Smith, B. R. The location of 11 am alleles in linkage group 5.

Analyses of random spores from crosses of the form

$$\frac{+ \quad am \quad +}{sp \quad + \quad inos}$$

were made to test the assumption that all 11 am alleles were located between spray (sp) and inositol (inos) in linkage group 5. The mutants used in these crosses were, sp B132, inos 37401, am am^1 am^2 am^3 am^4 am^5 am^6 am^7 am^8 am^9 am^{11} am^{211}.

Spores from the crosses were classified for the spray phenotype after 16 hours incubation on four selective media. (Table 1). The total viability for each cross was estimated on minimal medium supplemented with alanine and inositol. Sufficient spores were classified to ensure that a population of about 1000 viable spores were classified on each selective medium.

Table 1 shows the types of medium used, the spore types capable of growing on each and the proportions of sp, wild type and non-growing spores on each type of plate. The proportions given are those expected if P is the percentage of spores resulting from a single crossover between am and inos, Q is the percentage of spores resulting from a single crossover between sp and am and R is the percentage of spores resulting from a double crossover, one between sp and am and one between am and inos.

Table 2 gives experimental results expressed as percentages of a population of 1000 and calculated values for P, Q and R. In addition, values for the coefficient of coincidence and map distances are given.

TABLE 1

Spore genotype			Proportions	Vogels medium + alanine	Vogels medium + glycine	Vogels medium + glycine + inositol
+	am	+	} 100 (P+Q+R)	wild	–	–
sp	+	inos		–	–	spray
+	am	inos	} P	–	–	–
sp	+	+		spray	spray	spray
+	+	inos	} Q	–	–	wild
sp	am	+		spray	–	–
+	+	+	} R	wild	wild	wild
sp	am	inos		–	–	–
% sp colonies				$\frac{P+Q}{2}$	$\frac{P}{2}$	$\frac{100-(Q+R)}{2}$
% wild type colonies				$\frac{100-(P+Q)}{2}$	$\frac{R}{2}$	$\frac{Q+R}{2}$
% ungrown spores				50	$\frac{100-(P+R)}{2}$	50

TABLE 2

Cross	% viability estimated on minimal + alanine + inositol	Minimal + alanine % spray colonies $\frac{P+Q}{2}$	Minimal + glycine + inositol % wild type colonies $\frac{Q+R}{2}$	Minimal + glycine % wild type colonies $\frac{R}{2}$	Minimal + glycine % spray colonies $\frac{P}{2}$	P	Q	R	Co-efficient of Coincidence
$+ \quad am^1 \quad +$ / $sp \quad + \quad inos$ / 7.9 8.4	81.1	8.2	3.3	0.3	3.9	7.8	7.3	0.6	0.99
$+ \quad am^2 \quad +$ / $sp \quad + \quad inos$ / 5.3 4.6	97.8	3.8	3.6	0.1	2.2	4.4	5.1	0.2	0.82
$+ \quad am^3 \quad +$ / $sp \quad + \quad inos$ / 4.3 5.4	94.34	4.9	2.0	0.1	2.6	5.2	4.1	0.2	0.862
$+ \quad am^4 \quad +$ / $sp \quad + \quad inos$ / 5.1 5.4	84.8	5.0	2.6	0.1	2.6	5.2	4.9	0.2	0.727
$+ \quad am^5 \quad +$ / $sp \quad + \quad inos$ / 3.5 4.6	92.51	3.9	1.7	0.1	2.2	4.4	3.3	0.2	1.24
$+ \quad am^6 \quad +$ / $sp \quad + \quad inos$ / 4.0 4.8	87.9	4.1	2.1	0.1	2.3	4.6	3.8	0.2	1.04
$+ \quad am^7 \quad +$ / $sp \quad + \quad inos$ / 7.8 8.8	87.49	8.1	3.5	0.3	4.1	8.2	7.2	0.6	0.874
$+ \quad am^8 \quad +$ / $sp \quad + \quad inos$ / 4.8 8.0	92.68	6.3	2.3	0.1	3.9	7.8	4.6	0.2	0.52
$+ \quad am^9 \quad +$ / $sp \quad + \quad inos$ / 3.0 4.0	73.41	3.6	1.4	0.0	2.0	4.0	3.0	0.0	0.0
$+ \quad am^{11} \quad +$ / $sp \quad + \quad inos$ / 5.1 8.0	91.16	6.4	2.3	0.2	3.8	7.6	4.7	0.4	0.98
$+ \quad am^{211} \quad +$ / $sp \quad + \quad inos$ / 7.0 7.2	98.14	6.5	3.7	0.2	3.4	6.8	6.6	0.4	0.75

Per cent of germinated spores

The recombination values vary considerably from cross to cross but it is noticeable that the relative position of the _am_ alleles between _sp_ and _inos_ is remarkably constant. The average map distances for all the alleles are, _sp_ 5.3 _am_ 6.3 inos. Individual values for the coefficient of coincidence, being based on populations of 1000, are not accurate, but the average value, 0.8, is a fair indication of the intensity of positive interference in this region.