

GENETICAL ANALYSIS OF RYE (*SECALE CEREALE* L.)

I. RESULTS OF GENE LOCALIZATION ON RYE CHROMOSOMES USING-
PRIMARY TRISOMICS¹

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Summary. By trisomic analyses six genes of rye were localized on chromosomes. "Anthocyanless" (*an*) lies on chromosome 7R, "hairy peduncle" (*Hp*) on chromosome 5R, the compactum gene of "Moskowskij Karlik" (*cp*₄) and the dominant dwarf gene of "EM-1" (*Dw*₁) both on chromosome 3R and the genes of the dominant dwarf Type "K 10028" (*Dw*₂) and the compactum type "Gülzow kurz" (*cp*₃) both on chromosome 2R.

In comparison to other cereals only few informations are known about gene localization in rye. Communications were published for example by Riley and Chapman (1958), Sybenga and Wolters (1972) and Chang (1975). One method to localize genes is the trisomic analysis. Sets of trisomics were described by Kamanoi and Jenkins (1962), Balkandschiewa (1971), Zeller et al. (1977), Pilch (1978), Sturm (1978) and Kedrov-Zichman (1979), but trisomic analyses were carried out by the set of Sturm (1978) only. A short review and further results are presented in this paper.

MATERIAL AND METHODS

Using the trisomic set of the rye variety "Esto" first results were published by Sturm (1978) about mapping of genes. This trisomic set contains all possible trisomics with exception of 2R. At first we localized the gene "anthocyanless" in caryopses, coleoptils and nodes, the recessive short straw compactum genes "Moskowskij Karlik" and "Gülzow kurz", the dominant dwarf types "EM-1" and "K 10028" and the gene "hairy peduncle".

By using the trisomic lines as female parents and the testers as pollinators the *F*₁-progenies were selected from heterozygous trisomics by definition the number of chromosomes in root tops. These trisomics were pooled and grown in isolation for

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each line, while the F_2 -progenies were analysed for segregation in the disomic part for each line. In the case of recessive inheritance a segregation of 8 : 1 will be expected for the specific line of the trisomic set on which the gene is localized. If there takes place a dominant inheritance the segregation has the ratio of 5 : 4. The observed values were proved with Chi^2 -test against the 3 : 1 segregation in the case of crossing with trisomics in which the gene was not localized on extra chromosomes (Ta-

Table 1. Genetics of trisomic analyses in the case of sister pollination
 aa — recessive, — dominant Aa , AA

1. Dominant inheritance

Gene on extra chromosome		Gene not on extra chromosome																									
Parents:	$aaa \times AA$	$aa \times AA$																									
F_1 -plants:	Aaa	Aa																									
F_1 -gamets:	A, a, a, Aa, Aa, aa	A, a																									
F_2 -plants:	<table border="1" style="display: inline-table; vertical-align: middle;"> <tr><td></td><td>A</td><td>a</td><td>a</td></tr> <tr><td>A</td><td>AA</td><td>Aa</td><td>Aa</td></tr> <tr><td>a</td><td>Aa</td><td>aa</td><td>aa</td></tr> <tr><td>a</td><td>Aa</td><td>aa</td><td>aa</td></tr> </table>		A	a	a	A	AA	Aa	Aa	a	Aa	aa	aa	a	Aa	aa	aa	<table border="1" style="display: inline-table; vertical-align: middle;"> <tr><td></td><td>A</td><td>a</td></tr> <tr><td>A</td><td>AA</td><td>Aa</td></tr> <tr><td>a</td><td>Aa</td><td>aa</td></tr> </table>		A	a	A	AA	Aa	a	Aa	aa
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A	AA	Aa	Aa																								
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a	Aa	aa																									
of the disomic fraction:																											
Segregation:	5:4	3:1																									

2. Recessive inheritance

Gene on extra chromosome		Gene not on extra chromosome																									
Parents:	$AAA \times aa$	$AA \times aa$																									
F_1 -plants:	AAa	Aa																									
F_1 -gamets:	A, A, a, AA, Aa, Aa	a, A																									
F_2 -plants:	<table border="1" style="display: inline-table; vertical-align: middle;"> <tr><td></td><td>A</td><td>A</td><td>a</td></tr> <tr><td>A</td><td>AA</td><td>AA</td><td>Aa</td></tr> <tr><td>A</td><td>AA</td><td>AA</td><td>Aa</td></tr> <tr><td>a</td><td>Aa</td><td>Aa</td><td>aa</td></tr> </table>		A	A	a	A	AA	AA	Aa	A	AA	AA	Aa	a	Aa	Aa	aa	<table border="1" style="display: inline-table; vertical-align: middle;"> <tr><td></td><td>A</td><td>a</td></tr> <tr><td>A</td><td>AA</td><td>Aa</td></tr> <tr><td>a</td><td>AA</td><td>aa</td></tr> </table>		A	a	A	AA	Aa	a	AA	aa
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	A	a																									
A	AA	Aa																									
a	AA	aa																									
of the disomic fraction:																											
Segregation:	8:1	3:1																									

Table 2. Adaption of chromosome nomenclature of the trisomic sets "Esto" and "Danae" to the international nomenclature system (Schlegel 1983)

International system	Trisomic sets	
	"Esto" (Sturm 1978)	"Danae" (Balkandschlewa 1971)
1R	G	VII
2R	A	I
3R	B	II
4R	D	IV
5R	E	V
6R	F	VI
7R	C	III

ble 1). The nomenclature of rye chromosomes was determined by the First International Workshop-Meeting of Rye Cytogenetics in Wageningen (Netherlands) 1982. The present condition of the adaption is represented in Table 2.

