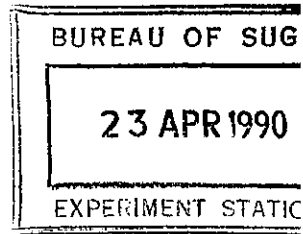


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PROJECT REPORT

Volume 7 of 7

PROJECT 409

BUNCH FAMILY SELECTION

Efficiency of bunch-planted and single-planted seedlings for selecting superior crosses in sugar cane

by

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1989

Table 112. Realized gains from selection of families in the Ts trial with evaluation based on the Re type in trial Te. Selection in Ss and Bs seedlings was based on only two replicates (KL).

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
B2STp	12	p	10.5	1.9	.6	2.5	2.9
		r	17.9	5.6	.1	5.7	6.4
		pr	21.0	3.8	.4	4.1	4.5
B2STp	6	p	13.8	2.6	.5	3.2	3.5
		r	37.2	9.2	-.3	8.9	9.2
		pr	45.8	6.1	.1	6.1	6.1
B2STp	4	p	-4.8	1.2	-1.3	-.3	-1.8
		r	55.2	16.6	-.3	16.4	16.1
		pr	39.7	9.4	-.8	8.3	6.3
B2STr	12	p	14.9	5.6	-.8	4.8	3.9
		r	21.5	8.8	-.7	8.0	6.8
		pr	31.9	7.3	-.7	6.4	5.2
B2STr	6	p	20.3	4.4	.7	5.2	5.3
		r	46.8	12.3	-.1	12.3	13.5
		pr	45.8	8.6	.3	8.8	9.0
B2STr	4	p	37.8	6.6	1.0	7.9	9.0
		r	40.8	13.4	.0	13.5	14.4
		pr	58.2	10.2	.5	10.8	11.4
B2STpr	12	p	9.4	2.0	.7	2.7	3.3
		r	17.9	6.1	.3	6.3	6.5
		pr	22.6	4.2	.5	4.6	4.8
B2STpr	6	p	20.3	4.4	.7	5.2	5.3
		r	46.8	12.3	-.1	12.3	13.5
		pr	45.8	8.6	.3	8.8	9.0
B2STpr	4	p	-4.8	1.2	-1.3	-.3	-1.8
		r	55.2	16.6	-.3	16.4	16.1
		pr	39.7	9.4	-.8	8.3	6.3
B2G_Bp	12	p	8.3	2.2	.4	2.7	2.8
		r	21.5	4.2	-.3	4.0	4.1
		pr	21.0	3.2	.1	3.3	3.4
B2G_Bp	6	p	31.2	8.7	3.5	12.4	15.0
		r	20.3	4.7	1.6	6.4	9.0
		pr	36.6	6.6	2.6	9.3	12.3

Table 112 continued 2/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
B2G_Br	12	p	9.4	4.2	1.2	5.5	6.2
		r	31.1	7.3	.6	7.9	8.1
		pr	27.3	5.8	.9	6.7	7.1
B2G_Br	6	p	26.9	7.1	1.8	9.2	10.6
		r	15.4	6.7	.9	7.4	9.0
		pr	21.0	6.9	1.3	8.3	9.9
B2G_Br	4	p	44.4	11.3	2.0	13.9	15.8
		r	19.0	10.2	.6	10.5	12.6
		pr	39.7	10.8	1.3	12.2	14.4
B2G_Bpr	12	p	15.9	4.3	.6	5.0	5.0
		r	28.7	7.0	-.3	6.7	6.3
		pr	25.7	5.8	.1	5.8	5.6
B2G_Bpr	6	p	18.1	6.5	2.1	8.9	10.8
		r	25.1	3.4	.9	4.2	5.3
		pr	24.1	4.9	1.5	6.5	8.3
B2G_Bpr	4	p	28.0	11.6	3.0	15.1	18.0
		r	22.7	6.1	2.2	8.1	10.6
		pr	39.7	8.7	2.6	11.5	14.7
B2GBp	12	p	1.7	5.4	1.4	6.9	7.8
		r	35.9	7.1	.7	7.9	7.5
		pr	25.7	6.3	1.1	7.4	7.7
B2GBp	6	p	26.8	9.5	3.6	13.4	16.2
		r	34.8	5.3	1.5	6.8	8.2
		pr	42.8	7.2	2.6	10.0	12.6
B2GBp	4	p	31.2	8.5	4.3	13.3	16.6
		r	48.1	5.5	2.1	8.0	9.3
		pr	49.0	6.9	3.3	10.6	13.3
B2GBr	12	p	10.5	3.7	1.4	5.2	6.4
		r	29.9	6.9	.9	7.8	8.8
		pr	25.7	5.4	1.2	6.5	7.5
B2GBr	6	p	11.5	8.9	1.8	11.0	12.4
		r	44.4	6.6	1.0	7.5	7.9
		pr	39.7	7.7	1.4	9.2	10.4
B2GBr	4	p	24.6	9.9	4.6	15.2	18.9

Table 112 continued 3/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
B2GBpr	6	p	13.7	8.0	4.1	12.5	15.3
		r	51.6	6.4	2.6	9.2	12.3
		pr	42.8	7.1	3.4	10.8	14.0
B2GBpr	4	p	34.4	9.1	6.0	15.6	20.6
		r	44.4	5.0	3.1	8.4	13.6
		pr	49.0	6.9	4.6	11.9	17.5
B2WSp	12	p	7.2	.4	1.7	2.1	3.3
		r	13.1	.5	.5	1.0	1.5
		pr	4.0	.4	1.1	1.5	2.5
B2WSp	6	p	5.0	3.5	3.3	7.2	9.4
		r	37.1	6.7	2.1	9.1	11.4
		pr	18.0	5.2	2.7	8.2	10.3
B2WSp	4	p	5.0	7.4	4.4	12.4	15.7
		r	33.4	4.0	2.7	6.9	9.2
		pr	11.7	5.6	3.5	9.5	12.8
B2WSr	12	p	12.6	1.0	2.5	3.7	5.8
		r	5.8	-1.1	1.5	.7	2.7
		pr	5.5	-.1	2.0	2.2	4.4
B2WSr	6	p	22.4	2.5	2.6	5.6	7.7
		r	3.4	-4.8	.9	-3.6	-2.9
		pr	5.6	-1.4	1.8	.9	3.0
B2WSr	4	p	-4.9	.0	2.6	2.8	4.9
		r	11.8	-2.1	1.5	-.4	-1.1
		pr	-11.5	-1.1	2.0	1.1	2.2
B2WSpr	12	p	13.7	2.2	1.8	4.2	5.4
		r	13.0	1.4	.6	2.2	3.1
		pr	11.7	1.8	1.2	3.2	4.4
B2WSpr	6	p	22.4	2.5	2.6	5.6	7.7
		r	3.4	-4.8	.9	-3.6	-2.9
		pr	5.6	-1.4	1.8	.9	3.0
B2WSpr	4	p	31.2	7.2	4.7	12.5	16.4
		r	11.8	.7	2.6	3.4	5.8
		pr	21.1	3.7	3.7	7.8	11.6
B2TCHp	12	p	12.7	3.1	1.1	4.3	5.0

Table 112 continued 4/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
B2TCHp	4	p	18.1	3.2	2.8	6.4	8.5
		r	44.4	7.9	1.2	9.4	9.0
		pr	35.1	5.7	2.0	8.0	8.7
B2TCHr	12	p	7.2	3.6	2.2	6.0	7.9
		r	26.3	5.4	1.6	7.1	8.4
		pr	21.0	4.5	1.9	6.5	8.1
B2TCHr	6	p	9.4	4.5	1.9	6.7	8.7
		r	27.5	3.8	.5	4.3	4.0
		pr	14.8	4.1	1.2	5.5	6.6
B2TCHr	4	p	11.5	6.9	4.3	11.9	15.7
		r	37.1	-.1	1.8	1.8	1.6
		pr	21.1	3.2	3.0	6.7	9.3
B2TCHpr	12	p	8.3	1.7	1.5	3.3	4.4
		r	22.7	4.7	.6	5.5	6.1
		pr	14.8	3.3	1.1	4.4	5.2
B2TCHpr	6	p	11.5	3.6	4.3	8.2	11.6
		r	34.7	3.5	2.1	6.0	8.4
		pr	18.0	3.6	3.2	7.1	10.1
B2TCHpr	4	p	18.1	7.3	6.1	14.1	19.2
		r	37.1	6.3	4.0	10.8	15.2
		pr	30.4	6.8	5.1	12.4	17.4
B2CCSp	12	p	3.9	4.1	1.7	6.0	7.2
		r	21.5	4.7	1.2	5.9	6.1
		pr	21.0	4.4	1.5	5.9	6.7
B2CCSp	6	p	-21.2	.9	2.0	3.0	4.5
		r	41.8	9.5	2.3	12.2	13.7
		pr	11.7	5.5	2.2	7.7	8.7
B2CCSp	4	p	-17.9	3.0	1.1	4.0	4.8
		r	40.6	8.8	1.7	10.5	12.7
		pr	20.9	6.0	1.4	7.3	8.3
B2CCSr	12	p	3.9	3.9	2.7	6.8	8.7
		r	28.6	4.6	1.9	6.7	8.9
		pr	16.4	4.3	2.3	6.7	8.8
B2CCSr	6	p	-8.1	3.9	2.1	6.0	7.7

Table 112 continued 5/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
B2CCSpr	12	p	-12.5	1.0	2.1	3.1	4.6
		r	20.2	2.4	1.9	4.5	5.7
		pr	4.0	1.7	2.0	3.8	5.1
B2CCSpr	6	p	-21.2	.9	2.0	3.0	4.5
		r	41.8	9.5	2.3	12.2	13.7
		pr	11.7	5.5	2.2	7.7	8.7
B2CCSpr	4	p	-4.8	2.9	2.9	5.7	8.3
		r	44.3	11.1	3.0	14.4	18.7
		pr	39.7	7.2	2.9	10.2	13.0
B2TSHp	12	p	13.7	2.4	1.9	4.4	5.8
		r	14.2	4.0	.8	4.9	6.2
		pr	14.8	3.2	1.4	4.6	6.0
B2TSHp	6	p	5.0	3.5	3.3	7.2	9.4
		r	37.1	6.7	2.1	9.1	11.4
		pr	18.0	5.2	2.7	8.2	10.3
B2TSHp	4	p	11.6	6.0	4.1	10.5	13.4
		r	47.9	10.1	2.5	13.1	15.0
		pr	25.7	8.2	3.3	11.9	14.1
B2TSHr	12	p	7.2	3.6	2.2	6.0	7.9
		r	26.3	5.4	1.6	7.1	8.4
		pr	21.0	4.5	1.9	6.5	8.1
B2TSHr	6	p	11.5	3.6	4.3	8.2	11.6
		r	34.7	3.5	2.1	6.0	8.4
		pr	18.0	3.6	3.2	7.1	10.1
B2TSHr	4	p	18.1	5.5	4.0	10.0	13.4
		r	51.6	6.0	1.5	8.0	7.4
		pr	35.1	5.8	2.8	9.0	10.7
B2TSHpr	12	p	6.1	3.4	2.1	5.6	7.3
		r	28.6	6.5	1.4	8.0	9.7
		pr	19.5	5.0	1.7	6.8	8.4
B2TSHpr	6	p	11.5	3.6	4.3	8.2	11.6
		r	34.7	3.5	2.1	6.0	8.4
		pr	18.0	3.6	3.2	7.1	10.1
B2TSHpr	4	p	18.1	7.3	6.1	14.1	19.2

Table 112 continued 6/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
B2GYOTp	6	p	2.8	5.9	4.6	11.0	14.6
		r	39.5	7.3	3.4	11.1	14.5
		pr	27.3	6.7	4.0	11.0	14.6
B2GYOTp	4	p	11.6	6.0	4.1	10.5	13.4
		r	47.9	10.1	2.5	13.1	15.0
		pr	25.7	8.2	3.3	11.9	14.1
B2GYOTr	12	p	7.2	3.6	2.2	6.0	7.9
		r	26.3	5.4	1.6	7.1	8.4
		pr	21.0	4.5	1.9	6.5	8.1
B2GYOTr	6	p	11.5	3.6	4.3	8.2	11.6
		r	34.7	3.5	2.1	6.0	8.4
		pr	18.0	3.6	3.2	7.1	10.1
B2GYOTr	4	p	18.1	5.5	4.0	10.0	13.4
		r	51.6	6.0	1.5	8.0	7.4
		pr	35.1	5.8	2.8	9.0	10.7
B2GYOTpr	12	p	6.1	3.4	2.1	5.6	7.3
		r	28.6	6.5	1.4	8.0	9.7
		pr	19.5	5.0	1.7	6.8	8.4
B2GYOTpr	6	p	13.7	4.5	4.4	9.4	13.7
		r	27.5	2.9	2.6	5.7	8.5
		pr	18.0	3.7	3.5	7.5	11.4
B2GYOTpr	4	p	18.1	7.3	6.1	14.1	19.2
		r	37.1	6.3	4.0	10.8	15.2
		pr	30.4	6.8	5.1	12.4	17.4
S2STp	12	p	16.0	4.7	.7	5.4	5.8
		r	22.7	8.9	.0	8.9	9.8
		pr	22.6	7.0	.4	7.2	7.6
S2STp	6	p	35.6	4.7	.7	5.6	6.6
		r	20.3	10.8	.0	10.7	11.7
		pr	33.4	8.0	.3	8.3	8.9
S2STp	4	p	37.8	5.9	-.3	6.0	6.9
		r	15.5	7.2	-.9	5.9	5.7
		pr	39.5	6.6	-.6	6.0	6.4
S2STr	12	p	13.8	4.7	.9	5.7	6.1

Table 112 continued 7/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2STr	4	p	14.9	.4	-1.6	-1.4	-2.9
		r	26.3	15.4	-1.1	14.4	13.1
		pr	21.1	8.3	-1.3	6.7	4.3
S2STpr	12	p	13.8	4.7	.9	5.7	6.1
		r	26.3	8.8	.4	9.0	10.1
		pr	22.6	6.9	.6	7.4	7.9
S2STpr	6	p	35.6	4.7	.7	5.6	6.6
		r	20.3	10.8	.0	10.7	11.7
		pr	33.4	8.0	.3	8.3	8.9
S2STpr	4	p	14.9	.4	-1.6	-1.4	-2.9
		r	26.3	15.4	-1.1	14.4	13.1
		pr	21.1	8.3	-1.3	6.7	4.3
S2G_Bp	12	p	7.2	4.3	.7	5.1	5.1
		r	25.1	5.6	.5	6.2	6.5
		pr	14.9	5.0	.6	5.7	5.7
S2G_Bp	6	p	11.5	7.5	3.8	11.7	14.1
		r	56.3	8.6	2.3	11.1	14.9
		pr	39.7	8.1	3.1	11.4	14.5
S2G_Bp	4	p	14.9	9.2	1.8	11.4	12.0
		r	69.6	8.5	.1	8.5	8.3
		pr	48.9	8.8	1.0	9.9	10.3
S2G_Br	12	p	14.9	6.0	.6	6.7	7.0
		r	21.5	7.8	.5	8.3	9.3
		pr	27.3	7.0	.5	7.5	8.1
S2G_Br	6	p	33.5	9.1	.7	10.0	10.8
		r	10.7	10.1	.6	10.6	13.6
		pr	33.5	9.6	.6	10.3	12.1
S2G_Br	4	p	47.6	10.0	5.5	16.1	20.2
		r	29.9	9.9	3.1	13.1	19.2
		pr	44.4	10.0	4.3	14.6	19.8
S2G_Bpr	12	p	13.7	4.9	.2	5.2	5.1
		r	26.3	8.0	.2	8.1	8.9
		pr	28.8	6.5	.2	6.7	6.8
S2G_Bpr	6	p	26.9	9.1	1.6	11.0	11.9

Table 112 continued 8/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2GBp	12	p	2.8	3.7	2.2	6.1	7.6
		r	31.1	4.8	1.6	6.6	7.9
		pr	19.5	4.3	1.9	6.3	7.8
S2GBp	6	p	-23.4	1.5	2.5	4.1	5.5
		r	51.5	7.6	2.1	10.1	11.4
		pr	5.6	4.7	2.3	7.2	8.2
S2GBp	4	p	-24.5	1.9	3.8	5.9	8.4
		r	51.5	9.5	3.6	13.7	16.9
		pr	11.9	5.9	3.7	9.9	12.3
S2GBr	12	p	9.4	4.3	1.8	6.3	7.7
		r	28.6	7.7	1.2	9.0	10.0
		pr	21.0	6.1	1.5	7.6	8.8
S2GBr	6	p	13.7	8.0	4.3	12.7	16.1
		r	56.3	7.8	2.6	10.6	14.1
		pr	55.2	7.9	3.5	11.6	15.2
S2GBr	4	p	28.0	10.9	5.8	17.2	21.3
		r	58.8	11.1	3.8	15.1	22.2
		pr	63.0	11.0	4.8	16.1	21.7
S2GBpr	12	p	5.0	3.2	1.6	4.9	6.2
		r	31.1	6.7	1.1	7.8	8.7
		pr	22.6	5.0	1.3	6.4	7.3
S2GBpr	6	p	13.7	8.0	4.3	12.7	16.1
		r	56.3	7.8	2.6	10.6	14.1
		pr	55.2	7.9	3.5	11.6	15.2
S2GBpr	4	p	28.0	10.9	5.8	17.2	21.3
		r	58.8	11.1	3.8	15.1	22.2
		pr	63.0	11.0	4.8	16.1	21.7
S2WSp	12	p	.7	5.4	.5	5.9	5.9
		r	23.9	3.5	.0	3.5	3.0
		pr	16.4	4.4	.2	4.7	4.6
S2WSp	6	p	-14.7	5.4	1.5	6.9	8.2
		r	27.5	2.1	.8	3.0	.5
		pr	11.8	3.7	1.2	4.9	4.7
S2WSp	4	n	-31.1	4.2	3.3	7.7	10.1

Table 112 continued 9/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2WSr	6	p	-1.6	-1.3	.4	-.8	-.8
		r	-11.0	-4.8	.6	-3.7	-4.5
		pr	-13.0	-3.2	.5	-2.3	-2.5
S2WSr	4	p	-24.5	-.9	.5	-.2	-.1
		r	1.0	-4.9	1.3	-3.0	-4.9
		pr	-16.1	-3.0	.9	-1.6	-2.3
S2WSpr	12	p	5.0	4.2	.2	4.4	4.4
		r	13.1	.2	-.3	.1	-.4
		pr	13.3	2.1	.0	2.2	2.2
S2WSpr	6	p	-19.1	1.9	2.0	4.1	5.7
		r	20.3	-1.3	1.6	.5	-.3
		pr	-3.7	.2	1.8	2.2	3.0
S2WSpr	4	p	-31.1	4.2	3.3	7.7	10.4
		r	22.6	1.1	3.6	5.0	5.7
		pr	-2.1	2.5	3.4	6.3	8.3
S2TCHp	12	p	9.4	4.7	.0	4.9	5.0
		r	22.7	5.1	-.5	4.4	2.7
		pr	16.4	4.9	-.2	4.7	3.9
S2TCHp	6	p	18.1	11.7	2.1	14.1	15.4
		r	44.4	5.3	.5	5.6	5.5
		pr	45.9	8.3	1.3	9.7	10.9
S2TCHp	4	p	37.8	15.9	3.5	19.8	22.4
		r	22.7	4.1	1.3	5.1	7.1
		pr	49.0	9.6	2.4	12.3	15.5
S2TCHr	12	p	17.1	5.0	.8	5.8	6.4
		r	20.3	7.8	.2	7.9	8.5
		pr	24.2	6.5	.5	6.9	7.3
S2TCHr	6	p	20.3	7.1	2.9	10.3	12.4
		r	41.9	11.2	1.8	13.2	17.7
		pr	42.7	9.3	2.4	11.8	14.8
S2TCHr	4	p	31.3	10.8	2.0	13.1	14.6
		r	62.4	17.5	1.1	18.8	21.4
		pr	72.2	14.4	1.6	16.0	17.7
S2TCHpr	12	p	10.5	4.6	.9	5.6	6.1

Table 112 continued 10/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2TCHpr	4	p	34.5	14.5	2.9	17.8	19.8
		r	47.9	9.0	.6	9.2	11.0
		pr	67.6	11.6	1.8	13.4	15.8
S2CCSp	12	p	-9.2	-.5	1.7	1.3	2.4
		r	11.8	.3	1.5	2.0	3.6
		pr	-.7	-.1	1.6	1.6	2.9
S2CCSp	6	p	-23.4	-1.8	2.5	.8	2.7
		r	34.7	2.6	1.5	4.5	5.1
		pr	5.6	.6	2.0	2.7	3.8
S2CCSp	4	p	-18.0	.1	4.0	4.3	7.7
		r	37.1	3.5	2.9	6.9	8.4
		pr	-2.1	1.9	3.5	5.7	8.0
S2CCSr	12	p	2.8	2.0	2.2	4.4	6.2
		r	22.7	2.3	1.3	3.8	4.7
		pr	19.5	2.2	1.8	4.1	5.6
S2CCSr	6	p	-21.3	2.8	1.9	4.8	6.4
		r	29.9	1.5	1.8	3.5	3.7
		pr	-3.7	2.1	1.9	4.1	5.2
S2CCSr	4	p	-4.9	4.3	3.0	7.4	10.4
		r	8.2	-2.8	2.4	-.3	2.8
		pr	-6.8	.6	2.7	3.4	6.9
S2CCSpr	12	p	-9.2	-.5	1.7	1.3	2.4
		r	11.8	.3	1.5	2.0	3.6
		pr	-.7	-.1	1.6	1.6	2.9
S2CCSpr	6	p	-21.3	2.8	1.9	4.8	6.4
		r	29.9	1.5	1.8	3.5	3.7
		pr	-3.7	2.1	1.9	4.1	5.2
S2CCSpr	4	p	-18.0	-.6	2.8	2.4	5.6
		r	11.8	-2.7	1.9	-.6	-.3
		pr	-20.8	-1.7	2.3	.8	2.9
S2TSHp	12	p	.6	4.4	1.1	5.6	6.3
		r	28.7	3.6	.3	3.9	3.1
		pr	17.9	4.0	.7	4.7	4.9
S2TSHp	6	p	7.2	10.5	2.2	13.1	14.4

Table 112 continued 11/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2TSHr	12	p	12.7	4.0	.7	4.7	5.3
		r	21.5	8.0	.0	8.0	7.8
		pr	19.5	6.1	.4	6.4	6.5
S2TSHr	6	p	20.3	5.4	3.4	9.1	11.8
		r	37.1	7.3	2.2	9.6	14.2
		pr	39.7	6.4	2.8	9.4	12.9
S2TSHr	4	p	28.0	10.9	5.8	17.2	21.3
		r	58.8	11.1	3.8	15.1	22.2
		pr	63.0	11.0	4.8	16.1	21.7
S2TSHpr	12	p	3.9	5.3	1.2	6.6	7.8
		r	33.5	6.9	.6	7.5	7.1
		pr	28.8	6.1	.9	7.1	7.5
S2TSHpr	6	p	13.8	8.2	2.4	10.9	13.1
		r	29.9	5.5	1.0	6.3	6.8
		pr	30.4	6.8	1.7	8.5	10.3
S2TSHpr	4	p	34.5	14.5	2.9	17.8	19.8
		r	47.9	9.0	.6	9.2	11.0
		pr	67.6	11.6	1.8	13.4	15.8
S2GYOTp	12	p	.6	4.4	1.1	5.6	6.3
		r	28.7	3.6	.3	3.9	3.1
		pr	17.9	4.0	.7	4.7	4.9
S2GYOTp	6	p	-1.6	7.8	2.9	11.2	13.1
		r	46.8	3.2	1.7	5.1	5.0
		pr	24.2	5.4	2.3	8.0	9.5
S2GYOTp	4	p	21.4	10.5	3.9	15.0	17.8
		r	58.8	4.7	1.6	6.2	8.5
		pr	53.6	7.4	2.7	10.4	13.6
S2GYOTr	12	p	14.9	3.7	1.0	4.8	5.7
		r	17.9	6.6	.3	6.9	7.4
		pr	21.0	5.3	.7	5.9	6.4
S2GYOTr	6	p	20.3	5.4	3.4	9.1	11.8
		r	37.1	7.3	2.2	9.6	14.2
		pr	39.7	6.4	2.8	9.4	12.9
S2GYOTr	4	p	28.0	10.2	4.5	15.2	19.2

Table 112 continued 12/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2GYOTpr	6	p	13.8	8.2	2.4	10.9	13.1
		r	29.9	5.5	1.0	6.3	6.8
		pr	30.4	6.8	1.7	8.5	10.3
S2GYOTpr	4	p	28.0	10.2	4.5	15.2	19.2
		r	33.4	4.9	2.8	7.6	13.5
		pr	44.3	7.4	3.7	11.3	16.6
S2SEL7p	12	p	8.3	4.0	1.8	5.9	7.2
		r	31.1	5.9	.8	6.7	7.1
		pr	25.7	5.0	1.3	6.3	7.2
S2SEL7p	6	p	5.0	4.6	3.2	8.3	11.4
		r	25.0	1.3	1.7	3.2	4.5
		pr	5.5	2.9	2.5	5.6	8.3
S2SEL7p	4	p	-8.2	1.6	2.7	4.4	7.0
		r	15.4	.2	1.9	2.1	5.7
		pr	-11.6	.9	2.3	3.2	6.4
S2SEL7r	12	p	14.8	5.1	1.1	6.3	7.0
		r	27.5	7.0	.5	7.4	8.0
		pr	27.2	6.1	.8	6.8	7.5
S2SEL7r	6	p	20.3	6.9	4.2	11.5	15.1
		r	41.9	6.1	2.5	8.7	13.2
		pr	39.7	6.5	3.3	10.0	14.2
S2SEL7r	4	p	41.0	8.7	6.6	15.9	22.0
		r	19.0	5.3	4.3	9.8	18.6
		pr	39.7	6.9	5.5	12.8	20.5
S2SEL8p	12	p	5.0	3.8	1.4	5.4	6.4
		r	28.7	6.1	1.1	7.3	8.1
		pr	16.4	5.0	1.3	6.4	7.2
S2SEL8p	6	p	-23.4	1.5	2.5	4.1	5.5
		r	51.5	7.6	2.1	10.1	11.4
		pr	5.6	4.7	2.3	7.2	8.2
S2SEL8p	4	p	-8.2	2.3	4.0	6.4	9.1
		r	40.7	6.3	2.9	9.7	14.4
		pr	7.1	4.5	3.4	8.1	11.5
S2SEL8r	12	p	22.5	3.6	1.2	5.0	5.6

Table 112 continued 13/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2SEL8r	4	p	47.5	8.9	4.5	14.1	17.8
		r	19.0	-6	1.7	1.0	4.2
		pr	39.7	3.9	3.1	7.3	11.7
S2S10p	12	p	6.1	1.5	1.6	3.2	4.1
		r	27.5	5.0	.6	5.7	6.6
		pr	8.6	3.3	1.1	4.5	5.2
S2S10p	6	p	5.0	3.9	2.3	6.6	8.5
		r	32.3	3.9	1.4	5.2	6.2
		pr	21.0	3.9	1.8	5.9	7.5
S2S10p	4	p	5.0	8.7	4.0	13.4	16.4
		r	51.5	5.9	2.5	8.5	10.2
		pr	35.1	7.2	3.3	10.9	13.6
S2S10r	12	p	18.1	3.6	.6	4.4	4.4
		r	14.2	2.3	-.1	2.1	2.1
		pr	14.9	2.9	.2	3.2	3.4
S2S10r	6	p	33.4	6.0	2.0	8.3	10.5
		r	1.0	-3.1	.0	-3.2	-1.8
		pr	21.0	1.1	1.0	2.4	4.9
S2S10r	4	p	41.0	12.7	3.1	16.3	19.1
		r	33.5	2.9	-.1	2.5	2.4
		pr	53.6	7.5	1.5	9.2	11.6
S2NMGp	12	p	10.5	4.1	1.0	5.2	5.9
		r	28.7	7.2	.3	7.4	7.4
		pr	22.6	5.7	.6	6.3	6.6
S2NMGp	6	p	11.5	7.0	3.0	10.3	12.8
		r	39.5	4.5	1.6	6.1	9.1
		pr	27.2	5.7	2.3	8.2	11.1
S2NMGp	4	p	-8.2	1.6	2.7	4.4	7.0
		r	15.4	.2	1.9	2.1	5.7
		pr	-11.6	.9	2.3	3.2	6.4
S2NMGr	12	p	17.0	4.1	1.0	5.2	5.8
		r	26.3	7.2	.1	7.2	8.4
		pr	25.7	5.7	.6	6.2	7.0
S2NMGr	6	p	20.3	5.4	3.4	9.1	11.8

Table 112 continued 14/15

Character	Number of families selected	Realized gain as per cent of General Mean					
		Crop	SEL8	TCH	CCS	TSH	NMGYOT
S2GVARp	12	p	-1.6	1.7	2.1	3.9	5.2
		r	29.9	3.5	1.3	4.9	5.3
		pr	19.5	2.6	1.7	4.4	5.2
S2GVARp	6	p	-32.2	-4.5	-.9	-5.5	-6.8
		r	37.1	2.2	-1.2	1.1	-3.0
		pr	-3.8	-1.0	-1.0	-2.1	-5.1
S2GVARp	4	p	-31.1	-8.9	-1.1	-10.0	-10.8
		r	15.5	-4.7	-2.1	-6.7	-13.4
		pr	-16.2	-6.6	-1.6	-8.3	-11.9
S2GVARr	12	p	18.1	3.8	1.0	5.0	5.1
		r	22.7	4.4	.2	4.6	5.0
		pr	21.1	4.1	.6	4.8	5.1
S2GVARr	6	p	29.0	4.0	2.5	7.0	8.7
		r	5.8	-2.9	1.0	-1.8	1.1
		pr	11.7	.3	1.8	2.5	5.3
S2GVARr	4	p	34.4	5.4	3.4	9.5	12.4
		r	8.2	-7.1	1.0	-5.8	-2.7
		pr	21.1	-1.2	2.2	1.6	5.6
S2STVp	12	p	2.8	-.4	.3	.0	-.1
		r	15.5	2.3	-.3	2.0	1.5
		pr	10.2	1.0	.0	1.1	.6
S2STVp	6	p	-23.4	-6.7	-.4	-7.2	-8.2
		r	17.8	3.2	-.2	3.3	4.4
		pr	2.4	-1.5	-.3	-1.8	-2.5
S2STVp	4	p	-31.1	-10.8	-2.5	-13.3	-15.7
		r	1.0	-3.5	-2.0	-5.6	-7.3
		pr	-2.2	-6.9	-2.3	-9.3	-11.9
S2STVr	12	p	-1.5	.6	-1.1	-.5	-2.0
		r	1.0	2.6	-.4	2.3	2.5
		pr	1.0	1.7	-.8	.9	.0
S2STVr	6	p	-8.1	-.8	1.9	1.4	2.3
		r	5.8	4.1	2.2	6.5	10.2
		pr	-9.9	1.8	2.1	4.0	5.8
S2STVr	4	p	-1.6	-3.3	.8	-2.3	-2.2

Table 112 continued 15/15

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B
including brix = GB

ST = stalks WS = weight per stalk (kg)

GVAR = within-plot variance for NMG

STV = within-plot variance for number of STALKS

Table 113. Realized gains from family selection in Bs or Ss seedlings in two (KL, Table 112) or three (KLM, Table 92) replicates. The value of the selected families was estimated by performance over PR crops of the Re type in trial Te. Gains are expressed as per cent of the Te trial character.

