

LINKAGE DATA

Cameron, H. R. Location of round spore (R), a dominant ascospore marker.

A mutant (R) producing round ascospores was reported by Mary Mitchell (1966 N.N.#10:6). When this mutant is carried by the fertilizing parent, all of the f₁ ascospores will be round (R has failed to function as a protoperithecial parent). Outcrosses of the f₁ to

wild type segregate in a 1:1 ratio for R. Calculations of second division segregation, based on unpublished data from Mary Mitchell, indicate on approximate distance of 33 units from centromere.

Round spore has not shown linkage with any of the seven reported linkage groups when tested with markers located near centromeres. Since R appeared to be well distal to centromere it was crossed to various outside markers. Use of the alcoy linkage testers suggested linkage to IR or IIR and a location of 38 units to the right or left of breakpoint. Succeeding crosses established the location of R on the right arm of linkage group I (Table 1).

Table 1. Map distances for R.

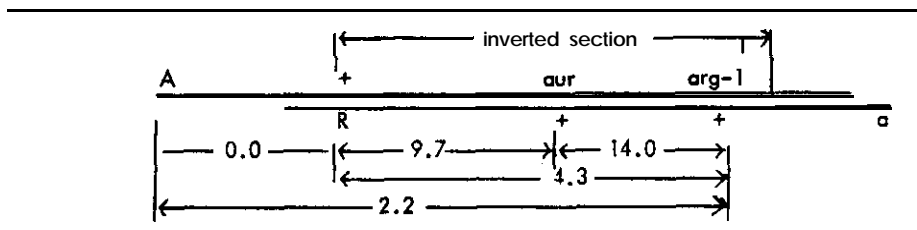
Zygote genotype and recombination percentage	Germination percentage
$\begin{array}{c} \text{al} \quad + \\ + \quad 42.9 \quad \text{R} \end{array}$	57.0
$\begin{array}{c} \text{A} \quad \text{al} \quad + \\ \text{a} \quad + \quad 38.0 \quad \text{R} \\ \leftarrow 53.6 \quad \quad \quad \rightarrow \end{array}$	74.0
$\begin{array}{c} \text{A} \quad \text{our} \quad + \\ 0 \quad + \quad 44.6 \quad \text{R} \\ \leftarrow 52.2 \quad \quad \quad \rightarrow \end{array}$	78.5
$\begin{array}{c} \text{aur} \quad \text{os} \quad + \\ + \quad 19.5 \quad 17.1 \quad \text{R} \\ \leftarrow 36.6 \quad \rightarrow \end{array}$	88.0
$\begin{array}{c} \text{aur} \quad \quad \text{nic-1} \quad \quad \text{os} \quad + \\ + \quad 5.2 \quad + \quad 19.8 \quad + \quad 23.2 \quad \text{R} \\ \quad \quad \quad \leftarrow 33.9 \quad \rightarrow \end{array}$	37.3

The following recombination percentages were obtained (Fig. 1) using on inversion (Newmeyer 1965 Genetics 52: 462) with the left break between arg-1 and mating type (A/a) and the right break distal to osmotic (os). Only the non-dark agar (DA) isolates were included. Dark agar mutants are the result of a viable duplication-deficiency class and were scored separately.

From the 4 point data (Table 1) round spore appears to be well out on the right arm of linkage group 1 and not near the mating type locus. From the non-dark agar data R must be near one of the breakpoints and since it is not near mating type it must be near the right break point. The low value for crossovers between R and arg-1 is because these are usually single crossovers in the inversion and therefore result in either DA's or inviable spores.

Conversely the DA's would be expected to result from single crossovers in the inversion and therefore usually be recombinants between R and arg-1. Indeed 16 out of 17 DA were crossovers between arg-1 and R.

Figure 1. Results of crossing R with pericentric inversion a/.



From the above data it appears that R is located about 20-25 units to the right of os. This would place R very close to so (Perkins 1959 Genetics 44: 1185). Four attempted reciprocal crosses with so have failed to produce perithecia.

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