

INTERSPECIFIC GENE TRANSFER IN *LOLIUM*

By

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DECLARATION

I hereby declare that the work contained in this thesis is the result of my own investigation, except production of hybrid clones, cytological screening and isozyme determination.

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I also declare that this work has not already been accepted in substance for any degree, and is not being concurrently submitted in candidature for any other degree.

W.N.P. Muesy.....

Date *30th April 1957*.....

Dedicated to

Florence

and

Mutheu

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SUMMARY

Nearly two thousand diploid hybrid plants originating from crosses between triploids (with two sets of Italian ryegrass chromosomes and one set of perennial ryegrass chromosomes) and diploid Italian ryegrass were clonally replicated and examined for their expression of five qualitative and five quantitative traits in a glasshouse. The qualitative traits were: presence of awns, red leaf base and three isozyme variants; phosphogluco isomerase (PGI), glutamate oxaloacetate transaminase (GOT) and superoxide dismutase (SOD). The quantitative traits were; leaf width, leaf length, per cent stem, regrowth score and days to ear emergence.

The purpose of using triploids during backcrossing was to reduce the proportion of genes originating from the donor parent. Assuming normal mendelian inheritance, the progeny would have $\frac{1}{6}$ or 17% of the genes of perennial ryegrass origin compared to $\frac{1}{4}$ or 25% in two generations of ordinary backcrossing: only a small advantage in using triploids. But loss of chromosomes of the donor species due to preferential pairing at meiosis in the triploid would greatly increase that advantage. The occurrence of such chromosome loss was best revealed by the frequency of hybrid plants with qualitative traits. The frequency of plants with the perennial ryegrass allele at the PGI/2 isozyme locus and with red base was much lower than expected but the frequency of plants with

the perennial ryegrass allele at the GOT locus was exactly as expected. Since these three loci were unlinked, the results suggest considerable loss of some chromosomes but not others.

There was a clear linkage between leaf length and red base, PGI and GOT suggesting that genes for leaf length were distributed widely over the genome. Genetic correlation between quantitative traits suggested linkage between early flowering and stemmy regrowth, both traits of Italian ryegrass.

Potentially useful hybrid clones which showed only a single perennial ryegrass trait were identified. Some had no awns, some with red base, some had entirely leafy regrowth and some were late flowering. However, because some of the quantitative traits had high coefficients of variation and because the traits examined only represent a small proportion of the ryegrass genome, further work is required to determine the value of these clones for breeding.

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INTRODUCTION

Italian and Perennial Ryegrass

The two ryegrasses, perennial ryegrass (Lolium perenne L.) and Italian ryegrass (Lolium multiflorum Lam.) are the most important grassland species in British Agriculture. Together they offer a most useful complementation of characters (Breese et al.,1981). They combine high yields under fertile conditions with high quality and satisfactory seed yields (Spedding and Diekmahns, 1972). In mixed farms the ryegrasses have been grown in rotation with arable crops, a practice called ley farming. Ley farming has been a means of weed control, however chemical methods of weed control have reduced the need for control by ley farming. Ley farming is, however, useful for improving soil structure where soils are poor due to the large quantity of fine roots produced by grass. On all grass farms ryegrasses are sown either to improve the yield, early spring growth and the quality of pastures for grazing or to provide crop for conservation which is followed and sometimes preceded by grazing.

Silage production is on the increase and may replace hay as the main source of winter feed (Wilkinson, 1981). For silage it is important to produce heavy crops at a predictable level of digestibility and with sufficient water-soluble carbohydrate, a task to which ryegrass is well suited.

Both perennial and Italian ryegrass are obligate out-breeders and are interfertile. Both are diploids ($2n = 14$) but several tetraploid cultivars have been produced by use of colchicine. The inflorescence is a simple spike of alternate sessile florets and the undersides of the leaves are glossy. Roots are fine and highly branched. There is genetic variation for a large number of morphological and physiological characteristics within both species and genetic interchange between species has occurred naturally. From the taxonomic point of view, the differences between Italian and perennial ryegrass probably are insufficient to justify their classification as distinct species (Bulinka-Radomska and Lester, 1985). From the agricultural point of view, however, the two species differ markedly in yield, steminess, persistency, winter hardiness and morphology.

Yield. Italian ryegrass seedlings grow more rapidly than those of perennial ryegrass and consequently crops establish more rapidly in the field (Spedding and Diekmahns, 1972). Italian ryegrass makes more growth in winter, early spring, early summer and autumn. Under dry conditions in late summer, perennial ryegrass sometimes outyields Italian ryegrass. In the first harvest year when cut 4-7 times, Italian ryegrass outyields perennial ryegrass by approximately 25% (Wilkins and Lovatt, 1983; Jones and Roberts, 1982; Jones, Rushton, Roberts and Stanley, 1984, 1985, 1986).

Stemminess. When the primary inflorescences of perennial ryegrass are removed, the regrowth is mainly vegetative, at least in cultivated varieties (cultivars). But with Italian ryegrass more than 50% of the regrowing tillers are reproductive. Consequently, at the second conservation cut Italian ryegrass gives much higher yields than perennial ryegrass, but the material is more fibrous and lower in digestibility. Under lax grazing, inflorescences of Italian ryegrass tend to accumulate with consequent reduction in pasture digestibility and in animal livestock weight gain. Less stemmy types such as the tetraploid hybrid Augusta have given higher liveweight gains than the typical ryegrass cultivar RvP (Jones and Roberts, 1984, 1985; Walters, Evans and Baker, 1982).

Persistency. The tiller density of Italian ryegrass declines steadily from the spring of the first harvest year onwards, whereas under good conditions that of the better perennial ryegrass cultivars will not decline and may even increase. In a typical experiment total annual production of Italian ryegrass "fell from 15 tonnes of dry matter per hectare in the first harvest year to 9 in the third harvest year (Hunt, 1962). The relatively poor persistence of Italian ryegrass could be due mainly to continued production of inflorescences and the consequently low numbers of vegetative meristems from which new tillers develop. However, it may be due also to its higher growth rate and greater dominance of large tillers over small ones in respect of

partitioning of assimilates. Studies in perennial ryegrass have shown that most tillers abort due to lack of assimilates (Ong, Marshall and Sagar, 1978). Tetraploid ryegrasses have larger tillers but fewer of them.

Winter hardiness. Perennial ryegrass is native to Britain whereas Italian ryegrass was introduced from Southern Europe (Clapham, Tutin and Warburg, 1962). Consequently, Italian ryegrasses are less winter hardy than the perennial varieties of British or continental origin (Anon, 1986).

Morphology. When grown under the same conditions, tillers of Italian ryegrass are larger than those of perennial ryegrass and its leaves longer and wider. All Italian ryegrasses have awned florets whereas most (but not all) perennial ryegrasses are awnless. In inter-species hybrids awns are dominant (Ahloowalia, 1977). Awn length is also under genetic control, awns in perennial ryegrass being shorter than those in Italian ryegrass. The two species differ in the intensity of red pigmentation shown by living leaf sheath, particularly at the base. Most perennial ryegrasses are highly pigmented while most Italian ryegrasses are very slightly pigmented (Terrel, 1966; Jenkin, 1930).

It has long been the aim of breeders to combine the high yield of Italian ryegrass with the persistency and winter hardiness of the better perennial ryegrasses by means of interspecies hybridization. Some potentially useful genes may occur only in

one species which gives further reason for interspecific gene transfer. True resistance to ryegrass mosaic virus has been found in perennial ryegrass but not in Italian ryegrass (Salehuzzaman and Wilkins, 1984). Italian ryegrass from the Po Valley region of Italy has a high net assimilation rate and has been used to increase conservation yields substantially (Wilkins and Lovatt, 1986). This germplasm shows very rapid regrowth after cutting. Additionally, marker traits such as awned florets in perennial ryegrass or red leaf base in Italian ryegrass could be a useful means of ensuring the distinctiveness of new cultivars. As the number of varieties increase, distinguishing them morphologically so that they can be awarded plant breeders rights becomes increasingly difficult.

Isozyme variation in ryegrass

Allelic variation is known to occur at several enzyme loci, five of which are used regularly as markers. These five are; phosphogluco isomerase (PGI), glutamate oxaloacetate transaminase (GOT), acid phosphatase (ACPH), superoxide dismutase (SOD) and amino peptidase (AMP). Apart from AMP which is monomeric, all these enzymes are dimers, that is in heterozygous state the phenotype has more than two bands.

TABLE 1. Isozymes at seven loci in perennial and Italian ryegrass

Species	Enzyme locus						
	PGI/2	GOT/2	GOT/3	ACPH/2	SOD	AMP/1	AMP/2
Perennial ryegrass	<u>a</u> <u>c</u> f	<u>a</u> c	a d	<u>a</u> <u>c</u>	<u>a</u> d	<u>a</u>	<u>a</u>
	<u>a</u> d g	<u>a</u>	<u>b</u>	a <u>d</u>	<u>b</u>	<u>b</u>	<u>b</u>
	<u>b</u> e	<u>b</u>	<u>c</u>	<u>b</u> e	c		
Italian ryegrass	a <u>c</u> f	a c	<u>a</u> <u>d</u>	a d	<u>a</u>	a	b e
	a <u>d</u>	<u>a</u>	<u>b</u>	b	a	c	c d
	<u>b</u> e	<u>b</u>	<u>c</u>	c	b	d	d

Table 1 shows the number of isozymes, that is the different allelic forms, that have been found so far at each enzyme locus in Italian and perennial ryegrass. Letters have been assigned to each allele depending upon its speed of migration across the gel, that is the 'a' isozymes move further than the 'd'. Those isozymes occurring most frequently in the various populations studied so far with each species have been underlined (McAdam, Humpreys and Michaelson-Yates, 1985). Over a dozen polymorphic enzyme systems are now available for genetic studies of the Lolium/Festuca complex. This has enabled the selection of Lolium and Festuca species with several contrasting isozymes phenotypes to be used in interspecific hybrid breeding programmes (Humpreys and Rogers, 1985). Isozyme polymorphism has been used as a measure of distinctiveness and stability in cultivars of perennial ryegrass (Hayward and McAdam, 1977; Almgard and Norman, 1970).

Methods of interspecific gene transfer in crop plants

The various methods of deliberate interspecific gene transfer used to combine in one crop variety the desirable genetic characteristics of different species have been reviewed by Lacadena (1977). These range from the creation of artificial amphiploids where the whole genomes of both parent species are combined to molecular manipulation where specific genes are isolated, cloned and inserted in the genome of a selected cultivar. The amphiploid method has the disadvantage that many undesirable dominant or additive genes inevitably are included in the hybrid and that its use is limited to instances where the amphiploid is fertile and stable. Theoretically, molecular manipulation is far superior in that only the desired genes are transferred and hybrid infertility poses no problem. However, so far very few desirable genes of crop plants have been isolated and cloned and so at present practical breeders have to rely primarily on methods which involve hybridization.

Usually the objective of such practical breeding work is to transfer genes controlling selected desired characteristics from a donor species while as far as possible discarding the rest of its genes. Where two species are so evolutionarily divergent that their hybrids are infertile the problem can be overcome sometimes by induced polyploidy (Thomas, 1986), sometimes by using other interspecific hybrids as genetic bridges as in *Nicotiana* (Mann, Gerstel and Apple, 1963), and possibly by somatic hybridization (Power, Cuning and Cocking, 1970). Backcrossing is commonly used.

For this to succeed it is essential to perform a large number of backcrosses in order to eliminate most of the undesirable genes of the donor species, time being the limiting factor. Consequently, backcrossing is used mostly in annual crops for the transfer of one or two genes controlling easily measured qualitative traits. The main alternative to backcrossing is the transfer of whole chromosomes or parts of chromosomes by cytological manipulation followed by an evaluation of the effects of the transfers on the phenotypes. Chromosomes may be added to create addition lines, substituted to create substitution lines, or (where there is crossing over) chromosome segments substituted to create translocation lines (Sears, 1966). Cytogenetic manipulation is easiest in crops such as wheat and oats where stained chromosomes can be distinguished by light microscopy. Alternatively, marker genes can be used to label specific chromosomes or blocks of closely linked genes.

The practical value of backcrossing and cytogenetic manipulation depends heavily on the number of genes controlling the required traits and their chromosomal location. If the genes are scattered over several chromosomes then undesirable linkages are virtually inevitable but if they are concentrated on one chromosome or one arm of a chromosome, then the likelihood of success is much higher.

Controlled gene transfer between
Italian and perennial ryegrass

These two diploid species produce fertile F1 progeny, but in the F2 and subsequent generations marked transgressive segregation occurs which leads to rapid genetic deterioration, including a degree of sterility. When allotetraploids are hybridized, segregation is greatly reduced (Breese and Thomas, 1977). Tetraploid Italian/perennial hybrids such as Augusta have been successful commercially as they combine much of the early spring growth and annual yield of Italian ryegrass with some of the leafiness and winter hardiness of perennial ryegrass. They are, however, similar in persistency to diploid Italian ryegrasses. Attempts to transfer specific traits have been less successful. Polygenic resistance to ryegrass mosaic virus was transferred from perennial to Italian ryegrass by repeated cycles of backcrossing, polycrossing and selection but the resultant variety was 11% lower yielding than the recurrent Italian ryegrass parent despite being indistinguishable in morphology, steminess and persistency (Wilkins, personal communication). However, recent work by Thomas et al. (1986) may enable the development of substitution and translocation lines. They produced triploid hybrids, by hybridising diploid perennial ryegrass with tetraploid Italian ryegrass, rescued the embryos by in vitro culture and hybridized the resultant triploid plants with diploid Italian ryegrass. Eighty-five per cent of the progeny were euploid with 14 chromosomes, the haploid pollen apparently having a marked selective advantage over aneuploid gametes so forming an

effective sieve to eliminate aneuploid gametes. If the pairing at meiosis of the three triploid hybrids was completely at random the chances of a perennial ryegrass gene being included in a gamete would be 1 in 3. However, in the perennial ryegrass x Italian ryegrass tetraploid there was strong evidence of preferential chromosome pairing (Lewis, 1980), and a degree of such chromosome pairing in triploid hybrids would reduce the frequency with which the perennial ryegrass alleles were included in the haploid gamete.

Aims and Objectives

The technique developed by Thomas et al. (1986) could be a good means of obtaining individuals which contain a single chromosome or part of a chromosome of Lolium perenne but are otherwise mainly Lolium multiflorum in origin. These can form the basis of substitution or translocation lines. Also it can provide a means of studying linkage relationships in Lolium. With these objectives in mind a large number of diploid clones provided by H.Thomas were characterized in a glasshouse experiment.