Table 113a. Mean gains.

Selection Class	Replicates	Estimated value in Te trial, PR crop					
		Number selected (SEL8)			NMGYOT		
		50%	25%	17%	50%	25%	17%
Bs	KLM	14.5	19.9	24.3	5.5	8.3	8.3
Bs	KL	18.8 <	23.5 <	30.6	6.2 <<	9.3 <<	11.6
Ss	KLM	18.2 <	28.3	26.0	6.1 <<	10.4	11.3
Ss	KL	15.5	21.1	24.2	5.8 <<	8.5 <<	11.2

Significance between types				SsKLM > SsKL
between rates				
Bs	KL	50 << 17		50 << 17
Ss	KLM			50 << 17
Ss	KL			50 << 17

Mean values were computed using the arcsin√% transformation, then reconverted to per cent. Each mean is based on 24 observations (8 characters * P, R, PR crops).

Significant differences involving more than one class (e.g. Ss KL50% vs Bs KL25%) are not included in the table.

NB. Means over all selection rates were as follows:-

Selection Class	Replicates	Estimated value in Te trial, PR crop	
		Number selected (SEL8)	NMGYOT
Bs	KLM	19.4	7.3
Bs	KL	24.2	8.9
Ss	KLM	24.0	9.1
Ss	KL	20.1	8.4

Significance	Ss KLM > Ss KL	Ss KLM > Ss KL

Table 113b. Gains for five important characters.

Character	Selection rate Selection Ts Rep. Class crop			Estimated value in Te trial, PR crop					
				Number selected (SEL8)			NMGYOT		
				50%	25%	17%	50%	25%	17%
TSH	P	KLM	Bs	14.8	18.0	25.7	3.2	10.3	14.1
			Ss	22.6	33.5	67.6	5.9	10.9	15.8
		KL	Bs	14.8	18.0	25.7	6.0	10.3	14.1
			Ss	17.9	33.5	49.0	4.9	10.9	15.5
NMGYOT	P	KLM	Bs	25.7	27.3	25.7	5.1	14.6	14.1
			Ss	28.8	33.5	35.1	7.6	12.4	13.6
		KL	Bs	27.2	27.3	25.7	8.0	14.6	14.1
			Ss	17.9	24.2	53.6	4.9	9.5	13.6
SEL8	P	KLM	Bs	8.6	24.1	20.9	3.0	13.9	15.8
			Ss	22.6	18.0	39.7	7.3	11.6	20.9
		KL	Bs						
			Ss	16.4	5.6	7.1	7.2	8.2	11.5
NMGplot_BR	P	KLM	Bs	21.0	36.6	44.4	6.4	16.3	20.1
			Ss	28.8	30.4	44.3	7.3	8.5	17.1
		KL	Bs	21.0	36.6	63.0	3.4	12.3	15.5
			Ss	14.9	39.7	48.9	5.7	14.5	10.3
NMGplot+BR	P	KLM	Bs	10.2	39.7	49.0	7.1	14.6	17.5
			Ss	24.2	27.3	21.1	7.6	14.5	15.7
		KL	Bs	25.7	42.8	49.0	7.7	12.6	13.3
			Ss	19.5	5.6	11.9	7.8	8.2	12.3

Table 113b continued 2/2

Character	Selection rate Selection Ts Rep. Class crop			Estimated value in Te trial, PR crop					
				Number selected (SEL8)			NMGYOT		
				50%	25%	17%	50%	25%	17%
TSH	R	KLM	Bs	21.0	24.1	25.7	8.0	10.6	11.9
			Ss	19.5	42.7	63.0	7.0	16.0	21.7
		KL	Bs	21.0	18.0	35.1	8.1	10.1	10.7
			Ss	19.5	39.7	63.0	6.5	12.9	21.7
NMGYOT	R	KLM	Bs	21.0	24.1	25.7	8.0	10.6	11.9
			Ss	14.9	39.7	39.7	6.6	12.9	20.5
		KL	Bs	21.0	18.0	35.1	8.1	10.1	10.7
			Ss	21.0	39.7	44.3	6.4	12.9	16.6
SEL8	R	KLM	Bs						
			Ss	18.0	30.4	30.3	6.5	12.9	14.7
		KL	Bs						
			Ss	21.1	30.4	39.7	4.9	12.9	11.7
NMGplot_BR	R	KLM	Bs	24.2	33.4	34.9	5.3	11.2	9.1
			Ss	27.3	49.0	44.3	7.4	10.4	6.7
		KL	Bs	27.3	21.0	39.7	7.1	9.9	14.4
			Ss	27.3	33.5	44.4	8.1	12.1	19.8
NMGplot+BR	R	KLM	Bs	22.6	33.4	16.3	4.7	11.2	8.2
			Ss	25.7	39.7	63.0	9.4	16.0	21.7
		KL	Bs	25.7	39.7	35.1	7.5	10.4	12.0
			Ss	21.0	55.2	63.0	8.8	15.2	21.7

Table 114. Correlations between family means in the Ts trial, based on three (KLM) or two (KL) replicates. DF = 22

Character in seedling trial		seedling trial			
		B2STp	B3STp	S2STp	S3STp
B2STp	25	1.0000			
B3STp	26	0.9495	1.0000		
S2STp	27	0.6742	0.6769	1.0000	
S3STp	28	0.6777	0.6711	0.9831	1.0000
B2STr	29	0.8207	0.7553	0.7957	0.8076
B3STr	30	0.7989	0.7955	0.7880	0.8003
S2STr	31	0.6471	0.6159	0.8750	0.8548
S3STr	32	0.5977	0.5681	0.8870	0.8891
B2STpr	33	0.9587	0.8983	0.7670	0.7748
B3STpr	34	0.9209	0.9452	0.7743	0.7779
S2STpr	35	0.6804	0.6637	0.9605	0.9411
S3STpr	36	0.6518	0.6320	0.9568	0.9658
B2G_Bp	37	0.5961	0.5636	0.5230	0.4818
B3G_Bp	38	0.5658	0.5485	0.5000	0.4827
S2G_Bp	39	0.5275	0.5665	0.5661	0.5808
S3G_Bp	40	0.4929	0.5348	0.5357	0.5657
B2G_Br	41	0.6953	0.6881	0.6536	0.6175
B3G_Br	42	0.6975	0.7440	0.5821	0.5556
S2G_Br	43	0.5949	0.5739	0.5997	0.6029
S3G_Br	44	0.5269	0.5105	0.6399	0.6586
B2G_Bpr	45	0.7011	0.6785	0.6372	0.5949
B3G_Bpr	46	0.7135	0.7316	0.6103	0.5855
S2G_Bpr	47	0.5879	0.6027	0.6138	0.6243
S3G_Bpr	48	0.5462	0.5661	0.6229	0.6503
B2GBp	49	0.5565	0.4927	0.4392	0.4319
B3GBp	50	0.5269	0.4832	0.4097	0.4190
S2GBp	51	0.5252	0.5818	0.5038	0.5394
S3GBp	52	0.5129	0.5466	0.4618	0.5102
B2GBr	53	0.6652	0.6490	0.6049	0.6011
B3GBr	54	0.7240	0.7498	0.5555	0.5512
S2GBr	55	0.6029	0.5867	0.6142	0.6256

Table 114 continued 2/5

Character in seedling trial		seedling trial		S2STr	S3STr	B2STpr	B3STpr	S2STpr
		B2STr	B3STr					
B2STr	29	1.0000						
B3STr	30	0.9370	1.0000					
S2STr	31	0.8525	0.8406	1.0000				
S3STr	32	0.8594	0.8451	0.9688	1.0000			
B2STpr	33	0.9493	0.9059	0.7804	0.7567	1.0000		
B3STpr	34	0.8950	0.9498	0.7710	0.7488	0.9521	1.0000	
S2STpr	35	0.8540	0.8437	0.9752	0.9628	0.7995	0.7975	1.0000
S3STpr	36	0.8601	0.8486	0.9439	0.9774	0.7868	0.7837	0.9803
B2G_Bp	37	0.4980	0.4605	0.4361	0.3959	0.5759	0.5393	0.4900
B3G_Bp	38	0.4875	0.4986	0.3867	0.3654	0.5539	0.5521	0.4510
S2G_Bp	39	0.5567	0.6270	0.3955	0.3981	0.5674	0.6306	0.4863
S3G_Bp	40	0.5313	0.6265	0.3843	0.3932	0.5356	0.6139	0.4660
B2G_Br	41	0.8163	0.7839	0.6584	0.6020	0.7889	0.7779	0.6775
B3G_Br	42	0.7269	0.7799	0.5497	0.5253	0.7456	0.8045	0.5823
S2G_Br	43	0.6869	0.6641	0.5353	0.4866	0.6692	0.6543	0.5819
S3G_Br	44	0.6575	0.6776	0.5764	0.5558	0.6172	0.6288	0.6240
B2G_Bpr	45	0.7054	0.6670	0.5890	0.5369	0.7368	0.7099	0.6301
B3G_Bpr	46	0.6889	0.7261	0.5307	0.5049	0.7355	0.7692	0.5843
S2G_Bpr	47	0.6466	0.6798	0.4803	0.4603	0.6453	0.6777	0.5568
S3G_Bpr	48	0.6275	0.6977	0.4976	0.4944	0.6129	0.6684	0.5709
B2GBp	49	0.4289	0.3777	0.3311	0.3020	0.5196	0.4581	0.3913
B3GBp	50	0.3941	0.3836	0.2545	0.2364	0.4860	0.4564	0.3337
S2GBp	51	0.4891	0.5679	0.3310	0.3364	0.5324	0.6066	0.4207
S3GBp	52	0.4663	0.5570	0.2974	0.3044	0.5143	0.5826	0.3822
B2GBr	53	0.7001	0.6850	0.5185	0.4888	0.7145	0.7045	0.5748
B3GBr	54	0.6810	0.7372	0.4728	0.4600	0.7373	0.7846	0.5260
S2GBr	55	0.5799	0.5775	0.4402	0.3961	0.6203	0.6143	0.5339
S3GBr	56	0.5086	0.5325	0.4203	0.3893	0.5473	0.5489	0.5120
B2GBpr	57	0.5931	0.5554	0.4475	0.4159	0.6539	0.6125	0.5104
B3GBpr	58	0.5873	0.6115	0.3967	0.3795	0.6700	0.6783	0.4704
S2GBpr	59	0.5476	0.5940	0.3914	0.3755	0.5913	0.6334	0.4863
S3GBpr	60	0.5088	0.5757	0.3655	0.3566	0.5553	0.5987	0.4577

Table 114 continued 3/5

Character in seedling trial		seedling trial						
		S3STpr	B2G_Bp	B3G_Bp	S2G_Bp	S3G_Bp	B2G_Br	B3G_Br
B2G_Bp	37	0.4469	1.0000					
B3G_Bp	38	0.4301	0.9011	1.0000				
S2G_Bp	39	0.4939	0.5318	0.6046	1.0000			
S3G_Bp	40	0.4842	0.4829	0.6031	0.9752	1.0000		
B2G_Br	41	0.6265	0.6773	0.6693	0.6661	0.6186	1.0000	
B3G_Br	42	0.5544	0.5644	0.5822	0.6583	0.6415	0.8146	1.0000
S2G_Br	43	0.5543	0.4313	0.4919	0.7807	0.7408	0.7260	0.7478
S3G_Br	44	0.6192	0.3455	0.4160	0.7116	0.7083	0.6109	0.7254
B2G_Bpr	45	0.5791	0.9274	0.8657	0.6487	0.5961	0.9033	0.7432
B3G_Bpr	46	0.5566	0.8145	0.8780	0.7111	0.7005	0.8379	0.9004
S2G_Bpr	47	0.5493	0.5182	0.5899	0.9611	0.9282	0.7312	0.7361
S3G_Bpr	48	0.5806	0.4613	0.5694	0.9376	0.9521	0.6637	0.7281
B2GBp	49	0.3706	0.9502	0.8658	0.5614	0.5312	0.5773	0.4771
B3GBp	50	0.3275	0.8838	0.9448	0.6235	0.6257	0.5725	0.4949
S2GBp	51	0.4398	0.5553	0.6357	0.9356	0.9389	0.5951	0.6032
S3GBp	52	0.4082	0.5382	0.6563	0.9088	0.9461	0.5661	0.5919
B2GBr	53	0.5547	0.7330	0.7494	0.7332	0.7136	0.9082	0.7345
B3GBr	54	0.5153	0.6334	0.6460	0.7043	0.6985	0.7841	0.9243
S2GBr	55	0.5135	0.5641	0.6339	0.8312	0.8136	0.6973	0.6607
S3GBr	56	0.5082	0.4815	0.5637	0.7425	0.7561	0.5627	0.6105
B2GBpr	57	0.4885	0.9199	0.8773	0.6882	0.6607	0.7820	0.6381
B3GBpr	58	0.4612	0.8422	0.8840	0.7322	0.7303	0.7441	0.7750
S2GBpr	59	0.4889	0.5806	0.6594	0.9262	0.9205	0.6626	0.6516
S3GBpr	60	0.4723	0.5420	0.6510	0.8853	0.9144	0.5943	0.6308

Character in seedling trial		seedling trial						
		S2G_Br	S3G_Br	B2G_Bpr	B3G_Bpr	S2G_Bpr	S3G_Bpr	B2GBp
S2G_Br	43	1.0000						
S3G_Br	44	0.9422	1.0000					
B2G_Bpr	45	0.6206	0.5120	1.0000				
B3G_Bpr	46	0.7035	0.6498	0.9009	1.0000			

Table 114 continued 4/5

Character in seedling trial		seedling trial		B2G_Bpr	B3G_Bpr	S2G_Bpr	S3G_Bpr	B2GBp
		S2G_Br	S3G_Br					
S2GBp	51	0.7023	0.6290	0.6263	0.6953	0.8868	0.8783	0.6382
S3GBp	52	0.6744	0.6288	0.6016	0.6997	0.8579	0.8829	0.6373
B2GBr	53	0.6898	0.5926	0.8891	0.8335	0.7566	0.7171	0.7171
B3GBr	54	0.7127	0.6833	0.7679	0.8900	0.7489	0.7467	0.6171
S2GBr	55	0.8982	0.8376	0.6834	0.7282	0.9090	0.8878	0.6192
S3GBr	56	0.8534	0.8748	0.5668	0.6611	0.8346	0.8668	0.5554
B2GBpr	57	0.5923	0.4919	0.9340	0.8452	0.6858	0.6394	0.9420
B3GBpr	58	0.6608	0.5948	0.8694	0.9294	0.7432	0.7289	0.8644
S2GBpr	59	0.8149	0.7443	0.6754	0.7365	0.9307	0.9163	0.6546
S3GBpr	60	0.7863	0.7670	0.6182	0.7198	0.8929	0.9223	0.6355

Character in seedling trial		seedling trial		S3GBp	B2GBr	B3GBr	S2GBr	S3GBr
		B3GBp	S2GBp					
S2GBp	51	0.7165	1.0000					
S3GBp	52	0.7429	0.9804	1.0000				
B2GBr	53	0.7313	0.7396	0.7327	1.0000			
B3GBr	54	0.6401	0.7397	0.7348	0.8397	1.0000		
S2GBr	55	0.7001	0.8502	0.8420	0.7970	0.7626	1.0000	
S3GBr	56	0.6461	0.7764	0.7989	0.6939	0.7187	0.9609	1.0000
B2GBpr	57	0.9111	0.7373	0.7333	0.9094	0.7723	0.7531	0.6652
B3GBpr	58	0.9127	0.8040	0.8165	0.8646	0.8982	0.8064	0.7524
S2GBpr	59	0.7370	0.9733	0.9579	0.7932	0.7783	0.9484	0.8868
S3GBpr	60	0.7403	0.9445	0.9664	0.7544	0.7663	0.9370	0.9267

Character in seedling trial		seedling trial		S2GBpr	S3GBpr
		B2GBpr	B3GBpr		
B2GBpr	57	1.0000			
B3GBpr	58	0.9319	1.0000		
S2GBpr	59	0.7726	0.8361	1.0000	
S3GBpr	60	0.7425	0.8317	0.9777	1.0000

Table 114 continued 5/5

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B
including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 115a. Correlations between family means of Bs and Ss seedlings in the Ts trial vs the Re type in trial Te. Means for families in the Ts trial are based on three (KLM) or two (KL) replicates. DF = 22. The correlation matrix consists of eight parts (a - h).

Character in seedling trial	Evaluation trial	A5, Random type						
		ReTCHp	ReTCHr	ReTCHpr	ReCCSp	ReCCSr	ReCCSpr	ReTSHp
B2STp	25	0.3875	0.7222	0.6333	-0.0349	-0.2017	-0.1101	0.3300
B3STp	26	0.3426	0.6779	0.5848	-0.0869	-0.2590	-0.1664	0.2715
S2STp	27	0.5124	0.7250	0.6925	0.0695	-0.1349	-0.0182	0.4716
S3STp	28	0.4993	0.7329	0.6916	0.0929	-0.0819	0.0192	0.4669
B2STr	29	0.4963	0.8006	0.7328	-0.0598	-0.1605	-0.1065	0.4095
B3STr	30	0.4850	0.8097	0.7333	-0.0362	-0.1263	-0.0773	0.4059
S2STr	31	0.3265	0.6785	0.5778	-0.1034	-0.1949	-0.1479	0.2493
S3STr	32	0.3385	0.6657	0.5752	-0.0798	-0.1607	-0.1187	0.2639
B2STpr	33	0.4602	0.7958	0.7132	-0.0490	-0.1909	-0.1136	0.3854
B3STpr	34	0.4384	0.7864	0.6972	-0.0644	-0.2018	-0.1276	0.3590
S2STpr	35	0.4220	0.7217	0.6489	-0.0277	-0.1738	-0.0934	0.3590
S3STpr	36	0.4225	0.7158	0.6454	-0.0024	-0.1290	-0.0585	0.3652
B2G_Bp	37	0.3786	0.4227	0.4406	0.3095	0.0163	0.1918	0.4516
B3G_Bp	38	0.4636	0.4345	0.4872	0.4105	0.1468	0.3098	0.5578
S2G_Bp	39	0.6927	0.7821	0.8115	0.1270	0.0630	0.1038	0.6449
S3G_Bp	40	0.6916	0.7538	0.7931	0.1788	0.1207	0.1602	0.6594
B2G_Br	41	0.5587	0.6565	0.6706	0.1182	-0.0603	0.0439	0.5341
B3G_Br	42	0.6574	0.6681	0.7234	-0.0008	-0.1242	-0.0552	0.5759
S2G_Br	43	0.7467	0.8043	0.8503	0.0618	0.0120	0.0424	0.6748
S3G_Br	44	0.7405	0.7535	0.8154	0.0342	-0.0244	0.0098	0.6592
B2G_Bpr	45	0.5048	0.5802	0.5978	0.2406	-0.0212	0.1342	0.5349
B3G_Bpr	46	0.6352	0.6259	0.6866	0.2192	0.0054	0.1333	0.6376
S2G_Bpr	47	0.7568	0.8373	0.8757	0.1056	0.0441	0.0826	0.6955
S3G_Bpr	48	0.7670	0.8127	0.8649	0.1302	0.0673	0.1077	0.7111
B2GBp	49	0.3466	0.4367	0.4347	0.3994	0.1793	0.3175	0.4518
B3GBp	50	0.4375	0.4421	0.4799	0.5328	0.2959	0.4486	0.5768
S2GBp	51	0.5587	0.7229	0.7125	0.3144	0.2523	0.2992	0.5929
S3GBp	52	0.5899	0.6992	0.7119	0.3745	0.3073	0.3594	0.6412
B2GBr	53	0.5683	0.5914	0.6341	0.3369	0.1699	0.2761	0.6169
B3GBr	54	0.5997	0.6583	0.6906	0.2027	0.0621	0.1485	0.5953
S2GBr	55	0.7195	0.7646	0.8128	0.3405	0.1956	0.2897	0.7494
S3GBr	56	0.7091	0.7038	0.7697	0.3621	0.2251	0.3156	0.7488

Table 115a continued 2/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReTSHr	ReTSHpr	ReGYOTp	ReGYOTr	ReGYOTpr	ReSEL7p	ReSEL7r
B2STp	25	0.6664	0.5600	0.2620	0.5527	0.4328	0.3410	0.5936
B3STp	26	0.6076	0.4954	0.2013	0.4716	0.3560	0.3541	0.5322
S2STp	27	0.6695	0.6347	0.4216	0.6228	0.5632	0.6905	0.5986
S3STp	28	0.6913	0.6450	0.4231	0.6535	0.5794	0.6640	0.6304
B2STr	29	0.7440	0.6463	0.3282	0.6398	0.5159	0.4210	0.6621
B3STr	30	0.7588	0.6531	0.3212	0.6420	0.5128	0.4164	0.6269
S2STr	31	0.6109	0.4860	0.1751	0.5612	0.3851	0.4663	0.4697
S3STr	32	0.6043	0.4897	0.1976	0.5563	0.3961	0.4841	0.4740
B2STpr	33	0.7370	0.6298	0.3075	0.6225	0.4949	0.3972	0.6562
B3STpr	34	0.7227	0.6078	0.2771	0.5895	0.4602	0.4073	0.6128
S2STpr	35	0.6575	0.5697	0.2935	0.6075	0.4789	0.5838	0.5438
S3STpr	36	0.6617	0.5754	0.3073	0.6171	0.4920	0.5811	0.5598
B2G_Bp	37	0.4320	0.4852	0.4362	0.3971	0.4591	0.4729	0.5784
B3G_Bp	38	0.4724	0.5635	0.5565	0.4653	0.5651	0.4690	0.5507
S2G_Bp	39	0.7840	0.7909	0.5551	0.6976	0.6804	0.4754	0.7520
S3G_Bp	40	0.7680	0.7890	0.5810	0.7062	0.7002	0.4592	0.7103
B2G_Br	41	0.6284	0.6427	0.4746	0.5311	0.5491	0.4300	0.6766
B3G_Br	42	0.6247	0.6620	0.4836	0.5082	0.5430	0.4940	0.4908
S2G_Br	43	0.7981	0.8145	0.5725	0.7366	0.7103	0.6127	0.6497
S3G_Br	44	0.7342	0.7691	0.5547	0.6803	0.6715	0.7125	0.5696
B2G_Bpr	45	0.5714	0.6096	0.4956	0.5015	0.5468	0.4944	0.6812
B3G_Bpr	46	0.6207	0.6913	0.5825	0.5482	0.6221	0.5419	0.5836
S2G_Bpr	47	0.8357	0.8472	0.5950	0.7554	0.7331	0.5637	0.7504
S3G_Bpr	48	0.8136	0.8422	0.6153	0.7503	0.7427	0.6050	0.7050
B2GBp	49	0.4901	0.5193	0.4595	0.4922	0.5206	0.3832	0.6412
B3GBp	50	0.5216	0.6020	0.6002	0.5412	0.6292	0.4051	0.6324
S2GBp	51	0.7773	0.7602	0.5557	0.7326	0.6983	0.3694	0.7678
S3GBp	52	0.7661	0.7785	0.6128	0.7342	0.7332	0.3561	0.7492
B2GBr	53	0.6258	0.6837	0.5961	0.5928	0.6525	0.4472	0.7360
B3GBr	54	0.6654	0.6958	0.5432	0.5757	0.6124	0.4333	0.6164
S2GBr	55	0.8040	0.8563	0.7046	0.7689	0.8054	0.5941	0.7802
S3GBr	56	0.7507	0.8248	0.7092	0.7376	0.7924	0.6416	0.7048
B2GBpr	57	0.5939	0.6388	0.5606	0.5793	0.6246	0.4434	0.7374