RESULTS AND DISCUSSION

The dominant dwarf gene of "EM-1" and the recessive compactum gene of "Moskowskij Karlik" are located on chromosome 3R (Sturm and Engel 1980, Sturm and Müller 1982). The gene of "Moskowskij Karlik" was named cp_4 . The gene which expresses anthocyanin was localized on chromosome 7R (Sturm et al. 1981). This result corresponds to the gene an described by Sybenga (1982). The gene "hairy peduncle" (Hp) lies on chromosome 5R (Table 3). This result agrees with the localization of Chang (1975). On the other hand it was not possible to localize the genes of "K 10028" and "Gülzow kurz" (Tables 4 and 5).

Table 3. F_2 -segregation of a cross trisomic line 5R × "hairy peduncle"
Hp ($\alpha=5\%$; $Chi^2=3.84$)

Line	No.	Observed segregation		Index	Chi^2 -test	
		hairy	normal		3:1	5:4
5R	191	118	73	1.6	33.1	3.05

Table 4. F_2 -segregations of crosses trisomics × recessive compactum type "Gülzow kurz"
 cp_3 ($\alpha=5\%$; $Chi^2=3.84$)

Line	No.	Observed segregat.		Index	Chi^2 -test	
		normal	compact		3:1	8:1
1R	227	171	56	3.0:1	0.02	43.19
3R	99	75	24	3.0:1	0.05	17.28
4R	149	121	28	4.3:1	2.91	8.03
5R	147	122	25	4.5:1	3.07	7.49
6R	142	113	29	3.9:1	1.37	11.90
7R	151	119	32	3.7:1	1.27	14.92

Table 5. F_2 -segregations of crosses trisomics × dominant dwarf type "K 10028"
 Dw_2 ($\alpha=5\%$; $Chi^2=3.84$)

Line	No.	Observed segregations		Index	Chi^2 -test	
		normal	dwarf		1:3	4:5
1R	102	28	74	1:2.8	0.32	11.49
3R*	50	16	34	1:2.1	1.31	2.92
4R	109	33	76	1:2.3	1.77	8.38
5R	102	28	74	1:2.6	0.32	11.49
6R	277	80	197	1:2.4	2.33	27.04
7R	110	21	89	1:4.2	2.05	28.85

* There is no linkage between the genes of "EM-1" and "K 10028"

That means, that these loci are on chromosome $2R$, which is absent in the set. The dominant dwarf genes of "EM-1" and "K 10028" were named Dw_1 and Dw_2 , respectively.

The localization of genes makes it possible to definite markers, which are linked to factors with high value for breeding purposes. There is a chance to reach a higher level of breeding effectivity by using the results described in this publication.

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ANALIZA GENETYCZNA ŻYTA (*SECALE CEREALE* L.)

I. WYNIKI LOKALIZACJI GENÓW W CHROMOSOMACH ŻYTA Z ZASTOSOWANIEM TRISOMIKÓW PIERWOTNYCH

Streszczenie

Zastosowano metodę analizy trisomicznej do lokalizacji genów w chromosomach u żyta. Określono, że gen „bezantocyjanowe” (*an*) znajduje się w chromosomie $7R$, gen omszenia dokłosa (*Hp*) na chromosomie $5R$, gen compactum typu „Moskowskij Karlik” (cp_4) i dominujący karłowatości „EM-1” (Dw_1) na chromosomie $3R$, gen dominujący karłowatości „K 10028” (Dw_2) i compactum typu „Gülzow kurz” (cp_3) w chromosomie $2R$.

ГЕНЕТИЧЕСКИЙ АНАЛИЗ РЖИ (*SECALE CEREALE* L.)
I. РЕЗУЛЬТАТЫ ЛОКАЛИЗАЦИИ ГЕНОВ НА ХРОМОСОМАХ
РЖИ С ПОМОЩЬЮ ПЕРВИЧНЫХ ТРИСОМИКОВ

Резюме

С помощью трисомических анализов шесть генов ржи были локализованы на хромосомах. Ген „anthocyanless” (*an*) лежит на хромосоме 7R, ген „hairy peduncle” (*Hp*) — на хромосоме 5R, компактный ген „Московского Карлика” (*cp₁*) и доминантный карликовый ген „ЕМ-1” (*Dw₁*) — на хромосоме 3R, а гены доминантного карликового типа „К 10028” (*Dw₂*) и типа компактный „Gülzow kurz” (*cp₂*) — на хромосоме 2R.