Kølmark, H. G. Linkage data for two "reose loci in linkage group V of Neurospora crassa.

The isolation of "reose defective mutants was reported previously (Kølmark 1965 Neurospora Newsl. 8: 6). The results presented here summarize linkage data, mostly of random spore isolations from 2-, 3-, and 4-point crosses with linked morken. As genetic symbol for "reose defective mutants, ure is "red here. The two mutants described ore desigmted as "re-1 (9) and ure-2 (47), where the hyphenated figures are locus numbers and the figures in parenthesis ore the original isolation numbers, now used as allelic designations (see note by Kølmark, this issue of Neurospora Newsl.).

The linkage group was first established as VR for bath of the ure mutants in crosses to bis (C-1810-1). The positions were then more precisely determined in crosses with sp (8 132), inos (37401), am (32213, 47305, and 52949) and hist-1 (C91). Both of the "reose mutants are closely linked to the am and hist-1 loci, and through 3-point analysis it was found that they ore located at opposite sides of am. Subsequently it was found that ure-1 and ure-2 complement in heterocaryons, giving a urease-positive mycelium. They also recombine in crosses to produce urease-positive offspring. Since each mutant is non-leaky, it appears that some combination of gene products (polypeptides) is a prerequisite for on active "reose enzyme, the system thus providing on example of a "two genes one enzyme" relationship.

Table 1. Summary of linkage data from 29 crosses involving markers in the region of linkage group VR where we-1 and ure-2 ore situated.

Recombinant loci		Number of crosses	Recombinants		Total	
			Total	%;map "nits	Tested	% Germination
Centr.	ure-2	5	134	27.9	480	72.0
Centr.	ure-1	1	68	29.8	228	80.0
sp	ure-1	1	13	9.2	141	94.0
ure-2	am (32213)	3	16	1.5	1055	67.5
ure-2	ure-1	3	28	3.1	891	79.0
ure-2	hist-1	4	60	4.1	1471	71.4
ure-2	inos	2	14	12.1	116	58.0
ure-2	bis	2	59	14.2	416	68.3
am (32213)	ure-1	3	7	1.1	629	61.2
am (47305)	ure-1	1	3	4.1	72	72.0
am (52949)	"re-1	1	6	1.2	489	98.0
am (322 13)	hist-1	8	91	3.9	2346	68.0
am (32213)	inos	1	5	7.2	69	69.0
am (47305)	inos	1	7	7.2	98	98.0
am (52949)	inos	1	8	8.8	91	91.0
ure-1	hist-1	3	11	4.1	780	61.5
ure-1	inos	1	13	5.6	231	92.5
ure-1	bis	3	72	9.0	803	89.3

All isolations were random, except those from which centromere distances were obtoined. The crosses include seventeen 2-point, nine 3-point ond three 4-point. Individual pairwise mop distances were obtained by summation of recombinants and number tested from crosses where the respective two markers were segregating.

The linkage data ore presented in Table 1 ond the relevant mop positions ore drown in Figure 1. The close positions of one ure locus on each side of the om locus seems interesting, and raises the question as to whether there three genes belong to a common operon. Urease, controlled by the ure loci, produces ommonio by its enzymatic *action*, while *glutamic* acid *dehydrogenase*, controlled by am, consumes ammonia by its action (see: Fincham and Day 1963 Fungal Genetics, p. 176. Blackwell Scientific Publications, Oxford). A coordinated control of the production of these enzymes would seem to be of advantage for the organism.

A detailed account of the ure mutants will be published elsewhere. This work was supported by grants from the Swedish Research Council.

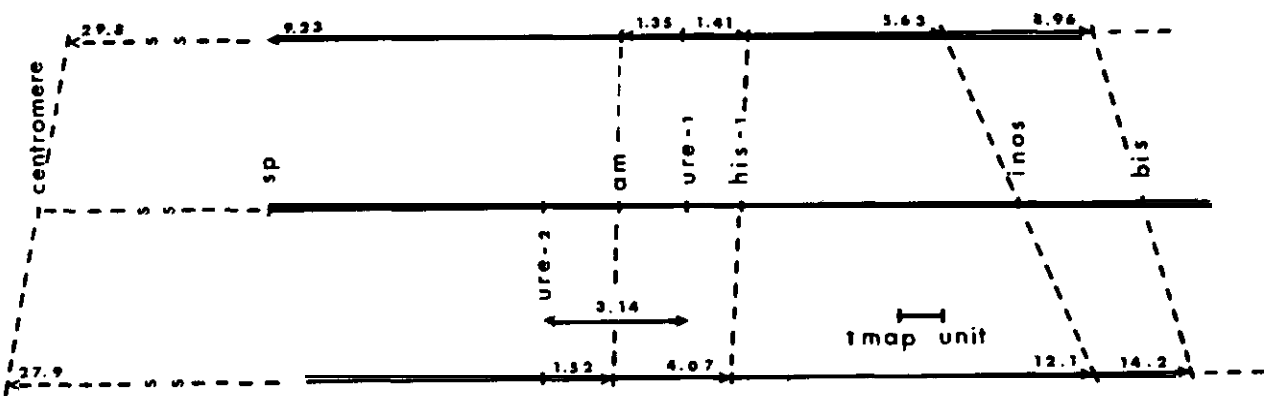

Figure 1. Map distances of group VR morken in relation to "re-1 and "re-2. Top line: Data from crosser with ure-1. All distances measured from the "re-1 position. Lower line: Data from crosses with "re-2. All distances measured from the ure-2 position. Middle line: Relative positions of "re-1 ond ure-2, and graphical mean positions of the various markers as determined from crosses with both ure-1 and ure-2.

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