Table 115a continued 3/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReS7plr	ReSEL8p	ReSEL8r	ReS8plr	ReSEL10p	ReSEL10r	ReS10p1
B2STp	25	0.4399	0.3220	0.5580	0.6036	0.2348	0.6605	0.5502
B3STp	26	0.4406	0.3030	0.4821	0.4789	0.1095	0.5712	0.3615
S2STp	27	0.6901	0.5660	0.4768	0.6170	0.3163	0.5714	0.4887
S3STp	28	0.6916	0.5144	0.5244	0.6201	0.2906	0.6181	0.5308
B2STr	29	0.5606	0.3432	0.6044	0.6620	0.2711	0.7124	0.5928
B3STr	30	0.5625	0.3027	0.6142	0.5765	0.1301	0.7109	0.5401
S2STr	31	0.4544	0.3425	0.3871	0.4748	0.2007	0.5221	0.4405
S3STr	32	0.4974	0.3503	0.4082	0.4846	0.1777	0.5248	0.4331
B2STpr	33	0.5211	0.3480	0.6078	0.6616	0.2641	0.7180	0.5978
B3STpr	34	0.5307	0.3196	0.5801	0.5579	0.1265	0.6781	0.4776
S2STpr	35	0.5768	0.4557	0.4406	0.5551	0.2600	0.5615	0.4767
S3STpr	36	0.6013	0.4361	0.4736	0.5610	0.2349	0.5830	0.4906
B2G_Bp	37	0.5590	0.4099	0.5118	0.5367	0.3616	0.3823	0.2805
B3G_Bp	38	0.5720	0.4146	0.5442	0.5850	0.3259	0.3868	0.2679
S2G_Bp	39	0.7643	0.3263	0.7590	0.6150	0.1259	0.5507	0.3809
S3G_Bp	40	0.7504	0.2907	0.7523	0.6114	0.1412	0.5493	0.3821
B2G_Br	41	0.5902	0.3769	0.5945	0.6061	0.2763	0.6296	0.3970
B3G_Br	42	0.6015	0.4626	0.4668	0.5679	0.2424	0.6186	0.3807
S2G_Br	43	0.7115	0.5232	0.5811	0.6952	0.3438	0.5581	0.5193
S3G_Br	44	0.7373	0.5846	0.5314	0.7020	0.4058	0.5591	0.5615
B2G_Bpr	45	0.6260	0.4306	0.6007	0.6211	0.3513	0.5430	0.3654
B3G_Bpr	46	0.6603	0.4943	0.5661	0.6475	0.3172	0.5712	0.3675
S2G_Bpr	47	0.7853	0.4323	0.7244	0.6861	0.2295	0.5859	0.4642
S3G_Bpr	48	0.8036	0.4408	0.7156	0.6986	0.2669	0.5966	0.4897
B2GBp	49	0.5618	0.2861	0.5723	0.5158	0.3317	0.3910	0.3221
B3GBp	50	0.5996	0.3282	0.6211	0.5704	0.3061	0.4058	0.3203
S2GBp	51	0.7395	0.1853	0.7892	0.5320	-0.0060	0.5415	0.3021
S3GBp	52	0.7185	0.1808	0.8045	0.5657	0.0663	0.5640	0.3724
B2GBr	53	0.6497	0.3138	0.6919	0.6192	0.2251	0.6769	0.3698
B3GBr	54	0.6543	0.3408	0.6321	0.5816	0.1372	0.6963	0.3795
S2GBr	55	0.8051	0.4643	0.7377	0.7309	0.3075	0.6066	0.5132
S3GBr	56	0.7853	0.4933	0.6869	0.7107	0.3511	0.5926	0.5647

Table 115a continued 4/5

Character in seedling trial		Evaluation trial, A5		
		ReSTp	ReSTr	ReSTp1r
B2STp	25	0.3857	0.5903	0.5583
B3STp	26	0.3478	0.5507	0.5150
S2STp	27	0.6539	0.7228	0.7546
S3STp	28	0.6275	0.7182	0.7402
B2STr	29	0.5632	0.8524	0.8063
B3STr	30	0.5349	0.8215	0.7720
S2STr	31	0.6342	0.8944	0.8667
S3STr	32	0.6628	0.9022	0.8829
B2STpr	33	0.4926	0.7491	0.7085
B3STpr	34	0.4677	0.7270	0.6819
S2STpr	35	0.6638	0.8449	0.8435
S3STpr	36	0.6654	0.8430	0.8422
B2G_Bp	37	0.3136	0.2401	0.2920
B3G_Bp	38	0.3435	0.2065	0.2760
S2G_Bp	39	0.3631	0.3998	0.4107
S3G_Bp	40	0.3720	0.3800	0.4001
B2G_Br	41	0.3985	0.5659	0.5409
B3G_Br	42	0.3643	0.4820	0.4759
S2G_Br	43	0.3665	0.5115	0.4958
S3G_Br	44	0.3966	0.5106	0.5106
B2G_Bpr	45	0.3854	0.4277	0.4452
B3G_Bpr	46	0.3984	0.3944	0.4280
S2G_Bpr	47	0.3857	0.4723	0.4721
S3G_Bpr	48	0.4118	0.4662	0.4792
B2GBp	49	0.2518	0.1635	0.2145
B3GBp	50	0.2168	0.0891	0.1451
S2GBp	51	0.2513	0.3244	0.3150
S3GBp	52	0.2485	0.2740	0.2790
B2GBr	53	0.2941	0.3837	0.3753
B3GBr	54	0.2083	0.3791	0.3426
S2GBr	55	0.2917	0.3416	0.3472
S3GBr	56	0.2536	0.2787	0.2924
B2GBpr	57	0.2920	0.2828	0.3091

Table 115a continued 5/5

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B
 including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 115b

Character in seedling trial	Evaluation trial	A5, Random type						
		ReTCHp	ReTCHr	ReTCHpr	ReCCSp	ReCCSr	ReCCSpr	ReTSHp
B2WSp	25	0.3483	0.1559	0.2585	0.5594	0.3177	0.4743	0.5038
B3WSp	26	0.4068	0.2049	0.3163	0.5432	0.2974	0.4556	0.5517
S2WSp	27	0.4298	0.1349	0.2826	0.1412	0.1026	0.1298	0.4216
S3WSp	28	0.5039	0.1994	0.3574	0.0773	0.0292	0.0592	0.4653
B2WSr	29	0.1675	-0.0534	0.0433	0.4693	0.3205	0.4217	0.3200
B3WSr	30	0.1494	-0.0375	0.0450	0.4073	0.3334	0.3904	0.2848
S2WSr	31	0.1681	-0.1509	-0.0178	0.3164	0.3499	0.3436	0.2593
S3WSr	32	0.1926	-0.1701	-0.0186	0.2185	0.2934	0.2602	0.2475
B2WSpr	33	0.2650	0.0236	0.1367	0.5729	0.3644	0.5030	0.4405
B3WSpr	34	0.2985	0.0681	0.1801	0.5507	0.3819	0.4975	0.4649
S2WSpr	35	0.3599	0.0164	0.1758	0.2418	0.2331	0.2475	0.3977
S3WSpr	36	0.4187	0.0429	0.2196	0.1584	0.1649	0.1676	0.4214
B2TCHp	37	0.5064	0.5180	0.5594	0.4419	0.1350	0.3233	0.6039
B3TCHp	38	0.4771	0.4852	0.5252	0.3762	0.0919	0.2651	0.5556
S2TCHp	39	0.7873	0.6724	0.7858	0.1836	-0.0432	0.0906	0.7502
S3TCHp	40	0.8201	0.7232	0.8329	0.1494	-0.0681	0.0592	0.7666
B2TCHr	41	0.5130	0.4756	0.5356	0.4287	0.2090	0.3483	0.6042
B3TCHr	42	0.5214	0.6031	0.6198	0.3419	0.1956	0.2906	0.5800
S2TCHr	43	0.7009	0.8051	0.8297	0.1981	0.0540	0.1421	0.6813
S3TCHr	44	0.7362	0.7883	0.8354	0.1758	0.0580	0.1307	0.7023
B2TCHpr	45	0.5541	0.5377	0.5937	0.4724	0.1906	0.3662	0.6563
B3TCHpr	46	0.5415	0.5918	0.6219	0.3879	0.1580	0.3014	0.6152
S2TCHpr	47	0.8039	0.7902	0.8677	0.2048	0.0023	0.1233	0.7727
S3TCHpr	48	0.8374	0.8076	0.8941	0.1734	-0.0101	0.0992	0.7899
B2CCSp	49	0.2974	0.4329	0.4097	0.3834	0.4165	0.4128	0.3902
B3CCSp	50	0.2948	0.4012	0.3884	0.5090	0.3888	0.4755	0.4364
S2CCSp	51	0.0924	0.1506	0.1374	0.5204	0.3789	0.4778	0.2608
S3CCSp	52	0.1860	0.2598	0.2492	0.5217	0.3971	0.4866	0.3472
B2CCSr	53	0.2427	0.3145	0.3098	0.3958	0.3882	0.4076	0.3473
B3CCSr	54	0.1231	0.3524	0.2787	0.4194	0.3562	0.4075	0.2521
S2CCSr	55	0.0848	0.0759	0.0868	0.5989	0.4279	0.5463	0.2831
S3CCSr	56	0.0645	0.1063	0.0966	0.5910	0.4527	0.5525	0.2658

Table 115b continued 2/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReTSHr	ReTSHpr	ReGYOTp	ReGYOTr	ReGYOTpr	ReSEL7p	ReSEL7r
B2WSp	25	0.2312	0.3944	0.5555	0.2899	0.4770	0.4426	0.3185
B3WSp	26	0.2762	0.4455	0.5949	0.3513	0.5312	0.4716	0.3794
S2WSp	27	0.1568	0.3086	0.3840	0.0633	0.2613	-0.1116	0.2108
S3WSp	28	0.2017	0.3574	0.4036	0.0953	0.2889	-0.0473	0.1924
B2WSr	29	0.0425	0.1894	0.3899	0.0752	0.2707	0.2182	0.2429
B3WSr	30	0.0639	0.1839	0.3426	0.0844	0.2469	0.1071	0.1799
S2WSr	31	-0.0476	0.1055	0.2857	-0.0356	0.1531	-0.0640	0.0288
S3WSr	32	-0.0801	0.0804	0.2473	-0.0640	0.1159	-0.0802	-0.1080
B2WSpr	33	0.1246	0.2995	0.5130	0.1725	0.3929	0.3412	0.3077
B3WSpr	34	0.1753	0.3417	0.5272	0.2256	0.4279	0.2985	0.3075
S2WSpr	35	0.0797	0.2512	0.3857	0.0241	0.2427	-0.1046	0.1513
S3WSpr	36	0.0892	0.2689	0.3817	0.0291	0.2428	-0.0704	0.0694
B2TCHp	37	0.5468	0.6307	0.6062	0.5325	0.6285	0.5748	0.5893
B3TCHp	38	0.5038	0.5807	0.5538	0.4953	0.5786	0.5500	0.5528
S2TCHp	39	0.6403	0.7607	0.6782	0.5199	0.6652	0.5119	0.6464
S3TCHp	40	0.6840	0.7948	0.6835	0.5701	0.6935	0.5533	0.6519
B2TCHr	41	0.5292	0.6206	0.6219	0.5068	0.6250	0.4913	0.6596
B3TCHr	42	0.6491	0.6785	0.5701	0.5854	0.6333	0.4147	0.6457
S2TCHr	43	0.8043	0.8214	0.6092	0.7425	0.7352	0.6530	0.6882
S3TCHr	44	0.7883	0.8229	0.6189	0.7383	0.7389	0.6708	0.6225
B2TCHpr	45	0.5838	0.6794	0.6680	0.5634	0.6809	0.5751	0.6819
B3TCHpr	46	0.6274	0.6838	0.6087	0.5871	0.6572	0.5190	0.6508
S2TCHpr	47	0.7713	0.8490	0.6951	0.6711	0.7509	0.6216	0.7167
S3TCHpr	48	0.7852	0.8660	0.7007	0.6949	0.7661	0.6515	0.6843
B2CCSp	49	0.5343	0.5137	0.4200	0.5230	0.5125	0.0048	0.4501
B3CCSp	50	0.4993	0.5169	0.4814	0.4833	0.5293	0.0802	0.5227
S2CCSp	51	0.2537	0.2827	0.3321	0.2930	0.3450	0.0691	0.3839
S3CCSp	52	0.3684	0.3943	0.4024	0.3750	0.4280	0.0439	0.4462
B2CCSr	53	0.4207	0.4251	0.3814	0.5060	0.4808	0.2108	0.4796
B3CCSr	54	0.4518	0.3943	0.2954	0.4801	0.4165	0.0919	0.5258
S2CCSr	55	0.1838	0.2532	0.3795	0.2307	0.3421	0.0943	0.3410
S3CCSr	56	0.2234	0.2675	0.3607	0.2403	0.3357	0.0140	0.3856

Table 115b continued 3/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReS7plr	ReSEL8p	ReSEL8r	ReS8plr	ReSEL10p	ReSEL10r	ReS10p
B2WSp	25	0.5635	0.3589	0.3621	0.3296	0.1331	0.1021	0.0229
B3WSp	26	0.5738	0.4058	0.4204	0.4440	0.2831	0.1830	0.1633
S2WSp	27	0.1821	-0.1285	0.3701	0.1818	-0.0908	0.2493	-0.0125
S3WSp	28	0.2173	-0.0402	0.3710	0.2687	0.0214	0.2659	0.0636
B2WSr	29	0.3449	0.1924	0.1543	0.0227	0.0826	0.0089	-0.0857
B3WSr	30	0.2139	0.1320	0.1370	-0.0264	0.0040	-0.0198	-0.0822
S2WSr	31	0.1092	-0.0349	0.1223	-0.0603	-0.1761	-0.0380	-0.1373
S3WSr	32	-0.0075	-0.0102	-0.0018	-0.1345	-0.1637	-0.1215	-0.1541
B2WSpr	33	0.4831	0.2886	0.2602	0.1511	0.1157	0.0479	-0.0536
B3WSpr	34	0.4240	0.2859	0.2960	0.1884	0.1343	0.0707	0.0160
S2WSpr	35	0.1700	-0.1018	0.2996	0.0891	-0.1438	0.1449	-0.0736
S3WSpr	36	0.1354	-0.0309	0.2367	0.1050	-0.0680	0.1098	-0.0360
B2TCHp	37	0.7038	0.5020	0.6033	0.6175	0.2662	0.4381	0.3248
B3TCHp	38	0.6548	0.4748	0.5554	0.5765	0.2771	0.4146	0.2934
S2TCHp	39	0.7350	0.4144	0.6894	0.6776	0.2218	0.6468	0.3947
S3TCHp	40	0.7559	0.4499	0.7048	0.7355	0.3050	0.6923	0.4916
B2TCHr	41	0.6896	0.4353	0.5363	0.4952	0.3093	0.4970	0.3535
B3TCHr	42	0.6232	0.3633	0.5915	0.4492	0.1391	0.5483	0.3846
S2TCHr	43	0.7871	0.5367	0.6606	0.6834	0.1971	0.7170	0.5214
S3TCHr	44	0.7560	0.5646	0.6173	0.6512	0.2051	0.6709	0.5166
B2TCHpr	45	0.7563	0.5059	0.6159	0.5985	0.3146	0.5109	0.3699
B3TCHpr	46	0.6909	0.4511	0.6215	0.5522	0.2220	0.5243	0.3690
S2TCHpr	47	0.8171	0.5072	0.7275	0.7321	0.2262	0.7312	0.4883
S3TCHpr	48	0.8103	0.5393	0.7120	0.7465	0.2773	0.7315	0.5395
B2CCSp	49	0.2950	-0.1158	0.5568	0.3934	0.1157	0.5252	0.5292
B3CCSp	50	0.3968	0.0198	0.5942	0.4180	0.1376	0.4800	0.5272
S2CCSp	51	0.3153	-0.0571	0.4384	0.1748	-0.1220	0.2615	0.0902
S3CCSp	52	0.2976	-0.0318	0.5154	0.2712	-0.0652	0.3498	0.2414
B2CCSr	53	0.3797	0.0535	0.4862	0.3106	0.0231	0.3913	0.2152
B3CCSr	54	0.3641	-0.0379	0.5752	0.2852	-0.0992	0.4322	0.2395
S2CCSr	55	0.2953	-0.0138	0.4055	0.1603	-0.1372	0.2731	0.0690
S3CCSr	56	0.2553	-0.0725	0.4443	0.1470	-0.1643	0.2790	0.1144

Table 115b continued 4/5

Character in seedling trial		Evaluation trial, A5		
		ReSTp	ReSTr	ReSTplr
B2WSp	25	0.1656	-0.0574	0.0224
B3WSp	26	0.2253	-0.0556	0.0492
S2WSp	27	-0.2111	-0.2932	-0.2940
S3WSp	28	-0.1491	-0.2418	-0.2314
B2WSr	29	-0.3688	-0.5075	-0.4924
B3WSr	30	-0.4838	-0.5159	-0.5428
S2WSr	31	-0.5417	-0.5652	-0.5999
S3WSr	32	-0.5706	-0.5971	-0.6340
B2WSpr	33	-0.2039	-0.3972	-0.3535
B3WSpr	34	-0.2455	-0.4008	-0.3712
S2WSpr	35	-0.3950	-0.4597	-0.4768
S3WSpr	36	-0.3799	-0.4524	-0.4642
B2TCHp	37	0.3349	0.2678	0.3139
B3TCHp	38	0.3400	0.2320	0.2921
S2TCHp	39	0.3398	0.2992	0.3327
S3TCHp	40	0.3815	0.3546	0.3888
B2TCHr	41	0.0807	0.1045	0.1029
B3TCHr	42	0.0565	0.2193	0.1703
S2TCHr	43	0.3962	0.6254	0.5879
S3TCHr	44	0.3846	0.5979	0.5640
B2TCHpr	45	0.2133	0.1943	0.2161
B3TCHpr	46	0.2080	0.2439	0.2474
S2TCHpr	47	0.3940	0.4856	0.4860
S3TCHpr	48	0.4105	0.5011	0.5039
B2CCSp	49	-0.0371	-0.0023	-0.0217
B3CCSp	50	-0.1407	-0.1305	-0.1502
S2CCSp	51	-0.1857	-0.2488	-0.2447
S3CCSp	52	-0.1918	-0.1765	-0.1972
B2CCSr	53	0.0159	-0.0458	-0.0253
B3CCSr	54	-0.1935	-0.0121	-0.0856
S2CCSr	55	-0.1907	-0.2812	-0.2722
S3CCSr	56	-0.2381	-0.2659	-0.2793

Table 115b continued 5/5

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B

including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 115c

Character in seedling trial		Evaluation trial, A5, Random type						
		ReTCHp	ReTCHr	ReTCHpr	ReCCSp	ReCCSr	ReCCSpr	ReTSHp
B2TSHp	25	0.5302	0.5798	0.6093	0.5039	0.2422	0.4078	0.6442
B3TSHp	26	0.4957	0.5220	0.5570	0.4793	0.1953	0.3723	0.6075
S2TSHp	27	0.6796	0.5968	0.6887	0.3364	0.1112	0.2500	0.7093
S3TSHp	28	0.7293	0.6681	0.7564	0.3320	0.1175	0.2501	0.7527
B2TSHr	29	0.4874	0.4693	0.5199	0.4733	0.2832	0.4077	0.5958
B3TSHr	30	0.4555	0.5788	0.5742	0.3943	0.2600	0.3503	0.5396
S2TSHr	31	0.6336	0.7174	0.7435	0.4047	0.2224	0.3398	0.6949
S3TSHr	32	0.6653	0.7289	0.7654	0.4083	0.2541	0.3559	0.7235
B2TSHpr	33	0.5448	0.5572	0.6017	0.5237	0.2854	0.4387	0.6641
B3TSHpr	34	0.5074	0.5919	0.6063	0.4634	0.2463	0.3854	0.6109
S2TSHpr	35	0.6933	0.6895	0.7534	0.3889	0.1729	0.3085	0.7405
S3TSHpr	36	0.7380	0.7349	0.8026	0.3879	0.1913	0.3160	0.7798
B2GYOTp	37	0.5414	0.6002	0.6274	0.5233	0.2854	0.4384	0.6599
B3GYOTp	38	0.5026	0.5376	0.5700	0.5159	0.2351	0.4118	0.6260
S2GYOTp	39	0.5851	0.5317	0.6041	0.3929	0.1732	0.3110	0.6463
S3GYOTp	40	0.6327	0.6075	0.6738	0.3996	0.1953	0.3248	0.6922
B2GYOTr	41	0.4589	0.4611	0.5016	0.4716	0.2945	0.4116	0.5695
B3GYOTr	42	0.4142	0.5571	0.5415	0.3969	0.2601	0.3518	0.5040
S2GYOTr	43	0.5466	0.6114	0.6367	0.4571	0.2315	0.3750	0.6388
S3GYOTr	44	0.5701	0.6314	0.6601	0.4758	0.2816	0.4083	0.6664
B2GYOTpr	45	0.5347	0.5642	0.6015	0.5341	0.3137	0.4574	0.6579
B3GYOTpr	46	0.4874	0.5865	0.5937	0.4840	0.2657	0.4062	0.6002
S2GYOTpr	47	0.5972	0.5994	0.6524	0.4455	0.2113	0.3592	0.6770
S3GYOTpr	48	0.6394	0.6546	0.7066	0.4598	0.2485	0.3842	0.7202
S2SEL7p	49	0.3821	0.4626	0.4672	0.4576	0.2679	0.3914	0.4934
S3SEL7p	50	0.4752	0.4926	0.5290	0.5031	0.3176	0.4405	0.5913
S2SEL8p	51	0.3659	0.5154	0.4931	0.4855	0.3506	0.4446	0.4897
S3SEL8p	52	0.4401	0.5111	0.5245	0.5586	0.3873	0.5044	0.5821
S2SEL10p	53	0.1869	0.2932	0.2706	0.2728	0.2185	0.2594	0.2639
S3SEL10p	54	0.2285	0.2581	0.2677	0.4002	0.2481	0.3485	0.3489
S2SEL7r	55	0.5007	0.5315	0.5652	0.4740	0.2906	0.4112	0.6044
S3SEL7r	56	0.4898	0.4981	0.5392	0.5060	0.3216	0.4440	0.6064

Table 115c continued 2/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReTSHr	ReTSHpr	ReGYOTp	ReGYOTr	ReGYOTpr	ReSEL7p	ReSEL7r
B2TSHp	25	0.6354	0.7034	0.6562	0.6244	0.7043	0.5175	0.6488
B3TSHp	26	0.5674	0.6447	0.6214	0.5616	0.6521	0.5098	0.6215
S2TSHp	27	0.6098	0.7219	0.6764	0.5273	0.6679	0.4244	0.6641
S3TSHp	28	0.6826	0.7868	0.7105	0.5989	0.7240	0.4429	0.6929
B2TSHr	29	0.5437	0.6248	0.6246	0.5492	0.6478	0.4699	0.6799
B3TSHr	30	0.6440	0.6547	0.5462	0.5986	0.6256	0.3588	0.6655
S2TSHr	31	0.7612	0.8032	0.6712	0.7331	0.7676	0.5975	0.7200
S3TSHr	32	0.7815	0.8298	0.6926	0.7510	0.7893	0.5889	0.7032
B2TSHpr	33	0.6284	0.7095	0.6870	0.6265	0.7238	0.5282	0.7170
B3TSHpr	34	0.6519	0.6959	0.6214	0.6227	0.6826	0.4581	0.6908
S2TSHpr	35	0.7186	0.8017	0.7105	0.6589	0.7540	0.5340	0.7280
S3TSHpr	36	0.7690	0.8514	0.7408	0.7069	0.7961	0.5393	0.7362
B2GYOTp	37	0.6662	0.7295	0.6757	0.6575	0.7325	0.4901	0.6644
B3GYOTp	38	0.5932	0.6693	0.6458	0.5879	0.6798	0.4893	0.6461
S2GYOTp	39	0.5644	0.6629	0.6341	0.5095	0.6337	0.3843	0.6469
S3GYOTp	40	0.6465	0.7346	0.6730	0.5875	0.6959	0.3845	0.6868
B2GYOTr	41	0.5394	0.6088	0.6011	0.5535	0.6359	0.4621	0.6801
B3GYOTr	42	0.6238	0.6246	0.5163	0.5828	0.5999	0.3502	0.6620
S2GYOTr	43	0.6586	0.7143	0.6422	0.6400	0.7037	0.5938	0.6654
S3GYOTr	44	0.6930	0.7486	0.6663	0.6737	0.7349	0.5851	0.6721
B2GYOTpr	45	0.6428	0.7148	0.6846	0.6471	0.7326	0.5121	0.7264
B3GYOTpr	46	0.6523	0.6907	0.6170	0.6260	0.6816	0.4440	0.7006
S2GYOTpr	47	0.6411	0.7236	0.6718	0.6012	0.7020	0.5086	0.6905
S3GYOTpr	48	0.7069	0.7844	0.7092	0.6636	0.7555	0.5041	0.7198
S2SEL7p	49	0.5249	0.5611	0.5223	0.4985	0.5614	0.3197	0.6897
S3SEL7p	50	0.5659	0.6355	0.6210	0.5458	0.6440	0.3172	0.6994
S2SEL8p	51	0.5984	0.6023	0.5169	0.6058	0.6117	0.3184	0.7360
S3SEL8p	52	0.6035	0.6528	0.6211	0.6184	0.6803	0.3449	0.7216
S2SEL10p	53	0.3458	0.3383	0.2648	0.3574	0.3369	0.1508	0.5275
S3SEL10p	54	0.3181	0.3658	0.3747	0.3397	0.3938	0.1973	0.4995
S2SEL7r	55	0.5930	0.6582	0.6191	0.6346	0.6871	0.6635	0.6480
S3SEL7r	56	0.5689	0.6451	0.6266	0.6264	0.6875	0.6886	0.5963

Table 115c continued 3/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReS7p1r	ReSEL8p	ReSEL8r	ReS8p1r	ReSEL10p	ReSEL10r	ReS10p
B2TSHp	25	0.7118	0.4179	0.6806	0.6447	0.2698	0.5073	0.4233
B3TSHp	26	0.6813	0.4301	0.6355	0.6075	0.2886	0.4671	0.3871
S2TSHp	27	0.7034	0.2981	0.7181	0.6073	0.1312	0.6235	0.3454
S3TSHp	28	0.7129	0.3308	0.7646	0.6883	0.2145	0.6920	0.4812
B2TSHr	29	0.6843	0.3830	0.5670	0.4891	0.2764	0.5069	0.3455
B3TSHr	30	0.6070	0.2850	0.6267	0.4300	0.0864	0.5530	0.3665
S2TSHr	31	0.7882	0.4507	0.7212	0.6501	0.1149	0.7262	0.4723
S3TSHr	32	0.7617	0.4566	0.7230	0.6294	0.1088	0.7046	0.5001
B2TSHpr	33	0.7493	0.4286	0.6639	0.5998	0.2941	0.5460	0.4085
B3TSHpr	34	0.6861	0.3763	0.6752	0.5476	0.1919	0.5500	0.4026
S2TSHpr	35	0.7839	0.3907	0.7586	0.6616	0.1302	0.7087	0.4277
S3TSHpr	36	0.7763	0.4110	0.7862	0.6972	0.1742	0.7363	0.5170
B2GYOTp	37	0.7056	0.3808	0.7087	0.6703	0.2851	0.5502	0.4791
B3GYOTp	38	0.6874	0.4085	0.6681	0.6300	0.2978	0.5007	0.4371
S2GYOTp	39	0.6693	0.2383	0.6986	0.5465	0.0776	0.5816	0.3007
S3GYOTp	40	0.6714	0.2557	0.7501	0.6223	0.1487	0.6583	0.4435
B2GYOTr	41	0.6742	0.3572	0.5654	0.4748	0.2561	0.5082	0.3316
B3GYOTr	42	0.5968	0.2637	0.6186	0.4117	0.0716	0.5476	0.3457
S2GYOTr	43	0.7455	0.4421	0.6493	0.5800	0.1219	0.6666	0.3944
S3GYOTr	44	0.7314	0.4466	0.6647	0.5663	0.1160	0.6442	0.4248
B2GYOTpr	45	0.7424	0.3965	0.6792	0.6063	0.2902	0.5688	0.4291
B3GYOTpr	46	0.6838	0.3540	0.6872	0.5495	0.1888	0.5631	0.4154
S2GYOTpr	47	0.7427	0.3520	0.7113	0.5922	0.1038	0.6546	0.3631
S3GYOTpr	48	0.7397	0.3630	0.7527	0.6316	0.1416	0.6900	0.4605
S2SEL7p	49	0.6170	0.1236	0.6916	0.4247	0.0543	0.4996	0.2764
S3SEL7p	50	0.6134	0.1623	0.7259	0.5351	0.1593	0.5597	0.4060
S2SEL8p	51	0.6423	0.0971	0.7299	0.4252	0.0273	0.4843	0.2994
S3SEL8p	52	0.6592	0.1716	0.7338	0.5400	0.1871	0.5165	0.4037
S2SEL10p	53	0.3799	-0.0750	0.5947	0.2604	-0.2055	0.6127	0.2731
S3SEL10p	54	0.3549	0.0249	0.5932	0.3759	0.0118	0.6706	0.4360
S2SEL7r	55	0.7652	0.4652	0.5954	0.5646	0.2291	0.5517	0.3885
S3SEL7r	56	0.7449	0.4746	0.5648	0.5640	0.2496	0.5226	0.3894

