	595	0.64
χ^2 for heterogeneity ($df=14$)					69.48**
χ^2 for heterogeneity except Mono-2A ($df=13$)					21.29

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

typically normal monosomics as the females to cross with Chinese Spring. In this cross, the normal ($n=21$) and chromosome deficient ($n=20$) gametes will be fertilized in the approximate ratio of 1:3. Consequently, about a 1:3 ratio of normal and chlorotic plants will be obtained by the test-cross. In contrast, the test-cross was carried out in the opposite direction in the present investigation, i.e. monosomic plants were used as the pollen parent. Since there is a great advantage of the normal pollen over the chromosome deficient type in fertilization, the segregation of normal and chlorotic plants in the test-cross should deviate from the 1:1 ratio, probably approaching a ratio of 1:9 even when 10% of the egg cells (a slight overestimation of the real frequency) is fertilized by the chromosome deficient pollen grains. Therefore, the author's design for monosomic analysis is more critical than that adopted by Hermesen and Waninge (1972).

Though this analytical difference existed in the procedure adopted, the present investigation confirmed the results of previous workers on the location of the Ch_1 gene.

SUMMARY

Monosomic analysis was carried out to locate one (Ch_1 gene) of the two complementary genes controlling the hybrid chlorosis type 1 in wheat. The result revealed that the Ch_1 gene is located on chromosome 2A; thus, confirming the previous report of Hermesen and Waninge (1972) based on a slightly different procedure.

LITERATURE CITED

- Hermesen, J. G. Th., 1966 Hybrid necrosis and red chlorosis in wheat. Proc. II Int. Wheat Genet. Symp. Hereditas Suppl. 2: 439-452.
- Hermesen, J. G. Th., and J. Waninge, 1972 Attempts to localize the gene Ch_1 for hybrid chlorosis in wheat. Euphytica 21: 204-208.
- Nishikawa, K., 1964 Further proof that Type 1 necrosis is controlled by the Ne -genetic system. Ann. Rep. Nat. Inst. Genet. Japan 41: 61.
- Tsunewaki, K., 1966 Gene analysis on chlorosis of the hybrid, *Triticum aestivum* var. Chinese Spring \times *T. macha* var. *subletschchumicum*, and its bearing on the genetic basis of necrosis and chlorosis. Japan. J. Genetics 41: 413-426.
- Tsunewaki, K., and H. Kihara, 1961 F_1 monosomic analysis of *Triticum macha*. Wheat Inf. Serv. 12: 1-3.