MATERIAL AND METHODS

The material under investigation consisted of nine hundred and ninety hybrid progeny between L.perenne and L.multiflorum. The seven parents consisting one clone of L.perenne and six clones of L.multiflorum were included as controls. The derivation of the material under investigation is described below.

Derivation of the triploid parents

The triploid plants P122/5 (2), P122/6 (12) and P122/6 (16) were obtained as a result of crossing diploid (2x) L.perenne (F5P8) with a tetraploid (4x) L.multiflorum (P87/5 (8)). Thus:

F5P8	X	P87/5 (8)
2x		4x
<u>L.perenne</u>	↓	<u>L.multiflorum</u> (Bb1276)
3x triploids, P122/5(2), P122/6(12) and P122/6(16)		

The phenotypes of the 2x and 4x parents used to make the 3x plants were as follows:

	<u>Isozymes</u>		
	PGI	GOT	SOD
F5P8 <u>L.perenne</u> 2n = 14	bb	ab	bb
P87/5(8) <u>L.multiflorum</u> 4x	bbdd	bbbb	aaaa

The phenotypes of the triploid plants P122/5(2), P122/6(12) and P122/6(16) were as follows:

	<u>Isozymes</u>		
	PGI	GOT	SOD
P122/5(2)	<u>abb</u>	<u>bba</u>	<u>aab</u>
P122/6(12)	<u>ddb</u>	<u>bba</u>	<u>aab</u>
P122/6(16)	<u>ddb</u>	<u>bba</u>	<u>aab</u>

Inheritance of the isozymes by P122/5(2), P122/6(12) and P122/6(16)
P122/6(12) and P122/6(16) (3x)

	<u>Isozymes</u>			X		<u>Isozymes</u>		
	PGI	GOT	SOD			PGI	GOT	SOD
F5P8	<u>bb</u>	<u>ab</u>	<u>bb</u>		P87/5(8)	bbdd	bbbb	aaaa
2n=14				↓	female parent			
male parent					<u>L.multiflorum</u>			
<u>L.perenne</u>								
	P122/6			3x				
					<u>Isozymes</u>			
					PGI	GOT	SOD	
					<u>ddb</u>	<u>bba</u>	<u>aab</u>	

The underlined alleles in P122/6 are those donated by L.perenne. At the PGI, locus it is possible to differentiate between ddb and dbb since there are two 'd' alleles in P122/6 one must have come from the 4x L.multiflorum parent and the other 'd' allele from the L.perenne 2x parent.

P122/5(2):

	<u>Isozymes</u>					<u>Isozymes</u>		
	PGI	GOT	SOD			PGI	GOT	SOD
F5P8	<u>bb</u>	<u>ab</u>	<u>bb</u>	X	P87/5(8)	abdd	bbbb	aaaa
2x				↓	4x			
<u>L.perenne</u>					<u>L.multiflorum</u>			
male parent					female parent			
				3x				
				P122/5		<u>adb</u>	<u>bba</u>	<u>aab</u>

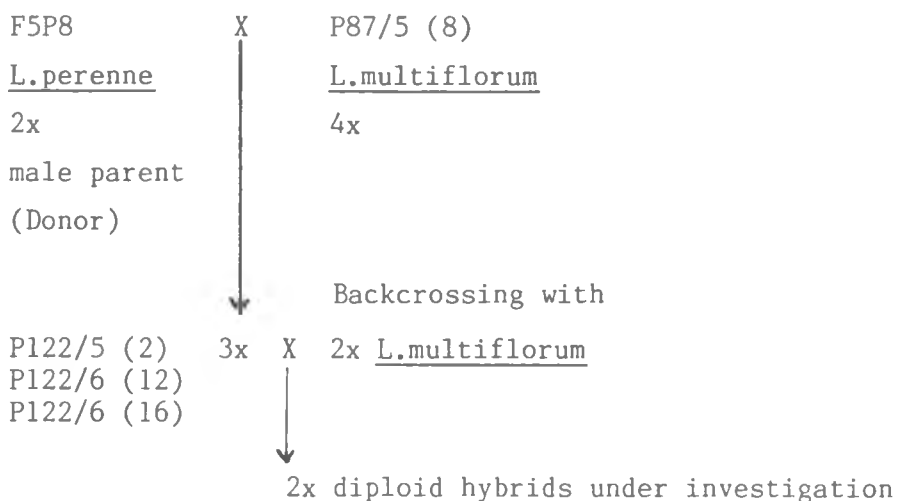
At the locus PGI the female gametes must be 'ad' and the allele 'b' is derived from the L.perenne parent. (Underlined alleles donated by L.perenne.)

Derivation of the diploid material
under investigation

The triploid plants P122/5 and P122/6 were backcrossed with the diploid L.multiflorum. Thus:

	<u>Isozymes</u>					<u>Isozymes</u>		
	PGI	GOT	SOD			PGI	GOT	SOD
<u>L.multiflorum</u>	ad	b	aa	X	Triploid	<u>adb</u>	<u>bba</u>	<u>aab</u>
2X	or	or		↓	3x			
	bb	bc						
	or							
	cd			↓				
				2n=14				

Chromosome counts were performed on all the progeny. Only diploid progeny were kept for this investigation.

Summary of hybridization schemeTHE EXPERIMENT

Before setting up the experiment a computer-generated randomization was made, one thousand clone numbers were fully randomized in each of four replicates as follows:

Replicate 1 positions	1-1000
Replicate 2 positions	1001-2000
Replicate 3 positions	2001-3000
Replicate 4 positions	3001-4000

In the glasshouse where the experiment was conducted, four thousand 3-inch pots were arranged in 160 boxes each containing 25 pots. Each pot had been previously filled with John Innes No.3 potting compost. Labels numbered from 1-4000 were placed in each pot starting from one end to the other in sequence. The number of the clone also was written on each label. After the arrangement of the four thousand pots in the glasshouse planting

started on 4 April 1986 and ended on 14 April 1986, a period of ten days.

Nine hundred and ninety hybrid plants had been previously grown in boxes in a glasshouse over the winter so that they were big enough to provide four approximately equal sized tillers. Seven parent plants were already grown in large pots. The nine hundred and ninety hybrids were each allocated a number and split into four or more equal tillers. One of each was planted in one pot in each of the four replicates, according to the position of the appropriate pot in the plan. Each of the seven parent plants were also planted, one tiller in each of the four replicates. Twelve pots remained empty, three in each replicate. To fill these pots three of the seven parents were split once more. The plants were watered by spraying water over them once each day. During the hot period of summer the pots were drying very fast. To help retain the water, capillary matting was placed under the pots in each box.

The following traits were recorded:

1. Leaf length and width. The length and width of the first fully expanded leaf was measured to the nearest millimeter for each of the 4000 plants. A ruler calibrated in millimeters was used.
2. Heading date. The date of each ear emergence was recorded for each plant. This was done by visual observation each day from the first plant to head to the last one. From the heading dates the number of days from planting to heading was calculated for each plant.

3.Red leaf base. All the plants were carefully observed for red leaf base. Where necessary senescent leaf sheaths were removed. Each of the plants with red leaf base was recorded.

4.Presence of awns and awn length. Close observation of each head was made. Presence of awns was recorded for each plant. The awns were put into two categories, long awns or short awns. Categorisation of short and long awns was by visual observation.

5.Rate of regrowth. After all the plants had headed and all the above records made, the plants were cut back at the height of two centimeters above the level of the soil. Fertilizer 20:10:10 NPK was applied at the rate of 0.08 grammes per pot. The fertilizer was dissolved in water. Altogether 320 gm of fertilizer were dissolved in 20 litres of water and 5 ml of the solution applied to each pot with an automatic syringe. The plants were allowed to regrow for two weeks. The rate of regrowth was assessed visually on a 0-5 scale, 0 for plants that did not regrow at all and 5 for plants that showed the best regrowth.

6.Per cent stem. Four weeks after cutting, the regrowth had begun to flower again. At this point the percentage stem was recorded. This was done by counting the total number of tillers in each pot, and the number of the stemmy ones. From the total number of tillers and the number of stemmy ones the percentage stem was calculated in each pot. The percentages were transformed into angular degrees using a transformation table,

A VAX computer was used to de-randomize the data and on the quantitative data to perform variance and co-variances analysis using GENSTAT.

RESULTSVariation Among Clones

Generally with all traits, the majority of the hybrid clones were similar to the Italian ryegrass parents but a minority of hybrids were similar to the perennial ryegrass parent.

Presence and absence of awns.

Presence or absence of awns in most of the clones was consistent over replicates (Table 2). In a few cases one of the four plants had been recorded as having awns. In such cases it was observed that one or two spikelets had very short awns. Most hybrid plants had awns but a small proportion were awnless. Assuming that no awns is a recessive gene at a single locus in the perennial ryegrass parent how would awnless hybrid plants appear in the progeny of the diploid and triploid cross? Several hypotheses can be proposed.

(1) If the triploid genotype was AAa and the diploid Italian ryegrass was homozygous, AA then the inheritance of awns would be as follows:

Triploid genotype		Diploid genotype
AAa	X	AA
$\frac{1}{3}$ of the gametes from the triploid will be a		All gametes from the diploid will be A

In this case all the hybrid plants will be either Aa or AA and all will have awns. In 8 out of 16 families all the plants had awns and the other 8 families had both awnless and awned plants

in various ratios (Table 3). This hypothesis is true in as far as eight families are concerned. However, the small numbers in these families should be borne in mind.

(2) There was self-fertilization. That is $AAa \times AAa$ in which the progeny genotypes would be AA , Aa and aa , where 1 in 9 would have no awns. This is an unlikely hypothesis since emasculation was carried out and only when Italian ryegrass was used as the female parent are the progeny likely to be diploid.

(3) Some of the diploid Italian ryegrass parents were heterozygous for the awned gene. That is:

AAa	X	Aa
$\frac{1}{3}$ of the gametes will be a		$\frac{1}{2}$ the gametes will be a

Therefore $\frac{1}{3} \times \frac{1}{2} = \frac{1}{6}$ chance of a progeny being of genotype aa , a ratio of 1:5. Or some of the tetraploid Italian ryegrass parents were heterozygous for the awned gene as well, giving some triploids with the genotype Aaa . Thus:

Aaa	X	Aa
$\frac{2}{3}$ of the gametes will be aa		$\frac{1}{2}$ of the gametes will be a

Therefore $\frac{2}{3} \times \frac{1}{2} = \frac{2}{6}$ or $\frac{1}{3}$ chance of a progeny being of genotype aa , a ratio of 1:2. Chi-square tests showed that there was no significant heterogeneity among families in the proportion of awnless plants but there were significantly (at $P = 0.001$) fewer awnless plants than would be expected assuming a 1:5 ratio (1:33, Table 3).

TABLE 2. Mean values for five quantitative and five qualitative traits in 990 hybrid plants and their Italian and perennial ryegrass parents