Table 115c continued 4/5

Character in seedling trial		Evaluation trial, A5		
		ReSTp	ReSTr	ReSTplr
B2TSHp	25	0.2954	0.2399	0.2780
B3TSHp	26	0.2688	0.1643	0.2164
S2TSHp	27	0.2077	0.1521	0.1800
S3TSHp	28	0.2306	0.2104	0.2305
B2TSHr	29	0.0665	0.0693	0.0730
B3TSHr	30	-0.0112	0.1705	0.1098
S2TSHr	31	0.2655	0.4300	0.4002
S3TSHr	32	0.2363	0.4120	0.3765
B2TSHpr	33	0.1794	0.1554	0.1754
B3TSHpr	34	0.1256	0.1800	0.1703
S2TSHpr	35	0.2478	0.2995	0.3000
S3TSHpr	36	0.2461	0.3214	0.3152
B2GYOTp	37	0.2825	0.2239	0.2616
B3GYOTp	38	0.2376	0.1347	0.1834
S2GYOTp	39	0.1444	0.0757	0.1034
S3GYOTp	40	0.1516	0.1302	0.1451
B2GYOTr	41	0.0637	0.0647	0.0690
B3GYOTr	42	-0.0346	0.1568	0.0915
S2GYOTr	43	0.1920	0.3288	0.3011
S3GYOTr	44	0.1708	0.3207	0.2879
B2GYOTpr	45	0.1745	0.1465	0.1674
B3GYOTpr	46	0.0979	0.1561	0.1430
S2GYOTpr	47	0.1757	0.2050	0.2068
S3GYOTpr	48	0.1698	0.2300	0.2227
S2SEL7p	49	0.0804	0.0227	0.0410
S3SEL7p	50	0.1207	0.0077	0.0465
S2SEL8p	51	0.1033	0.1230	0.1196
S3SEL8p	52	0.1607	0.0796	0.1133
S2SEL10p	53	-0.1387	0.0651	-0.0145
S3SEL10p	54	-0.1016	0.0005	-0.0449
S2SEL7r	55	0.2680	0.2971	0.3123
S3SEL7r	56	0.2849	0.2805	0.3076
S2SEL8r	57	0.1297	0.0192	0.0650

Table 115c continued 5/5

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B

including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 115d

Character in seedling trial		Evaluation trial, A5, Random type						
		ReTCHp	ReTCHr	ReTCHpr	ReCCSp	ReCCSr	ReCCSpr	ReTSHp
S2NMGp	25	0.5106	0.6363	0.6359	0.3489	0.1773	0.2865	0.5670
S3NMGp	26	0.5534	0.6215	0.6462	0.4178	0.2358	0.3535	0.6290
S2NMGr	27	0.5613	0.6282	0.6541	0.4209	0.1963	0.3379	0.6400
S3NMGr	28	0.5208	0.5880	0.6101	0.4719	0.2618	0.3973	0.6210
S2NMGpr	29	0.5495	0.6520	0.6636	0.3925	0.1914	0.3188	0.6170
S3NMGpr	30	0.5653	0.6361	0.6609	0.4620	0.2587	0.3899	0.6550
S2GVARp	31	-0.1008	0.0296	-0.0278	0.4134	0.2798	0.3701	0.0630
S3GVARp	32	-0.0961	-0.0188	-0.0560	0.3998	0.2602	0.3534	0.0620
S2GVARr	33	0.3119	0.0687	0.1867	0.4250	0.2911	0.3823	0.4290
S3GVARr	34	0.3214	0.1386	0.2352	0.4724	0.2675	0.4001	0.4550
S2GVARpr	35	0.2164	0.0662	0.1412	0.4965	0.3388	0.4459	0.3710
S3GVARpr	36	0.2185	0.1036	0.1658	0.5439	0.3220	0.4668	0.3900
S2STVp	37	-0.3586	-0.0848	-0.2183	-0.0649	-0.1091	-0.0871	-0.3270
S3STVp	38	-0.2509	-0.0379	-0.1392	-0.1985	-0.1498	-0.1848	-0.2870
S2STVr	39	0.1227	0.2611	0.2210	-0.0896	-0.0412	-0.0717	0.0790
S3STVr	40	0.2323	0.4353	0.3812	-0.1889	-0.1550	-0.1812	0.1370
S2STVpr	41	0.0259	0.2106	0.1446	-0.0932	-0.0612	-0.0828	-0.0040
S3STVpr	42	0.1550	0.3821	0.3121	-0.2112	-0.1704	-0.2014	0.0620
		1	2	3	4	5	6	7

Character in seedling trial		Evaluation trial, A5, Random type						
		ReTSHr	ReTSHpr	ReGYOTp	ReGYOTr	ReGYOTpr	ReSEL7p	ReSEL7r
S2NMGp	25	0.6714	0.6849	0.5557	0.6373	0.6506	0.4455	0.7410
S3NMGp	26	0.6708	0.7164	0.6278	0.6408	0.6955	0.4243	0.7460
S2NMGr	27	0.6645	0.7183	0.6346	0.6786	0.7184	0.6620	0.6690
S3NMGr	28	0.6395	0.6942	0.6333	0.6575	0.7071	0.6511	0.6350
S2NMGpr	29	0.6887	0.7211	0.6089	0.6757	0.7016	0.5585	0.7310
S3NMGpr	30	0.6887	0.7406	0.6603	0.6788	0.7339	0.5462	0.7320
S2GVARp	31	0.1114	0.0980	0.1088	0.1004	0.1152	-0.0933	0.2970
S3GVARp	32	0.0576	0.0656	0.1189	0.0351	0.0887	-0.1110	0.1130
S2GVARr	33	0.1386	0.3020	0.4466	0.2163	0.3750	0.4495	0.3190
S3GVARr	34	0.2037	0.3534	0.4791	0.2904	0.4315	0.6294	0.3240

Table 115d Continued 2/3

Character in seedling trial		Evaluation trial, A5, Random type						
		ReTCHp	ReTCHr	ReTCHpr	ReCCSp	ReCCSr	ReCCSpr	ReTSHr
S2STVr	39	0.2416	0.1825	0.0209	0.2694	0.1470	0.2644	0.1183
S3STVr	40	0.3828	0.2952	0.0598	0.3916	0.2314	0.3854	0.1943
S2STVpr	41	0.1880	0.1078	-0.0542	0.2164	0.0756	0.2044	0.1133
S3STVpr	42	0.3265	0.2235	-0.0041	0.3457	0.1703	0.3493	0.1553
		8	9	10	11	12	13	14

Character in seedling trial		Evaluation trial, A5, Random type						
		ReS7plr	ReSEL8p	ReSEL8r	ReS8plr	ReSEL10p	ReSEL10r	ReS10p
S2NMGp	25	0.7086	0.2474	0.7183	0.5226	0.0860	0.6213	0.3733
S3NMGp	26	0.6974	0.2515	0.7614	0.5958	0.1565	0.6528	0.4513
S2NMGr	27	0.7679	0.4901	0.6205	0.5979	0.1781	0.6766	0.4233
S3NMGr	28	0.7453	0.4772	0.6162	0.5887	0.1681	0.6323	0.4163
S2NMGpr	29	0.7574	0.3663	0.6952	0.5732	0.1309	0.6658	0.4073
S3NMGpr	30	0.7522	0.3648	0.7326	0.6211	0.1692	0.6748	0.4573
S2GVARp	31	0.0607	-0.2269	0.4453	0.0753	-0.1368	0.1828	0.0763
S3GVARp	32	-0.0283	-0.1793	0.2647	0.0795	0.0073	0.1271	0.1393
S2GVARr	33	0.5058	0.2570	0.3018	0.2233	0.1715	0.1248	0.0433
S3GVARr	34	0.5645	0.4290	0.3030	0.3223	0.2456	0.1294	0.1173
S2GVARpr	35	0.4325	0.1262	0.4073	0.2089	0.0891	0.1683	0.0623
S3GVARpr	36	0.4412	0.2689	0.3532	0.2915	0.1999	0.1573	0.1523
S2STVp	37	-0.2252	-0.2202	0.0683	-0.0100	-0.0469	0.0706	0.1203
S3STVp	38	-0.1897	-0.0652	-0.1572	0.0152	0.0100	0.0995	0.0903
S2STVr	39	0.1176	0.1673	0.0386	0.1144	0.1511	0.0367	0.2123
S3STVr	40	0.2415	0.3058	0.0823	0.2823	0.2379	0.2222	0.3683
S2STVpr	41	0.0523	0.0970	0.0501	0.0990	0.1227	0.0490	0.2143
S3STVpr	42	0.1760	0.2604	0.0404	0.2565	0.2156	0.2202	0.3493
		15	16	17	18	19	20	21

Table 115d Continued 3/3

Character in seedling trial		Evaluation trial, A5		
		ReSTp	ReSTr	ReSTplr
S2NMGp	25	0.2330	0.2345	0.2481
S3NMGp	26	0.2192	0.1837	0.2073
S2NMGr	27	0.3292	0.3937	0.4000
S3NMGr	28	0.3304	0.3992	0.4034
S2NMGpr	29	0.2843	0.3148	0.3254
S3NMGpr	30	0.2796	0.2891	0.3052
S2GVARp	31	-0.3779	-0.2043	-0.2970
S3GVARp	32	-0.2325	-0.2373	-0.2606
S2GVARr	33	-0.0220	-0.1386	-0.0985
S3GVARr	34	0.0594	-0.0443	-0.0018
S2GVARpr	35	-0.1558	-0.1867	-0.1882
S3GVARpr	36	-0.0488	-0.1340	-0.1095
S2STVp	37	0.0474	0.2084	0.1609
S3STVp	38	0.3698	0.3121	0.3600
S2STVr	39	0.3859	0.5123	0.5104
S3STVr	40	0.6115	0.7494	0.7636
S2STVpr	41	0.3507	0.4987	0.4861
S3STVpr	42	0.6267	0.7384	0.7613
		22	23	24

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = (p+r)/2 where p,r are plot values

plr = (p+r)/2 where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B

including brix = GB

ST = stalks

WS = weight per stalk (kg)

GVAR = within-plot variance for NMG

Table 115e

Character in seedling trial	Evaluation trial	A5, Random type						
		ReBRiXp	ReBRiXr	ReBRp1r	ReHARDp	ReHARDr	ReHp1r	ReNMGr
B2STp	25	0.0816	0.2572	0.2033	-0.0673	-0.0022	-0.0378	0.4420
B3STp	26	0.0303	0.2510	0.1654	-0.0009	0.0558	0.0297	0.4020
S2STp	27	0.2774	0.1817	0.2799	0.1158	-0.0427	0.0400	0.6290
S3STp	28	0.2749	0.1994	0.2879	0.1479	-0.0357	0.0608	0.6070
B2STr	29	0.1950	0.0198	0.1247	0.0429	0.0932	0.0733	0.5310
B3STr	30	0.1874	0.0839	0.1574	0.1396	0.1643	0.1650	0.5290
S2STr	31	0.2038	-0.0542	0.0888	0.0470	0.0280	0.0398	0.4690
S3STr	32	0.2722	-0.0660	0.1260	0.1386	0.0787	0.1173	0.4890
B2STpr	33	0.1419	0.1513	0.1739	-0.0156	0.0452	0.0157	0.5070
B3STpr	34	0.1168	0.1750	0.1704	0.0750	0.1176	0.1045	0.4930
S2STpr	35	0.2440	0.0520	0.1791	0.0799	-0.0035	0.0411	0.5570
S3STpr	36	0.2811	0.0547	0.2043	0.1469	0.0281	0.0946	0.5580
B2G_Bp	37	0.2980	0.4353	0.4633	-0.0545	-0.1524	-0.1061	0.5180
B3G_Bp	38	0.3432	0.3733	0.4478	0.0195	-0.1150	-0.0457	0.5790
S2G_Bp	39	0.0471	0.5074	0.3227	0.2801	0.2926	0.3094	0.5440
S3G_Bp	40	0.1150	0.4876	0.3541	0.3114	0.2977	0.3278	0.5780
B2G_Br	41	0.1745	0.1554	0.1940	-0.0725	-0.0427	-0.0590	0.5440
B3G_Br	42	0.2309	0.1391	0.2339	0.2355	0.1432	0.2065	0.6170
S2G_Br	43	0.1809	0.2748	0.2786	0.2536	0.2147	0.2510	0.6520
S3G_Br	44	0.2845	0.2361	0.3287	0.4021	0.2266	0.3367	0.7400
B2G_Bpr	45	0.2625	0.3329	0.3688	-0.0686	-0.1106	-0.0919	0.5780
B3G_Bpr	46	0.3197	0.2817	0.3773	0.1490	0.0227	0.0971	0.6730
S2G_Bpr	47	0.1090	0.4340	0.3219	0.2847	0.2752	0.3015	0.6230
S3G_Bpr	48	0.1975	0.4169	0.3709	0.3751	0.2902	0.3573	0.6940
B2GBp	49	0.3034	0.5508	0.5367	-0.0851	-0.1492	-0.1226	0.4420
B3GBp	50	0.3559	0.5525	0.5669	-0.0416	-0.1684	-0.1092	0.5030
S2GBp	51	0.1627	0.6408	0.4827	0.1541	0.1742	0.1767	0.4400
S3GBp	52	0.2130	0.6411	0.5157	0.1728	0.1480	0.1723	0.4860
B2GBr	53	0.3345	0.4223	0.4667	-0.0536	-0.0385	-0.0472	0.5700
B3GBr	54	0.3604	0.3924	0.4750	0.1279	0.0793	0.1127	0.5700
S2GBr	55	0.2998	0.5918	0.5493	0.1223	0.0279	0.0796	0.6490
S3GBr	56	0.3929	0.5890	0.6152	0.2383	0.0226	0.1384	0.6900

Table 115e continued 2/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReNMGr	ReNMGplr	ReFIBREp	ReFIBREr	ReFIBRpr	ReSTVp	ReSTVr
B2STp	25	0.6368	0.6423	0.2828	0.5167	0.4246	-0.1072	0.057
B3STp	26	0.5758	0.5805	0.3072	0.5248	0.4411	-0.1891	0.072
S2STp	27	0.6075	0.7127	0.1875	0.3396	0.2800	-0.0228	0.312
S3STp	28	0.6246	0.7122	0.1660	0.3259	0.2618	-0.0002	0.271
B2STr	29	0.6911	0.7165	0.3140	0.5060	0.4342	0.0511	0.392
B3STr	30	0.6759	0.7030	0.3831	0.5408	0.4875	-0.0098	0.476
S2STr	31	0.4778	0.5470	0.3374	0.4839	0.4336	0.0152	0.457
S3STr	32	0.4795	0.5573	0.3103	0.4237	0.3870	0.0704	0.479
B2STpr	33	0.6944	0.7100	0.3119	0.5362	0.4498	-0.0335	0.226
B3STpr	34	0.6617	0.6787	0.3653	0.5625	0.4906	-0.1033	0.294
S2STpr	35	0.5526	0.6405	0.2797	0.4336	0.3774	-0.0016	0.406
S3STpr	36	0.5603	0.6448	0.2526	0.3907	0.3403	0.0398	0.397
B2G_Bp	37	0.4948	0.5938	0.2501	0.2308	0.2508	-0.2788	-0.140
B3G_Bp	38	0.5139	0.6295	0.1954	0.1747	0.1929	-0.2477	-0.036
S2G_Bp	39	0.8066	0.7958	0.4401	0.4466	0.4636	-0.0788	0.187
S3G_Bp	40	0.7637	0.7842	0.4121	0.4255	0.4382	-0.0821	0.189
B2G_Br	41	0.6810	0.7139	0.2473	0.4016	0.3437	-0.1249	0.322
B3G_Br	42	0.5782	0.6962	0.3763	0.5028	0.4631	-0.0339	0.269
S2G_Br	43	0.7202	0.8058	0.3985	0.5232	0.4855	-0.1083	0.154
S3G_Br	44	0.6327	0.7996	0.3918	0.4976	0.4681	-0.0416	0.206
B2G_Bpr	45	0.6347	0.7092	0.2716	0.3387	0.3209	-0.2261	0.082
B3G_Bpr	46	0.6154	0.7468	0.3262	0.3896	0.3760	-0.1525	0.139
S2G_Bpr	47	0.8152	0.8464	0.4472	0.5064	0.5002	-0.0965	0.183
S3G_Bpr	48	0.7668	0.8524	0.4356	0.4900	0.4855	-0.0710	0.211
B2GBp	49	0.5290	0.5778	0.1553	0.1509	0.1599	-0.2321	-0.259
B3GBp	50	0.5679	0.6289	0.1168	0.0864	0.1054	-0.2665	-0.252
S2GBp	51	0.7946	0.7367	0.3231	0.2980	0.3240	-0.1922	-0.034
S3GBp	52	0.7725	0.7457	0.2805	0.2804	0.2932	-0.1683	-0.051
B2GBr	53	0.7088	0.7500	0.1517	0.2637	0.2204	-0.2760	0.123
B3GBr	54	0.6797	0.7407	0.2983	0.3692	0.3509	-0.1842	0.100
S2GBr	55	0.8175	0.8670	0.2444	0.3320	0.3039	-0.2331	-0.071
S3GBr	56	0.7308	0.8380	0.2219	0.3072	0.2791	-0.2180	-0.120

Table 115e continued 3/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReSTVp1r	ReBRVp	ReBRVr	ReBRVp1r	ReGVp	ReGVr	ReGVp
B2STp	25	-0.0478	-0.0374	-0.0542	0.0368	-0.0692	0.4047	0.269
B3STp	26	-0.0968	-0.0230	-0.0222	0.0983	-0.1640	0.3319	0.147
S2STp	27	0.1424	-0.3653	-0.0699	-0.2442	-0.2017	0.4188	0.230
S3STp	28	0.1366	-0.3582	-0.0406	-0.2523	-0.2233	0.4537	0.264
B2STr	29	0.2213	-0.2825	-0.1467	-0.1956	-0.2349	0.4878	0.253
B3STr	30	0.2573	-0.3809	-0.0953	-0.2044	-0.3511	0.5593	0.255
S2STr	31	0.2262	-0.3634	-0.2894	-0.3614	-0.2255	0.3496	0.144
S3STr	32	0.2862	-0.4331	-0.1960	-0.3624	-0.2659	0.3711	0.157
B2STpr	33	0.0839	-0.1612	-0.1028	-0.0771	-0.1550	0.4655	0.274
B3STpr	34	0.0885	-0.2173	-0.0626	-0.0594	-0.2741	0.4728	0.213
S2STpr	35	0.1953	-0.3760	-0.1984	-0.3195	-0.2220	0.3926	0.188
S3STpr	36	0.2254	-0.4109	-0.1298	-0.3219	-0.2539	0.4200	0.211
B2G_Bp	37	-0.2913	-0.0541	-0.1653	-0.2044	-0.1175	0.3388	0.093
B3G_Bp	38	-0.1581	-0.2040	-0.0203	-0.2119	-0.2243	0.4099	0.119
S2G_Bp	39	0.0540	-0.1008	-0.1560	-0.0976	-0.3910	0.4203	0.071
S3G_Bp	40	0.0717	-0.2169	-0.1672	-0.1909	-0.4712	0.4369	0.056
B2G_Br	41	0.0230	-0.2274	-0.2404	-0.2402	-0.1846	0.4490	0.184
B3G_Br	42	0.1117	-0.2283	-0.0916	-0.0270	-0.1519	0.5259	0.297
S2G_Br	43	0.0104	-0.0850	-0.0919	-0.0247	-0.0816	0.4016	0.258
S3G_Br	44	0.0934	-0.2249	-0.0692	-0.1107	-0.0810	0.4602	0.318
B2G_Bpr	45	-0.1582	-0.1472	-0.2186	-0.2413	-0.1624	0.4258	0.148
B3G_Bpr	46	-0.0188	-0.2437	-0.0649	-0.1294	-0.2095	0.5290	0.239
S2G_Bpr	47	0.0379	-0.0997	-0.1367	-0.0711	-0.2769	0.4364	0.158
S3G_Bpr	48	0.0868	-0.2374	-0.1379	-0.1711	-0.3392	0.4813	0.174
B2GBp	49	-0.3199	-0.0121	-0.1901	-0.2606	-0.1048	0.3232	0.107
B3GBp	50	-0.2964	-0.1103	-0.0511	-0.2392	-0.1936	0.3997	0.137
S2GBp	51	-0.1432	-0.1309	-0.1642	-0.1971	-0.4778	0.3786	-0.016
S3GBp	52	-0.1268	-0.2077	-0.1610	-0.2670	-0.4810	0.4344	0.044
B2GBr	53	-0.1444	-0.3169	-0.1405	-0.3394	-0.2413	0.4451	0.135
B3GBr	54	-0.0582	-0.2922	-0.0558	-0.1663	-0.2282	0.5465	0.231
S2GBr	55	-0.1989	-0.1736	-0.0907	-0.1922	-0.1905	0.4346	0.196
S3GBr	56	-0.2030	-0.2485	-0.0399	-0.2453	-0.1448	0.4695	0.266

Table 115e continued 4/5

Character in seedling trial		Evaluation trial, A5, Random type		
		ReWSp	ReWSr	ReWSpr
B2STp	25	0.0383	0.2759	0.1483
B3STp	26	0.0422	0.2901	0.1569
S2STp	27	-0.1522	0.0756	-0.0621
S3STp	28	-0.1382	0.0966	-0.0437
B2STr	29	-0.0669	0.0396	-0.0248
B3STr	30	-0.0673	0.0969	0.0008
S2STr	31	-0.3048	-0.2202	-0.2929
S3STr	32	-0.3212	-0.2429	-0.3133
B2STpr	33	-0.0122	0.1715	0.0692
B3STpr	34	-0.0143	0.2022	0.0817
S2STpr	35	-0.2450	-0.0921	-0.1969
S3STpr	36	-0.2458	-0.0931	-0.1977
B2G_Bp	37	0.0789	0.2966	0.1839
B3G_Bp	38	0.0806	0.3705	0.2182
S2G_Bp	39	0.2646	0.6089	0.4427
S3G_Bp	40	0.2413	0.5931	0.4207
B2G_Br	41	0.1192	0.2339	0.1809
B3G_Br	42	0.3033	0.3469	0.3489
S2G_Br	43	0.3510	0.4673	0.4339
S3G_Br	44	0.3168	0.3817	0.3740
B2G_Bpr	45	0.1066	0.2918	0.1992
B3G_Bpr	46	0.2216	0.4025	0.3221
S2G_Bpr	47	0.3181	0.5817	0.4645
S3G_Bpr	48	0.2929	0.5481	0.4335
B2GBp	49	0.1162	0.4064	0.2573
B3GBp	50	0.1951	0.5238	0.3602
S2GBp	51	0.2671	0.6296	0.4536
S3GBp	52	0.2873	0.6564	0.4785
B2GBr	53	0.2188	0.3722	0.3067
B3GBr	54	0.3873	0.4699	0.4578
S2GBr	55	0.3793	0.6366	0.5283
S3GBr	56	0.4140	0.6142	0.5406

Table 115e continued 5/5

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B
including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 115f

Character in seedling trial		Evaluation trial, A5, Random type						
		ReBRIXp	ReBRIXr	ReBRp1r	ReHARDp	ReHARDr	ReHp1r	ReNMG
B2WSp	25	0.3879	0.3299	0.4522	0.1847	-0.1582	0.0184	0.428
B3WSp	26	0.4121	0.3135	0.4604	0.1936	-0.1400	0.0313	0.545
S2WSp	27	-0.1262	0.4112	0.1605	0.0846	0.1664	0.1355	0.098
S3WSp	28	-0.0844	0.3677	0.1647	0.1609	0.2068	0.1975	0.201
B2WSr	29	0.2687	0.4287	0.4530	0.0533	-0.1887	-0.0716	0.149
B3WSr	30	0.2284	0.3982	0.4101	0.0349	-0.1169	-0.0453	0.063
S2WSr	31	0.1656	0.4106	0.3785	0.1637	0.1139	0.1499	-0.049
S3WSr	32	0.0669	0.2631	0.2219	0.2457	0.2014	0.2411	-0.068
B2WSpr	33	0.3558	0.4488	0.5170	0.1147	-0.2041	-0.0455	0.284
B3WSpr	34	0.3601	0.4356	0.5140	0.1168	-0.1500	-0.0175	0.301
S2WSpr	35	-0.0056	0.4628	0.2828	0.1323	0.1625	0.1592	0.039
S3WSpr	36	-0.0205	0.3666	0.2162	0.2256	0.2329	0.2467	0.094
B2TCHp	37	0.3677	0.4052	0.4825	0.1125	-0.1369	-0.0099	0.612
B3TCHp	38	0.3301	0.3556	0.4288	0.1377	-0.0911	0.0272	0.621
S2TCHp	39	0.1429	0.5098	0.3901	0.1967	0.0866	0.1537	0.624
S3TCHp	40	0.1799	0.4550	0.3821	0.2670	0.1076	0.2015	0.691
B2TCHr	41	0.3852	0.3669	0.4773	0.0393	-0.1536	-0.0600	0.515
B3TCHr	42	0.3212	0.3637	0.4298	0.0922	-0.0180	0.0403	0.470
S2TCHr	43	0.4184	0.3640	0.4940	0.2162	0.1167	0.1798	0.674
S3TCHr	44	0.4435	0.2783	0.4577	0.3550	0.2279	0.3144	0.708
B2TCHpr	45	0.4099	0.4176	0.5212	0.0789	-0.1585	-0.0403	0.607
B3TCHpr	46	0.3523	0.3895	0.4647	0.1234	-0.0573	0.0369	0.587
S2TCHpr	47	0.2918	0.4756	0.4718	0.2214	0.1083	0.1785	0.697
S3TCHpr	48	0.3241	0.3998	0.4473	0.3300	0.1752	0.2722	0.749
B2CCSp	49	0.0906	0.6284	0.4321	-0.1592	-0.1714	-0.1799	0.104
B3CCSp	50	0.1349	0.7471	0.5385	-0.1900	-0.3076	-0.2690	0.138
S2CCSp	51	0.3007	0.7986	0.6913	-0.0620	-0.1279	-0.1039	0.126
S3CCSp	52	0.2734	0.8064	0.6778	-0.1282	-0.1508	-0.1518	0.139
B2CCSr	53	0.2871	0.5978	0.5545	0.0208	0.0892	0.0578	0.272
B3CCSr	54	0.3200	0.6365	0.6011	-0.1329	-0.0150	-0.0831	0.150
S2CCSr	55	0.3170	0.7996	0.6979	-0.1563	-0.2753	-0.2327	0.110
S3CCSr	56	0.2846	0.8367	0.7013	-0.2147	-0.2953	-0.2744	0.033

