The genetics of *Phytophthora dreschleri*

D. SHAW, B. JANSSEN and I. KHAKI
School of Plant Biology
University College of North Wales
Bangor (U.K.)

I. THE GENETICS OF DRUG RESISTANCE

Mutants resistant to *p*-fluorophenylalanine (*p*-fp) and chloramphenicol were selected from the wild type isolates 6503 and 6500. The sensitivity of zoospores to the mutagens UV, ethylmethane sulphanate, EMS and nitrosoguanidine was tested and kill curves are shown in figure 1. The plateau on the UV kill curve, figure 1A, is thought to be due to the presence of a small proportion of more resistant binucleate spores. Mutants used in matings and their origin are shown in Table I. F_1 progeny of matings to wild type were all resistant whereas progeny from backcrosses to the sensitive parent segregated into equal frequencies of resistant and sensitive phenotypes. F2 progeny segregated into 3 resistant : 1 sensitive. Clearly this pattern of inheritance is to be expected if the organism is diploid. This working hypothesis of diploidy is further strengthened by finding that backcrosses of F2 to the sensitive parent segregate 1:1.

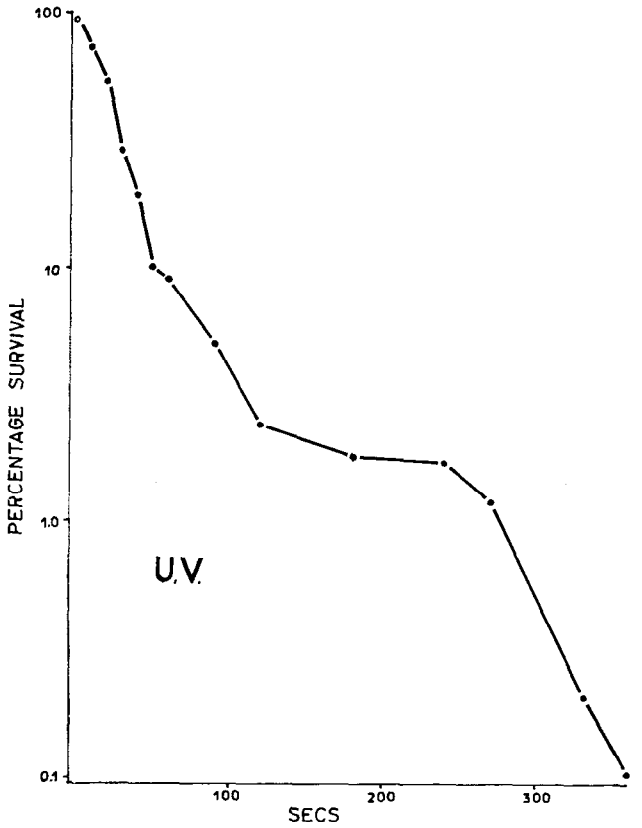

Fig. 1A.

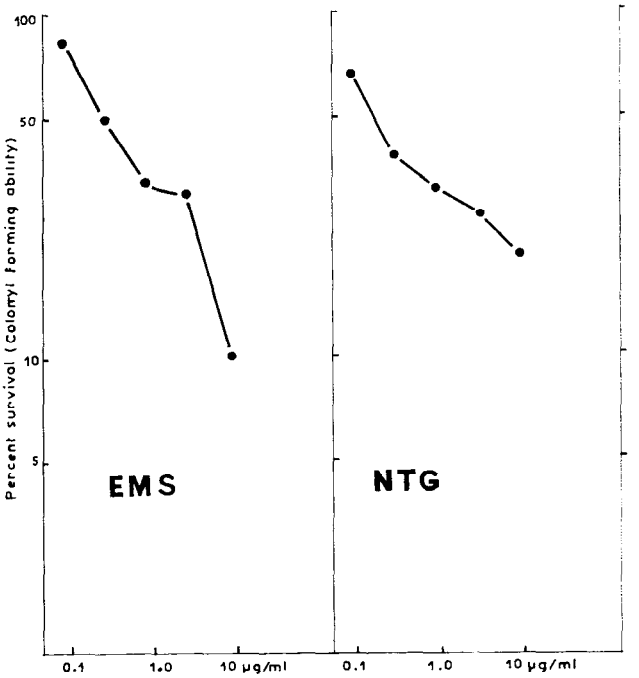

Fig. 1B.

Kill curved of zoospores exposed to different doses of mutagen.

TABLE I

CROSSES BETWEEN RESISTANT MUTANTS, SENSITIVE WILD TYPES AND THEIR PROGENY

Mutant	Derived from	Resistant to (μg/ml)	Origin	Mating	Progeny R:S or R:I:S	Mating type of progeny				Germination of oospores %
						A^1	A^2	Neuter	A^1A^2	
FA1	6503	100 *p*-fp	Spontaneous (zoospore)	×6500	125:0	—	—	—	—	100
				F1 ×6500	68:57					100
				F1 ×FA1	65:0					100
				F1 ×F1	35:11					—
FA4	6500	100 *p*-fp	Spontaneous (sector)	×6503	?	0	48	9		100
				F1 ×6503	0:14:20					?
				F1 ×FA4	0:37:11					100
				F1 ×F1	0:38:26					100
C1	6503	100 chlor-amphenicol	NTG	×6500	:66:0	14	2	0	0	51
				F1 ×6500	:60:48					76
				F1 ×C_1	:59:0					47
				F1 ×F_1	:51:17					58
				F2 (1) ×6500	25:19					44
				F2 (2) ×6500	18:23					41
C2	6503	100 chlor-amphenicol	NTG	×6500	71:0	72	2	4	0	97
				F1 ×6500	43:32					75
				F1 ×C2	60:0					69
				F1 ×F1	40:13					53
C3	6503	100 chlor-amphenicol	NTG	×6500	57:0	31	0	3	0	57
				F1 ×6500	—					—
				F1 ×C3	?:0					50

II. THE GENETICS OF MATING TYPE

A cross of wild type 6500A_1 with 6503A_2 gave 67A_1 : 41A_2 : 4 A_1A_2 phenotypes. However crosses involving mutants of the same wild types give very different ratios. Mutants C1 (A_2), C2 (A_2) and C3 (A_2) when crossed with wild type gave a marked excess of mating A_1 — the mating type of the wild type parent. Mutant FA4 (A_1) gave only A_2 phenotype in the F1 progeny — again the mating type of the wild type parent. Although matings of these mutants to wild type are fertile, matings of FA4 to C1, C2 and C3 are sterile. This last result may offer an explanation of the excess of the wild type mating types found above based upon a deficiency of female function in the mutant strains.

The A_1A_2 phenotypes have been further examined :

(1) Colonies from hyphal inocula produced sterile sectors with abundant aerial mycelium. Sectors were either A_1 or A_2 in phenotype ;

(2) Thirteen single zoospore isolates were made from an A_1A_2 culture. All isolates were self sterile, nine were A_1 and four were A_2 ;

(3) From 100 hyphal tips from a self fertile A_1A_2 colony two gave rise to A_1A_2 phenotypes ;

(4) Fifty zoosporangia were isolated from an A_1A_2 culture. Forty-four were self sterile but six were self fertile.

The above evidence strongly suggests that A_1A_2 cultures are heterokaryotic for nuclei bearing A_1 and A_2 determinants.