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									PGI	GOT	SOD
1	BC/18/1	8.00	336.00	35.78	3.50	43.50	0	0	0	0	0
2	BC/18/2	7.50	333.00	50.08	3.00	48.50	0	0	0	0	0
3	BC/18/4	8.00	382.50	26.58	5.00	52.75	0	0	0	0	1
4	BC/18/5	8.50	421.00	40.33	2.50	49.50	0	0	1	0	0
5	BC/18/6	8.50	335.75	34.13	3.25	49.00	0	0	1	0	0
6	BC/18/8	7.50	305.75	30.53	4.00	53.00	0	0	0	0	0
7	BC/18/9	7.00	292.75	22.58	3.50	44.25	0	0	1	0	0
8	BC/18/10	8.50	389.00	42.00	4.25	47.75	0	0	0	0	0
9	BC/18/11	7.50	329.50	36.83	4.25	39.00	0	0	0	0	1
10	BC/18/12	7.50	278.50	28.98	3.25	51.33	0	0	0	0	1
11	BC/18/13	9.75	318.50	33.85	3.25	40.67	0	0	1	0	0
12	BC/18/14	7.25	322.25	38.35	4.25	50.33	0	0	0	0	0
13	BC/18/15	9.00	350.25	31.00	4.50	52.00	0	0	0	0	1
14	BC/18/16	8.25	335.00	30.23	4.50	52.25	0	0	0	0	1
15	BC/18/17	7.50	349.00	21.08	3.75	50.00	0	0	0	0	1
16	BC/18/19	8.00	368.25	38.08	3.75	44.00	0	1	0	0	0
17	BC/18/20	7.75	296.50	26.05	3.00	38.75	0	0	0	0	1
18	BC/18/21	8.00	390.50	33.20	3.50	49.00	0	0	0	0	0
19	BC/18/22	6.50	308.25	30.10	4.25	51.00	0	0	0	0	0
20	BC/18/23	7.50	364.25	22.20	4.50	53.50	0	1	0	0	0
21	BC/18/24	8.25	317.75	26.90	4.50	47.00	0	0	0	0	1
22	BC/18/25	7.50	316.75	7.00	4.50	60.25	0	0	0	0	0
23	BC/18/26	7.25	342.00	22.45	4.50	50.0	0	0	1	0	0
24	BC/18/27	7.75	358.00	30.83	3.00	40.25	0	1	1	0	0
25	BC/18/28	9.00	338.50	27.45	4.50	57.67	0	0	0	1	0
26	BC/18/29	6.50	330.00	33.85	3.75	57.50	0	0	0	1	0
27	BC/18/32	8.75	307.50	36.30	3.67	70.67	0	1	0	0	0
28	BC/18/33	7.75	317.75	33.42	4.00	45.25	1	0	0	0	1
29	BC/18/34	7.75	318.50	37.05	4.25	54.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn l=Presence o=Absence	Mean red base O=Green l=Red	Isozymes		
									O=Absence of alleles from F5P8 l=Presence of alleles from F5P8	PGI	GOT
30	BC/18/35	8.25	315.75	35.35	3.50	48.50	0	0	1	1	0
31	BC/18/36	7.75	309.25	36.23	4.00	50.00	0	0	1	0	0
32	BC/18/37	8.25	350.25	29.18	4.00	44.00	0	0	0	0	0
33	BC/18/38	5.75	327.25	15.18	4.75	57.75	0	0	0	0	0
34	BC/18/39	7.75	332.75	34.08	4.00	43.75	0	0	0	0	1
35	BC/18/40	9.25	330.00	18.27	4.00	52.25	0	0	0	0	1
36	BC/18/41	8.50	369.25	42.98	4.25	41.00	0	0	0	0	0
37	BC/18/42	7.75	385.75	28.00	4.00	49.75	0	0	1	1	0
38	BC/18/43	7.75	322.25	36.10	4.50	44.00	0	0	0	1	0
39	BC/18/44	8.75	356.00	41.67	4.50	48.25	0	0	0	0	0
40	BC/18/45	8.00	345.00	38.77	3.25	46.00	1	0	0	1	0
41	BC/18/46	7.50	324.25	18.08	3.75	51.25	0	0	0	0	1
42	BC/18/47	7.50	281.50	26.95	3.50	47.33	0	0	0	0	1
43	BC/18/48	8.00	333.75	15.80	4.00	52.75	0	0	0	1	1
44	BC/18/49	7.25	285.00	43.20	2.75	44.67	0	0	0	0	1
45	BC/18/50	7.75	303.25	30.55	4.50	58.75	0	0	0	0	0
46	BC/18/51	7.75	315.75	29.97	4.25	67.25	0	0	0	0	0
47	BC/18/52	7.25	332.25	31.90	3.75	49.67	0	0	1	0	0
48	BC/18/54	9.00	319.00	19.27	3.75	47.00	0	0	0	0	1
49	BC/18/55	8.00	333.75	31.85	3.25	51.75	0	0	0	0	1
50	BC/20/2	8.00	335.00	38.00	4.00	53.00	0	1	0	0	0
51	BC/20/3	6.50	259.00	4.60	2.25	51.75	0	0	0	0	1
52	BC/20/4	8.00	294.50	41.97	3.50	44.75	0	0	0	1	0
53	BC/20/5	8.50	318.75	30.02	3.75	50.00	0	0	0	0	0
54	BC/20/7	8.00	316.25	35.90	4.00	51.75	0	0	0	1	0
55	BC/20/9	7.50	283.75	22.67	3.00	43.33	0	0	0	0	1
56	BC/20/10	7.75	306.25	42.95	2.25	44.25	0	0	0	1	0
57	BC/20/12	8.50	321.75	31.90	2.75	47.25	0	1	0	0	1
58	BC/20/13	8.50	345.75	38.25	3.25	51.00	0	0	0	0	0
59	BC/20/14	7.50	334.75	49.10	3.50	50.25	0	0	0	0	0
60	BC/20/15	8.75	292.25	39.6	3.25	46.00	0	0	0	1	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
61	BC/20/16	7.50	278.00	46.67	4.00	48.50	0	0	0	1	0
62	BC/20/17	7.25	292.75	0.00	2.25	59.25	0	0	0	1	1
63	BC/20/19	6.50	277.75	21.60	4.25	41.75	0	0	0	0	0
64	BC/20/20	6.25	270.75	20.70	4.00	51.5	0	0	0	1	0
65	BC/20/21	8.25	315.25	33.13	3.25	49.25	0	0	0	0	0
66	BC/20/22	9.00	291.75	49.18	2.75	50.5	0	0	0	1	0
67	BC/20/23	6.75	316.00	41.85	4.25	55.75	0	0	0	0	0
68	BC/20/24	7.75	322.50	38.08	3.75	51.50	0	0	0	1	0
69	BC/20/25	8.75	343.50	36.45	3.50	44.50	0	0	0	0	0
70	BC/20/27	9.00	285.00	31.75	3.75	52.50	0	0	0	1	0
71	BC/20/29	7.25	299.25	39.00	3.25	48.75	0	0	0	1	1
72	BC/20/31	7.75	307.25	47.60	3.75	55.75	0	0	0	0	0
73	BC/20/32	7.25	287.50	32.65	3.25	48.33	0	0	0	0	0
74	BC/20/33	7.75	295.75	38.53	3.50	47.00	0	0	0	1	0
75	BC/20/34	8.00	301.25	52.28	3.00	48.75	0	0	0	1	0
76	BC/19/2	6.50	338.50	39.45	2.50	45.50	0	0	0	0	1
77	BC/19/3	7.00	331.75	35.17	3.75	46.50	0	0	0	1	0
78	BC/19/4	8.75	370.75	35.42	3.50	56.00	0	0	0	0	0
79	BC/19/5	7.00	315.00	29.10	3.50	52.75	0	0	0	1	0
80	BC/19/9	7.00	335.00	40.95	4.00	51.25	0	0	0	0	0
81	BC/19/10	6.75	376.50	40.15	4.25	44.75	0	0	0	0	0
82	BC/19/11	6.50	345.75	32.95	4.00	46.25	0	0	0	0	0
83	BC/19/12	6.25	317.50	25.98	2.75	46.75	0	0	0	0	0
84	BC/19/13	7.50	281.00	28.83	3.00	49.75	0	0	1	1	0
85	BC/19/14	7.50	291.00	37.75	4.25	42.50	0	0	0	0	0
86	BC/19/15	7.75	313.75	27.30	4.00	52.75	0	0	0	0	0
87	BC/19/16	8.25	391.25	34.88	4.00	44.75	0	0	0	0	0
88	BC/19/19	7.25	344.50	18.10	4.50	49.00	0	0	0	1	0
89	BC/19/20	6.75	278.50	27.63	3.75	49.25	0	0	0	0	0
90	BC/19/22	7.75	340.75	32.33	2.75	49.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
91	BC/19/23	8.50	297.00	47.83	3.5	40.75	0	0	0	0	0
92	BC/19/24	7.00	312.50	25.05	4.75	50.00	0	0	0	1	0
93	BC/19/25	7.25	341.00	23.53	3.00	51.33	0	0	0	0	1
94	BC/19/26	7.00	354.25	20.93	4.50	60.33	0	0	0	0	0
95	BC/19/28	5.75	377.50	25.52	4.00	48.50	0	0	0	0	1
96	BC/19/30	8.50	325.75	36.67	3.50	46.00	0	0	0	1	0
97	BC/19/32	7.00	348.00	41.90	3.75	44.25	1	0	0	0	0
98	BC/19/33	7.25	314.50	26.63	3.75	50.00	0	0	0	0	1
99	BC/19/34	8.25	302.50	32.22	4.25	55.00	0	0	0	1	0
100	BC/19/35	6.25	318.50	29.40	3.25	52.25	0	0	0	0	0
101	BC/19/36	7.00	325.25	33.42	4.00	42.25	0	0	0	1	0
102	BC/19/37	6.75	308.00	31.18	4.25	55.50	0	0	0	1	0
103	BC/19/38	7.33	271.00	36.15	3.75	47.00	0	0	0	1	0
104	BC/19/39	9.00	384.75	34.88	4.00	45.67	0	0	0	1	0
105	BC/19/41	5.75	333.25	33.33	3.50	58.75	0	0	0	0	0
106	BC/19/42	6.75	310.75	36.33	3.75	52.5	0	0	0	0	0
107	BC/19/44	7.75	339.50	33.95	4.00	54.67	0	0	0	0	0
108	BC/19/45	7.75	321.50	36.55	3.75	50.25	0	0	0	0	0
109	BC/19/46	7.33	316.00	28.45	4.50	44.25	0	0	0	1	0
110	BC/19/47	7.25	328.25	32.47	4.25	47.75	0	0	0	0	0
111	BC/19/48	7.75	351.00	42.75	3.75	52.75	0	0	0	0	0
112	BC/19/49	8.00	341.00	48.62	3.75	47.75	0	0	0	0	0
113	BC/19/50	7.75	336.25	34.10	3.75	49.50	0	0	1	0	0
114	BC/19/52	7.00	333.75	41.35	4.50	52.00	0	0	0	0	0
115	BC/19/54	6.75	302.00	28.83	4.00	62.75	0	0	1	0	0
116	BC/19/55	9.00	356.75	50.33	3.50	47.67	0	0	0	1	0
117	BC/19/36	7.25	306.25	33.5	3.75	48.67	0	0	0	0	0
118	BC/19/57	7.75	312.00	24.17	4.50	43.75	0	0	1	0	0
119	BC/19/58	8.50	358.75	32.78	3.75	55.33	1	0	0	0	0
120	BC/19/59	7.25	303.00	36.67	4.00	48.67	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
121	BC/19/60	8.75	370.75	26.52	3.25	62.00	0	0	0	0	0
122	BC/19/62	7.75	314.50	33.75	3.75	48.00	0	1	0	0	0
123	BC/19/63	7.25	318.25	31.88	4.00	48.75	0	0	0	0	0
124	BC/19/64	7.25	325.00	23.48	4.00	47.75	0	0	0	0	0
125	BC/19/65	7.75	335.75	33.73	3.25	56.33	0	0	0	1	0
126	BC/19/66	6.75	284.25	27.83	3.50	54.50	0	0	0	0	0
127	BC/19/67	9.25	346.75	34.85	3.50	48.75	0	0	1	1	0
128	BC/19/68	7.00	317.75	27.08	4.50	44.50	0	0	0	0	0
129	BC/19/70	6.00	295.50	19.98	3.75	49.50	0	0	1	0	0
130	BC/19/71	5.75	340.50	34.60	3.75	58.25	0	0	0	0	0
131	BC/19/72	6.50	310.25	30.30	3.75	52.75	0	0	0	0	1
132	BC/19/73	7.50	301.00	40.45	3.25	49.00	0	0	0	1	0
133	BC/19/74	7.75	327.75	34.48	3.00	51.75	0	0	0	0	0
134	BC/19/75	6.50	299.67	50.13	3.00	43.75	0	0	0	0	1
135	BC/19/77	7.00	370.50	30.10	4.50	53.50	0	0	1	0	1
136	BC/19/78	8.00	329.25	34.28	3.50	48.75	0	0	1	1	0
137	BC/19/79	7.50	331.75	31.20	4.25	46.00	0	0	0	1	0
138	BC/19/80	6.50	313.50	20.42	4.50	55.33	0	0	0	0	0
139	BC/19/81	8.50	322.75	28.30	3.50	53.33	0	0	0	0	0
140	BC/19/82	9.00	326.75	50.35	4.00	40.00	0	0	0	1	0
141	BC/19/83	6.50	279.25	31.95	3.25	44.67	1	0	0	1	0
142	BC/19/84	8.50	342.00	22.28	4.50	53.33	0	0	0	0	0
143	BC/19/85	6.00	341.25	30.45	3.50	47.33	0	0	1	0	0
144	BC/19/86	7.50	342.75	32.20	4.25	43.75	0	0	0	1	0
145	BC/19/87	6.50	339.75	37.37	4.00	52.75	0	0	0	0	0
146	BC/19/88	7.00	326.75	45.30	3.75	45.75	0	0	1	1	0
147	BC/19/89	7.50	340.75	27.90	3.25	50.75	0	0	0	1	0
148	BC/19/90	6.50	288.75	35.73	4.00	57.75	0	0	0	1	0
149	BC/19/91	5.50	323.50	11.50	4.75	53.50	0	0	0	1	0
150	BC/19/92	8.25	331.50	38.25	3.00	41.75	0	0	0	1	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn l=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
151	BC/19/93	8.00	361.00	32.20	2.75	46.00	0	0	1	0	0
152	BC/19/94	6.75	346.25	28.77	4.50	40.25	0	0	0	0	1
153	BC/19/95	7.50	299.75	23.48	4.50	55.25	0	1	0	1	1
154	BC/19/96	7.25	315.25	33.25	4.25	46.00	0	0	0	0	0
155	BC/19/97	6.75	317.75	21.77	4.00	46.00	1	0	0	0	1
156	BC/19/98	7.75	357.75	36.42	4.00	45.75	0	0	1	0	0
157	BC/19/100	6.50	329.75	31.73	4.25	42.33	0	0	1	0	0
158	BC/19/101	6.50	298.25	37.33	4.00	46.50	1	0	0	0	0
159	BC/19/102	8.00	349.25	29.55	3.50	52.50	0	0	0	1	0
160	BC/19/103	7.25	341.50	20.23	4.25	42.25	0	0	0	0	1
161	BC/19/104	8.25	381.00	41.23	3.25	51.25	0	0	0	0	0
162	BC/19/105	7.25	334.75	33.83	3.75	49.33	0	0	0	0	0
163	BC/19/107	7.00	297.25	40.50	3.50	40.25	0	0	1	1	1
164	BC/19/108	7.75	359.00	31.73	4.25	39.00	0	0	0	0	1
165	BC/19/109	7.75	300.50	36.38	3.50	55.00	0	0	0	1	0
166	BC/19/110	7.75	363.75	27.02	4.50	51.00	0	0	1	0	0
167	BC/19/111	8.00	287.25	28.45	4.00	49.67	0	0	0	0	1
168	BC/19/112	8.25	359.25	31.27	3.00	41.50	1	0	0	0	0
169	BC/19/113	7.00	374.75	36.48	4.00	44.50	0	0	0	0	0
170	BC/19/114	6.75	301.75	34.75	3.00	42.00	0	0	1	0	1
171	BC/21/1	8.75	287.50	26.33	4.75	49.00	0	0	0	0	1
172	BC/21/2	9.50	314.50	32.75	3.75	38.25	0	0	0	0	0
173	BC/21/3	9.00	355.75	31.65	4.50	42.75	0	0	0	1	0
174	BC/21/5	7.25	286.75	30.28	3.25	35.5	1	0	0	1	0
175	BC/21/8	7.00	297.50	31.02	3.75	38.50	0	0	0	0	0
176	BC/21/10	7.50	307.00	19.52	4.00	35.00	0	0	0	0	1
177	BC/21/12	9.25	377.00	40.65	4.00	44.00	0	0	0	0	0
178	BC/21/14	8.50	291.25	7.65	3.00	35.75	0	0	0	0	1
179	BC/21/15	9.75	361.50	35.98	4.00	36.75	0	0	1	0	0
180	BC/21/19	8.50	270.50	13.98	4.25	46.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn l=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
181	BC/21/20	8.75	298.50	27.90	4.25	53.25	0	0	0	0	0
182	BC/21/21	9.25	311.00	22.80	3.75	43.00	0	0	0	0	0
183	BC/21/22	9.25	283.25	41.00	4.25	36.00	0	0	1	0	1
184	BC/21/23	8.00	296.00	34.08	3.75	44.25	0	0	0	0	0
185	BC/21/24	8.75	328.25	36.98	4.75	42.00	0	0	0	0	1
186	BC/21/25	6.50	302.00	19.85	3.50	58.00	0	0	0	0	0
187	BC/21/27	7.75	317.50	34.45	3.50	37.50	0	0	0	1	1
188	BC/21/28	8.50	283.00	15.10	4.50	47.75	0	0	0	0	1
189	BC/21/29	7.25	262.75	28.60	4.00	35.50	0	0	0	0	0
190	BC/21/30	9.50	300.00	24.10	4.25	34.50	0	0	1	0	0
191	BC/21/31	7.75	268.50	29.02	4.00	35.00	0	0	0	0	0
192	BC/21/33	7.50	264.50	24.92	3.00	34.75	1	0	0	0	0
193	BC/21/24	7.25	260.00	23.80	4.00	46.25	0	0	0	0	0
194	BC/21/36	8.00	336.50	43.60	3.75	48.33	0	0	0	0	0
195	BC/21/37	7.50	291.50	26.57	4.00	39.00	0	0	0	0	0
196	BC/21/38	9.75	286.75	26.70	4.00	43.00	0	0	0	1	0
197	BC/21/40	7.50	269.00	21.65	3.50	43.25	0	0	0	0	1
198	BC/21/42	8.25	336.00	30.70	3.75	46.00	1	0	0	0	1
199	BC/21/43	9.00	268.75	34.23	4.75	34.75	0	0	0	0	0
200	BC/21/45	7.50	309.25	34.33	4.75	34.00	0	0	0	0	0
201	BC/21/46	8.50	322.25	34.92	4.00	46.25	0	0	0	0	0
202	BC/21/47	8.50	276.75	22.68	4.50	38.50	0	0	0	1	1
203	BC/21/48	8.25	295.75	13.55	4.75	39.75	0	0	1	0	1
204	BC/21/49	9.50	346.75	24.80	4.25	40.75	0	0	0	1	1
205	BC/21/50	4.00	200.75	13.75	3.25	55.75	0	0	1	0	0
206	BC/21/51	8.75	276.75	33.33	5.00	36.25	0	0	0	0	0
207	BC/21/52	8.00	290.25	34.38	4.25	43.50	0	0	0	0	1
208	BC/21/54	8.00	270.75 ^f	17.65	3.25	34.00	0	0	0	0	0
209	BC/21/56	8.50	305.00	28.75	4.25	37.00	0	0	0	0	0
210	BC/21/57	8.75	280.00	35.67	4.50	43.50	0	0	0	0	1