Table 115f continued 2/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReNMGr	ReNMGplr	ReFIBREp	ReFIBREr	ReFIBRpr	ReSTVp	ReSTVr
B2WSp	25	0.2993	0.4106	0.0419	-0.2038	-0.0917	-0.1963	-0.203
B3WSp	26	0.3421	0.5025	-0.0028	-0.1398	-0.0785	-0.1372	-0.134
S2WSp	27	0.3338	0.2616	0.2339	0.1710	0.2097	-0.2116	-0.196
S3WSp	28	0.3400	0.3231	0.3214	0.2669	0.3058	-0.1353	-0.144
B2WSr	29	0.1377	0.1812	-0.2276	-0.2854	-0.2699	-0.2693	-0.493
B3WSr	30	0.1240	0.1309	-0.1971	-0.2314	-0.2251	-0.2792	-0.509
S2WSr	31	0.0769	0.0424	0.0086	-0.2150	-0.1144	-0.2490	-0.518
S3WSr	32	-0.0318	-0.0407	0.0989	-0.1095	-0.0116	-0.2313	-0.419
B2WSpr	33	0.2225	0.3003	-0.1509	-0.2933	-0.2363	-0.2772	-0.445
B3WSpr	34	0.2497	0.3300	-0.1444	-0.2346	-0.2007	-0.2666	-0.432
S2WSpr	35	0.2543	0.1900	0.1562	0.0095	0.0822	-0.2550	-0.373
S3WSpr	36	0.2019	0.1867	0.2552	0.1164	0.1901	-0.2019	-0.301
B2TCHp	37	0.5932	0.6986	0.2046	0.1263	0.1707	-0.2514	-0.144
B3TCHp	38	0.5415	0.6705	0.1570	0.1551	0.1631	-0.2248	-0.070
S2TCHp	39	0.7606	0.8080	0.3424	0.3884	0.3832	-0.1857	0.057
S3TCHp	40	0.7615	0.8449	0.3733	0.4483	0.4316	-0.1152	0.086
B2TCHr	41	0.5861	0.6520	-0.0492	0.0331	-0.0061	-0.1788	-0.154
B3TCHr	42	0.6409	0.6626	0.0812	0.1837	0.1414	-0.1924	-0.009
S2TCHr	43	0.7670	0.8510	0.3994	0.4209	0.4295	-0.1983	0.135
S3TCHr	44	0.7053	0.8272	0.4479	0.4617	0.4759	-0.1865	0.212
B2TCHpr	45	0.6403	0.7315	0.0721	0.0821	0.0809	-0.2303	-0.162
B3TCHpr	46	0.6422	0.7214	0.1272	0.1840	0.1643	-0.2251	-0.041
S2TCHpr	47	0.8218	0.8911	0.3971	0.4343	0.4356	-0.2061	0.101
S3TCHpr	48	0.7883	0.8969	0.4371	0.4871	0.4845	-0.1590	0.155
B2CCSp	49	0.4803	0.3636	-0.0470	-0.0008	-0.0235	0.0563	-0.323
B3CCSp	50	0.5418	0.4252	-0.0411	-0.0564	-0.0513	-0.0982	-0.545
S2CCSp	51	0.3482	0.3004	-0.0625	-0.0779	-0.0738	-0.4848	-0.665
S3CCSp	52	0.4477	0.3732	-0.0091	0.0111	0.0017	-0.4831	-0.698
B2CCSr	53	0.4165	0.4169	-0.0549	0.0058	-0.0239	-0.2616	-0.226
B3CCSr	54	0.4938	0.4073	-0.0054	-0.0240	-0.0159	-0.3393	-0.313
S2CCSr	55	0.3203	0.2681	-0.2014	-0.2254	-0.2237	-0.4589	-0.600
S3CCSr	56	0.3631	0.2590	-0.1969	-0.2129	-0.2146	-0.4370	-0.654

Table 115f continued 3/5

Character in seedling trial	Evaluation trial, A5, Random type							
		ReSTVp1r	ReBRVp	ReBRVr	ReBRVp1r	ReGVp	ReGVr	ReGV1r
B2WSp	25	-0.2118	-0.2597	0.0785	-0.1805	-0.5022	0.2680	-0.101
B3WSp	26	-0.1358	-0.3119	0.0359	-0.2303	-0.4158	0.2883	-0.039
S2WSp	27	-0.2145	0.0346	-0.0103	0.1125	-0.4659	0.2239	-0.161
S3WSp	28	-0.1252	0.0082	-0.0656	0.0876	-0.4054	0.2759	-0.093
B2WSr	29	-0.4858	0.1267	0.1300	0.0375	0.0717	0.0789	0.039
B3WSr	30	-0.4877	0.1817	0.1383	0.0713	0.1463	0.0129	0.017
S2WSr	31	-0.4186	0.1868	0.2569	0.2618	-0.0308	-0.0045	-0.080
S3WSr	32	-0.3127	0.2401	0.2977	0.3444	0.0456	-0.0014	-0.016
B2WSpr	33	-0.4432	-0.0123	0.1283	-0.0450	-0.1504	0.1678	-0.010
B3WSpr	34	-0.4167	-0.0153	0.1188	-0.0556	-0.0892	0.1444	-0.005
S2WSpr	35	-0.3376	0.1120	0.1146	0.1978	-0.3188	0.1445	-0.143
S3WSpr	36	-0.2360	0.1247	0.1064	0.2277	-0.2370	0.1761	-0.068
B2TCHp	37	-0.2229	-0.2165	0.0477	-0.1172	-0.4294	0.4384	0.064
B3TCHp	38	-0.1723	-0.2410	0.0162	-0.1274	-0.3976	0.3773	0.032
S2TCHp	39	-0.0795	-0.2573	-0.0376	-0.0798	-0.5019	0.5208	0.075
S3TCHp	40	-0.0090	-0.2902	-0.0643	-0.1266	-0.4714	0.5785	0.151
B2TCHr	41	-0.2466	-0.1104	0.0368	-0.1055	-0.0911	0.4238	0.242
B3TCHr	42	-0.1478	-0.1711	0.0415	-0.1086	-0.1633	0.4728	0.246
S2TCHr	43	-0.0505	-0.3265	-0.0325	-0.1501	-0.2885	0.5297	0.224
S3TCHr	44	0.0388	-0.3754	0.0586	-0.1375	-0.2759	0.5463	0.261
B2TCHpr	45	-0.2563	-0.1724	0.0454	-0.1205	-0.2663	0.4677	0.175
B3TCHpr	46	-0.1726	-0.2215	0.0318	-0.1273	-0.2982	0.4624	0.155
S2TCHpr	47	-0.0710	-0.3115	-0.0380	-0.1211	-0.4332	0.5648	0.156
S3TCHpr	48	0.0141	-0.3536	-0.0077	-0.1412	-0.4080	0.6040	0.217
B2CCSp	49	-0.0673	-0.0243	-0.0563	-0.2500	-0.0907	0.5595	0.431
B3CCSp	50	-0.3251	0.0848	0.0195	-0.1036	-0.0694	0.5151	0.390
S2CCSp	51	-0.6580	-0.0679	0.1424	-0.0832	-0.2464	0.0892	-0.095
S3CCSp	52	-0.6856	-0.0039	0.1233	-0.0396	-0.2016	0.1716	-0.002
B2CCSr	53	-0.2161	-0.1272	0.1214	-0.1567	-0.0804	0.1796	0.069
B3CCSr	54	-0.3218	-0.0860	0.1068	-0.1731	-0.1151	0.2378	0.053
S2CCSr	55	-0.6197	-0.1599	0.1612	-0.1623	-0.1833	0.1210	-0.021
S3CCSr	56	-0.6621	-0.0784	0.1240	-0.1604	-0.1363	0.1293	-0.002

Table 115f continued 4/5

Character in seedling trial		Evaluation trial, A5, Random type		
		ReWSp	ReWSr	ReWSpr
B2WSp	25	0.1315	0.3117	0.2245
B3WSp	26	0.1224	0.3718	0.2456
S2WSp	27	0.5635	0.6184	0.6362
S3WSp	28	0.5816	0.6313	0.6535
B2WSr	29	0.5797	0.6175	0.6470
B3WSr	30	0.6835	0.6510	0.7279
S2WSr	31	0.7265	0.5318	0.7016
S3WSr	32	0.7639	0.5379	0.7280
B2WSpr	33	0.4801	0.5811	0.5675
B3WSpr	34	0.5528	0.6460	0.6426
S2WSpr	35	0.7122	0.6564	0.7481
S3WSpr	36	0.7533	0.6723	0.7814
B2TCHp	37	0.1463	0.4102	0.2781
B3TCHp	38	0.1136	0.4170	0.2600
S2TCHp	39	0.3724	0.5908	0.5029
S3TCHp	40	0.3687	0.5816	0.4965
B2TCHr	41	0.4550	0.5719	0.5472
B3TCHr	42	0.4769	0.6076	0.5770
S2TCHr	43	0.2994	0.3173	0.3338
S3TCHr	44	0.3323	0.3268	0.3589
B2TCHpr	45	0.3418	0.5415	0.4615
B3TCHpr	46	0.3281	0.5590	0.4604
S2TCHpr	47	0.3641	0.4986	0.4563
S3TCHpr	48	0.3771	0.4967	0.4638
B2CCSp	49	0.3064	0.5899	0.4615
B3CCSp	50	0.4176	0.7140	0.5880
S2CCSp	51	0.2933	0.5493	0.4340
S3CCSp	52	0.3985	0.6028	0.5249
B2CCSr	53	0.2136	0.5070	0.3644
B3CCSr	54	0.3163	0.5281	0.4391
S2CCSr	55	0.2559	0.4891	0.3833
S3CCSr	56	0.3061	0.5099	0.4247

Table 115f continued 5/5

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B

including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 115g

Character in seedling trial		Evaluation trial, A5, Random type						
		ReBRIXp	ReBRIXr	ReBRp1r	ReHARDp	ReHARDr	ReHp1r	ReNM
B2TSHp	25	0.3607	0.5225	0.5470	0.0673	-0.1557	-0.0455	0.574
B3TSHp	26	0.3382	0.4943	0.5177	0.0758	-0.1617	-0.0447	0.580
S2TSHp	27	0.2035	0.6950	0.5468	0.1183	0.0152	0.0723	0.530
S3TSHp	28	0.2361	0.6707	0.5546	0.1415	0.0080	0.0798	0.590
B2TSHr	29	0.4002	0.4445	0.5345	0.0251	-0.1277	-0.0543	0.497
B3TSHr	30	0.3355	0.4437	0.4885	0.0304	-0.0333	-0.0021	0.411
S2TSHr	31	0.4720	0.6202	0.6863	0.1102	-0.0183	0.0497	0.611
S3TSHr	32	0.4990	0.5986	0.6913	0.2025	0.0591	0.1413	0.621
B2TSHpr	33	0.4121	0.5152	0.5812	0.0469	-0.1504	-0.0542	0.571
B3TSHpr	34	0.3606	0.4997	0.5373	0.0546	-0.0984	-0.0232	0.527
S2TSHpr	35	0.3490	0.6952	0.6463	0.1206	-0.0008	0.0648	0.604
S3TSHpr	36	0.3787	0.6721	0.6526	0.1794	0.0337	0.1146	0.638
B2GYOTp	37	0.3500	0.5843	0.5769	0.0316	-0.1775	-0.0770	0.557
B3GYOTp	38	0.3337	0.5667	0.5587	0.0365	-0.2004	-0.0870	0.567
S2GYOTp	39	0.2282	0.7651	0.6088	0.0924	-0.0139	0.0423	0.480
S3GYOTp	40	0.2518	0.7522	0.6178	0.0850	-0.0366	0.0252	0.514
B2GYOTr	41	0.3966	0.4736	0.5503	0.0138	-0.1135	-0.0530	0.482
B3GYOTr	42	0.3400	0.4643	0.5048	0.0035	-0.0433	-0.0222	0.393
S2GYOTr	43	0.4979	0.6197	0.7034	0.0505	-0.1263	-0.0407	0.585
S3GYOTr	44	0.5362	0.6192	0.7299	0.1206	-0.0618	0.0322	0.588
B2GYOTpr	45	0.4055	0.5644	0.6066	0.0235	-0.1534	-0.0688	0.550
B3GYOTpr	46	0.3604	0.5492	0.5677	0.0206	-0.1243	-0.0556	0.500
S2GYOTpr	47	0.3738	0.7338	0.6880	0.0766	-0.0703	0.0035	0.558
S3GYOTpr	48	0.4042	0.7319	0.7083	0.1072	-0.0509	0.0301	0.580
S2SEL7p	49	0.2403	0.7297	0.5935	0.0485	-0.0993	-0.0271	0.370
S3SEL7p	50	0.2460	0.7606	0.6153	0.0171	-0.1462	-0.0692	0.410
S2SEL8p	51	0.2422	0.7392	0.5996	0.0275	-0.1101	-0.0458	0.337
S3SEL8p	52	0.2926	0.7262	0.6259	-0.0127	-0.2006	-0.1154	0.420
S2SEL10p	53	-0.0424	0.6151	0.3434	-0.0968	-0.1823	-0.1508	0.062
S3SEL10p	54	0.0285	0.5679	0.3597	-0.1728	-0.3609	-0.2867	0.174
S2SEL7r	55	0.5841	0.5935	0.7472	0.1371	-0.1061	0.0159	0.639
S3SEL7r	56	0.5983	0.5638	0.7380	0.1904	-0.1183	0.0390	0.655

Table 115g continued 2/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReNMGr	ReNMGplr	ReFIBREp	ReFIBREr	ReFIBRpr	ReSTVp	ReSTVr
B2TSHp	25	0.6543	0.7184	0.1621	0.1063	0.1387	-0.2145	-0.211
B3TSHp	26	0.6087	0.6968	0.1129	0.1048	0.1135	-0.2237	-0.200
S2TSHp	27	0.7452	0.7561	0.2522	0.2805	0.2792	-0.3102	-0.180
S3TSHp	28	0.7815	0.8101	0.2812	0.3410	0.3269	-0.2576	-0.190
B2TSHr	29	0.5939	0.6485	-0.0843	-0.0011	-0.0423	-0.2044	-0.188
B3TSHr	30	0.6496	0.6395	0.0423	0.1200	0.0871	-0.2284	-0.082
S2TSHr	31	0.7808	0.8288	0.2611	0.2633	0.2742	-0.3410	-0.120
S3TSHr	32	0.7659	0.8235	0.3010	0.3019	0.3153	-0.3414	-0.100
B2TSHpr	33	0.6677	0.7309	0.0259	0.0498	0.0403	-0.2252	-0.215
B3TSHpr	34	0.6753	0.7127	0.0803	0.1214	0.1066	-0.2421	-0.145
S2TSHpr	35	0.8034	0.8334	0.2702	0.2870	0.2918	-0.3425	-0.160
S3TSHpr	36	0.8169	0.8613	0.3065	0.3406	0.3392	-0.3131	-0.158
B2GYOTp	37	0.6765	0.7241	0.1337	0.0946	0.1183	-0.1846	-0.256
B3GYOTp	38	0.6384	0.7068	0.0912	0.0848	0.0918	-0.2176	-0.269
S2GYOTp	39	0.7017	0.7013	0.1993	0.2182	0.2187	-0.3708	-0.294
S3GYOTp	40	0.7510	0.7541	0.2170	0.2717	0.2570	-0.3281	-0.318
B2GYOTr	41	0.5857	0.6355	-0.0951	-0.0079	-0.0514	-0.2218	-0.197
B3GYOTr	42	0.6349	0.6196	0.0235	0.0981	0.0657	-0.2528	-0.104
S2GYOTr	43	0.6924	0.7562	0.1410	0.1687	0.1627	-0.3992	-0.176
S3GYOTr	44	0.6941	0.7605	0.1669	0.1918	0.1883	-0.3975	-0.175
B2GYOTpr	45	0.6755	0.7282	0.0068	0.0404	0.0257	-0.2215	-0.240
B3GYOTpr	46	0.6814	0.7067	0.0597	0.0990	0.0841	-0.2540	-0.195
S2GYOTpr	47	0.7344	0.7658	0.1810	0.2053	0.2027	-0.4046	-0.252
S3GYOTpr	48	0.7674	0.8013	0.2055	0.2490	0.2389	-0.3809	-0.267
S2SEL7p	49	0.6281	0.5956	0.0191	0.0742	0.0503	-0.2959	-0.252
S3SEL7p	50	0.6695	0.6457	-0.0133	0.0715	0.0328	-0.2379	-0.322
S2SEL8p	51	0.6647	0.6028	0.0746	0.0896	0.0863	-0.2876	-0.308
S3SEL8p	52	0.6659	0.6474	0.0010	0.0299	0.0170	-0.2010	-0.360
S2SEL10p	53	0.5181	0.3712	0.1509	0.0457	0.0998	-0.2500	-0.272
S3SEL10p	54	0.4793	0.4017	0.0323	-0.0223	0.0037	-0.2248	-0.314
S2SEL7r	55	0.6039	0.7294	0.0482	0.0874	0.0721	-0.2987	-0.093
S3SEL7r	56	0.5462	0.6991	0.0637	0.0787	0.0750	-0.3135	-0.137

Table 115g continued 3/5

Character in seedling trial		Evaluation trial, A5, Random type						
		ReSTVp1r	ReBRVp	ReBRVr	ReBRVp1r	ReGVp	ReGVr	ReGVp
B2TSHp	25	-0.2209	-0.2070	0.0273	-0.1796	-0.4247	0.5190	0.147
B3TSHp	26	-0.2363	-0.2009	0.0183	-0.1529	-0.3792	0.4528	0.113
S2TSHp	27	-0.2893	-0.2253	-0.0088	-0.1106	-0.5061	0.4602	0.022
S3TSHp	28	-0.2597	-0.2326	-0.0351	-0.1397	-0.4656	0.5333	0.116
B2TSHr	29	-0.2620	-0.1219	0.0519	-0.1364	-0.0992	0.3977	0.217
B3TSHr	30	-0.1953	-0.1538	0.0524	-0.1327	-0.1725	0.4501	0.213
S2TSHr	31	-0.2808	-0.3305	0.0185	-0.1956	-0.3190	0.5020	0.184
S3TSHr	32	-0.2490	-0.3496	0.0878	-0.1947	-0.2943	0.5288	0.229
B2TSHpr	33	-0.2628	-0.1715	0.0444	-0.1672	-0.2605	0.4853	0.201
B3TSHpr	34	-0.2291	-0.1879	0.0387	-0.1523	-0.2858	0.4829	0.179
S2TSHpr	35	-0.3008	-0.2902	0.0044	-0.1591	-0.4399	0.5060	0.104
S3TSHpr	36	-0.2688	-0.3031	0.0236	-0.1745	-0.4069	0.5605	0.178
B2GYOTp	37	-0.2171	-0.1960	0.0115	-0.2033	-0.3919	0.5563	0.206
B3GYOTp	38	-0.2677	-0.1729	0.0161	-0.1546	-0.3498	0.4856	0.163
S2GYOTp	39	-0.3893	-0.2006	0.0207	-0.1100	-0.4863	0.3977	-0.013
S3GYOTp	40	-0.3757	-0.1946	-0.0042	-0.1286	-0.4450	0.4766	0.084
B2GYOTr	41	-0.2717	-0.1185	0.0574	-0.1397	-0.0913	0.3768	0.206
B3GYOTr	42	-0.2214	-0.1433	0.0592	-0.1356	-0.1572	0.4298	0.201
S2GYOTr	43	-0.3597	-0.3467	0.0427	-0.2402	-0.2604	0.4651	0.186
S3GYOTr	44	-0.3462	-0.3543	0.0932	-0.2482	-0.2279	0.4789	0.220
B2GYOTpr	45	-0.2667	-0.1658	0.0406	-0.1816	-0.2437	0.4933	0.222
B3GYOTpr	46	-0.2611	-0.1676	0.0425	-0.1539	-0.2646	0.4881	0.196
S2GYOTpr	47	-0.3954	-0.2834	0.0326	-0.1802	-0.4002	0.4522	0.085
S3GYOTpr	48	-0.3835	-0.2833	0.0426	-0.1942	-0.3660	0.5056	0.155
S2SEL7p	49	-0.3282	-0.1961	0.0169	-0.2875	-0.3734	0.3940	0.044
S3SEL7p	50	-0.3224	-0.1862	0.0336	-0.2555	-0.3236	0.4517	0.147
S2SEL8p	51	-0.3895	-0.1470	-0.1482	-0.3762	-0.3992	0.3288	-0.015
S3SEL8p	52	-0.3485	-0.1668	-0.1305	-0.3566	-0.3696	0.4186	0.094
S2SEL10p	53	-0.3545	0.0634	-0.1570	-0.1296	-0.3662	0.3631	0.015
S3SEL10p	54	-0.3336	-0.0125	-0.0765	-0.1511	-0.3223	0.5291	0.210
S2SEL7r	55	-0.2665	-0.4428	-0.0481	-0.4443	-0.1392	0.3652	0.176
S3SEL7r	56	-0.2761	-0.4476	0.0176	-0.4267	-0.1759	0.4044	0.207

Table 115g continued 4/5

Character in seedling trial		Evaluation trial, A5, Random type		
		ReWSp	ReWSr	ReWSpr
B2TSHp	25	0.2067	0.5230	0.3674
B3TSHp	26	0.2017	0.5465	0.3746
S2TSHp	27	0.4118	0.6744	0.5657
S3TSHp	28	0.4453	0.6889	0.5935
B2TSHr	29	0.4383	0.6054	0.5517
B3TSHr	30	0.4778	0.6364	0.5905
S2TSHr	31	0.3539	0.4531	0.4296
S3TSHr	32	0.4130	0.4893	0.4835
B2TSHpr	33	0.3626	0.6124	0.5068
B3TSHpr	34	0.3758	0.6367	0.5259
S2TSHpr	35	0.4052	0.6001	0.5282
S3TSHpr	36	0.4539	0.6285	0.5720
B2GYOTp	37	0.2282	0.5653	0.4003
B3GYOTp	38	0.2391	0.6008	0.4230
S2GYOTp	39	0.3919	0.6796	0.5554
S3GYOTp	40	0.4408	0.7044	0.5976
B2GYOTr	41	0.4142	0.5988	0.5334
B3GYOTr	42	0.4636	0.6247	0.5763
S2GYOTr	43	0.3408	0.4479	0.4190
S3GYOTr	44	0.3916	0.4822	0.4667
B2GYOTpr	45	0.3566	0.6295	0.5108
B3GYOTpr	46	0.3851	0.6576	0.5413
S2GYOTpr	47	0.3875	0.6010	0.5174
S3GYOTpr	48	0.4428	0.6381	0.5693
S2SEL7p	49	0.2639	0.6611	0.4659
S3SEL7p	50	0.3077	0.7092	0.5155
S2SEL8p	51	0.2311	0.5894	0.4129
S3SEL8p	52	0.2484	0.6314	0.4429
S2SEL10p	53	0.2787	0.3315	0.3271
S3SEL10p	54	0.2671	0.3621	0.3335
S2SEL7r	55	0.2064	0.3518	0.2906
S3SEL7r	56	0.1753	0.3241	0.2585

Table 115g continued 5/5

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = $(p+r)/2$ where p,r are plot values

plr = $(p+r)/2$ where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B
including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 115h

Character in seedling trial		Evaluation trial, A5, Random type						
		ReBRIXp	ReBRIXr	ReBRp1r	ReHARDp	ReHARDr	ReHp1r	ReNMGP
S2NMGp	25	0.2178	0.6697	0.5406	0.1192	-0.0265	0.0500	0.4746
S3NMGp	26	0.2600	0.7004	0.5872	0.0953	-0.0671	0.0150	0.5087
S2NMGr	27	0.4719	0.5233	0.6249	0.1151	-0.1403	-0.0123	0.6414
S3NMGr	28	0.5336	0.4899	0.6438	0.1393	-0.1560	-0.0071	0.6335
S2NMGpr	29	0.3410	0.6228	0.5957	0.1207	-0.0796	0.0227	0.5656
S3NMGpr	30	0.3951	0.6393	0.6405	0.1196	-0.1101	0.0058	0.5890
S2GVARp	31	0.0773	0.4883	0.3434	-0.2039	-0.1723	-0.2023	-0.0132
S3GVARp	32	0.0456	0.4010	0.2699	-0.2202	-0.2671	-0.2588	-0.0110
S2GVARr	33	0.4521	0.4677	0.5953	0.2330	-0.0986	0.0717	0.4299
S3GVARr	34	0.5247	0.4422	0.6252	0.2784	-0.1356	0.0768	0.5406
S2GVARpr	35	0.3960	0.5570	0.6085	0.1141	-0.1433	-0.0161	0.3444
S3GVARpr	36	0.4391	0.5210	0.6129	0.1320	-0.2192	-0.0456	0.4285
S2STVp	37	-0.1912	-0.0326	-0.1517	-0.3014	-0.2599	-0.3017	-0.1750
S3STVp	38	-0.2746	-0.1898	-0.3071	-0.2390	-0.2171	-0.2428	-0.1470
S2STVr	39	0.1563	-0.1566	0.0064	0.0767	0.1290	0.1103	0.2374
S3STVr	40	0.1561	-0.2589	-0.0581	0.1408	0.1200	0.1409	0.3458
S2STVpr	41	0.0939	-0.1449	-0.0288	-0.0021	0.0534	0.0274	0.1692
S3STVpr	42	0.0822	-0.2727	-0.1171	0.0749	0.0612	0.0742	0.2788

Character in seedling trial		Evaluation trial, A5, Random type						
		ReNMGr	ReNMGpr	ReFIBREp	ReFIBREr	ReFIBRpr	ReSTVp	ReSTVr
S2NMGp	25	0.7203	0.7091	0.1630	0.2503	0.2185	-0.2501	-0.1322
S3NMGp	26	0.7385	0.7388	0.1136	0.2092	0.1715	-0.2339	-0.1936
S2NMGr	27	0.6681	0.7662	0.1600	0.2152	0.1978	-0.3028	-0.0338
S3NMGr	28	0.6287	0.7346	0.1058	0.1375	0.1282	-0.2772	-0.0333
S2NMGpr	29	0.7183	0.7569	0.1666	0.2418	0.2157	-0.2819	-0.0910
S3NMGpr	30	0.7245	0.7721	0.1155	0.1871	0.1603	-0.2644	-0.1309
S2GVARp	31	0.2222	0.1353	0.1082	-0.0073	0.0494	-0.5254	-0.3049
S3GVARp	32	0.0699	0.0356	0.0287	-0.0568	-0.0171	-0.3396	-0.3666
S2GVARr	33	0.2271	0.3837	0.0823	-0.0398	0.0188	-0.3136	-0.1806
S3GVARr	34	0.2359	0.4443	0.0899	-0.0297	0.0281	-0.4157	-0.2279

Table 115h continued 2/3

Character in seedling trial		Evaluation trial, A5, Random type						
		ReNMGr	ReNMGp1r	ReFIBREp	ReFIBREr	ReFIBRpr	ReSTVp	ReSTVr
S2GVARpr	35	0.2652	0.3608	0.1057	-0.0357	0.0326	-0.4469	-0.2568
S3GVARpr	36	0.2187	0.3712	0.0841	-0.0471	0.0156	-0.4732	-0.3346
S2STVp	37	-0.0467	-0.1255	0.0581	0.0602	0.0620	-0.1230	0.0218
S3STVp	38	-0.1252	-0.1689	-0.1729	-0.0611	-0.1190	0.1985	0.1483
S2STVr	39	0.0901	0.1835	0.2658	0.2866	0.2894	-0.0303	0.4880
S3STVr	40	0.1958	0.3068	0.2930	0.3756	0.3520	0.1480	0.5205
S2STVpr	41	0.0690	0.1332	0.2468	0.2658	0.2686	-0.0551	0.4342
S3STVpr	42	0.1488	0.2392	0.2260	0.3235	0.2901	0.1748	0.4985
Character in seedling trial		Evaluation trial, A5, Random type						
		ReSTVp1r	ReBRVp	ReBRVr	ReBRVp1r	ReGVp	ReGVr	ReGVp1r
S2NMGp	25	-0.2358	-0.1964	-0.0392	-0.2325	-0.3659	0.4540	0.1137
S3NMGp	26	-0.2502	-0.2300	-0.0079	-0.2492	-0.3600	0.4959	0.1609
S2NMGr	27	-0.2183	-0.3908	-0.0071	-0.3079	-0.2346	0.5071	0.2432
S3NMGr	28	-0.1958	-0.4561	0.0511	-0.3608	-0.2439	0.5140	0.2631
S2NMGpr	29	-0.2348	-0.2916	-0.0256	-0.2741	-0.3167	0.4923	0.1767
S3NMGpr	30	-0.2377	-0.3424	0.0181	-0.3111	-0.3252	0.5276	0.2143
S2GVARp	31	-0.4739	-0.0235	0.0050	-0.2571	-0.2698	0.2301	-0.0600
S3GVARp	32	-0.3490	0.0092	0.0903	-0.1094	-0.1994	0.3541	0.1649
S2GVARr	33	-0.3758	-0.3208	-0.2533	-0.5148	-0.1681	0.1121	-0.1153
S3GVARr	34	-0.4137	-0.3397	-0.0247	-0.4136	-0.1597	0.1669	-0.0272
S2GVARpr	35	-0.4774	-0.2701	-0.2027	-0.5120	-0.2349	0.1753	-0.1153
S3GVARpr	36	-0.4760	-0.2683	0.0171	-0.3770	-0.2111	0.2811	0.0464
S2STVp	37	-0.1068	0.0563	-0.1691	-0.1954	-0.0485	0.0001	-0.0552
S3STVp	38	0.2278	0.0784	0.0488	0.0782	0.0514	0.0067	0.1174
S2STVr	39	0.2325	-0.3375	-0.2984	-0.4163	-0.0777	0.0517	-0.0299
S3STVr	40	0.3600	-0.3122	-0.2469	-0.2724	-0.0795	0.1769	0.1213
S2STVpr	41	0.1799	-0.2842	-0.3013	-0.4113	-0.0795	0.0457	-0.0388
S3STVpr	42	0.3712	-0.2638	-0.2114	-0.2284	-0.0601	0.1600	0.1337

Table 115h continued 3/3

Character in seedling trial		Evaluation trial, A5, Random type		
		ReWSp	ReWSr	ReWSpr
S2NMGp	25	0.2478	0.6190	0.4367
S3NMGp	26	0.2913	0.6609	0.4832
S2NMGr	27	0.2018	0.3752	0.2979
S3NMGr	28	0.1553	0.3170	0.2423
S2NMGpr	29	0.2342	0.5259	0.3862
S3NMGpr	30	0.2442	0.5381	0.3982
S2GVARp	31	0.1966	0.3441	0.2799
S3GVARp	32	0.0946	0.3006	0.1958
S2GVARr	33	0.2831	0.2493	0.2930
S3GVARr	34	0.2101	0.2278	0.2371
S2GVARpr	35	0.3013	0.3271	0.3395
S3GVARpr	36	0.2083	0.3077	0.2719
S2STVp	37	-0.4482	-0.4072	-0.4684
S3STVp	38	-0.6187	-0.4828	-0.6104
S2STVr	39	-0.2989	-0.3739	-0.3582
S3STVr	40	-0.3730	-0.4327	-0.4317
S2STVpr	41	-0.3660	-0.4221	-0.4226
S3STVpr	42	-0.4660	-0.4911	-0.5170

DF = 22

Correlation is significantly different from zero if > 0.404 (5%), 0.515 (1%)

The prefixes B2, S2, B3, S3, and Re are defined as follows:

	D1X rep KLM	D1X rep KL	A5 RANDOM
Single	S3	S2	Re
Bunch	B3	B2	

p = plant crop r = ratoon crop

pr = (p+r)/2 where p,r are plot values

plr = (p+r)/2 where p,r are values for each seedling or clone

SEL7, 8, 10 = Number of clones with visual NMG 7+, 8+, 10+

NMG = Visual net merit grade, GYOT = NMGYOT

Visual net merit grade of whole plot, omitting brix = G_B

including brix = GB

ST = stalks

WS = weight per stalk (kg)

Table 116. AOV` of correlations between family means in trial Ts based on two (KL) or three (KLM) replicates vs the Re type in the Te trial. Variance ratios (F) for a fixed model are presented in this table, with means and significant differences in Table 117.

