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Three-point tests on barley chromosome 1.

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In a previous paper (Søgaard, 1974) a linkage map of chromosome 1 comprising the five genes cer-f, ac_2, ert-d, ert-a and ert-m has been reported. In all three-point tests involving these genes, negative interference was found. This result was surprising. The three tests have been repeated and confirmed the occurrence of negative interference in this region of chromosome 1 ($\gamma = 10.5$; 2.6; 3.4).

In order to investigate whether negative interference is a common characteristic for chromosome 1, a different region on chromosome 1 has been studied by two three-point tests. These two tests comprised the four genes cer-a, br, fc and yc, and normal positive interference was obtained ($\gamma = 0.4$; 0.6).

The combinations in the five crosses were as follows:

	markers in parent 1		marker in parent 2
cross number	m	c	r
1	ert-d	cer-f	ac_2
2	ert-m	cer-f	ac_2
3	ert-a	cer-f	ac_2
4	br	cer-a	yc
5	br	cer-a	fc

The letters m and c designate the markers which are in coupling, and r designates the marker which is in repulsion with respect to m and c. The observed number of plants in the 18 viable genotype classes of the three-point tests numbers 1-4 and in 27 viable genotype classes in test number 5 are listed in Table 1. In test number 5, plants homozygous for fc are of poor viability in mixed stands with phenotypically normal plants. Only 205 of the 275 chlorina plants in the F_2 generation reached maturity and could be tested in F_3. Assuming equal lethality in all nine fcfc genotypes, the distribution of the 275 chlorina plants can be calculated and is given in parenthesis in Table 1.

From the data in Table 1, the order of the loci in each cross was determined and the recombination percentages were calculated (Figure 1). A linkage map comprising the 9 genes is given in Figure 2.

The details of the analysis are published in:

Søgaard, B., 1977: The localization of eceriferum loci in barley. V. Three-point tests of genes on chromosome 1 and 3. Carlsberg Res. Commun. 42, 67-75.

Table 1. Observed number of F_2 plants.

M = wild type allele; m = the mutant allele which is in coupling with c
C = " " " ; c = " " " " " " " " m
R = " " " ; r = " " " in repulsion to m and c

Data in parenthesis under test 5 refer to the number of plants after correction.

	Test number					
Genotype	1	2	3	4	5	
MmCcRr	824	547	504	309	415	
mmccRR	409	270	248	127	197	
MMCCrr	-	-	-	-	153	(205)
MmCCrr	-	-	-	-	34	(52)
MmccRR	17	83	48	45	58	
MMCcRr	18	83	46	48	59	
mmCcRr	23	81	48	40	56	
mmccRr	4	5	7	93	15	
MMCCRr	7	4	2	97	18	
MmCcRR	5	6	4	102	19	
MmCcrr	-	-	-	-	9	(14)
MMCcrr	-	-	-	-	1	(1)
mmCcRR	20	11	12	10	2	
MmCCRr	19	15	16	27	4	
MmccRr	22	13	14	26	4	
MMCcRR	0	0	0	16	2	
mmCcrr	-	-	-	-	1	(1)
mmCCrr	-	-	-	-	1	(2)
MMccRR	0	5	6	2	6	(0)
mmccrr	-	-	-	-	0	
MMCCRR	0	0	0	18	0	
mmCCRr	0	0	0	0	0	
MMccRr	0	1	2	2	0	
MmCCRR	0	0	0	3	0	
Mmccrr	-	-	-	-	0	(0)
mmCCRR	0	0	0	1	0	
MMccrr	-	-	-	-	0	(0)

References:

Søgaard, B., 1974: The localization of eceriferum loci in barley. III. Three-point tests of genes on chromosome 1 in barley. Hereditas 76, 41-48.

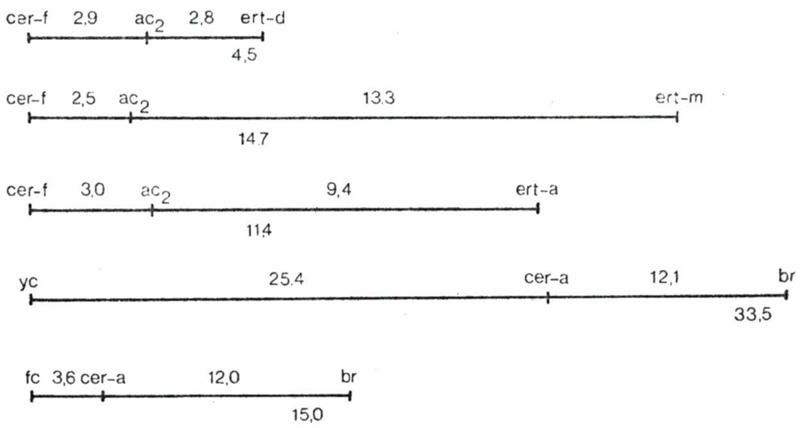

Figure 1. Distances between the marker genes in the five three-point tests

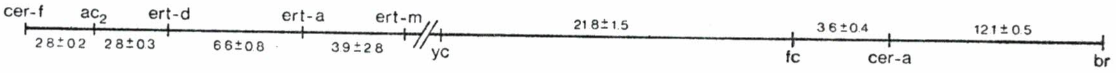

Figure 2. Sequence, distances and standard deviations in chromosome 1