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									PGI	GOT	SOD
211	BC/21/58	7.50	344.25	17.20	3.5	39.67	0	0	0	1	1
212	BC/21/59	8.00	286.00	22.30	4.50	43.25	0	0	0	0	0
213	BC/21/60	7.25	233.50	15.33	3.25	45.50	0	0	0	1	1
214	BC/21/62	7.25	327.75	34.90	4.00	45.00	0	0	1	0	1
215	BC/21/61	8.75	317.75	27.67	4.00	47.00	0	0	0	0	1
216	BC/21/64	9.00	322.50	26.60	4.50	40.00	0	0	0	0	1
217	BC/21/65	7.75	318.25	30.15	4.50	58.00	0	0	0	0	0
218	BC/21/67	9.00	356.00	28.50	4.00	47.75	0	0	0	0	0
219	BC/21/68	8.50	347.50	36.30	4.25	47.33	0	0	0	0	0
220	BC/21/69	8.50	332.25	32.90	4.50	42.33	0	0	0	0	0
221	BC/21/70	7.25	292.25	21.70	3.75	39.75	0	0	1	1	1
222	BC/21/72	9.50	328.25	27.40	4.00	43.50	0	0	0	0	0
223	BC/21/75	7.50	320.50	32.75	3.75	37.67	0	0	0	0	0
224	BC/21/76	8.50	335.25	20.88	2.50	46.00	0	0	0	0	0
225	BC/21/78	5.75	283.25	9.38	4.75	56.75	0	0	0	0	1
226	BC/21/79	6.00	247.00	4.10	3.00	47.25	1	0	0	0	1
227	BC/21/80	9.50	318.00	11.75	4.00	37.75	0	0	0	0	1
228	BC/21/82	9.50	344.00	23.17	4.00	40.25	0	0	0	0	0
229	BC/21/84	8.25	388.75	29.18	4.25	57.25	0	1	0	0	0
230	BC/21/85	7.75	298.50	27.42	4.50	53.33	0	0	0	0	0
231	BC/21/86	7.50	273.00	34.33	4.00	54.75	0	0	0	0	1
232	BC/21/87	8.25	324.00	25.30	3.75	40.75	0	0	0	0	1
233	BC/21/89	9.25	320.50	0.00	3.50	40.75	0	0	0	0	0
234	BC/21/91	8.50	324.25	34.90	4.00	48.75	0	0	1	0	1
235	BC/21/92	8.75	365.25	25.70	4.00	40.25	0	0	0	0	0
236	BC/21/93	8.50	338.25	24.70	4.25	41.75	0	0	0	0	0
237	BC/21/94	9.25	338.00	31.40	4.25	41.75	0	0	0	0	1
238	BC/21/95	7.25	281.00	25.60	4.00	40.25	0	0	0	0	1
239	BC/21/96	8.75	283.00	17.95	4.50	38.50	0	0	1	0	0
240	BC/21/97	7.67	306.75	34.98	3.25	48.25	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn l=Presence O=Absence	Mean red base O=Green l=Red	Isozymes		
									O=Absence of alleles from F5P8 l=Presence of alleles from F5P8		
									PGI	GOT	SOD
241	BC/21/100	9.50	294.00	38.60	4.25	39.67	0	0	0	0	1
242	BC/21/102	7.50	297.25	0.00	2.50	51.33	0	0	0	0	1
243	BC/21/103	7.50	256.75	32.85	3.75	47.00	0	0	0	0	1
244	BC/21/104	7.75	272.25	21.33	4.25	37.50	0	0	0	0	0
245	BC/21/105	7.50	317.25	23.08	4.25	44.50	0	0	0	0	1
246	BC/21/106	6.25	378.75	20.15	4.00	42.00	0	0	0	0	1
247	BC/21/107	7.50	260.00	29.35	3.75	41.00	0	0	0	0	0
248	BC/21/108	8.75	291.75	19.80	4.00	41.33	0	0	0	0	1
249	BC/21/109	8.50	265.25	13.25	3.25	37.00	0	0	0	0	1
250	BC/22/1	8.25	304.50	47.47	3.25	42.33	0	0	0	1	0
251	BC/22/2	7.50	325.50	33.20	2.75	51.67	0	0	0	0	0
252	BC/22/3	6.25	282.00	17.03	3.75	51.75	0	0	0	1	1
253	BC/22/4	8.50	280.00	48.08	3.50	35.50	0	0	0	0	0
254	BC/22/5	9.75	319.25	26.48	3.50	45.25	0	0	0	1	0
255	BC/22/6	6.75	261.00	29.40	3.50	66.00	0	0	0	0	0
256	BC/22/7	11.00	291.50	10.75	3.75	45.25	0	0	0	1	0
257	BC/22/8	8.00	288.00	27.25	3.50	42.50	0	0	0	1	0
258	BC/22/9	9.00	345.25	5.50	3.50	42.50	0	0	0	1	0
259	BC/22/10	7.75	306.50	39.60	3.75	48.00	0	0	0	0	0
260	BC/22/11	7.25	249.25	38.40	2.00	40.00	0	1	0	1	1
261	BC/22/12	8.25	299.25	26.23	4.25	47.25	0	0	0	0	0
262	BC/22/13	7.25	328.75	18.20	4.5	51.00	0	0	0	0	0
263	BC/22/14	7.00	275.00	16.73	4.00	36.00	0	0	1	0	1
264	BC/22/15	9.25	284.75	17.13	3.75	37.50	0	1	0	1	0
265	BC/22/16	7.75	246.50	27.45	3.25	38.00	0	0	0	1	0
266	BC/22/17	8.25	298.25	29.23	4.25	37.00	0	0	0	0	0
267	BC/22/18	7.00	272.75	25.45	3.25	36.00	0	0	0	0	1
268	BC/22/19	6.50	295.25	30.15	4.25	41.75	0	0	0	1	1
269	BC/22/20	10.50	292.00	41.90	3.25	41.67	0	1	0	0	0
270	BC/22/21	8.75	282.00	24.05	3.25	42.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days
271	BC/22/22	7.50	304.75	37.13	3.75	37.50
272	BC/22/23	9.00	345.75	34.43	4.00	38.50
273	BC/22/24	7.50	292.25	33.10	3.50	36.50
274	BC/22/25	7.25	240.25	20.33	3.25	38.75
275	BC/22/26	9.25	295.25	25.43	4.00	42.75
276	BC/22/27	7.00	261.75	41.20	3.75	39.67
277	BC/22/28	7.00	267.00	35.75	4.00	39.50
278	BC/22/30	8.75	309.50	40.90	4.25	41.75
279	BC/22/31	8.25	326.75	28.80	4.50	44.00
280	BC/22/32	7.25	310.50	34.55	3.75	50.50
281	BC/22/33	8.00	286.00	31.73	3.00	37.75
282	BC/22/34	7.50	292.25	46.37	4.25	38.00
283	BC/22/35	10.00	317.50	30.75	4.00	36.75
284	BC/22/36	10.25	320.25	28.63	3.75	45.25
285	BC/22/37	9.25	333.75	35.58	3.75	45.50
286	BC/22/38	7.75	286.00	26.37	4.00	38.50
287	BC/22/39	8.75	295.50	29.57	2.50	40.00
288	BC/22/40	7.75	299.00	39.78	3.50	42.75
289	BC/22/41	9.25	295.75	28.65	3.50	44.25
290	BC/22/42	8.50	299.50	36.05	3.75	48.25
291	BC/22/43	7.5	307.50	38.90	3.75	46.25
292	BC/22/44	9.25	337.50	35.17	4.00	38.67
293	BC/22/45	8.75	339.00	39.20	3.75	45.75
294	BC/22/46	8.50	302.50	30.37	4.25	44.75
295	BC/22/47	7.50	333.25	26.80	4.50	50.25
296	BC/22/48	7.50	310.50	41.95	3.75	37.75
297	BC/22/49	8.00	305.50	17.82	4.75	43.00
298	BC/22/50	10.50	314.00	37.15	4.00	42.67
299	BC/22/52	8.00	290.25	9.45	3.75	46.50
300	BC/22/53	7.75	293.00	45.40	3.00	42.50

Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
		0=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
0	0	0	1	0
0	0	0	1	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	1	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	1
0	0	0	1	0
0	0	1	0	1
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
1	0	0	1	1
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	1	1	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	1

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn l=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 l=Presence of alleles from F5P8		
									PGI	GOT	SOD
301	BC/22/55	8.75	318.75	18.10	4.25	46.50	0	0	0	0	0
302	BC/22/56	10.00	329.25	45.35	3.75	44.50	0	0	1	1	0
303	BC/22/57	10.00	278.00	0.00	3.25	45.75	0	0	0	0	0
304	BC/22/58	6.00	242.25	27.77	3.25	37.75	0	0	0	0	1
305	BC/23/1	5.50	290.25	30.05	4.25	52.25	0	0	0	1	0
306	BC/23/2	6.50	291.00	28.70	4.25	37.75	0	0	0	0	1
307	BC/23/3	6.75	323.50	41.98	4.00	51.00	0	0	1	1	1
308	BC/23/4	6.50	307.75	16.33	4.25	39.00	0	0	0	0	0
309	BC/23/5	6.75	252.50	32.72	4.00	59.50	0	0	0	1	0
310	BC/23/7	7.50	296.00	25.65	4.25	59.50	0	0	0	0	0
311	BC/23/8	6.25	308.50	23.40	3.75	46.50	0	0	0	1	0
312	BC/23/9	7.50	289.25	25.77	3.50	37.00	0	0	0	0	0
313	BC/23/10	7.75	283.00	35.30	3.50	37.00	0	0	0	1	0
314	BC/23/11	7.25	336.0	32.48	4.00	46.50	0	0	0	0	0
315	BC/23/12	7.50	341.25	34.75	3.75	40.00	0	0	1	1	0
316	BC/23/14	8.50	351.50	22.07	3.50	41.00	0	0	0	0	1
317	BC/23/16	7.75	299.25	18.60	4.25	41.75	0	0	0	0	1
318	BC/22/18	6.50	297.25	37.35	4.25	36.50	0	0	0	0	0
319	BC/23/19	8.00	331.00	26.98	3.50	39.00	0	0	0	0	0
320	BC/23/20	7.50	318.25	37.25	4.00	38.67	0	0	0	0	0
321	BC/23/22	7.75	306.50	32.28	4.25	39.25	0	0	0	0	0
322	BC/23/23	6.75	322.00	34.88	3.50	40.25	0	0	0	0	0
323	BC/23/24	7.00	299.75	31.00	3.75	35.00	0	0	0	1	0
324	BC/23/25	5.75	299.00	21.85	5.00	43.75	0	0	0	1	0
325	BC/23/27	8.25	370.75	22.48	3.00	42.25	0	0	0	0	0
326	BC/23/29	6.75	348.25	30.35	4.00	42.75	0	0	0	1	0
327	BC/23/31	6.00	293.50	23.15	4.75	45.33	0	0	0	0	0
328	BC/23/33	8.75	343.75	28.90	3.75	51.50	0	0	0	0	0
329	BC/23/34	7.75	263.00	31.07	2.75	46.00	0	0	0	0	0
330	BC/23/35	8.25	338.50	38.33	4.00	42.75	0	0	0	0	1