Character in seedling trial	F values			F values			
	Crops	Class	Rep	Crops * Class	Crops * Rep	Class * Rep	Crops * Class * Rep
STALKS	0.9	3.1	0.5	35.4**	0.7	3.5	0.5
KG/STALK	26.7**	12.0**	1.8	0.4	1.3	0.0	0.0
NMGplot_BR	20.2**	238.7**	4.5*	2.8	0.4	6.8**	0.1
NMGplot+BR	41.4**	198.0**	6.7**	0.2	1.1	5.2*	0.1
TCH	13.5**	222.0**	1.2	1.1	0.1	2.2	1.7
CCS	10.1**	166.2**	1.4	0.6	2.0	3.6	0.1
TSH	10.9**	173.6**	3.0	10.1**	0.0	14.1**	2.0
NMGYOT	11.0**	35.9**	2.6	14.4**	0.0	22.2**	1.8
df	2	1	1	2	2	1	2

` Factorial AOV with three crop levels (P, R, PR) * two seedling classes (Class = Bs, Ss) * two replicate levels (Rep = KL, KLM) in the Ts trial. There were 48 replicates, namely 16 characters * 3 crop classes (P, R, PR) in the Re type in the Te trial. Each mean in the Te trial was based on all three replications. A Z transformation was used.
Error df = 517

Table 117. Means and significant differences for the factorial AOV of correlations, F values for which are presented in Table 116. A Z transformation was used in the analysis, and Z values rather than correlations are presented in this Table.

Character in seedling trial	General mean	Crops P	R	PR	Class Bs	Ss	Rep Kl	KLM
STALKS	0.3573	0.3525	0.3534	0.3661	0.3655	0.3492	0.3605	0.3541
					P 0.3110 << 0.3940			
					R 0.4059 >> 0.3009			
					PR 0.3795 0.3528			
					PR,R>>P P>PR>>R			
KG/STALK	0.1318	0.1853 >> 0.0671 << 0.1430			0.1550 >> 0.1086		0.1229	0.1407
		P>PR						
NMGplot_BR	0.4271	0.3845 << 0.4394 = 0.4575			0.3517 << 0.5025		0.4168 <	0.4374
							Bs 0.3286 << 0.3748	
							Ss 0.5049 = 0.5001	
							Ss>>Bs Ss>>Bs	
NMGplot+BR	0.4239	0.3697 << 0.4584 = 0.4438			0.3639 << 0.4840		0.4129 <<	0.4350
							Bs 0.3431 << 0.3847	
							Ss 0.4826 = 0.4853	
							Ss>>Bs Ss>>Bs	
TCH	0.4401	0.4069 << 0.4415 < 0.4717			0.3643 << 0.5158		0.4345	0.4456
CCS	0.1893	0.2068 >> 0.1620 << 0.1991			0.2455 >> 0.1331		0.1842	0.1944
TSH	0.4279	0.4075 = 0.4250 << 0.4513			0.3772 << 0.4787		0.4213	0.4346
					P 0.3784 << 0.4367		Bs 0.3850 = 0.3693	
					R 0.3535 << 0.4964		Ss 0.4576 << 0.4998	
					PR 0.3995 << 0.5031		Ss>>Bs Ss>>Bs	
					PR>>R PR,R>>P			
NMGYOT	0.3985	0.3936 = 0.3822 << 0.4197			0.3785 << 0.4185		0.3932	0.4039
					P 0.3952 0.3921		Bs 0.3889 > 0.3681	
					R 0.3399 << 0.4245		Ss 0.3975 << 0.4396	
					PR 0.4005 << 0.4390		Ss>>Bs Ss>>Bs	
					PR,P>>R PR,R>>P			

Table 118. AOV of correlations between family means of Ss seedlings in trial Ts based on two (KL) or three (KLM) replicates vs the Re type in trial Te.

Character in seedling trial	F values			Means General mean	Crops			Rep KL	KLM
	Crops	Rep	Crops * Rep		P	R	PR		
Visual NMG	3.6*	0.7	2.5	0.4150	0.4006 p<<pr	0.4162	0.4281	0.4114	0.4186
NMG_VAR	47.8**	2.1	1.3	0.1196	0.0230 <<	0.1815 =	0.1543	0.1093	0.1299
ST_VAR	92.6**	18.3**	1.8	0.0412	-0.1062 <<	0.1343 >	0.0955	0.0081 <<	0.0743 p<<pr
SEL7	13.6**	1.6	2.8	0.3557	0.3255 <<	0.3858		0.3452	0.3661
SEL8	5.9*	1.0	0.7	0.304	0.329 >	0.280		0.294	0.314
SEL10	23.8**	1.3	0.1	0.238	0.178 <<	0.298		0.224	0.252

Factorial AOV with two or three crop levels (P, R, PR) * two replicate levels (Rep = KL, KLM) in the Ts trial. Only two crop levels (P,R) were included for number of selections. There were 48 replicates, namely 16 characters * 3 crop classes (P, R, PR) in the Re type in the Te trial. Each mean in the Te trial was based on all three replications. A Z transformation was used.

Crop levels	Degrees of freedom			
	Crops	Rep	Crops*Rep	Error
3	2	1	2	235
2	1	1	1	141

The term a >> b = c shows that a >> c. The = is used for a non-significant difference in some cases to give a clearer presentation. >> shows $P \leq 0.01$, > shows $P \leq 0.05$

NMG_VAR = within-family variance for visual net merit grade. ST = number of stalks
SEL8 = number of seedlings with visual NMG 8.0 or higher.

Table 119. Performance of Ss seedlings in the P and R crops of trial Ts and the same clones in 4-sett plots in the Tm trial.

Character	Trial	A`	B	C	D	E
BRIX	SsP	22.48 ± 0.87	22.31 ± 0.93	21.59 ± 1.35	21.92 ± 1.71	20.96 ± 1.84
BRIX	SsR	23.23 ± 0.97	22.54 ± 1.13	22.97 ± 0.95	22.41 ± 1.39	21.74 ± 1.74
BRIX	TmP	19.805 ± 1.438	19.329 ± 1.367	19.168 ± 1.728	19.503 ± 1.238	18.525 ± 1.810
STALKS	SsP	8.70 ± 2.04	8.07 ± 2.13	7.35 ± 2.36	8.10 ± 2.99	6.82 ± 2.66
STALKS	SsR	11.45 ± 3.60	8.56 ± 3.52	11.01 ± 4.00	7.62 ± 2.98	7.27 ± 4.12
STALKS	TmP	19.216 ± 6.031	18.407 ± 5.763	19.182 ± 6.126	18.379 ± 5.486	18.072 ± 6.620
HARDNESS	SsP	5.16 ± 0.96	5.07 ± 0.88	5.25 ± 0.96	5.10 ± 0.98	4.98 ± 0.97
HARDNESS	SsR	5.01 ± 1.00	4.73 ± 0.88	4.98 ± 0.97	4.74 ± 1.13	4.67 ± 0.97
HARDNESS	TmP	5.267 ± 1.060	5.088 ± 1.111	5.030 ± 1.012	5.000 ± 0.926	4.947 ± 1.110
Visual NMG	SsP	9.15 ± 1.16	8.76 ± 0.90	6.46 ± 1.32	8.00 ± 0.00	5.91 ± 2.44
Visual NMG	SsR	9.62 ± 1.91	6.07 ± 1.39	9.01 ± 1.62	5.62 ± 1.53	5.29 ± 2.64
Visual NMG	TmP	6.344 ± 2.215	6.076 ± 2.407	5.815 ± 2.067	6.000 ± 1.871	4.831 ± 2.140
SEL8	TmP	44 (25.0)	51 (23.6)	41 (19.2)	5 (17.2)	27 (11.4)
SEL10	TmP	17 (9.7)	13 (6.0)	4 (1.9)	1 (3.4)	3 (1.3)

Class

- A Selected in plant crop, also selected independently in ratoon. 176 clones.
- B Selected in plant crop, rejected in ratoon. 216 clones.
- C Rejected in plant crop, selected in ratoon. 216 clones.
- D Surplus for crop (= plant) with higher natural selection rate. 29 clones.
- E Random 239 clones in the seedling trial, 237 clones in the mass selection trial.

The mean ± standard deviation are shown for each character, except for number of selections (SEL8, SEL10) which show the total number of selections in each class, expressed % of the number in the class, in (). Variances for SsP and SsR are not normal, so the standard deviations presented for them are not reliable. Standard deviations for TmP are based on normal variances, and are satisfactory.

Table 120. Performance of Ss seedlings in the P and R crops of trial Ts and the same clones in 4-sett plots in the Tm trial. Results are expressed as difference from the random group (E).

Character	Trial	A`	B	C	D
BRIX	SsP	+1.52 7.3	+1.35 6.4	+0.63 3.0	+0.96 4.6
BRIX	SsR	+1.49 6.9	+0.80 3.7	+1.23 5.7	+0.67 3.1
BRIX	TmP	+1.280 6.9	+0.804 4.3	+0.643 3.5	+0.978 5.3
STALKS	SsP	+1.88 27.6	+1.25 18.3	+0.53 7.8	+1.28 18.8
STALKS	SsR	+4.18 57.5	+1.29 17.7	+3.74 51.4	+0.35 4.8
STALKS	TmP	+1.144 6.3	+0.335 1.9	+1.11 6.1	0.307 1.7
HARDNESS	SsP	+0.18 3.6	+0.09 1.8	+0.27 5.4	+0.12 2.4
HARDNESS	SsR	+0.34 7.3	+0.06 1.3	+0.31 6.6	+0.07 1.5
HARDNESS	TmP	+0.320 6.5	+0.141 2.8	+0.083 1.7	0.053 1.1
Visual NMG	SsP	+3.24 54.8	+2.85 48.2	+0.55 9.3	+2.09 35.4
Visual NMG	SsR	+4.33 81.9	+0.78 14.7	+3.72 70.3	+0.33 6.2
Visual NMG	TmP	+1.513 31.3	+1.245 25.8	+0.984 20.4	1.169 24.2
SEL8 (A% - E%)	TmP	25.0% 13.6	23.6% 12.2	19.2% 7.8	17.2% 5.8
SEL10 (A% - E%)	TmP	9.7% 8.4	6.0% 4.7	1.9% 0.6	3.4% 2.1

Class

- A Selected in plant crop, also selected independently in ratoon. 176 clones.
- B Selected in plant crop, rejected in ratoon. 216 clones.
- C Rejected in plant crop, selected in ratoon. 216 clones.
- D Surplus for crop (= plant) with higher natural selection rate. 29 clones.
- E Random 239 clones in the seedling trial, 237 clones in the mass selection trial.

Except for number of selections (SEL8 SEL10) the first line = (Class - Random).

Table 121. Realized gains from individual (mass) selection in the Ts trial, based on visual NMG in P, R and PR crops.

Ts crop selected	Number (n)	Performance in 4-sett plots in trial Tm		
		Visual NMG Mean \pm SE [`]	Number of selections from trial Tm Graded 8+	Number of selections from trial Tm Graded 10+
P	390	6.196 \pm 0.118	95 (24.4%)	30 (7.7%)
R	390	6.054 \pm 0.109	85 (21.8%)	21 (5.4%)
PR	390	6.255	95 (24.4%)	28 (7.2%)
Random	237	4.831 \pm 0.139	27 (11.4%)	3 (1.3%)
Significance [~]		P,R >> Random	P,R,PR >> Random	P,PR >> Random R > Random

[`] SE = standard error of the mean = SD/ \sqrt{n}

[~] > significantly greater than ($P \leq 0.05$)

>> significantly greater than ($P \leq 0.01$)

For Means, significant differences were determined by t-tests

For number of selections, Chisquare tests were used, with a contingency correction of 0.25

Table 122. Correlations between performance of individual Ss seedlings in the Ts trial and the same clones in 4-sett plots in the Tm trial.

Character	Class	NMG SsP	NMG SsR	NMG SsPR	NMG Tm	BRIX SsP	BRIX SsR	BRIX Tm	STALK SsP	STALK SsR	STALK Tm	HARD SsP	HARD SsR	HARD Tm
NMG														
SsP	A+B	1.000	0.258	0.582	-0.017	0.211	0.143	0.058	0.301	0.179	-0.018	0.030	-0.032	-0.031
	A+C	1.000	0.246	0.796	0.114	0.450	0.184	0.226	0.435	0.117	0.014	-0.041	-0.021	0.099
	random	1.000	0.634	0.896	0.307	0.517	0.394	0.334	0.587	0.480	0.109	0.056	-0.037	0.123
SsR	A+B	0.258	1.000	0.936	0.096	0.100	0.313	0.176	0.267	0.579	0.128	0.106	0.106	0.081
	A+C	0.246	1.000	0.783	0.111	0.096	0.115	0.080	0.237	0.468	0.105	0.052	0.037	0.051
	random	0.634	1.000	0.912	0.344	0.346	0.383	0.227	0.538	0.750	0.336	0.131	0.082	0.041
SsPR	A+B	0.582	0.936	1.000	0.075	0.161	0.315	0.169	0.335	0.568	0.101	0.100	0.078	0.061
	A+C	0.796	0.783	1.000	0.142	0.349	0.190	0.195	0.427	0.367	0.075	0.006	0.010	0.091
	random	0.896	0.912	1.000	0.361	0.473	0.429	0.308	0.621	0.686	0.251			
Tm	A+B	-0.017	0.096	0.075	1.000	0.134	0.139	0.403	0.063	0.148	0.631	0.128	0.029	0.281
	A+C	0.114	0.111	0.142	1.000	0.190	0.135	0.413	0.186	0.197	0.590	0.096	0.113	0.351
	random	0.307	0.344	0.361	1.000	0.207	0.230	0.409	0.328	0.291	0.622	0.059	0.122	0.291
BRIX														
SsP	A+B	0.211	0.100	0.161	0.134	1.000	0.549	0.422	-0.046	-0.058	-0.015	0.010	-0.032	0.031
	A+C	0.450	0.096	0.349	0.190	1.000	0.602	0.463	0.093	-0.079	0.009	0.035	-0.004	0.101
	random	0.517	0.346	0.473	0.207	1.000	0.714	0.533	0.125	0.127	0.001	0.066	-0.118	0.061
SsR	A+B	0.143	0.313	0.315	0.139	0.549	1.000	0.420	-0.030	-0.033	-0.006	0.049	0.025	0.081
	A+C	0.184	0.115	0.190	0.135	0.602	1.000	0.389	0.029	-0.133	0.025	-0.003	-0.007	0.011
	random	0.394	0.383	0.429	0.230	0.714	1.000	0.505	0.063	0.123	0.039	0.029	-0.119	-0.031
Tm	A+B	0.058	0.176	0.169	0.403	0.422	0.420	1.000	-0.020	0.058	-0.003	0.114	-0.029	0.261
	A+C	0.226	0.080	0.195	0.413	0.463	0.389	1.000	0.054	-0.023	0.036	0.119	-0.023	0.351
	random	0.334	0.227	0.308	0.409	0.533	0.505	1.000	0.092	0.095	0.035	0.069	-0.027	0.271
STALKS														
SsP	A+B	0.301	0.267	0.335	0.063	-0.046	-0.030	-0.020	1.000	0.573	0.315	0.026	0.039	0.001
	A+C	0.435	0.237	0.427	0.186	0.093	0.029	0.054	1.000	0.633	0.388	0.057	0.020	0.101
	random	0.587	0.538	0.621	0.328	0.125	0.063	0.092	1.000	0.693	0.470	-0.009	-0.068	0.071
SsR	A+B	0.179	0.597	0.568	0.148	-0.058	-0.033	0.058	0.573	1.000	0.300	0.106	0.077	0.131
	A+C	0.117	0.468	0.367	0.197	-0.079	-0.133	-0.023	0.633	1.000	0.402	0.129	0.050	0.161
	random	0.480	0.750	0.686	0.291	0.127	0.123	0.095	0.693	1.000	0.451	0.143	0.035	0.081
Tm	A+B	-0.018	0.128	0.101	0.631	-0.015	-0.006	-0.003	0.315	0.300	1.000	-0.026	0.023	0.041
	A+C	0.014	0.105	0.075	0.590	0.009	0.025	0.036	0.388	0.402	1.000	0.008	0.039	0.081
	random	0.109	0.336	0.251	0.622	0.001	0.039	0.035	0.470	0.451	1.000	-0.002	0.060	0.061

Table 122 continued 2/2

Character	Ts crop selected	NMG SsP	NMG SsR	NMG SsPR	NMG Tm	BRIX SsP	BRIX SsR	BRIX Tm	STALK SsP	STALK SsR	STALK Tm	HARD SsP	HARD SsR	HARD Tm
HARDNESS														
SsP	A+B	0.030	0.106	0.100	0.128	0.010	0.049	0.114	0.026	0.106	-0.026	1.000	0.347	0.456
	A+C	-0.041	0.052	0.006	0.096	0.035	-0.003	0.119	0.057	0.129	0.008	1.000	0.320	0.395
	random	0.056	0.131		0.059	0.066	0.029	0.069	-0.009	0.143	-0.002	1.000	0.462	0.437
SsR	A+B	-0.032	0.106	0.078	0.029	-0.032	0.025	-0.029	0.039	0.077	0.023	0.347	1.000	0.365
	A+C	-0.021	0.037	0.010	0.113	-0.004	-0.007	-0.023	0.020	0.050	0.039	0.320	1.000	0.328
	random	-0.037	0.082		0.122	-0.118	-0.119	-0.027	-0.068	0.035	0.060	0.462	1.000	0.400
Tm	A+B	-0.031	0.088	0.063	0.283	0.031	0.081	0.268	0.002	0.135	0.042	0.456	0.369	1.000
	A+C	0.095	0.052	0.093	0.352	0.105	0.014	0.358	0.101	0.165	0.083	0.399	0.328	1.000
	random	0.123	0.049		0.299	0.066	-0.033	0.273	0.072	0.088	0.060	0.437	0.400	1.000

Ts Crop selected	DF	Correlation significant at	
		P ≤ 0.05	P ≤ 0.01
A+B, A+C	388	0.100	0.131
random	235	0.130	0.169

Class

A	Selected in P crop, also selected independently in R	176 clones.
B	Selected in P crop, rejected in R	216 clones.
C	Rejected in P crop, selected in R	216 clones.
D	Surplus for crop (= P) with higher natural selection rate	29 clones.
E	Random	239 clones.

A+B Selected in TsP crop, 390 clones (2 missing).

A+C Selected in TsR crop, 390 clones (2 missing).

E random, 237 clones (2 missing).

Distributions for selected Ss seedlings (A+B, A+C) are not normal for visual NMG in the Ts trial, so correlations involving them are not valid. There are also doubts about characters such as brix and number of stalks in the Ts trial. All correlations in the Tm trial are valid, as are those between the Tm trial vs the random group in the Ts trial.

Table 123. Selection differentials in the trial Ts, realized gains in trial Tm, with broad sense heritabilities.

Table 123a. Selection differential (Dif), with realized gains from selection (Gain), expressed as per cent of the mean for the random group. Means presented in Table 124 are used in these calculations.

Crop	Class`	Selection differential or realized gain			
		BRIX	STALKS	HARDNESS	Visual NMG
TsP	Dif = (A+B) - E	6.860	22.149	2.425	50.666
TsR	Dif = (A+C) - E	6.234	53.478	6.885	75.255
TmP	Gain = (A+B) - E	5.490	3.862	4.467	28.255

Table 123b Realized broad sense heritability (realized $h^2 = \text{Gain} / \text{Dif}$), compared with $h^2 = \text{the correlation TmP vs Ts in } ()$

Ts trial Crop	Class	Broad sense heritability			
		BRIX	STALKS	HARDNESS	Visual NMG
TsP	A+B	0.800 (0.422)	0.174 (0.315)	1.842 (0.456)	0.558 (-0.017)
TsR	A+C	0.881 (0.389)	0.072 (0.402)	0.649 (0.328)	0.375 (0.111)
TsP	E	(0.533)	(0.470)	(0.437)	(0.307)
TsR	E	(0.505)	(0.451)	(0.400)	(0.344)

Class

- A Selected in P crop, also selected independently in R 176 clones.
- B Selected in P crop, rejected in R 216 clones.
- C Rejected in P crop, selected in R 216 clones.
- D Surplus for crop (= P) with higher natural selection rate 29 clones.
- E Random 239 clones.

	n	DF	Correlation	significant
			$P \leq 0.05$	$P \leq 0.01$
A+B Selected in TsP crop,	390 clones (2 missing)	388	0.100	0.131
A+C Selected in TsR crop,	390 clones (2 missing)	388	0.100	0.131
E random,	237 clones (2 missing)	235	0.130	0.169

The class is used as the X1 variable for correlations, X2 being the value for the same class in the Tm trial. For example, the correlation of 0.422 is (A+B, TsP vs A+B, TmP). Correlations for (A+B) and (A+C) are not valid for visual NMG, and those for brix and number of stalks are doubtful, because the distributions for (A+B) and (A+C) in the Ts trial are abnormal.

Table 124. Mean \pm standard deviation, with CV in (), for each character in the Ts and Tm trials

Crop	Class`	Character [mean \pm standard deviation, with CV in ()]			
		BRIX	STALKS	HARDNESS	Visual NMG
TsP	A+B	22.385 \pm 0.907 (4)	8.355 \pm 2.111 (25)	5.110 \pm 0.915 (18)	8.936 \pm 1.045 (12)
	A+C	21.993 \pm 1.243 (6)	7.959 \pm 2.324 (29)	5.209 \pm 0.958 (18)	7.677 \pm 1.833 (24)
	random	20.948 \pm 1.841 (9)	6.840 \pm 2.665 (39)	4.989 \pm 0.973 (20)	5.931 \pm 2.439 (41)
TsR	A+B	22.851 \pm 1.115 (5)	9.855 \pm 3.830 (39)	4.857 \pm 0.945 (19)	7.663 \pm 2.416 (32)
	A+C	23.092 \pm 0.963 (4)	11.210 \pm 3.836 (34)	4.999 \pm 0.982 (20)	9.292 \pm 1.783 (19)
	random	21.737 \pm 1.746 (8)	7.304 \pm 4.415 (60)	4.677 \pm 0.962 (21)	5.302 \pm 2.640 (50)
TmP	A+B	19.542 \pm 1.417 (7)	18.770 \pm 5.891 (31)	5.168 \pm 1.090 (21)	6.196 \pm 2.324 (38)
	A+C	19.455 \pm 1.633 (8)	19.197 \pm 6.076 (32)	5.137 \pm 1.039 (20)	6.054 \pm 2.149 (35)
	random	18.525 \pm 1.815 (10)	18.072 \pm 6.629 (37)	4.947 \pm 1.112 (22)	4.831 \pm 2.145 (44)

Class

- A Selected in P crop, also selected independently in R. 176 clones.
- B Selected in P crop, rejected in R. 216 clones.
- C Rejected in P crop, selected in R. 216 clones.
- D Surplus for crop (= P) with higher natural selection rate. 29 clones.
- E Random 239 clones in the Ts trial, 237 clones in the Tm trial.

A+B Selected in TsP crop, 392 clones

A+C Selected in TsR crop, 390 clones (2 missing).

Standard deviations for A+B and A+C in the Ts trial are not valid for visual NMG, and those for brix and number of stalks are doubtful, because the variances are not normal.

All standard deviations for random, and all standard deviations in the TmP crop, are valid.

Table 125. Performance of Ss seedlings in trial Tm.

Visual NMG Ts	SsP, A+B`		SsR, A+C`		SsP, random		SsR, random		SsPR, random	
	Sum	NMG 8+ in Tm No. (%)	Sum	NMG 8+ in Tm No. (%)	Sum	NMG 8+ in Tm No. (%)	Sum	NMG 8+ in Tm No. (%)	Sum	NMG 8+ in Tm No. (%)
1					7	0 (0)	16	0 (0)	8	0 (0)
2					12	0 (0)	22	0 (0)	15	0 (0)
3					22	1 (5)	22	0 (0)	33	1 (1)
4					42	3 (7)	38	6 (16)	41	4 (10)
5					29	4 (14)	32	2 (6)	31	4 (13)
6					27	2 (7)	28	3 (11)	42	3 (7)
7					41	5 (12)	41	6 (15)	29	5 (17)
8	208	50 (24)	197	37 (19)	26	5 (19)	16	3 (19)	19	4 (21)
9	121	30 (25)	72	13 (18)	17	3 (18)	10	3 (30)	7	3 (43)
10	26	7 (27)	50	17 (34)	6	2 (33)	3	3 (100)	7	2 (29)
11	24	6 (25)	22	7 (32)	7	2 (29)	3	0 (0)	5	1 (20)
12	10	2 (20)	23	6 (26)	1	0 (0)	2	0 (0)		
13	3	0 (0)	12	3 (25)			2	1 (50)		
14-18			14	2 (14)			2	0 (0)		
Total	392	95 (24)	390	85 (22)	237	27 (11)	237	27 (11)	237	27 (11)
NMG8+					57	12 (21)	38	10 26	38	10 26
NMG7+					98	17 (17)	79	16 20	67	15 22

Class

- A Selected in P crop, also selected independently in R 176 clones.
 B Selected in P crop, rejected in R 216 clones.
 C Rejected in P crop, selected in R 216 clones.
 D Surplus for crop (= P) with higher natural selection rate 29 clones.
 E Random 239 clones.

Table 126. Performance of random Ss seedlings (class E) in trials TsP and TmP.

