

2002-2003

Analysed the soil from under the five year old, kanamycin resistance gene-containing transgenic pines at Rotorua for evidence kanamycin gene transfer to soil bacteria or increase in kanamycin resistance in the soil bacteria. Soils were screened from around both transgenic and non-transgenic pines, firstly on selective (kan⁵⁰ or kan¹⁰⁰) or non-selective media. No differences were found in the number of bacteria on kanamycin selection plates from under transgenic or non-transgenic pines. Where possible, 50 individual colonies were taken from each plate and probed with radio-labelled nptII gene. Eleven hundred individual colonies from kan⁵⁰ or kan¹⁰⁰ respectively, and a further 675 from kan⁰ were probed. Several weakly positive colonies were detected, none of which were found to have the nptII gene when colonies were re-probed using fresh cultures. Colonies which appeared weakly positive were mainly *Pseudomonas* sp., which routinely probe positive to most radioactively labelled probes.

2005-2006

Forest Research soils (June 2006)

Method

Soils were dilution plated on to three selective agars: Plate count agar (Difco) with Cycloheximide 100 mg/L plus either no Kanamycin, Kanamycin 10 mg/L or Kanamycin 100 mg/L. Total bacterial numbers were enumerated after 48hr incubation at 30°C.

Results

Tree	ID	Bacterial numbers (cfu/g dry soil)			% 10mg to total	%100mg to total	Soil Moisture
		Kanamycin none	Kanamycin 10mg/ml	Kanamycin 100mg/ml			%
Control	27	2.73E+06	3.95E+05	4.95E+05	14.47	18.13	44.37
Control	29	1.55E+06	1.41E+05	2.74E+04	9.10	1.77	48.57
Control	42	4.00E+06	3.32E+05	3.09E+04	8.30	0.77	51.08
Control	46	4.93E+06	7.14E+05	3.02E+04	14.48	0.61	47.18
Control	85	2.58E+06	1.36E+06	2.89E+04	52.71	1.12	54.01
	mean	3.16E+06	5.88E+05	1.22E+05	19.81	3.88	
	sd	1.32E+06	4.78E+05	2.08E+05			
GM1	10	6.19E+07	4.85E+06	7.81E+05	7.84	1.26	39.74
GM1	16	9.26E+07	3.94E+07	1.21E+05	42.55	0.13	35.43
GM1	18	4.22E+06	1.81E+05	4.75E+04	4.29	1.13	51.41
GM1	19	4.44E+07	1.73E+07	4.51E+05	38.96	1.02	47.55
GM1	23	1.61E+07	4.56E+06	1.01E+06	28.32	6.27	45.33

	mean	4.38E+07	1.33E+07	4.82E+05	24.39	1.96	
	sd	3.55E+07	1.59E+07	4.15E+05			
GM2	4	1.60E+07	2.73E+06	1.17E+05	17.06	0.73	77.31
GM2	20	3.99E+06	5.66E+04	8.06E+04	1.42	2.02	45.21
GM2	25	1.19E+07	3.30E+06	2.55E+05	27.73	2.14	55.04
GM2	36	4.04E+06	6.38E+05	4.32E+04	15.79	1.07	42.76
GM2	51	5.70E+05	7.91E+05	2.78E+04	138.77	4.88	41.78
	mean	7.30E+06	1.50E+06	1.05E+05	40.16	2.17	
	sd	6.40E+06	1.42E+06	9.09E+04			