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
331	BC/23/36	8.25	365.50	36.05	3.75	41.67	0	0	0	1	0
332	BC/23/37	6.25	338.00	18.83	4.75	49.75	0	0	0	0	0
333	BC/23/38	7.75	268.50	34.20	3.50	35.25	0	0	0	1	0
334	BC/23/39	7.50	309.50	34.13	3.25	36.50	0	0	0	1	0
335	BC/23/41	8.25	373.25	19.25	4.25	39.25	0	0	0	1	0
336	BC/23/42	7.00	328.25	27.65	4.25	45.67	0	0	0	0	0
337	BC/23/45	7.25	336.50	23.33	4.50	45.50	0	0	0	0	0
338	BC/23/46	7.25	354.50	31.02	4.00	49.50	0	0	0	1	0
339	BC/23/47	8.25	339.25	27.17	5.00	52.25	0	0	0	0	0
340	BC/23/48	7.75	313.00	15.60	4.00	36.50	0	0	0	0	0
341	BC/23/49	7.00	294.00	10.55	3.25	44.50	0	0	0	1	0
342	BC/23/52	5.50	264.50	36.10	4.00	36.00	0	0	0	0	0
343	BC/23/53	8.00	280.25	34.67	4.25	33.75	0	0	0	0	0
344	BC/23/54	8.25	332.25	19.08	5.00	44.75	0	0	0	0	0
345	BC/23/55	8.50	326.25	29.78	4.00	41.25	0	0	0	0	0
346	BC/23/56	8.25	314.75	28.00	4.25	35.25	1	0	1	1	1
347	BC/23/57	7.00	278.25	33.45	3.50	38.67	1	0	0	1	1
348	BC/23/58	7.50	323.00	17.40	4.25	44.00	0	0	0	0	0
349	BC/23/59	8.00	329.25	13.55	4.50	43.75	0	0	0	0	0
350	BC/23/60	9.25	285.60	36.50	3.25	43.25	0	0	0	0	0
351	BC/23/61	7.25	276.75	43.80	3.25	35.50	0	0	1	1	0
352	BC/23/62	7.50	283.25	20.63	4.50	37.25	0	0	1	1	0
353	BC/23/63	7.25	341.75	28.83	3.50	42.50	0	0	0	0	0
354	BC/23/64	8.00	282.25	28.90	4.25	47.00	1	0	0	0	1
355	BC/23/65	8.00	353.00	24.77	4.25	43.50	0	0	0	0	0
356	BC/23/66	7.50	315.75	37.20	3.75	49.25	0	0	0	0	0
357	BC/23/67	6.25	231.00	22.27	2.50	42.25	0	0	0	1	0
358	BC/23/68	7.00	341.00	27.30	4.75	45.75	0	0	0	0	0
359	BC/23/69	7.75	331.00	20.88	3.75	44.25	0	0	0	0	0
360	BC/23/72	7.50	288.25	31.75	3.50	37.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
361	BC/23/73	7.25	295.00	19.53	4.00	37.50	1	0	0	1	0
362	BC/23/74	9.50	315.75	16.33	4.50	40.33	0	0	0	0	0
363	BC/23/75	8.00	292.00	5.07	3.50	43.00	0	0	0	1	0
364	BC/23/76	7.75	267.25	23.77	3.00	34.00	0	0	1	1	0
365	BC/23/77	7.25	282.75	28.35	3.75	37.50	0	0	0	0	1
366	BC/23/78	8.75	323.25	32.88	4.00	39.75	0	0	0	0	0
367	BC/23/79	7.00	305.25	27.05	4.25	40.75	0	0	0	1	0
368	BC/23/80	6.50	281.25	27.38	4.25	41.75	0	0	0	0	0
369	BC/23/81	7.50	326.75	5.70	5.00	47.00	0	0	0	0	1
370	BC/23/82	8.00	327.00	25.73	4.75	43.25	0	0	0	0	0
371	BC/23/83	7.75	298.75	31.77	2.75	41.00	0	0	0	0	0
372	BC/23/84	6.00	262.00	30.75	4.00	39.33	0	0	0	0	1
373	BC/23/85	9.00	362.25	29.30	4.00	45.50	0	0	0	0	0
374	BC/23/86	6.75	311.75	28.67	4.25	35.00	0	0	0	1	1
375	BC/23/88	7.00	326.75	25.53	4.00	39.75	0	0	0	0	1
376	BC/23/89	7.50	318.25	36.13	4.00	47.50	0	0	0	1	0
377	BC/23/90	9.75	343.50	19.18	3.75	41.67	0	0	0	0	1
378	BC/23/91	9.00	311.50	27.62	4.25	42.67	0	0	0	0	0
379	BC/23/92	6.25	280.00	18.70	4.50	53.67	0	0	0	0	0
380	BC/23/93	8.25	343.00	15.93	4.75	46.50	0	0	0	0	0
381	BC/23/94	7.75	346.00	31.70	4.25	37.00	0	0	1	0	0
382	BC/23/95	6.50	307.75	37.18	3.75	41.25	0	0	0	0	1
383	BC/23/97	7.75	333.75	29.80	3.50	42.67	0	0	0	0	0
384	BC/23/98	7.75	299.75	36.25	3.00	41.75	0	0	0	1	0
385	BC/23/99	5.75	243.75	4.10	2.00	35.33	0	1	0	0	1
386	BC/23/100	7.50	317.75	39.98	4.25	40.00	0	0	0	0	0
387	BC/23/101	9.00	330.00	32.60	4.00	44.75	0	0	0	0	0
388	BC/23/104	9.00	350.00	34.65	3.00	33.67	1	0	0	1	0
389	BC/23/106	8.25	322.00	20.33	3.00	41.50	0	0	0	0	0
390	BC/23/107	8.25	295.75	31.18	3.25	37.00	1	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
391	BC/23/110	6.50	301.25	37.22	3.25	40.00	0	0	0	1	0
392	BC/23/112	6.75	339.50	37.98	4.25	45.75	0	0	0	0	0
393	BC/23/114	7.25	329.25	29.63	4.25	43.25	0	0	0	0	0
394	BC/23/115	6.00	294.25	32.15	3.75	39.75	0	0	0	0	0
395	BC/23/116	6.75	317.00	26.88	4.25	44.25	0	0	0	0	0
396	BC/23/117	6.50	290.75	34.80	3.25	37.5	0	0	0	0	0
397	BC/23/118	5.50	263.50	7.38	2.75	40.00	0	0	0	0	1
398	BC/23/119	8.50	359.25	17.33	4.00	42.50	0	0	0	0	0
399	BC/23/121	6.75	306.25	16.32	4.25	47.50	0	0	0	0	0
400	BC/23/122	6.50	300.00	37.50	3.50	33.50	0	0	0	1	0
401	BC/23/123	6.25	292.25	20.30	4.25	38.75	0	0	0	1	0
402	BC/23/124	6.75	367.25	12.73	4.50	44.75	0	0	0	0	0
403	BC/23/126	8.25	306.50	21.15	4.25	34.00	0	0	0	1	0
404	BC/23/127	7.75	333.75	34.85	3.00	37.00	0	0	0	0	0
405	BC/23/129	7.50	319.00	16.18	4.50	43.5	1	0	0	0	1
406	BC/23/130	7.00	303.00	22.20	2.75	36.00	0	1	0	1	0
407	BC/23/133	7.50	369.25	34.15	4.25	42.50	0	0	0	1	0
408	BC/23/134	7.00	311.00	41.70	4.75	36.00	0	0	0	0	0
409	BC/23/135	6.75	284.00	10.38	2.75	39.50	0	1	0	0	1
410	BC/23/136	8.50	358.50	36.55	4.25	41.25	0	0	0	0	0
411	BC/23/137	11.00	298.00	27.25	3.50	36.75	0	0	0	1	0
412	BC/23/138	6.25	293.00	19.75	2.75	39.25	0	1	1	0	1
413	BC/23/139	9.00	389.75	31.13	3.25	49.33	0	0	0	0	0
414	BC/23/140	7.75	305.25	34.17	3.75	43.00	0	0	0	0	0
415	BC/23/142	8.25	326.75	32.20	2.00	39.25	0	0	1	1	0
416	BC/23/143	7.00	280.50	23.20	4.25	39.25	0	0	0	0	0
417	BC/23/144	6.25	282.75	29.45	4.50	41.50	0	0	0	0	0
418	BC/23/145	7.50	326.00	34.53	4.00	34.00	0	0	0	0	0
419	BC/23/147	8.25	356.50	19.90	4.00	44.75	0	0	0	0	0
420	BC/23/148	7.25	313.25	18.85	4.67	47.00	0	0	0	1	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
421	BC/23/149	6.50	328.00	19.77	4.00	39.75	0	0	0	0	1
422	BC/23/151	6.00	275.00	43.78	3.75	36.00	0	0	1	0	0
423	BC/23/153	7.25	336.50	24.08	4.00	35.75	0	1	0	1	0
424	BC/23/154	6.50	363.50	36.50	3.25	42.75	0	0	0	0	1
425	BC/23/156	8.33	315.33	5.10	3.33	34.67	0	0	0	1	1
426	BC/23/157	9.00	309.75	14.70	3.50	40.75	1	0	0	0	0
427	BC/23/158	7.50	361.25	24.23	4.25	41.00	0	0	1	0	0
428	BC/23/159	8.25	364.25	35.05	4.00	40.67	0	0	0	0	0
429	BC/23/160	6.00	262.75	30.42	4.00	36.5	0	0	0	0	0
430	BC/23/161	7.25	324.75	34.33	4.00	50.25	0	0	1	0	0
431	BC/23/162	6.25	312.00	31.85	4.25	41.00	0	0	0	1	0
432	BC/23/163	7.75	287.50	35.67	4.00	36.75	0	0	0	0	0
433	BC/23/164	7.25	288.25	25.43	4.00	40.25	0	0	0	1	0
434	BC/23/165	7.75	314.25	11.03	3.50	47.00	0	0	0	0	0
435	BC/23/166	6.75	291.75	26.65	4.25	44.33	0	0	1	1	1
436	BC/23/168	8.75	312.50	46.67	3.50	40.00	0	0	0	0	0
437	BC/23/169	5.75	288.75	34.27	3.50	35.00	0	0	0	0	0
438	BC/23/170	7.00	346.25	17.52	3.25	52.00	0	0	0	0	1
439	BC/23/172	7.00	307.25	32.22	3.75	42.75	0	0	0	0	0
440	BC/23/173	8.50	350.25	30.58	3.25	41.00	0	0	1	0	0
441	BC/23/174	8.50	311.25	22.85	3.75	42.00	0	0	0	1	0
442	BC/23/175	6.25	300.25	32.22	4.50	37.50	0	0	0	0	0
443	BC/23/177	8.25	300.50	29.48	3.25	43.00	0	0	0	0	0
444	BC/23/176	8.00	309.50	23.23	4.25	39.75	0	0	0	0	0
445	BC/23/179	6.25	295.25	21.30	4.50	41.25	0	0	0	0	0
446	BC/23/180	7.75	334.75	31.40	4.25	41.00	0	0	1	0	0
447	BC/23/181	6.75	287.00	37.40	3.75	38.5	0	0	0	1	0
448	BC/23/182	7.75	284.00	28.95	4.50	44.00	1	0	0	1	0
449	BC/24/1	8.75	398.75	21.75	3.25	53.00	0	0	0	0	0
450	BC/24/4	7.50	365.25	13.80	4.25	56.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn base 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes 0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
451	BC/24/5	7.25	379.00	7.87	1.50	54.50	0	0	0	1	1
452	BC/24/6	9.50	385.00	24.77	4.25	44.33	0	0	0	0	0
453	BC/24/8	7.50	336.50	2.50	4.00	62.50	0	0	0	1	1
454	BC/24/9	7.75	338.00	21.17	3.00	45.50	0	0	0	0	1
455	BC/24/10	7.50	387.25	13.68	4.25	59.25	0	0	0	0	0
456	BC/24/11	8.25	360.50	0.00	3.00	60.50	0	0	0	0	0
457	BC/24/12	7.75	351.75	2.88	3.75	44.75	0	0	0	0	0
458	BC/24/14	8.00	352.00	3.22	3.50	58.75	0	0	0	1	0
459	BC/24/15	7.75	337.75	15.65	4.25	49.75	0	0	0	0	0
460	BC/24/16	10.00	429.25	16.20	3.25	54.50	0	0	1	0	0
461	BC/24/18	6.00	294.50	8.15	4.25	58.00	0	0	1	0	0
462	BC/24/19	9.25	385.50	15.80	2.50	47.00	0	0	1	1	1
463	BC/24/22	9.00	407.75	0.00	3.25	50.50	0	0	0	0	0
464	BC/24/23	8.25	360.00	2.88	4.00	55.50	0	0	0	0	0
465	BC/24/24	6.75	297.00	32.30	2.50	54.50	0	0	0	0	1
466	BC/24/26	7.75	311.25	0.00	4.25	61.00	0	0	0	0	0
467	BC/24/27	7.50	338.50	11.00	4.25	43.75	0	0	0	1	0
468	BC/24/28	8.00	399.75	7.73	3.75	48.25	0	0	1	0	0
469	BC/24/29	8.50	365.75	15.08	3.00	48.50	0	0	0	0	0
470	BC/24/30	9.25	426.50	21.95	4.00	55.67	0	0	0	0	0
471	BC/24/31	7.75	281.00	35.20	3.25	53.00	0	0	1	0	0
472	BC/24/33	7.25	359.00	17.40	3.75	52.67	0	0	1	0	0
473	BC/24/34	8.50	349.00	26.00	3.75	48.00	0	0	0	0	0
474	BC/24/35	8.75	387.75	0.00	3.25	60.67	0	0	0	0	0
475	BC/24/36	7.25	363.00	36.33	3.75	51.50	0	0	1	0	0
476	BC/24/37	7.75	357.50	15.25	3.75	50.25	0	0	0	0	0
477	BC/24/38	8.75	322.75	5.72	3.25	49.75	0	0	0	1	0
478	BC/24/39	7.00	291.50	0.00	2.25	44.25	0	0	0	0	0
479	BC/24/40	8.00	348.50	15.40	3.00	49.00	0	0	0	0	0
480	BC/24/42	7.25	312.00	25.30	4.25	50.25	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes of alleles from F5P8		
									PGI	GOT	SOD
481	BC/24/43	7.25	291.50	2.23	4.25	57.5	0	0	1	0	0
482	BC/24/44	7.75	352.50	13.80	3.25	42.25	0	0	0	0	0
483	BC/24/45	8.00	343.00	23.05	4.00	51.67	0	0	0	0	0
484	BC/24/47	7.25	370.50	26.60	4.00	58.50	0	0	0	0	1
485	BC/24/48	6.50	305.00	0.00	4.00	55.75	0	0	0	0	1
486	BC/24/49	7.25	387.50	0.00	4.00	55.00	0	0	0	0	0
487	BC/24/50	7.50	316.25	8.20	3.75	55.00	0	0	0	0	0
488	BC/24/51	7.50	352.75	14.78	4.25	65.25	0	0	0	0	0
489	BC/24/52	7.50	390.75	0.00	4.25	57.75	0	0	0	1	0
490	BC/24/53	8.25	363.50	10.55	3.50	54.00	0	0	0	1	0
491	BC/24/54	7.25	298.75	12.22	4.25	57.33	0	0	0	0	0
492	BC/24/57	8.25	364.0	14.70	4.00	45.67	1	0	0	0	1
493	BC/24/59	7.50	349.75	4.85	4.00	59.33	0	0	0	0	0
494	BC/24/60	10.75	372.25	18.88	2.25	49.50	0	0	1	0	0
495	BC/24/61	7.25	300.75	4.05	4.75	55.00	0	0	1	1	0
496	BC/24/62	8.00	344.75	21.63	4.00	53.00	0	0	0	0	0
497	BC/24/64	6.50	348.0	9.13	4.25	52.00	0	0	0	0	0
498	BC/24/65	10.25	344.25	15.57	3.50	44.00	0	0	0	0	1
499	BC/24/66	7.50	307.25	0.00	2.50	41.00	0	0	0	0	1
500	BC/24/67	8.00	315.50	18.23	4.00	52.33	0	0	0	1	0
501	BC/24/68	7.25	354.00	6.88	5.00	55.00	0	0	0	1	0
502	BC/24/69	7.75	294.25	19.02	3.00	48.00	0	0	0	0	0
503	BC/24/70	8.00	330.50	2.03	4.00	61.00	0	0	0	1	1
504	BC/24/71	8.50	326.75	14.53	4.00	54.25	0	0	0	0	1
505	BC/24/72	7.50	349.50	9.57	4.00	63.00	0	0	0	1	0
506	BC/24/73	8.50	354.25	13.55	4.00	50.33	0	0	0	0	1
507	BC/24/74	7.75	346.00	11.15	4.00	59.50	0	0	0	0	0
508	BC/24/75	6.50	327.75	10.10	3.75	66.50	0	0	0	0	0
509	BC/24/77	8.25	381.00	30.32	3.50	50.67	0	0	0	0	0
510	BC/24/78	8.00	401.00	15.23	4.25	62.75	0	0	1	0	0