MG in trial TsP	Trial Tm		3	4	5	6	7	8	9	10	11	12+	Sum	NMG 8+ No. (%)
	1	2												
.	1	2	2		2								7	0 (0)
1	1	2	3	2	1	2	1						12	0 (0)
2	3	2	8	2	4	1	1		1				22	1 (5)
3	3	7	6	8	5	3	7	1	2				42	3 (7)
4	2	3	5	4	6	5		3	1				29	4 (14)
5		2	4	6	5	4	4	1	1				27	2 (7)
6	1		4	10	9	9	3	2	2	1			41	5 (12)
7	1		2	8	3	2	5	3	1		1		26	5 (19)
8	1		1	4	4	2	2	2		1			17	3 (18)
9			1	2			1	1	1				6	2 (33)
10		1		1	2	2		1	1				8	2 (25)
Total	13	19	36	47	41	30	24	14	10	2	1		237	27 (11)
NMG8+	2	1	4	15	9	6	8	7	3	1	1		57	12 (21)

Table 127. Performance of random Ss seedlings (class E) in trials TsR and TmP.

NMG in Trial TsR	Trial Tm												Sum	NMG 8+ No. (%	
	1	2	3	4	5	6	7	8	9	10	11	12+			
1	4	3	2	4	3									16	0 (0
2	3	5	6	3	3	1	1							22	0 (0
3		2	8	4	2	3	3							22	0 (0
4	2	4	5	5	6	5	5	2	4					38	6 (16
5	2	1	7	6	5	5	4	1	1					32	2 (6
6	1	2	1	8	8	2	3	3						28	3 (11
7	1	1	4	7	11	6	5	1	4	1				41	6 (15
8			1	5	1	3	3	2		1				16	3 (19
9		1		2	1	3		2			1			10	3 (30
10								2	1					3	3 (100
11+			2	3	1	2		1						9	1 (11
Total	13	19	36	47	41	30	24	14	10	2	1			237	27 (11
NMG8+	0	1	3	10	3	8	3	7	1	1	1			38	10 (26

Table 128. Performance of random Ss seedlings (class E) in trials TsPR and TmP.

NMG in Trial TsPR	Trial Tm												Sum	NMG 8+ No. (%	
	1	2	3	4	5	6	7	8	9	10	11	12+			
1	2	2	1	1	2									8	0 (0
2	2	2	8	2	1									15	0 (0
3	3	7	6	5	3	3	5			1				33	1 (3
4	3	4	8	5	7	7	3	2	2					41	4 (10
5		2	4	7	7	3	4	2	2					31	4 (13
6	2	1	5	12	11	5	3	2	1					42	3 (7
7			1	5	5	6	7	2	2	1				29	5 (17
8	1		1	5	3	3	2	2		1	1			19	4 (21
9				2	1	1		1	2					7	3 (43
10		1	1	3				2						7	2 (29
11+			1		1	2		1						5	1 (20
Total	13	19	36	47	41	30	24	14	10	2	1		237	27 (11	
NMG8+	1	1	3	10	5	6	2	6	2	1	1		38	10 (20	

Table 129. Effect of selection in random (E) Ss seedlings on number of selections (SEL8) lost at the next stage of selection (Tm trial).

NMG	Ss seedlings, P crop		Ss seedlings, R crop		Ss seedlings, PR crop			
	Discarded No. (%)	Lost from Tm trial No. (%)	Discarded No. (%)	Lost from Tm trial No. (%)	Discarded No. (%)	Lost from Tm trial No. (%)	Discarded No. (%)	Lost from Tm trial No. (%)
2	19 (8)	0 (0)			23	10	0	0
3	41 (17)	1 (4)	60 (25)	0 (0)	56	24	1	4
4	83 (35)	4 (15)	98 (41)	6 (22)	97	41	5	19
5	112 (47)	8 (30)	130 (55)	8 (30)	128	54	9	33
6	139 (59)	10 (37)	158 (67)	11 (41)	170	72	12	44
7	180 (76)	15 (56)	199 (84)	17 (63)	199	84	17	63
8.0	196 (83)	18 (67)	215 (91)	20 (74)	218	92	21	78
8.5	206 (87)	20 (74)						
9	223 (94)	23 (85)	225 (95)	23 (85)	225	95	24	89
10	229 (97)	25 (93)			232	98	26	96
11	236 (100)	27 (100)						
12	237 (100)	27 (100)	233 (98)	26 (96)	237	100	27	100
14			237 (100)	27 (100)				

Table 130. Mean \pm standard deviation, with CV in (), for each character in clones of the Re type (n=646) compared with the same clones in Ss seedlings.

Type	Character [mean \pm standard deviation, with CV in ()]			
	BRIX	STALKS	HARDNESS	Visual NMG
SsP	20.762 \pm 1.856 (9)	6.338 \pm 2.625 (41)	4.697 \pm 0.933 (20)	5.603 \pm 2.296 (41)
SsR	21.813 \pm 1.719 (8)	7.113 \pm 4.311 (61)	4.773 \pm 1.048 (22)	5.252 \pm 2.779 (53)
ReP	23.685 \pm 1.700 (7)	17.685 \pm 6.307 (36)	5.036 \pm 1.026 (20)	6.257 \pm 2.259 (36)
ReR	20.020 \pm 1.632 (8)	23.762 \pm 8.833 (37)	5.093 \pm 1.075 (21)	5.972 \pm 2.786 (47)

Table 131. Correlations between clones of the Re type and the Ss seedlings which provided their planting material. The crop (P, R) is included in the name of the character

		1	2	3	4	5	6	7
BrixSsP	1	1.0000						
StalkSsP	2	0.0860	1.0000					
HardSsP	3	0.1153	0.1537	1.0000				
NmgSsP	4	0.5177	0.6097	0.2217	1.0000			
BrixSsR	5	0.6553	0.0372	0.0709	0.3380	1.0000		
StalkSsR	6	0.1212	0.7011	0.2551	0.5192	0.1193	1.0000	
HardSsR	7	0.0720	0.1074	0.3511	0.1161	0.1553	0.1997	1.0000
NmgSsR	8	0.2733	0.5237	0.2583	0.6099	0.3557	0.7874	0.2458
StalkReP	9	0.0314	0.4193	0.0571	0.2565	0.0302	0.4978	0.0868
BrixReP	10	0.3141	0.0540	0.0917	0.2240	0.3259	0.1489	0.1850
HardReP	11	-0.0251	0.0864	0.3420	0.0859	-0.0087	0.1382	0.3677
NmgReP	12	0.1767	0.2180	0.1521	0.3566	0.0998	0.3651	0.1335
StalkReR	13	0.0610	0.4427	0.1541	0.2231	0.0628	0.5627	0.1282
BrixReR	14	0.4991	0.0642	0.0654	0.2858	0.5494	0.0944	0.0784
HardReR	15	0.0282	0.0629	0.3400	0.0516	0.0459	0.1191	0.3445
NmgReR	16	0.2823	0.2100	0.1890	0.3790	0.2624	0.3612	0.1395
		1	2	3	4	5	6	7
NmgSsR	8	1.0000						
StalkReP	9	0.3473	1.0000					
BrixReP	10	0.2461	0.1299	1.0000				
HardReP	11	0.1457	0.0566	0.3172	1.0000			
NmgReP	12	0.3860	0.5761	0.3515	0.2434	1.0000		
StalkReR	13	0.3898	0.6300	0.1005	0.1345	0.4299	1.0000	
BrixReR	14	0.2360	0.1080	0.3812	0.0910	0.1472	0.1223	1.0000
HardReR	15	0.1084	0.0823	0.1671	0.3959	0.1454	0.1306	0.2749
NmgReR	16	0.4273	0.4265	0.1920	0.2100	0.5411	0.6022	0.4119
		8	9	10	11	12	13	14
HardReR	15	1.0000						
NmgReR	16	0.1975	1.0000					
		15	16					

Table 132. Visual net merit grades given to clones in the Re type compared with grades given to the same clones in Ss seedlings. The lower limit of each class is shown, e.g. 4 = 4.0 to 4.99.

Table 132a

NmgSsP	NmgReP															% of total	
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+	
1	5	1	5	7	4	0	3	1	0	0	0	26	1	4	4	1	
2	3	3	4	4	9	8	4	0	3	0	0	38	3	8	6	2	
3	1	4	10	11	13	16	4	3	7	1	0	70	11	16	11	6	
4	0	0	10	14	21	22	14	12	7	1	2	103	22	21	16	12	
5	0	2	4	14	10	17	16	11	7	3	2	86	23	27	13	13	
6	1	1	2	5	14	11	21	10	10	6	3	84	29	35	13	16	
7	0	3	3	11	13	27	17	26	10	2	3	115	41	36	18	22	
8	0	2	4	5	8	15	10	13	8	7	2	74	30	41	11	16	
9	1	1	1	1	5	8	5	8	3	3	3	39	17	44	6	9	
10	0	0	0	0	1	0	1	1	0	1	1	5	3	60	1	2	
11+	0	0	0	0	1	1	1	0	0	1	2	6	3	50	1	2	
Sum	11	17	43	72	99	125	96	85	55	25	18	646	183	28	100	100	
8+	1	3	5	6	15	24	17	22	11	12	8	124	53	43			

Table 132b

NngSsP	NmgReR															% of total	
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+	
1	8	3	3	6	2	2	0	1	0	1	0	26	2	8	4	1	
2	5	9	6	5	4	2	3	4	0	0	0	38	4	11	6	2	
3	3	7	7	15	11	4	5	8	4	3	3	70	18	26	11	11	
4	4	5	17	19	16	12	18	4	4	1	3	103	12	12	16	7	
5	0	8	10	14	16	7	13	5	5	2	6	86	18	21	13	11	
6	3	3	6	10	14	11	14	11	6	3	3	84	23	27	13	14	
7	1	1	6	8	20	27	19	11	5	6	11	115	33	29	18	20	
8	0	2	5	6	5	7	18	10	4	5	12	74	31	42	11	19	
9	0	2	1	2	5	4	4	7	5	2	7	39	21	54	6	13	
10	0	0	0	1	0	1	1	0	1	0	1	5	2	40	1	1	
11+	0	0	0	1	2	1	0	0	0	1	1	6	2	33	1	1	
Sum	24	40	61	87	95	78	95	61	34	24	47	646	166	26	100	100	
8+	0	4	6	10	12	13	23	17	10	8	21	124	56	45			

Table 132c

NmgSSP	NmgRePR												% of total			
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+
1	5	5	4	6	3	1	1	0	1	0	0	26	1	4	4	1
2	4	4	5	10	6	4	3	2	0	0	0	38	2	5	6	2
3	3	4	12	9	13	10	10	5	3	1	0	70	9	13	11	7
4	0	4	9	26	20	19	14	4	6	0	1	103	11	11	16	9
5	0	2	9	14	20	13	11	8	4	4	1	86	17	20	13	13
6	1	1	3	13	13	14	17	14	6	1	1	84	22	26	13	17
7	0	1	5	13	19	23	31	6	9	5	3	115	23	20	18	18
8	0	1	3	5	12	13	16	6	9	6	3	74	24	32	11	19
9	1	0	0	2	5	9	7	4	7	3	1	39	15	38	6	12
10	0	0	0	0	1	1	0	1	0	2	0	5	3	60	1	2
11+	0	0	0	1	0	2	1	0	0	1	1	6	2	33	1	2
Sum	14	22	50	99	112	109	111	50	45	23	11	646	129	20	100	100
8+	1	1	3	8	18	25	24	11	16	12	5	124	44	35		

Table 132d

NmgSsR	NmgReP													% of total		
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+
1	5	6	11	13	11	7	4	4	3	0	0	64	7	11	10	4
2	0	2	5	9	18	9	6	4	6	2	0	61	12	20	9	7
3	1	2	5	15	11	13	11	3	2	2	0	65	7	11	10	4
4	1	1	9	8	11	15	9	2	6	2	3	67	13	19	10	7
5	2	1	3	9	13	14	6	17	7	2	2	76	28	37	12	15
6	0	1	2	8	8	16	14	19	2	3	1	74	25	34	11	14
7	1	4	4	4	17	38	27	15	15	4	5	134	39	29	21	21
8	1	0	4	2	8	7	14	9	6	3	3	57	21	37	9	11
9	0	0	0	3	0	5	1	3	5	1	0	18	9	50	3	5
10	0	0	0	0	2	0	2	1	2	3	0	10	6	60	2	3
11+	0	0	0	1	0	1	2	8	1	3	4	20	16	80	3	9
Sum	11	17	43	72	99	125	96	85	55	25	18	646	183	28	100	100
8+	1	0	4	6	10	13	19	21	14	10	7	105	52	50		

Table 132e

NmgSsR	NmgReR															% of total	
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+	
1	14	9	12	12	5	9	1	2	0	0	0	64	2	3	10	1	
2	4	8	9	9	10	4	6	1	6	2	2	61	11	18	9	7	
3	2	9	8	17	3	3	10	9	2	1	1	65	13	20	10	8	
4	0	4	12	12	16	7	6	4	3	0	3	67	10	15	10	6	
5	2	3	6	9	8	15	13	7	7	2	4	76	20	26	12	12	
6	1	0	5	9	13	11	15	9	3	5	3	74	20	27	11	12	
7	1	5	7	12	26	17	18	19	6	7	16	134	48	36	21	29	
8	0	2	2	3	9	6	16	6	4	2	7	57	19	33	9	11	
9	0	0	0	2	3	3	4	1	0	2	3	18	6	33	3	4	
10	0	0	0	1	1	1	1	1	1	1	3	10	6	60	2	4	
11+	0	0	0	1	1	2	5	2	2	2	5	20	11	55	3	7	
Sum	24	40	61	87	95	78	95	61	34	24	47	646	166	26	100	100	
8+	0	2	2	7	14	12	26	10	7	7	18	105	42	40			

Table 132f

NmgSsR	NmgRePR												% of total			
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+
1	7	10	11	17	9	5	4	1	0	0	0	64	1	2	10	1
2	0	5	6	18	11	7	4	5	4	0	1	61	10	16	9	8
3	2	0	13	15	10	11	8	4	2	0	0	65	6	9	10	5
4	1	3	8	10	18	15	3	4	3	1	1	67	9	13	10	7
5	2	1	5	11	13	9	20	6	7	2	0	76	15	20	12	12
6	0	0	2	7	17	16	18	8	3	2	1	74	14	19	11	11
7	1	3	3	15	24	24	28	11	16	8	1	134	36	27	21	28
8	1	0	2	2	8	16	13	5	4	3	3	57	15	26	9	12
9	0	0	0	3	1	3	4	3	2	1	1	18	7	39	3	5
10	0	0	0	1	0	1	3	1	1	3	0	10	5	50	2	4
11+	0	0	0	0	1	2	6	2	3	3	3	20	11	55	3	9
Sum	14	22	50	99	112	109	111	50	45	23	11	646	129	20	100	100
8+	1	0	2	6	10	22	26	11	10	10	7	105	38	36		

Table 132g

NngSsPR	NngRePR												% of total			
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+
1	6	7	4	8	4	2	1	0	1	0	0	33	1	3	5	1
2	2	6	10	14	8	5	6	4	0	0	0	55	4	7	9	3
3	4	4	16	23	14	11	5	3	2	1	1	84	7	8	13	5
4	0	2	8	19	17	19	16	8	4	0	0	93	12	13	14	9
5	0	0	3	7	24	16	12	7	11	2	0	82	20	24	13	16
6	0	2	6	14	21	18	25	9	5	4	3	107	21	20	17	16
7	1	1	2	9	16	22	27	11	11	6	2	108	30	28	17	23
8	1	0	1	2	7	9	10	5	7	4	2	48	18	38	7	14
9	0	0	0	3	0	5	4	2	2	2	1	19	7	37	3	5
10	0	0	0	0	1	2	4	0	2	2	0	11	4	36	2	3
11+	0	0	0	0	0	0	1	1	0	2	2	6	5	83	1	4
Sum	14	22	50	99	112	109	111	50	45	23	11	646	129	20	100	100
8+	1	0	1	5	8	16	19	8	11	10	5	84	34	40		

Table 133. Correlation matrix for random clones common to Ss seedlings, the Re type in Trial Te, and trial Tm

BrixTm	1	1.0000							
StalkTm	2	0.1515	1.0000						
HardTm	3	0.4422	0.1575	1.0000					
NmgTm	4	0.4684	0.7249	0.3391	1.0000				
BrixSsP	5	0.3215	-0.0812	-0.0571	0.0883	1.0000			
StalkSsP	6	0.2597	0.4961	0.1037	0.3751	0.0810	1.0000		
HardSsP	7	0.3033	-0.1909	0.3729	0.0453	0.0992	0.0699	1.0000	
NmgSsP	8	0.3897	0.1031	0.0724	0.1894	0.5958	0.5614	0.1964	
BrixSsR	9	0.4039	-0.0071	-0.1288	0.2457	0.7391	-0.0103	0.0561	
StalkSsR	10	0.2590	0.4770	0.1455	0.4507	0.0857	0.7418	0.2498	
HardSsR	11	0.0872	-0.0319	0.1963	0.1235	-0.1801	-0.2463	0.2917	
NmgSsR	12	0.3467	0.3412	0.0315	0.3916	0.3705	0.5556	0.2805	
LiveRe	13	0.1761	0.3490	0.3339	0.3017	-0.0111	0.1393	0.2586	
StalkReP	14	0.2417	0.5766	0.1722	0.5198	0.0318	0.5568	0.0755	
BrixReP	15	0.4230	0.0164	0.1295	0.1077	0.4148	0.2208	0.1378	
HardReP	16	0.3647	-0.0116	0.5387	0.2059	-0.1125	0.0680	0.5558	
NmgReP	17	0.2728	0.2485	0.0966	0.3778	-0.0036	0.3746	0.1430	
StalkReR	18	0.0591	0.5219	0.0579	0.4753	-0.0811	0.3374	0.0327	
BrixReR	19	0.5002	0.0737	0.0943	0.3115	0.5538	0.0531	0.1668	
HardReR	20	0.2876	-0.0604	0.4411	0.2078	-0.2539	-0.1274	0.4451	
NmgReR	21	0.2261	0.3310	0.1883	0.5227	0.1420	0.2732	0.2929	
		1	2	3	4	5	6	7	
NmgSsP	8	1.0000							
BrixSsR	9	0.4401	1.0000						
StalkSsR	10	0.4834	0.1131	1.0000					
HardSsR	11	-0.1754	-0.0876	0.0062	1.0000				
NmgSsR	12	0.7001	0.3945	0.7308	0.1383	1.0000			
LiveRe	13	0.1073	-0.0573	0.2523	0.0408	0.2120	1.0000		
StalkReP	14	0.2550	0.0847	0.6016	-0.0717	0.3434	0.4774	1.0000	
BrixReP	15	0.5461	0.4330	0.1353	-0.1613	0.3216	0.2566	0.1985	
HardReP	16	0.1716	-0.1092	0.1360	0.2780	0.1476	0.1398	-0.0139	
NmgReP	17	0.4062	0.1668	0.3745	0.0482	0.3680	0.2337	0.5815	
StalkReR	18	-0.0100	0.0672	0.4483	0.0381	0.1876	0.3193	0.6276	
BrixReR	19	0.3598	0.6936	0.1099	-0.0583	0.2942	0.0197	0.1135	
HardReR	20	-0.2233	-0.1233	-0.0241	0.3619	-0.0658	0.1886	-0.0172	
NmgReR	21	0.3285	0.3585	0.4426	0.1154	0.4760	0.2095	0.4392	
		8	9	10	11	12	13	14	
BrixReP	15	1.0000							
HardReP	16	0.2330	1.0000						
NmgReP	17	0.3511	0.1577	1.0000					
StalkReR	18	0.0035	-0.0135	0.4213	1.0000				
BrixReR	19	0.5257	0.1209	0.1188	0.1465	1.0000			

Table 134. Visual net merit grades given to clones in the Re type compared with grades given to the same clones in the Tm trial. The lower limit of each class is shown, e.g. 4 = 4.0 to 4.99.

Table 134a

NngReP	NngTmP											% of total					
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	2	0	0	0	0	0	0	0	0	0	2	0	0	3	0	0
4	0	1	1	2	0	3	0	0	0	0	0	7	0	0	10	0	0
5	1	1	1	1	3	0	1	0	1	0	0	9	1	11	13	10	0
6	2	1	1	4	4	2	1	0	0	0	0	15	0	0	22	0	0
7	1	1	4	0	3	1	3	0	3	0	0	16	3	19	24	30	0
8	0	1	0	2	2	0	1	3	0	0	0	9	3	33	13	30	0
9	0	0	0	1	0	1	2	0	0	0	1	5	1	20	7	10	0
10	0	0	0	1	1	0	0	1	0	0	0	3	1	33	4	10	0
11+	0	0	0	0	0	1	0	0	1	0	0	2	1	50	3	10	0
Sum	4	7	7	11	13	8	8	4	5	0	1	68	10	15	100	100	0
8+	0	1	0	4	3	2	3	4	1	0	1	19	6	32			0

Table 134b

NmgReR	NmgTnP												% of total				
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	1	3	1	1	1	0	0	0	0	0	0	7	0	0	10	0	0
3	1	1	0	0	2	0	1	0	1	0	0	6	1	17	9	10	0
4	0	1	2	4	1	1	1	0	0	0	0	10	0	0	15	0	0
5	1	2	2	0	3	2	1	0	0	0	0	11	0	0	16	0	0
6	0	0	0	2	0	0	0	1	0	0	0	3	1	33	4	10	0
7	0	0	2	0	5	0	3	1	1	0	0	12	2	17	18	20	0
8	0	0	0	3	0	2	0	0	1	0	0	6	1	17	9	10	0
9	0	0	0	1	0	1	0	0	1	0	0	3	1	33	4	10	0
10	1	0	0	0	0	1	1	0	0	0	0	3	0	0	4	0	0
11+	0	0	0	0	1	1	1	2	1	0	1	7	4	57	10	40	0
Sum	4	7	7	11	13	8	8	4	5	0	1	68	10	15	100	100	0
8+	1	0	0	4	1	5	2	2	3	0	1	19	6	32			

Table 134c

NmgRePR	NmgTmP											% of total				
	1	2	3	4	5	6	7	8	9	10	11+	Sum	8+	%8+	Ss	Re8+
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0
3	0	2	0	1	0	0	0	0	0	0	0	3	0	0	4	0
4	2	1	3	1	3	3	1	0	0	0	0	14	0	0	21	0
5	0	2	1	2	3	0	1	0	1	0	0	10	1	10	15	10
6	1	1	1	3	3	0	2	0	0	0	0	11	0	0	16	0
7	1	0	2	2	2	2	2	2	2	0	0	15	4	27	22	40
8	0	0	0	1	1	1	0	0	0	0	0	3	0	0	4	0
9	0	0	0	1	1	0	1	1	2	0	0	6	3	50	9	30
10	0	0	0	0	0	2	0	1	0	0	0	3	1	33	4	10
11+	0	0	0	0	0	0	1	0	0	0	1	2	1	50	3	10
Sum	4	7	7	11	13	8	8	4	5	0	1	68	10	15	100	100
8+	0	0	0	2	2	3	2	2	2	0	1	14	5	36		

Table 135. Number of selections from trial Tm which reached advanced stages.

(a) A comparison of normal mass selection in SsP and SsR seedlings.

Ss crop selected	Class	4-sett No.	30-sett No. (%)	YOT No. (%)	SYT No. (%)
P	A+B	392	56 (14.3%)	11 (2.8%)	5 (1.3%)
R	A+C	390	52 (13.3)	8 (2.1)	3 (0.8)
Random	E	237	5 (2.1)	2 (0.8)	0 (0.0)

P,R >> Random

(b) A comparison of classes A, B and C.

Ss crop selected	Class	4-sett No.	30-sett No. (%)	YOT No. (%)	SYT No. (%)
P & R	A	176	34 (19.3%)	6 (3.4%)	2 (1.1%)
P only	B	216	22 (10.1)	5 (2.3)	3 (1.4)
R only	C	214	18 (8.4)	2 (0.9)	1 (0.5)

A > B
A >> C

Table 136. Number of selections from trial Te which reached advanced stages.

(a) Comparison of types produced by modified mass selection

Type	30-sett	YOT	SYT
Re	103	17	8
Be	130	17	7
Se	124	26	6

(b) Comparison of selection levels (L1 = best 3 per plot, L3 = worst)

Level	30-sett	YOT	SYT
L1	127	15	9
L2	116	18	5
L3	114	27	7

Chisquare tests showed that there were no significant differences between types (Re, Be, Se), or between the three selection levels within the Be and Se types.

Table 137. Value in Ts trial of families with highest and lowest cross ratios in 1989. Cross ratios are the mean of 79N to latest series, omitting 80N which were used in the experiment.

