The resistance genes were derived from samples of the International Rust Monogenic lines developed by Hooker and supplied by Dr. K. S. McWhirter. All lines carrying a gene for resistance were homozygous for the $\underline{Cx-F}$ allele of catechol oxidase. Six of those lines showing resistance to the local rust strain were crossed and backcrossed reciprocally to the two null lines, P3 and P4. If CX activity is a necessary component of the resistance mechanism then only 25% of the backcross progeny will carry the gene for resistance with an active CX and will show resistance. Conversely, if CX is not involved, 50% of the progeny will be resistant and 50% susceptible. The results are presented in Table 1 and indicate 50% resistant progeny for all alleles and the three loci tested. This result indicates that CX is not involved with the expression of resistance with one reservation. This would arise if the genes for resistance and CX were tightly Rp, Rp5 and Cx are on chromosome 10 but should be some 33 recombination units apart (\overline{Rp} is at position 0 and \overline{Cx} is very close (<0.2% recombination) to dull endosperm (\underline{du}) at position 33). $\underline{Rp4}$ is unlinked on chromosome 4. For reasons mentioned previously (Pryor and Schwartz 1973) it was not possible to assay unambiguously for resistance and catechol oxidase in the same plants. Thus, seedlings from the backcross involving the $\underline{\mathsf{Rp-g}}$ gene were grown to maturity and the selfed progeny were scored for Cx genotype:

Recombination between \underline{Rp} and \underline{Cx} is estimated at 34%. But, more significantly, 6 of 14 resistant plants were also homozygous for the null gene $(C\tilde{x}-N)$ for catechol oxidase.

Conclusion: Catechol oxidase activity is not required for the expression of genes for resistance to rust.

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Genetics of fertility restoration for male sterile cytoplasms

Crosses were made between homozygous male sterile (rf rf) and homozygous restored (Rf Rf) plants to produce a series of plants heterozygous for the pollenrestoring genes (Rf rf) for each of 26 different sources of cytoplasmic male sterility. These heterozygous F_1 plants were crossed onto their respective cytoplasmic male sterile parent; Table 1 presents the data on the number of fertile versus sterile plants in each backcross. All of the cms-S type cytoplasms and cms-K, -L, -B, and -D (which are similar to cms-S but have shown some fertility restoration differences) gave no sterile plants. Therefore, all of the cms-S type cytoplasms exhibited gametophytic restoration in which the recessive (\underline{rf}) fertility restoration alleles produced by the Rf rf parent were not functional. The cms-T cytoplasms gave the 1:1 ratio between fertile and sterile plants expected of the sporophytic type of fertility restoration in which both rf as well as Rf pollen grains are functional. The cms-C type cytoplasms also follow the sporophytic pattern of restoration.

Table 1. Ratio of fertile and male sterile plants from the backcross of heterozygous (Rf rf) F₁s to homozygous (rf rf) parental cytoplasmic male sterile lines.

Cytoplasm	Reaction Type	Fertile	Male Sterile
T	sporophytic	20	23
Р	"	17	25
RS	ti	22	16
Q	18	21	19
нА	it .	21	25
С	11	23	24
RB	11	14	11
S	gametophytic	38	0
S G	11	38	0
I J	11	32	0
	11	36	0
М	11	35	0
R	it	23	0
ML	11	50	0
VG	If	36	0
H	l)	30	0
EK	U	36	0
IA	ll .	36	1
MY	Bt .	38	0
PS	11	37	0
SD	11	40	0
TA	II	25	0
K	16	37	0
L	II	45	0
В	It	33	0
D	II	35	Ō

Although all of the <u>cms-S</u> group of cytoplasms show the gametophytic type of restoration and exhibit similar patterns of fertility restoration reactions, we have observed a number of exceptional reactions within the <u>cms-S</u> group (Gracen and Grogan, Agron. J. 66:654, 1974), which seem to be due to the involvement of genes other than <u>Rf3</u>. Studies are underway to determine whether other alleles are involved in <u>cms-S</u> restoration or whether the exceptional reactions observed result from the differential action of modifying genes which control the degree of fertility restoration (full versus partial) of <u>cms-S</u> cytoplasms in different environments.

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