TABLE 2 continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
511	BC/24/79	7.50	335.25	11.90	3.75	45.50	0	0	0	0	0
512	BC/24/82	7.50	309.50	26.15	4.50	41.75	0	0	1	0	1
513	BC/24/83	9.50	316.50	20.57	4.50	49.50	0	0	0	0	1
514	BC/24/84	8.25	364.75	16.10	4.50	50.33	0	0	0	1	0
515	BC/24/85	6.75	285.00	2.30	2.25	54.33	0	0	0	1	1
516	BC/24/87	8.00	299.25	15.80	4.00	44.25	0	0	0	0	0
517	BC/24/88	8.00	343.50	23.88	3.50	50.00	0	0	0	0	0
518	BC/24/89	8.00	304.00	2.88	3.25	56.25	0	0	1	1	0
519	BC/24/90	9.50	370.00	19.88	3.50	49.00	0	0	0	1	0
520	BC/24/91	9.00	368.75	26.08	3.75	51.50	0	1	0	1	0
521	BC/24/92	7.25	278.00	0.00	3.00	77.25	0	1	1	1	0
522	BC/24/93	8.75	350.25	21.73	3.50	50.00	0	0	0	0	0
523	BC/24/94	7.75	306.25	9.93	3.75	55.25	0	0	0	0	0
524	BC/24/95	9.00	396.25	30.20	3.25	52.50	0	0	1	0	1
525	BC/24/96	7.25	322.75	11.95	4.50	54.25	0	0	0	1	0
526	BC/24/97	7.25	365.00	24.90	3.50	57.50	0	0	0	0	1
527	BC/24/98	8.25	309.75	16.40	4.25	58.67	0	0	0	0	0
528	BC/24/99	7.75	329.00	0.00	2.00	46.50	0	0	0	0	0
529	BC/24/100	7.75	323.75	16.23	4.25	53.75	0	0	1	0	1
530	BC/24/101	9.00	356.25	23.38	3.25	46.67	0	0	0	0	0
531	BC/24/103	8.50	338.50	29.88	4.00	46.75	0	0	0	0	0
532	BC/24/104	7.75	392.50	20.90	3.75	53.00	0	0	0	0	0
533	BC/24/105	7.50	373.50	28.90	4.00	47.50	0	0	0	0	0
534	BC/24/107	9.00	325.25	25.88	4.25	41.25	0	0	0	1	1
535	BC/24/109	7.75	341.75	31.95	4.00	48.33	0	0	0	1	0
536	BC/24/110	8.75	361.50	6.45	3.50	47.25	0	0	0	1	0
537	BC/24/112	6.50	369.25	0.00	2.00	54.00	0	0	0	0	1
538	BC/24/113	5.75	305.50	12.35	2.25	53.33	1	0	0	0	1
539	BC/24/114	8.25	265.25	10.55	1.75	45.00	0	0	0	1	1
540	BC/24/115	8.50	351.75	20.03	4.00	50.75	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
541	BC/24/116	7.50	388.75	17.95	4.25	53.67	0	0	1	0	0
542	BC/24/117	8.00	323.50	12.60	5.00	51.00	0	0	0	1	0
543	BC/24/118	8.25	331.75	4.38	4.00	60.67	0	0	0	0	0
544	BC/24/119	6.75	311.75	11.90	4.25	57.25	0	0	0	0	0
545	BC/24/120	7.25	317.25	2.03	4.50	57.67	0	0	0	0	0
546	BC/24/121	8.25	303.25	26.65	4.25		0	0	0	0	0
547	BC/24/122	8.00	310.50	15.70	3.75	55.25	0	0	1	1	0
548	BC/24/123	8.75	316.75	33.93	4.00	53.50	0	0	0	1	0
549	BC/24/125	7.25	331.5	18.30	4.50	56.00	0	0	0	0	0
550	BC/24/126	7.75	370.75	5.83	1.75	52.50	0	0	0	0	0
551	BC/24/127	8.25	324.50	23.67	4.25	55.00	0	0	0	0	1
552	BC/24/128	6.75	333.50	23.80	4.25	50.00	0	0	0	1	0
553	BC/24/129	8.25	320.25	23.98	2.00	55.50	0	0	0	1	0
554	BC/24/130	8.75	352.75	0.00	4.00	54.50	0	0	0	0	0
555	BC/24/131	8.50	356.25	9.88	3.00	48.50	0	0	1	0	0
556	BC/24/132	8.00	288.50	17.30	4.25	53.75	0	0	0	0	0
557	BC/24/133	8.25	330.75	17.78	4.00	49.33	0	0	0	0	0
558	BC/24/135	7.75	302.75	8.68	4.75	58.50	0	0	0	0	0
559	BC/24/138	8.00	328.50	15.43	3.50	52.50	0	0	0	0	0
560	BC/24/139	8.5	309.5	13.00	3.75	49.75	0	0	0	1	0
561	BC/24/140	7.25	333.00	9.68	4.25	53.25	0	0	0	0	0
562	BC/24/141	7.50	359.75	15.55	3.75	54.00	0	0	1	0	0
563	BC/24/142	9.50	354.25	19.73	4.00	54.50	0	0	0	0	0
564	BC/24/143	8.75	383.00	38.75	4.25	51.33	0	0	0	0	0
565	BC/24/144	7.50	342.50	22.30	3.00	53.33	0	0	0	1	0
566	BC/24/145	8.00	349.00	28.40	3.50	53.67	0	0	0	0	0
567	BC/24/147	8.25	398.00	14.03	3.75	51.00	0	0	0	0	0
568	BC/24/148	9.25	351.50	20.38	4.00	51.75	0	0	0	0	0
569	BC/24/149	6.5	303.00	18.73	3.50	49.75	0	0	0	1	0
570	BC/24/153	8.00	352.25	24.20	4.25	57.50	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
571	BC/24/154	7.50	304.50	6.88	3.25	52.25	0	0	0	0	0
572	BC/24/155	8.00	343.00	18.35	4.00	51.75	0	0	0	1	0
573	BC/24/156	8.50	345.50	24.67	3.25	51.50	0	0	0	0	0
574	BC/24/157	9.00	379.25	22.50	3.50	54.50	0	0	0	0	0
575	BC/24/158	8.25	315.50	5.38	2.75	54.00	0	0	0	0	1
576	BC/24/159	7.25	308.25	2.88	4.00	55.33	1	0	0	1	1
577	BC/24/160	8.75	369.75	2.88	4.00	66.00	0	0	0	0	0
578	BC/24/161	7.25	314.25	**	1.00	54.00	0	0	0	0	0
579	BC/24/162	8.25	347.25	7.57	4.00	50.75	0	0	0	0	0
580	BC/24/163	7.50	327.00	16.32	4.00	52.33	0	0	0	0	0
581	BC/24/164	8.50	315.00	15.08	3.75	48.50	0	0	0	1	0
582	BC/24/166	7.50	333.00	13.07	4.25	54.67	0	0	0	0	0
583	BC/24/167	8.75	374.00	25.53	4.00	50.50	0	0	0	0	0
584	BC/24/168	8.50	388.00	35.20	3.50	53.25	0	0	0	0	0
585	BC/24/169	8.50	375.25	26.18	4.00	51.67	0	0	0	0	0
586	BC/24/174	8.50	335.00	11.17	3.50	55.00	0	0	0	0	0
587	BC/24/175	7.25	367.25	20.53	3.50	49.75	0	0	0	0	0
588	BC/24/176	9.00	331.75	21.83	3.50	54.00	0	0	0	1	0
589	BC/24/177	8.00	343.00	16.28	4.00	50.75	0	0	0	0	0
590	BC/24/178	6.75	363.00	2.50	3.50	63.00	0	0	1	1	1
591	BC/24/180	6.25	272.25	0.00	1.75	56.50	0	0	0	0	0
592	BC/24/182	6.75	378.25	13.58	4.00	60.67	0	0	0	0	1
593	BC/24/183	7.75	349.25	14.38	3.75	54.00	0	0	1	0	0
594	BC/24/184	7.75	313.25	19.05	4.25	50.75	0	0	0	0	0
595	BC/24/185	7.25	318.00	14.73	4.00	52.25	0	0	0	0	0
596	BC/24/186	7.00	413.50	8.38	4.25	56.00	0	0	0	1	1
597	BC/24/187	7.75	332.25	6.10	3.25	48.75	0	0	0	0	0
598	BC/24/188	6.75	299.50	20.58	4.25	58.33	0	0	0	0	0
599	BC/24/189	8.50	391.75	0.00	4.00	56.00	0	0	0	1	0
600	BC/24/190	8.50	352.00	19.73	4.00	55.50	0	1	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn l=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
601	BC/24/192	8.75	357.00	12.97	3.75	56.00	0	0	0	1	0
602	BC/24/193	6.50	353.75	9.67	4.25	52.75	0	0	0	0	0
603	BC/24/195	5.75	360.50	14.05	4.50	63.75	0	0	0	0	0
604	BC/24/196	8.75	374.00	18.80	4.00	58.50	0	0	1	0	0
605	BC/24/197	7.25	304.50	4.38	3.00	54.75	0	1	0	0	0
606	BC/24/200	9.00	352.25	23.70	3.75	53.75	0	0	0	1	0
607	BC/24/201	8.25	378.00	6.43	4.50	51.00	0	0	0	0	1
608	BC/24/202	8.25	389.00	23.77	4.00	50.75	0	0	0	0	0
609	BC/24/203	9.00	368.00	6.70	3.75	57.50	0	0	0	0	0
610	BC/24/204	9.25	347.50	23.67	3.75	60.25	0	0	1	0	0
611	BC/24/205	7.00	253.75	18.95	3.50	60.75	0	0	1	0	0
612	BC/24/206	9.00	384.75	0.00	3.50	59.50	0	0	0	0	0
613	BC/24/207	8.50	358.25	9.18	3.50	58.67	0	0	0	0	0
614	BC/24/208	8.25	347.25	24.88	3.00	49.67	0	0	0	0	1
615	BC/24/209	8.25	377.50	10.23	4.25	53.50	0	1	1	1	0
616	BC/24/211	7.50	340.25	0.00	4.25	46.00	0	1	0	0	0
617	BC/24/212	9.00	358.75	27.32	3.50	48.67	0	1	0	1	1
618	BC/24/215	8.00	365.00	28.75	4.25	53.00	0	0	1	1	0
619	BC/24/216	7.75	338.25	10.65	3.25	51.25	0	0	0	0	0
620	BC/24/217	6.75	302.25	6.88	4.25	52.00	0	0	0	1	0
621	BC/24/218	8.50	350.25	20.23	4.00	48.25	0	0	1	0	0
622	BC/24/219	8.25	352.75	18.70	4.00	55.00	0	0	0	0	0
623	BC/24/221	7.25	302.00	23.33	4.00	55.25	0	0	0	1	1
624	BC/24/222	7.25	327.25	16.32	3.75	54.67	0	0	0	1	0
625	BC/24/224	8.00	332.25	30.95	3.00	54.67	0	0	0	1	0
626	BC/24/225	7.25	338.00	7.18	2.25	50.25	0	0	0	0	0
627	BC/24/226	8.25	374.00	30.20	3.00	55.50	0	0	0	1	0
628	BC/24/227	8.50	323.00	18.63	4.00	54.00	0	0	0	1	0
629	BC/24/229	8.25	362.25	21.08	3.25	57.75	0	0	0	1	0
630	BC/24/230	7.25	341.50	2.88	4.25	58.67	0	0	0	1	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes 0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
631	BC/24/231	10.00	377.75	10.55	3.75	59.75	0	0	0	0	0
632	BC/24/232	7.25	351.00	5.75	3.25	53.75	0	0	0	0	0
633	BC/24/233	7.50	346.25	6.43	3.75	55.75	0	0	0	0	0
634	BC/24/234	7.00	343.50	12.6	3.75	56.50	0	0	0	0	0
635	BC/24/235	7.75	338.25	18.33	4.25	41.75	0	0	0	0	1
636	BC/24/236	6.75	406.25	0.00	2.75	60.33	0	0	1	1	1
637	BC/24/237	8.25	330.00	13.28	3.75	49.25	0	0	0	0	0
638	BC/24/238	7.25	296.75	0.00	4.25	60.33	0	0	0	0	0
639	BC/24/239	7.50	322.25	22.73	4.00	63.33	0	0	0	0	0
640	BC/24/242	8.25	308.50	2.50	3.50	62.00	0	0	0	0	0
641	BC/24/244	8.75	336.00	12.80	3.75	61.25	0	0	0	0	0
642	BC/24/245	8.25	372.50	20.85	4.33	49.50	0	0	0	0	0
643	BC/24/246	8.25	341.50	2.88	2.50	49.50	0	0	0	0	1
644	BC/24/247	9.00	399.50	3.55	3.25	59.67	0	0	0	0	0
645	BC/24/248	9.75	369.75	29.50	2.00	54.50	0	0	0	0	0
646	BC/24/249	7.00	295.00	16.38	3.75	50.75	0	0	0	0	0
647	BC/24/253	7.25	319.50	25.00	4.50	53.25	0	0	0	0	0
648	BC/24/254	7.50	350.00	3.83	4.75	70.75	0	0	1	0	0
649	BC/24/255	7.25	346.25	12.68	3.75	52.67	0	0	0	0	0
650	BC/24/256	5.75	337.25	0.00	4.25	62.50	0	0	0	0	1
651	BC/24/257	8.75	361.00	20.77	3.75	54.00	0	0	0	0	0
652	BC/24/260	9.00	352.00	2.88	3.25	50.00	0	0	0	1	0
653	BC/24/261	7.75	325.25	9.58	4.00	53.75	0	0	1	0	0
654	BC/24/262	8.50	367.25	20.68	4.00	58.67	0	0	0	1	0
655	BC/24/263	9.75	348.25	16.47	3.75	56.25	0	0	0	1	0
656	BC/24/264	8.00	354.25	13.15	4.50	54.75	0	0	1	0	0
657	BC/24/265	8.50	331.25	0.00	1.75	46.75	0	0	0	0	1
658	BC/24/266	8.50	370.25	23.38	4.25	51.75	0	0	0	1	0
659	BC/24/267	8.00	278.75	24.02	3.50	55.33	0	0	0	0	0
660	BC/24/268	7.50	414.50	22.45	3.25	53.33	0	0	1	0	1