Character	Mean values			Top - Worst (% worst)	Top - GM (%GM)	Families including	
	GM	Worst 4	Top 3			Top 5	Top 3
tsSTpr	46.5275	41.4175	49.3867	7.9692 (19)	2.8592 (6)	21	15
tsSTp	52.1804	47.1675	54.2200	7.0525 (15)	2.0396 (4)	19	13
tsSTr	40.8746	35.6650	44.5533	8.8883 (25)	3.6787 (9)	20	10
tsBRIXpr	21.9325	21.5960	22.3110	0.7150 (3)	0.3785 (2)	13	13
tsBRIXp	21.6264	21.0753	22.0887	1.0134 (5)	0.4622 (2)	18	14
tsBRIXr	22.2390	22.1168	22.5337	0.4169 (2)	0.2946 (1)	16	16
tsHARDpr	5.2362	5.1043	5.1667	0.0624 (1)	-0.0695 (-1)	23	23
tsHARDp	5.4931	5.3750	5.1667	-0.2083 (-4)	-0.3264 (-6)	24	24
tsHARDr	4.9791	4.8333	5.1667	0.3334 (7)	0.1875 (4)	20	20
tsG_Bpr	7.2014	6.3543	8.1390	1.7848 (28)	0.9376 (13)	16	13
tsG_Bp	6.6180	6.0000	7.9443	1.9443 (32)	1.3264 (20)	18	4
tsG_Br	7.7847	6.7083	8.3333	1.6251 (24)	0.5487 (7)	21	21
tsGBpr	6.3958	5.6025	7.5967	1.9942 (36)	1.2008 (19)	15	7
tsGBp	6.0083	5.2525	7.7233	2.4708 (47)	1.7150 (29)	13	4
tsGBr	6.7850	5.9575	7.4767	1.5192 (26)	0.6917 (10)	18	18
tsWSpr	0.7624	0.7625	0.8963	0.1338 (18)	0.1339 (18)	10	9
tsWSp	0.5936	0.5943	0.7743	0.1801 (30)	0.1807 (30)	12	4
tsWSr	0.9313	0.9305	1.0187	0.0882 (9)	0.0874 (9)	12	12
tsTCHpr	65.8563	58.1900	83.3433	25.1533 (43)	17.4871 (27)	13	4
tsTCHp	59.3225	54.2625	80.1400	25.8775 (48)	20.8175 (35)	16	4
tsTCHr	72.3875	62.1175	86.5467	24.4292 (39)	14.1592 (20)	11	8
tsCCSpr	14.6138	14.2350	15.0397	0.8047 (6)	0.4259 (3)	13	13
tsCCSp	14.2693	13.6493	14.7893	1.1401 (8)	0.5200 (4)	18	14
tsCCSr	14.9580	14.8205	15.2890	0.4685 (3)	0.3310 (2)	16	16
tsTSHpr	9.6954	8.3875	12.5500	4.1625 (50)	2.8546 (29)	12	4
tsTSHp	8.4846	7.4175	11.8367	4.4192 (60)	3.3521 (40)	13	5
tsTSHr	10.9067	9.3600	13.2633	3.9033 (42)	2.3567 (22)	12	7
tsGYOTpr	6.5833	5.5725	8.7600	3.1875 (57)	2.1767 (33)	12	4
tsGYOTp	5.8992	4.9550	8.5200	3.5650 (72)	2.6208 (44)	15	5

Table 137 continued 2/4

Parameter	Mean values			Top - Worst (% worst)	Top - GM (%GM)	Families including	
	GM	Worst 4	Top 3			Top 5	Top 3
IsS7p1r	9.3333	8.5833	16.2220	7.6387 (89)	6.8887 (74)	21	3
IsS8p1r	4.5694	4.0833	9.7778	5.6944 (139)	5.2083 (114)	21	4
IsI0p1r	0.8750	1.0000	2.3333	1.3333 (133)	1.4583 (167)	24	9
IsBRVp1r	1.5751	1.7148	1.5210	-0.1938 (-11)	-0.0541 (-3)	15	15
IsBRVpr	2.0023	2.3080	1.9123	-0.3957 (-17)	-0.0900 (-4)	19	19
IsBRVp	2.0852	2.2910	2.0120	-0.2790 (-12)	-0.0732 (-4)	19	19
IsBRVr	1.9195	2.3258	1.8127	-0.5131 (-22)	-0.1068 (-6)	20	16
IsLBRVpr	1.0611	1.1558	1.0520	-0.1037 (-9)	-0.0091 (-1)	17	17
IsLBRVp	1.0869	1.1623	1.0840	-0.0782 (-7)	-0.0029 (-0)	19	19
IsLBRVr	1.0355	1.1490	1.0200	-0.1290 (-11)	-0.0155 (-1)	19	16
IsG_Bpr	7.6125	6.7085	8.8890	2.1805 (33)	1.2765 (17)	17	6
IsG_Bp	7.5137	6.3748	8.9443	2.5696 (40)	1.4306 (19)	16	7
IsG_Br	7.7112	7.0418	8.8333	1.7916 (25)	1.1222 (15)	19	8
IsGBpr	6.6035	5.7543	8.3667	2.6124 (45)	1.7632 (27)	17	4
IsGBp	6.6028	5.5250	8.5113	2.9863 (54)	1.9085 (29)	14	8
IsGBr	6.6042	5.9835	8.2223	2.2388 (37)	1.6181 (25)	20	3
IsWSpr	0.9450	0.9060	0.9449	0.0390 (4)	-0.0001 (-0)	24	24
IsWSp	0.9388	0.8755	0.9463	0.0708 (8)	0.0075 (1)	24	24
IsWSr	0.9511	0.9364	0.9436	0.0072 (1)	-0.0075 (-1)	19	19
IsTCHpr	67.8088	60.5200	77.0333	16.5133 (27)	9.2246 (14)	19	12
IsTCHp	64.3754	56.8725	73.9967	17.1242 (30)	9.6213 (15)	18	17
IsTCHr	71.2425	64.1650	80.0633	15.8983 (25)	8.8208 (12)	14	10
IsCCSpr	14.1111	14.0935	14.7677	0.6742 (5)	0.6565 (5)	20	16
IsCCSp	13.5978	13.3988	14.3993	1.0006 (7)	0.8015 (6)	19	13
IsCCSr	14.6245	14.7880	15.1360	0.3480 (2)	0.5115 (3)	22	15
IsTSHpr	9.6040	8.5850	11.3550	2.7700 (32)	1.7510 (18)	15	7
IsTSHp	8.7841	7.6608	10.6120	2.9513 (39)	1.8279 (21)	17	13
IsTSHr	10.4240	9.5093	12.0980	2.5888 (27)	1.6740 (16)	14	4
IsGYOTpr	6.2848	5.6128	7.7957	2.1829 (39)	1.5109 (24)	16	9
IsGYOTp	5.8552	5.0350	7.4553	2.4203 (48)	1.6001 (27)	19	10
IsGYOTr	6.7140	6.1900	8.1357	1.9457 (31)	1.4217 (21)	11	4

Table 137 continued 3/4

Parameter	Mean values					Families including	
	GM	Worst 4	Top 3	Top - Worst (% worst)	Top - GM (%GM)	Top 5	Top 3
ssSEL7pr	12.0142	11.0850	17.7200	6.6350 (60)	5.7058 (47)	21	4
ssSEL7p	12.2500	10.5000	18.1133	7.6133 (73)	5.8633 (48)	19	8
ssSEL7r	11.7775	11.6650	17.3333	5.6683 (49)	5.5558 (47)	17	3
ssSEL8pr	5.8192	5.3775	11.1100	5.7325 (107)	5.2908 (91)	20	4
ssSEL8p	6.1942	5.0000	11.8900	6.8900 (138)	5.6958 (92)	18	3
ssSEL8r	5.4446	5.7500	10.3333	4.5833 (80)	4.8888 (90)	18	6
ssSEL10pr	1.2783	1.1675	2.9967	1.8292 (157)	1.7183 (134)	19	10
ssSEL10p	0.8742	0.6650	1.8900	1.2250 (184)	1.0158 (116)	19	10
ssSEL10r	1.6804	1.6675	4.1133	2.4458 (147)	2.4329 (145)	17	13
ssVISGpr	5.2939	4.9768	6.2813	1.3046 (26)	0.9875 (19)	16	6
ssVISGp	5.4021	4.9668	6.4383	1.4716 (30)	1.0363 (19)	17	7
ssVISGr	5.1855	4.9865	6.1240	1.1375 (23)	0.9385 (18)	14	5
ssGVARpr	6.0292	6.3250	7.7633	1.4383 (23)	1.7342 (29)	22	6
ssGVARp	5.0658	4.7350	5.5467	0.8117 (17)	0.4808 (9)	19	10
ssGVARr	6.9925	7.9150	9.9800	2.0650 (26)	2.9875 (43)	23	8
ssLGVpr	1.8998	1.9333	2.1130	0.1798 (9)	0.2132 (11)	22	5
ssLGVp	1.7719	1.7165	1.8713	0.1548 (9)	0.0994 (6)	19	10
ssLGVr	2.0276	2.1503	2.3547	0.2044 (10)	0.3270 (16)	23	8
ssSTVpr	11.1379	10.3225	12.4800	2.1575 (21)	1.3421 (12)	21	13
ssSTVp	6.3892	6.4300	6.5467	0.1167 (2)	0.1575 (2)	24	17
ssSTVr	15.8867	14.2125	18.4133	4.2008 (30)	2.5267 (16)	21	13
ssLSVpr	2.3695	2.3330	2.4820	0.1490 (6)	0.1125 (5)	21	13
ssLSTVp	1.9699	1.9743	2.0140	0.0397 (2)	0.0441 (2)	24	16
ssLSTVr	2.7690	2.6913	2.9503	0.2591 (10)	0.1813 (7)	21	12
ssSQRGpr	2.3379	2.2576	2.5392	0.2816 (12)	0.2013 (9)	16	6
ssSQRGp	2.3685	2.2662	2.5886	0.3224 (14)	0.2201 (9)	17	7
ssSQGR	2.3073	2.2491	2.4899	0.2408 (11)	0.1826 (8)	13	5
ssSQGVpr	0.2975	0.3229	0.3340	0.0112 (3)	0.0365 (12)	22	10
ssSQGVp	0.2504	0.2533	0.2353	-0.0180 (-7)	-0.0151 (-6)	21	20
ssSQGVr	0.3447	0.3925	0.4327	0.0402 (10)	0.0880 (26)	23	11
ssLSQGr	0.2575	0.2766	0.2838	0.0072 (3)	0.0263 (10)	22	10

Table 137 continued 4/4

Parameter	Mean values					Families including	
	GM	Worst 4	Top 3	Top - Worst (% worst)	Top - GM (%GM)	Top 5	Top 3

KEY

 p = plant crop, r = ratoon crop, pr = (p+r)/2 where p,r are plot values
 sBRVpr = (p+r)/2 of each seedling was used to compute within plot brix
 variance
 VAR = within plot variance
 SEL7 (8, 10) = Number of selections (seedlings) graded 7+ (8+, 10+)
 ST = number of stalks, HARD = Hardness
 %B = Visual NMG of whole plot, omitting brix
 %B = Visual NMG of whole plot, adjusted for brix
 WS = Weight per stalk (kg)
 % = net merit grade, VISG = Visual NMG
 %YOT = NMGYOT vs standard variety Q82
 %QRG, %SQG = SQRT(Visual NMG of each seedling + 0.5)
 %SELST = Number of selectable stalks in each bunch-planted family

Table 138. Value in Re families with highest and lowest cross ratios in 1989. Cross ratios are the mean of 79N to latest series, omitting 80N which were used in the experiment.

Parameter	Mean values					Families including	
	GM	Worst 4	Top 3	Top - Worst (% worst)	Top - GM (%GM)	Top 5	Top 3
ReFIBREp	13.4213	13.2145	12.9613	-0.2532 (-2)	-0.4600 (-3)	18	18
ReFIBREr	14.1730	13.6568	13.6330	-0.0237 (-0)	-0.5400 (-4)	20	20
ReFIBRpr	13.7971	13.4353	13.2973	-0.1379 (-1)	-0.4997 (-4)	19	19
ReTCHp	66.0237	58.7550	74.0700	15.3150 (26)	8.0463 (12)	18	13
ReTCHr	74.2838	62.6225	80.3833	17.7608 (28)	6.0996 (8)	17	17
ReTCHpr	70.1533	60.6850	77.2300	16.5450 (27)	7.0767 (10)	18	12
ReCCSp	14.7536	14.5675	15.9390	1.3715 (9)	1.1854 (8)	10	3
ReCCSr	13.9238	13.7690	14.6190	0.8500 (6)	0.6952 (5)	14	8
ReCCSpr	14.3386	14.1680	15.2790	1.1110 (8)	0.9404 (7)	12	3
ReTSHp	9.7487	8.5443	11.7957	3.2514 (38)	2.0470 (21)	18	8
ReTSHr	10.3326	8.5870	11.7330	3.1460 (37)	1.4004 (14)	15	9
ReTSHpr	10.0407	8.5658	11.7643	3.1986 (37)	1.7237 (17)	16	4
ReNMGYp	7.4968	6.5098	9.5600	3.0503 (47)	2.0632 (28)	17	3
ReNMGYr	6.1651	5.0073	7.5873	2.5801 (52)	1.4222 (23)	12	6
ReNMGYpr	6.8309	5.7587	8.5737	2.8149 (49)	1.7427 (26)	15	3
ReSEL7p	3.8758	3.5825	5.5567	1.9742 (55)	1.6808 (43)	17	7
ReSEL7r	3.6250	2.9975	5.1100	2.1125 (70)	1.4850 (41)	19	11
ReSEL7plr	3.3338	2.9150	4.7767	1.8617 (64)	1.4429 (43)	13	6
ReSEL8p	2.5425	2.0825	3.7767	1.6942 (81)	1.2342 (49)	15	15
ReSEL8r	2.3056	1.9168	3.2223	1.3056 (68)	0.9168 (40)	19	15
ReS8plr	1.7917	1.1668	2.8890	1.7223 (148)	1.0973 (61)	20	15
ReSEL10p	0.5972	0.4168	1.1110	0.6943 (167)	0.5138 (86)	24	18
ReSEL10r	0.9861	0.4168	1.4443	1.0276 (247)	0.4582 (46)	21	15
ReS10plr	0.4722	0.0833	0.7777	0.6944 (834)	0.3055 (65)	24	24
ReSTp	17.6242	16.1925	19.3733	3.1808 (20)	1.7492 (10)	20	7
ReSTr	23.7229	21.7150	24.9767	3.2617 (15)	1.2538 (5)	18	15
ReSTplr	20.6888	19.0425	22.1733	3.1308 (16)	1.4846 (7)	15	12
ReBRIXp	23.6801	24.0148	24.7563	0.7416 (3)	1.0762 (5)	16	4
ReBRIXr	20.0174	19.8985	20.5210	0.6225 (3)	0.5036 (3)	22	15

Table 138 continued 2/2

Parameter	Mean values			Top - Worst (% worst)	Top - GM (%GM)	Families including	
	GM	Worst 4	Top 3			Top 5	Top 3
reVISGp	6.2423	5.9720	7.3150	1.3430 (22)	1.0727 (17)	12	5
reVISGr	5.9608	5.2298	6.7287	1.4989 (29)	0.7679 (13)	19	12
reVISGplr	6.1095	5.6493	7.0213	1.3721 (24)	0.9118 (15)	15	9
reSTVp	35.7792	32.2500	26.4667	-5.7833 (-18)	-9.3125 (-26)	23	23
reSTVr	70.0708	65.1250	55.4333	-9.6917 (-15)	-14.6375 (-21)	21	21
reSTVplr	42.3250	35.9250	31.5667	-4.3583 (-12)	-10.7583 (-25)	23	23
reBRVp	2.0742	1.8800	1.1733	-0.7067 (-38)	-0.9008 (-43)	24	24
reBRVr	2.0856	2.1493	2.0187	-0.1306 (-6)	-0.0670 (-3)	22	22
reBRVplr	1.4531	1.1860	1.0027	-0.1833 (-15)	-0.4504 (-31)	24	24
reHVp	0.8940	0.7628	0.7160	-0.0468 (-6)	-0.1780 (-20)	24	19
reHVr	0.9846	1.0120	0.5680	-0.4440 (-44)	-0.4166 (-42)	24	24
reHVplr	0.6376	0.5933	0.3757	-0.2176 (-37)	-0.2619 (-41)	24	24
reGVp	4.5996	4.6525	3.5333	-1.1192 (-24)	-1.0663 (-23)	24	24
reGVr	7.0700	4.5175	8.2067	3.6892 (82)	1.1367 (16)	17	17
reGVplr	4.5788	3.1425	4.7067	1.5642 (50)	0.1279 (3)	23	23
reWSp	1.2703	1.2478	1.2823	0.0346 (3)	0.0120 (1)	20	20
reWSr	1.0491	0.9695	1.0743	0.1048 (11)	0.0252 (2)	19	16
reWSpr	1.1598	1.1088	1.1787	0.0699 (6)	0.0188 (2)	18	18

= plant crop

= ratoon crop

r = (p+r)/2 crop, where p, r are whole plot values

lr = (p+r)/2 crop, where p, r are individual seedling values

p = (r-p)/2 crop

MGY = NMGYOT

ISG = visual net merit grade

EL7 = number of selections graded 7+

EL8 = number of selections graded 8+

EL10 = number of selections graded 10+

T = number of stalks

S = weight per stalk

IV = within plot variance for number of stalks

RV = within plot variance for BRIX

V = within plot variance for HARDNESS

V = within plot variance for visual net merit grade

Table 139. Value in Be families with highest and lowest cross ratios in 1989. Cross ratios are the mean of 79N to latest series, omitting 80N which were used in the experiment.

Parameter	Mean values			Top - Worst (% worst)	Top - GM (%GM)	Families including	
	GM	Worst 4	Top 3			Top 5	Top 3
BeFIBREp	13.4061	12.9950	12.8180	-0.1770 (-1)	-0.5881 (-4)	22	22
BeFIBREr	14.1382	14.0520	13.3530	-0.6990 (-5)	-0.7852 (-6)	21	21
BeFIBRpr	13.7722	13.5233	13.0857	-0.4376 (-3)	-0.6865 (-5)	22	22
BeTCHp	73.8208	69.7550	84.4133	14.6583 (21)	10.5925 (14)	19	19
BeTCHr	83.9900	72.8075	91.7967	18.9892 (26)	7.8067 (9)	15	12
BeTCHpr	78.9050	71.2775	88.1033	16.8258 (24)	9.1983 (12)	13	13
BeCCSp	14.7858	14.8268	15.5013	0.6746 (5)	0.7155 (5)	12	7
BeCCSr	13.9504	13.7940	14.7257	0.9317 (7)	0.7753 (6)	14	13
BeCCSpr	14.3680	14.3105	15.1133	0.8028 (6)	0.7453 (5)	12	9
BeTSHp	10.9270	10.3360	13.0997	2.7637 (27)	2.1727 (20)	14	14
BeTSHr	11.6758	10.0040	13.4423	3.4383 (34)	1.7665 (15)	13	10
BeTSHpr	11.3013	10.1698	13.2710	3.1013 (30)	1.9697 (17)	11	10
BeNMGyp	8.4615	8.0482	10.4763	2.4281 (30)	2.0148 (24)	12	12
BeNMGYr	7.0209	5.8060	8.3073	2.5013 (43)	1.2864 (18)	11	6
BeNMGYpr	7.7412	6.9270	9.3920	2.4650 (36)	1.6508 (21)	8	7
BeSEL7p	4.9438	4.4150	6.6667	2.2517 (51)	1.7229 (35)	10	10
BeSEL7r	4.3338	3.5850	5.3333	1.7483 (49)	0.9996 (23)	22	13
BeS7plr	4.2213	3.3325	5.8867	2.5542 (77)	1.6654 (39)	12	8
BeSEL8p	3.1108	2.9175	5.2200	2.3025 (79)	2.1092 (68)	10	7
BeSEL8r	3.0556	2.3335	4.1110	1.7775 (76)	1.0554 (35)	18	12
BeS8plr	2.3611	2.0000	3.9997	1.9997 (100)	1.6385 (69)	14	6
BeSEL10p	0.9027	0.8335	2.5553	1.7218 (207)	1.6526 (183)	9	7
BeSEL10r	1.0418	0.8335	1.5557	0.7222 (87)	0.5139 (49)	20	20
BeS10plr	0.5694	0.6665	1.4447	0.7782 (117)	0.8753 (154)	16	9
BeSTp	17.1958	17.0925	18.6800	1.5875 (9)	1.4842 (9)	19	14
BeSTr	23.5325	22.3700	24.4700	2.1000 (9)	0.9375 (4)	22	14
BeSTplr	20.3800	19.7300	21.5767	1.8467 (9)	1.1967 (6)	23	14
BeBRIXp	23.6210	23.8360	24.1283	0.2923 (1)	0.5074 (2)	13	14
BeBRIXr	19.7492	19.6758	20.0393	0.3636 (2)	0.2902 (1)	20	14

Table 139 continued 2/2

Character	Mean values			Top - Worst (% worst)	Top - GM (%GM)	Families including	
	GM	Worst 4	Top 3			Top 5	Top 3
3eVISGp	6.8657	6.7083	8.1663	1.4581 (22)	1.3007 (19)	10	9
3eVISGr	6.5627	5.9723	7.3393	1.3671 (23)	0.7766 (12)	19	10
3eVISGp1r	6.7192	6.3403	7.7530	1.4128 (22)	1.0338 (15)	14	9
3eSTVp	32.3333	45.6000	30.9667	-14.6333 (-32)	-1.3667 (-4)	23	15
3eSTVr	65.8750	75.9250	79.1333	3.2083 (4)	13.2583 (20)	23	23
3eSTVp1r	39.5292	51.5000	42.9000	-8.6000 (-17)	3.3708 (9)	20	20
3eBRVp	1.6492	1.6550	2.1867	0.5317 (32)	0.5375 (33)	21	20
3eBRVr	1.8168	2.2660	1.8050	-0.4610 (-20)	-0.0118 (-1)	23	23
3eBRVp1r	1.2246	1.4000	1.3213	-0.0787 (-6)	0.0968 (8)	18	12
3eHVp	1.0973	0.8865	1.2500	0.3635 (41)	0.1527 (14)	18	11
3eHVr	1.0113	0.9352	1.0587	0.1234 (13)	0.0474 (5)	24	24
3eHVp1r	0.7373	0.6065	0.7613	0.1548 (26)	0.0241 (3)	24	19
3eGVp	3.7067	4.6400	4.8933	0.2533 (5)	1.1867 (32)	23	8
3eGVr	5.7533	6.2850	8.1867	1.9017 (30)	2.4333 (42)	21	23
3eGVp1r	3.3483	4.2600	4.3367	0.0767 (2)	0.9883 (30)	12	12
3eWSp	1.4463	1.3868	1.5103	0.1236 (9)	0.0641 (4)	18	18
3eWSr	1.1972	1.1090	1.2607	0.1517 (14)	0.0635 (5)	18	16
3eWSpr	1.3217	1.2478	1.3857	0.1379 (11)	0.0640 (5)	19	19

p = plant crop

r = ratoon crop

p_r = (p+r)/2 crop, where p, r are whole plot values

1r = (p+r)/2 crop, where p, r are individual seedling values

_p = (r-p)/2 crop

MGY = NMGYOT

ISG = visual net merit grade

EL7 = number of selections graded 7+

EL8 = number of selections graded 8+

EL10 = number of selections graded 10+

T = number of stalks

S = weight per stalk

TV = within plot variance for number of stalks

RV = within plot variance for BRIX

V = within plot variance for HARDNESS

V = within plot variance for visual net merit grade

Table 140. Value in Se families with highest and lowest cross ratios in 1989. Cross ratios are the mean of 79N to latest series, omitting 80N which were used in the experiment.

Parameter	Mean values					Families including	
	GM	Worst 4	Top 3	Top - Worst (% worst)	Top - GM (%GM)	Top 5	Top 3
SeFIBREp	13.5382	13.4508	13.2387	-0.2121 (-2)	-0.2995 (-2)	20	20
SeFIBREr	14.3179	14.3323	13.3603	-0.9719 (-7)	-0.9575 (-7)	23	23
SeFIBRpr	13.9281	13.8918	13.2993	-0.5924 (-4)	-0.6287 (-5)	22	22
SeTCHp	69.3604	66.1525	73.4733	7.3208 (11)	4.1129 (6)	13	13
SeTCHr	78.7113	67.6800	87.4267	19.7467 (29)	8.7154 (11)	16	16
SeTCHpr	74.0354	66.9150	80.4533	13.5383 (20)	6.4179 (9)	16	9
SeCCSp	15.1252	15.1583	15.6043	0.4461 (3)	0.4791 (3)	17	17
SeCCSr	14.4031	13.9615	15.2790	1.3175 (9)	0.8759 (6)	11	9
SeCCSpr	14.7642	14.5603	15.4417	0.8814 (6)	0.6775 (5)	14	14
SeTSHp	10.4830	10.0068	11.4680	1.4613 (15)	0.9850 (9)	16	16
SeTSHr	11.3225	9.3897	13.3320	3.9423 (42)	2.0095 (18)	15	4
SeTSHpr	10.9028	9.6980	12.4003	2.7023 (28)	1.4976 (14)	9	1
SeNMGyp	8.1908	7.8360	9.1693	1.3333 (17)	0.9785 (12)	14	14
SeNMGyr	6.8981	5.5083	8.6103	3.1021 (56)	1.7122 (25)	10	4
SeNMGypr	7.5444	6.6723	8.8897	2.2174 (33)	1.3453 (18)	8	8
SeSEL7p	4.8617	4.0825	5.4467	1.3642 (33)	0.5850 (12)	15	15
SeSEL7r	4.2092	3.0850	4.8867	1.8017 (58)	0.6775 (16)	16	16
SeS7pir	4.1813	3.0000	5.2233	2.2233 (74)	1.0421 (25)	13	13
SeSEL8p	3.1942	2.5825	4.3333	1.7508 (68)	1.1392 (36)	17	17
SeSEL8r	2.8333	1.9168	3.5553	1.6386 (85)	0.7220 (25)	16	16
SeS8pir	2.3194	1.3333	2.9997	1.6664 (125)	0.6803 (29)	18	18
SeSEL10p	0.7778	0.4165	1.4443	1.0278 (247)	0.6665 (86)	16	16
SeSEL10r	0.9027	0.4165	1.4443	1.0278 (247)	0.5417 (60)	20	20
SeS10pir	0.5000	0.1665	0.8890	0.7225 (434)	0.3890 (78)	13	13
SeSTp	17.6588	17.3150	18.0867	0.7717 (4)	0.4279 (2)	19	19
SeSTr	24.3854	22.6825	25.3567	2.6742 (12)	0.9712 (4)	19	19
SeSTpir	21.0233	20.0000	21.7233	1.7233 (9)	0.7000 (3)	18	18
SeBRIXp	24.1201	24.3850	24.4790	0.0940 (0)	0.3589 (1)	21	21
SeBRITyr	20.2930	20.2783	20.5457	0.2674 (1)	0.2527 (1)	18	18

Table 140 continued 2/2

Character	Mean values			Top - Worst (% worst)	Top - GM (%GM)	Families including	
	GM	Worst 4	Top 3			Top 5	Top 3
SeVISGp	6.7606	6.4078	7.4443	1.0366 (16)	0.6837 (10)	12	7
SeVISGr	6.4402	5.5950	6.8397	1.2447 (22)	0.3994 (6)	16	16
SeVISGplr	6.6023	6.0128	7.1420	1.1293 (19)	0.5397 (8)	13	13
SeSTVp	38.6208	35.1500	46.6333	11.4833 (33)	8.0125 (21)	19	13
SeSTVr	77.8625	70.8250	76.1667	5.3417 (8)	-1.6958 (-2)	24	18
SeSTVplr	47.1042	44.1500	52.7000	8.5500 (19)	5.5958 (12)	23	15
SeBRVp	1.6571	1.1825	1.4500	0.2675 (23)	-0.2071 (-12)	23	23
SeBRVr	1.5246	2.0138	1.3937	-0.6201 (-31)	-0.1310 (-9)	22	20
SeBRVplr	1.0516	1.0300	0.8790	-0.1510 (-15)	-0.1726 (-16)	22	19
SeHVp	0.9452	0.9492	0.8427	-0.1066 (-11)	-0.1025 (-11)	22	22
SeHVr	0.8952	0.8530	0.5463	-0.3067 (-36)	-0.3488 (-39)	24	24
SeHVplr	0.6436	0.6863	0.4560	-0.2303 (-34)	-0.1876 (-29)	23	23
SeGVp	4.4442	3.6175	5.1800	1.5625 (43)	0.7358 (17)	16	16
SeGVr	5.2063	4.3450	6.3133	1.9683 (45)	1.1071 (21)	17	17
SeGVplr	3.4733	2.7700	4.5233	1.7533 (63)	1.0500 (30)	19	14
SeWSp	1.3193	1.2865	1.3647	0.0782 (6)	0.0454 (3)	15	15
SeWSr	1.0826	1.0075	1.1620	0.1545 (15)	0.0794 (7)	15	15
SeWSplr	1.2009	1.1470	1.2630	0.1160 (10)	0.0621 (5)	14	14

= plant crop
 = ratoon crop
 r = (p+r)/2 crop, where p, r are whole plot values
 lr = (p+r)/2 crop, where p, r are individual seedling values
 _p = (r-p)/2 crop
 MGY = NMGYOT
 ISG = visual net merit grade
 EL7 = number of selections graded 7+
 EL8 = number of selections graded 8+
 EL10 = number of selections graded 10+
 T = number of stalks
 S = weight per stalk
 TV = within plot variance for number of stalks
 RV = within plot variance for BRIX
 V = within plot variance for HARDNESS
 V = within plot variance for visual net merit grade

Table 141. Value in Ts trial (Bs and Ss seedlings) and Te trial (Re, Be, and Se types) of families with highest and lowest cross ratios in 1989. Cross ratios are the mean of 79N to latest series, omitting 80N series which was used in the experiment.

Character	Crop	Gain in top 3 families as %GM					Families selected for top 3`				
		Bs	Ss	Re	Be	Se	Bs	Ss	Re	Be	Se
SEL8	P	43**	92**	49*	68**	36*	19 >>	3 <<	15 >	7	6
	R		90**	40	35*	25		6 <	15	12	16
	PR		91**	61*	69**	29		4 <<	15 >	6	13
NMGYOT	P	44**	27**	28**	24**	12*	5	10 >	3 <<	12	14
	R	24*	21**	23**	18**	25**	7	4	6	6	4
	PR	33**	24**	26**	21**	18**	4	5	3	7	8
TSH	P	40**	21**	21**	20**	9*	5 <	13 >	5 <	14	16
	R	22**	16**	14**	15**	18**	7	4	9	10	4
	PR	29**	18**	17**	17**	14**	4	7	4	10	7
TCH	P	35**	15**	12**	14**	6	4 <<	17	13	19	13
	R	20**	12**	8*	9**	11**	8	10	17	12	10
	PR	27**	14**	10**	12**	9*	4 <	12	12	13	9
GB	P	29**	29**				4	8			
	R	10	25**				18 >>	3			
	PR	19*	27**				7	4			
G_B	P	20**	19**				4	7			
	R	7	15**				21 >>	8			
	PR	13*	17**				13	6			
WS	P	30**	1	1	4	3	4 <<	24	20	18	15
	R	9	-1	2	5	7	12 <<	24 >>	16	16	15
	PR	18**	0	2	5	5	9 <<	19	18	19	14
STALKS	P	4	13**	10*	9	2	13	10	7	14	19
	R	9	9**	5	4	4	10	12	15	13	17
	PR	6	11**	7*	6	3	15	12	12	13	17
CCS	P	4	6**	8**	5**	3*	14	13 >>	3	7 <<	17
	R	2	3**	5**	6**	6**	16	15	8	13	9
	PR	3	5**	7**	5**	5**	13	16 >>	3	9	14

` The number of families which must be selected to include the top 3. Significant differences are shown for adjoining columns. If n1 is the lower value, the second one is significantly higher if the difference is:-

n1 P≤0.05 n1 P≤0.01 (chi-square test on 2x2 table, continuity correction = 0.25)