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score
661	BC/24/270	8.25	415.00	8.63	4.00
662	BC/24/273	9.50	378.75	20.05	3.75
663	BC/24/277	9.25	322.75	7.73	3.75
664	BC/24/279	6.50	310.00	5.70	3.50
665	BC/24/280	8.00	369.00	37.03	3.25
666	BC/24/281	9.75	330.00	26.65	3.75
667	BC/24/282	10.25	407.25	16.38	3.50
668	BC/24/283	7.50	368.50	0.00	4.00
669	BC/24/284	7.25	329.50	11.43	3.75
670	BC/24/285	8.00	352.75	8.63	4.00
671	BC/24/288	7.00	302.00	23.05	4.25
672	BC/24/289	6.50	336.75	7.73	3.75
673	BC/24/290	8.50	407.50	21.80	3.75
674	BC/24/291	9.00	312.00	21.55	4.25
675	BC/24/292	8.50	377.25	4.85	3.50
676	BC/24/293	8.75	321.50	18.60	3.50
677	BC/24/296	8.50	377.50	6.43	3.25
678	BC/24/297	6.75	380.25	11.97	4.75
679	BC/24/298	8.25	322.25	19.63	4.25
680	BC/24/299	6.50	347.50	12.18	4.50
681	BC/24/300	5.75	338.75	0.00	3.25
682	BC/24/301	7.75	373.50	0.00	3.00
683	BC/24/302	7.50	368.75	12.88	3.25
684	BC/24/303	9.00	362.00	21.08	3.50
685	BC/24/304	9.25	341.25	5.28	4.00
686	BC/24/307	8.50	306.00	21.70	3.50
687	BC/24/308	7.50	338.25	17.33	4.25
688	BC/24/309	8.00	310.50	24.28	3.25
689	BC/24/310	8.75	329.50	3.22	4.75
690	BC/24/311	6.50	330.75	2.03	4.00

Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
			0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
			PGI	GOT	SOD
62.70	0	0	0	0	0
57.00	0	0	0	0	0
60.33	0	0	1	0	0
61.50	0	0	0	0	0
45.50	0	0	0	1	0
46.50	0	0	1	0	0
50.67	0	0	0	0	0
56.25	0	0	1	0	0
51.75	0	0	0	0	0
57.50	0	0	1	0	0
55.25	0	0	0	0	0
34.00	0	0	0	0	0
53.50	0	0	0	0	0
54.50	0	0	0	0	0
53.67	0	0	0	0	1
58.00	0	0	0	1	0
52.50	0	0	0	0	0
67.25	0	0	0	0	0
50.75	0	0	0	0	0
57.33	0	0	0	0	0
57.50	0	0	0	0	0
56.00	0	0	0	0	0
54.00	0	0	1	0	0
48.50	0	0	0	0	0
55.00	0	0	0	0	0
51.75	0	0	0	0	0
65.50	0	0	1	0	0
49.25	0	0	0	1	0
62.25	0	0	0	0	0
47.00	0	1	0	1	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
691	BC/24/312	7.50	327.00	2.03	4.00	51.00	0	0	0	0	0
692	BC/24/313	7.75	365.25	11.55	3.50	55.00	0	0	0	0	0
693	BC/24/316	8.75	353.00	11.50	1.75	46.75	0	0	0	0	1
694	BC/24/317	8.75	335.25	33.45	3.75	50.50	0	0	0	1	1
695	BC/24/318	8.50	331.75	8.15	3.00	57.75	0	0	0	0	0
696	BC/24/320	8.25	324.75	26.68	4.00	44.00	0	0	0	1	0
697	BC/24/321	7.50	341.00	11.40	4.00	54.25	0	0	0	0	0
698	BC/24/322	7.75	337.25	22.52	4.00	44.50	0	0	0	0	0
699	BC/24/324	6.75	326.75	18.30	4.50	48.50	0	0	0	0	0
700	BC/24/326	8.00	386.75	5.73	3.75	47.00	1	0	0	0	1
701	BC/24/327	8.00	325.25	25.43	4.25	50.00	0	1	0	1	0
702	BC/24/328	9.50	355.50	11.55	3.67	51.50	0	0	0	1	0
703	BC/24/329	7.75	330.75	24.15	4.25	47.25	0	0	1	0	0
704	BC/24/330	6.50	307.50	14.68	4.00	51.00	0	0	0	0	0
705	BC/24/332	6.75	333.00	22.73	4.00	60.50	0	0	1	1	0
706	BC/24/333	6.00	329.25	9.65	3.25	54.50	0	0	0	0	0
707	BC/24/334	6.50	397.00	0.00	4.75	58.75	0	0	0	1	0
708	BC/24/336	8.50	403.50	17.48	4.75	49.75	0	0	0	0	0
709	BC/24/337	7.75	358.00	2.88	3.75	59.75	0	0	0	1	0
710	BC/24/338	7.50	426.50	33.75	4.00	57.50	0	0	1	0	0
711	BC/24/339	8.75	381.75	31.20	3.50	51.75	0	0	1	0	0
712	BC/24/340	8.25	309.00	3.23	4.00	56.75	0	0	0	0	0
713	BC/24/341	6.00	266.75	0.00	2.25	49.67	0	0	0	0	1
714	BC/24/342	7.00	359.75	0.00	3.25	50.67	0	0	0	1	1
715	BC/24/343	8.75	404.25	16.25	3.50	49.75	0	0	1	0	0
716	BC/25/3	7.25	346.50	10.57	3.25	55.75	0	0	0	0	0
717	BC/25/5	10.00	338.25	29.08	4.00	53.25	0	0	0	0	0
718	BC/25/6	8.00	375.75	31.88	3.75	51.00	0	0	0	1	0
719	BC/25/9	7.50	349.25	22.50	3.50	47.25	0	0	0	1	1
720	BC/25/10	8.50	285.75	31.15	4.25	48.67	0	0	0	1	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence 1=Presence of alleles from F5P8	O=Absence 1=Presence of alleles from F5P8	O=Absence 1=Presence of alleles from F5P8
									PGI	GOT	SOD
721	BC/25/11	9.25	292.75	13.90	4.00	50.00	0	0	0	0	0
722	BC/25/13	7.25	290.25	16.33	3.75	42.50	0	0	0	0	1
723	BC/25/14	8.00	330.00	14.60	4.75	53.25	0	0		0	1
724	BC/25/16	9.25	423.25	9.53	3.75	46.00	0	0	0	1	0
725	BC/25/17	9.25	330.75	7.93	3.50	47.00	0	0	0	0	0
726	BC/25/18	7.75	370.25	30.85	4.00	45.50	0	0	0	0	0
727	BC/25/19	9.75	311.25	18.05	3.50	44.75	0	0	0	0	0
728	BC/25/20	8.75	336.75	29.33	4.25	39.50	0	0	0	0	0
729	BC/25/22	8.75	330.50	25.35	3.75	46.00	0	0	1	0	0
730	BC/25/23	6.50	284.75	23.92	4.50	51.00	0	0	0	0	1
731	BC/25/24	8.75	342.25	11.25	2.75	46.30	0	1	1	1	0
732	BC/25/25	8.75	367.75	2.50	4.25	52.25	0	0	0	0	0
733	BC/25/26	9.25	280.50	40.45	3.75	47.33	0	0	0	0	0
734	BC/25/29	6.75	299.25	0.00	2.00	47.25	0	0	1	1	1
735	BC/25/30	8.25	314.50	5.75	4.00	48.67	0	0	0	0	0
736	BC/25/31	8.50	312.50	22.13	4.50	49.00	0	0	0	0	0
737	BC/25/33	8.50	331.25	0.00	4.50	63.32	0	1	0	0	0
738	BC/25/36	9.50	362.75	27.95	2.00	56.00	0	1	0	0	0
739	BC/25/38	7.25	312.75	14.20	4.50	53.00	0	0	0	1	0
740	BC/25/40	8.00	302.25	22.02	3.75	54.00	0	0	0	0	0
741	BC/25/41	7.00	319.00	0.00	3.25	54.67	0	0	0	0	1
742	BC/25/42	8.75	375.75	6.43	3.75	49.50	0	0	0	0	1
743	BC/25/43	8.50	311.00	28.15	4.00	49.25	0	0	0	1	0
744	BC/25/44	6.25	291.00	20.83	3.25	54.50	0	0	0	1	0
745	BC/25/45	9.25	359.25	5.07	3.50	50.75	0	0	1	0	0
746	BC/25/46	6.00	329.50	12.33	4.50	48.00	0	1	1	1	1
747	BC/25/48	9.00	287.00	25.53	2.75	54.33	0	0	0	0	0
748	BC/25/49	7.75	363.00	10.05	3.00	58.75	0	0	0	1	0
749	BC/25/50	6.75	279.00	24.65	1.25	49.75	0	0	0	0	1
750	BC/25/51	9.00	340.25	15.98	3.75	43.00	0	0	0	1	1

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
751	BC/25/52	9.50	310.00	34.53	3.00	47.67	0	0	0	1	0
752	BC/25/53	9.00	316.00	34.38	3.25	46.00	1	0	0	0	0
753	BC/25/54	7.25	327.75	9.10	3.50	57.75	0	0	0	0	0
754	BC/25/56	6.25	312.00	10.35	3.75	57.75	0	0	0	1	0
755	BC/25/57	8.75	344.50	0.00	3.75	51.00	0	0	0	0	0
756	BC/25/58	7.50	297.25	37.13	3.50	48.50	0	0	0	1	0
757	BC/25/59	9.00	327.25	14.90	4.00	59.75	0	0	0	0	0
758	BC/25/60	7.50	319.50	19.90	3.25	53.75	0	0	0	0	1
759	BC/25/61	10.50	367.75	30.30	3.00	45.00	0	0	0	1	1
760	BC/25/63	9.75	336.50	28.20	3.75	46.50	0	0	0	1	0
761	BC/25/65	7.50	296.75	8.20	4.50	66.50	0	0	0	0	0
762	BC/25/66	10.75	391.50	27.20	3.75	62.25	0	0	0	0	0
763	BC/25/67	5.75	269.00	24.75	4.00	68.75	0	0	0	1	0
764	BC/25/68	8.50	351.75	24.25	3.67	46.50	0	0	0	0	1
765	BC/25/69	7.75	353.75	15.05	4.25	51.50	0	0	0	0	0
766	BC/25/70	8.50	382.00	13.75	4.25	60.50	0	0	0	0	0
767	BC/25/71	9.00	426.75	31.55	3.50	51.25	0	0	0	0	0
768	BC/25/72	8.25	313.50	23.68	3.25	51.50	0	0	0	0	0
769	BC/25/74	7.75	299.50	20.35	4.50	51.00	0	0	0	0	0
770	BC/25/76	8.50	351.75	0.00	1.75	48.75	0	0	0	1	1
771	BC/25/77	7.00	318.50	14.35	4.00	57.00	0	0	0	0	1
772	BC/25/78	10.25	355.75	34.08	3.25	43.00	0	0	0	0	1
773	BC/25/79	8.25	336.75	0.00	4.25	62.33	0	0	0	0	0
774	BC/25/80	9.25	398.00	29.20	3.50	51.67	0	0	0	0	0
775	BC/25/81	8.00	312.00	10.20	2.75	50.00	0	0	0	1	0
776	BC/25/82	9.50	366.00	9.17	3.75	63.00	0	0	0	1	0
777	BC/25/83	9.25	320.75	43.13	3.75	47.75	0	0	0	1	0
778	BC/25/84	8.75	342.50	19.80	4.25	51.50	0	0	0	0	0
779	BC/25/86	9.25	350.00	17.20	3.75	48.00	0	1	0	1	0
780	BC/25/87	8.25	331.50	11.10	3.75	63.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes 0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	-SOD*
781	BC/25/88	6.75	333.50	27.13	3.75	55.50	0	0	0	0	0
782	BC/25/90	8.00	336.50	5.28	4.00	51.00	0	0	0	0	1
783	BC/25/91	8.25	301.25	20.33	2.75	47.75	0	1	0	0	0
784	BC/25/92	9.50	359.50	19.43	3.25	64.33	0	1	0	0	0
785	BC/25/93	8.00	312.00	13.95	3.00	45.33	0	0	0	1	0
786	BC/25/94	8.50	332.50	16.13	3.75	50.25	0	0	0	1	0
787	BC/25/96	9.25	349.25	12.88	4.50	45.75	0	0	0	0	1
788	BC/25/97	9.50	280.25	32.80	3.25	47.25	0	0	0	1	0
789	BC/25/98	6.25	283.50	0.00	1.50	53.25	0	0	0	1	1
790	BC/25/99	8.00	331.00	11.63	4.75	43.00	0	0	0	1	0
791	BC/25/100	6.50	334.75	5.07	4.00	53.30	0	0	0	0	0
792	BC/25/101	8.50	278.75	7.60	4.25	49.25	0	0	0	1	0
793	BC/25/102	8.25	334.00	2.50	4.25	50.67	0	1	0	0	0
794	BC/25/103	7.25	350.00	8.60	1.75	47.25	0	0	0	1	1
795	BC/25/105	8.25	324.25	6.10	3.00	45.50	0	0	0	0	0
796	BC/25/106	9.25	329.75	14.40	3.75	50.25	0	0	0	0	0
797	BC/25/108	8.00	371.50	0.00	3.50	50.75	0	0	0	0	0
798	BC/25/109	6.25	359.50	5.28	2.75	54.25	0	0	0	0	1
799	BC/25/110	9.25	346.25	43.92	2.75	45.25	0	0	0	0	1
800	BC/25/111	8.75	279.25	0.00	1.50	57.67	0	0	1	0	0
801	BC/25/112	7.50	345.00	23.48	4.25	51.00	0	0	0	0	0
802	BC/25/113	7.25	360.00	6.10	3.75	54.50	0	0	0	0	0
803	BC/25/115	9.00	312.75	0.00	3.25	51.25	0	0	0	0	0
804	BC/25/116	7.00	346.25	29.13	4.00	59.00	0	0	0	1	0
805	BC/25/117	8.00	314.75	0.00	2.25	42.25	0	1	0	1	1
806	BC/25/119	10.75	389.25	20.25	3.25	51.00	0	0	0	0	0
807	BC/25/122	8.25	385.75	29.40	4.50	49.75	0	0	0	0	0
808	BC/26/1	10.75	319.00	32.67	3.75	44.75	0	0	0	0	0
809	BC/26/2	8.75	286.25	38.88	4.25	48.00	0	1	0	1	0
810	BC/26/3	9.25	346.50	32.42	4.25	44.33	0	1	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
811	BC/26/4	7.00	239.00	9.88	3.50	39.50	0	0	0	0	1
812	BC/26/8	9.25	295.75	38.90	3.25	42.00	0	0	0	0	0
813	BC/26/9	7.25	343.00	38.20	4.25	46.00	0	0	0	0	0
814	BC/26/10	7.25	303.50	26.02	4.75	48.75	0	0	0	0	0
815	BC/26/11	8.00	299.00	4.38	4.00	57.75	0	1	0	0	0
816	BC/26/13	6.50	308.50	5.07	2.75	42.50	0	0	0	0	1
817	BC/26/14	8.25	315.50	10.32	5.00	45.50	0	0	0	0	1
818	BC/26/15	7.00	303.00	4.38	4.75	51.00	0	0	0	0	0
819	BC/26/16	8.75	290.75	37.97	3.50	53.00	0	1	0	0	0
820	BC/26/17	8.50	302.00	49.88	3.75	54.33	0	0	0	0	0
821	BC/26/19	7.50	308.25	13.05	4.00	52.50	0	0	0	0	0
822	BC/26/21	7.25	300.50	53.68	2.50	48.67	0	0	0	1	0
823	BC/26/22	7.50	312.25	23.68	3.25	49.33	0	0	0	1	1
824	BC/26/23	6.75	278.75	39.63	3.25	47.75	0	0	1	1	0
825	BC/26/24	7.00	309.25	23.88	4.25	47.75	0	0	0	1	0
826	BC/26/25	7.25	300.75	31.10	4.25	45.50	0	0	0	0	0
827	BC/26/26	6.00	295.50	28.92	4.25	44.00	0	0	0	1	0
828	BC/26/27	7.25	275.25	24.73	4.25	44.50	0	0	0	0	0
829	BC/26/30	10.00	295.50	30.98	3.00	41.00	0	0	0	1	0
830	BC/26/32	8.25	313.75	33.98	3.75	45.67	0	0	0	1	0
831	BC/26/33	8.25	315.75	8.75	4.00	52.75	0	1	0	1	0
832	BC/26/34	7.75	287.75	26.05	4.00	50.75	0	0	0	1	0
833	BC/26/35	7.00	303.75	25.43	3.33	**	**	0	0	0	0
834	BC/26/38	7.00	281.25	40.30	3.50	53.25	0	0	0	0	0
835	BC/26/39	7.75	305.50	39.60	4.00	42.00	0	0	0	1	0
836	BC/26/40	9.25	293.00	35.45	3.75	35.75	0	0	0	1	0
837	BC/26/41	9.75	349.00	32.10	4.25	42.75	0	0	0	0	0
838	BC/26/44	8.75	313.50	33.17	4.00	42.75	1	0	0	1	0
839	BC/26/45	8.00	324.00	35.98	4.50	44.75	0	0	0	1	0
840	BC/26/46	7.50	285.75	20.75	4.25	43.50	0	0	0	1	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
841	BC/26/50	7.00	281.75	35.73	3.75	40.75	0	1	0	1	0
842	BC/26/51	9.00	306.50	48.43	3.75	51.67	0	0	0	0	0
843	BC/26/52	6.50	276.75	33.55	3.75	34.25	0	0	0	1	0
844	BC/26/53	8.25	283.25	49.17	3.75	39.75	0	0	0	0	0
845	BC/26/54	6.50	253.50	22.48	4.50	39.00	0	0	0	0	1
846	BC/26/55	7.00	291.00	27.22	4.25	65.75	0	0	0	0	0
847	BC/26/56	9.00	276.00	18.95	4.25	54.25	0	0	0	0	0
848	BC/26/58	6.50	328.75	0.00	3.00	57.33	0	0	0	0	0
849	BC/26/59	7.00	326.25	27.42	2.50	39.00	0	0	0	0	1
850	BC/26/60	8.25	287.00	31.40	3.50	45.67	0	0	0	1	0
851	BC/26/61	10.00	343.75	27.40	3.25	44.50	0	0	0	1	0
852	BC/26/62	6.50	273.75	33.88	4.75	44.00	0	0	0	1	0
853	BC/26/66	8.25	294.00	27.88	4.50	43.25	0	0	0	1	1
854	BC/26/67	8.25	334.25	9.52	3.25	40.50	0	0	0	1	0
855	BC/26/70	9.50	337.75	26.35	3.25	38.25	0	0	0	0	1
856	BC/26/71	7.00	294.00	44.43	3.25	42.50	0	0	0	1	1
857	BC/26/72	6.50	275.00	26.47	3.50	42.75	0	0	0	0	0
858	BC/26/73	8.50	349.00	20.68	4.50	47.00	0	0	0	1	1
859	BC/26/76	9.00	296.25	32.90	3.00	40.50	0	0	0	0	0
860	BC/26/77	9.00	370.50	38.75	3.75	50.00	0	0	0	1	0
861	BC/26/78	8.00	343.25	23.75	4.00	51.00	0	0	0	1	0
862	BC/26/79	11.25	341.75	51.08	3.00	41.50	0	0	0	1	0
863	BC/26/81	8.75	303.00	26.93	3.00	48.50	0	0	0	0	0
864	BC/26/84	8.00	270.75	30.38	4.00	52.50	0	0	1	1	0
865	BC/26/85	8.25	334.25	37.43	3.25	47.00	0	0	1	1	0
866	BC/26/86	7.75	349.25	21.38	3.00	51.67	0	0	0	0	0
867	BC/26/87	8.00	309.50	21.43	4.25	48.75	0	0	0	1	0
868	BC/26/88	7.50	326.25	50.90	3.50	47.25	0	0	0	1	0
869	BC/26/89	7.50	326.50	30.83	4.25	44.75	0	0	0	1	0
870	BC/26/90	7.25	351.25	39.42	4.75	44.00	0	0	0	0	1

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days
871	BC/26/91	8.75	357.50	20.70	4.75	54.00
872	BC/26/92	9.00	333.00	34.45	4.00	45.33
873	BC/26/93	7.75	300.50	41.38	4.00	47.67
874	BC/26/94	9.25	333.00	12.03	4.50	47.75
875	BC/26/95	8.50	325.75	31.53	4.00	47.25
876	BC/26/97	9.50	367.50	56.75	3.00	43.00
877	BC/26/98	10.00	348.00	44.28	3.25	49.00
878	BC/26/99	7.75	309.00	36.03	3.50	45.00
879	BC/26/102	9.00	309.00	24.35	4.75	45.00
880	BC/26/103	8.00	293.50	37.55	3.50	40.50
881	BC/26/105	7.75	356.25	22.75	4.50	66.75
882	BC/26/107	9.50	306.25	43.97	4.00	43.25
883	BC/26/108	6.75	277.50	23.90	3.00	43.75
884	BC/26/109	8.50	281.00	30.65	3.00	42.75
885	BC/26/111	8.00	346.75	38.55	4.75	40.50
886	BC/26/112	9.50	327.50	21.30	4.25	42.75
887	BC/26/113	8.00	298.25	34.70	3.75	44.75
888	BC/26/114	8.00	295.75	49.30	3.00	45.00
889	BC/26/115	8.50	320.75	40.67	3.50	41.25
890	BC/26/116	7.75	275.25	48.10	3.25	37.67
891	BC/26/117	8.00	352.00	22.95	4.50	48.25
892	BC/26/118	7.75	271.75	32.53	3.50	48.75
893	BC/26/119	9.00	286.00	36.00	3.00	45.50
894	BC/26/120	8.00	316.75	32.78	4.00	48.75
895	BC/26/122	8.25	299.25	24.25	4.25	44.33
896	BC/26/123	7.25	331.25	26.25	3.75	53.50
897	BC/26/124	9.75	326.75	24.83	3.25	50.33
898	BC/26/126	8.00	315.75	39.38	4.25	47.50
899	BC/27/1	7.75	265.75	22.33	3.00	36.00
900	BC/27/4	6.50	261.00	31.52	4.25	53.00

Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
		0=Absence of alleles from F5P8 1=Presence of alleles from F5P8	PGI	GOT
0	0	0	0	0
0	0	0	1	1
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	0
0	0	0	0	1
0	0	0	0	0
0	0	0	1	0
0	0	1	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	0
0	0	1	0	0
0	0	0	1	0
0	0	0	0	0
0	0	0	1	1
0	0	0	1	0
1	0	0	1	0
0	0	0	0	0
0	0	0	1	1
0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes 0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
901	BC/27/5	7.25	255.75	23.40	4.00	43.50	0	0	0	0	1
902	BC/27/6	7.00	304.00	34.50	4.00	43.50	0	0	0	0	1
903	BC/27/9	7.00	260.50	24.68	3.50	44.25	0	0	0	0	1
904	BC/27/11	5.50	170.75	32.30	3.25	54.75	0	0	1	0	1
905	BC/27/12	7.25	266.00	51.28	3.50	46.33	0	0	0	0	0
906	BC/27/13	7.00	332.00	41.60	4.25	36.33	0	0	0	0	0
907	BC/27/14	7.50	321.25	49.05	3.00	43.50	0	0	1	1	0
908	BC/27/15	7.25	273.75	35.90	4.25	45.00	0	0	0	1	1
909	BC/27/18	7.00	284.00	42.78	3.75	45.00	0	0	0	0	0
910	BC/27/21	7.25	273.00	43.60	3.75	41.75	0	0	0	0	0
911	BC/27/23	8.00	294.75	33.40	4.25	44.75	0	0	0	1	1
912	BC/27/24	7.00	286.25	46.28	4.00	41.50	0	0	0	0	0
913	BC/27/25	8.75	278.00	32.48	3.50	41.75	0	0	0	0	1
914	BC/27/26	6.50	310.00	38.35	3.75	42.00	0	0	0	0	0
915	BC/27/27	7.75	255.75	37.53	3.50	44.67	0	0	1	0	0
916	BC/27/28	7.75	309.50	42.55	3.75	42.67	0	0	1	0	1
917	BC/27/29	6.50	295.75	15.38	4.50	52.00	0	0	0	0	0
918	BC/27/30	7.25	282.75	22.17	3.00	43.25	0	0	0	0	1
919	BC/27/31	5.50	230.75	16.23	2.50	40.00	0	0	0	0	1
920	BC/28/1	5.75	238.50	34.13	3.25	45.25	0	0	1	0	1
921	BC/28/2	7.50	310.00	43.55	4.00	35.50	0	0	0	1	0
922	BC/28/3	6.75	288.25	37.90	3.75	46.50	0	0	0	0	0
923	BC/28/4	6.75	263.50	49.50	3.25	35.50	0	0	0	0	0
924	BC/28/5	8.25	290.75	34.75	3.75	40.00	0	0	0	0	1
925	BC/28/6	7.25	287.50	24.48	3.25	42.87	0	0	1	0	0
926	BC/28/7	6.00	280.50	32.25	3.50	40.67	0	0	0	0	0
927	BC/28/8	7.00	290.25	41.40	2.75	43.25	0	0	0	1	0
928	BC/28/9	8.00	278.50	30.70	4.25	46.67	0	0	0	0	0
929	BC/28/10	4.25	146.75	33.57	2.25	38.50	0	0	0	0	1
930	BC/28/11	5.50	238.25	36.80	3.50	43.00	0	0	0	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days
931	BC/28/12	5.57	266.50	36.95	3.00	35.50
932	BC/28/13	6.25	279.75	23.55	3.50	43.50
933	BC/28/14	7.00	244.00	42.80	3.75	37.33
934	BC/28/15	6.25	210.25	0.00	2.50	38.75
935	BC/28/16	6.25	311.75	31.38	2.50	36.50
936	BC/28/18	6.25	294.50	40.05	3.75	41.00
937	BC/28/19	6.25	242.00	34.58	3.00	34.75
938	BC/29/1	7.25	247.00	51.18	2.50	40.25
939	BC/29/2	8.75	291.25	44.30	2.00	35.00
940	BC/29/3	7.25	321.00	44.85	3.50	42.75
941	BC/29/5	6.75	300.00	38.90	3.25	39.33
942	BC/29/6	8.00	294.75	58.38	1.75	48.25
943	BC/29/7	9.25	270.50	42.40	3.50	55.00
944	BC/29/8	8.25	300.25	39.03	3.75	42.33
945	BC/29/10	7.50	269.75	38.93	3.25	37.25
946	BC/29/11	7.25	286.50	53.25	3.00	44.00
947	BC/29/13	7.25	288.50	36.88	4.00	38.33
948	BC/29/14	7.00	301.25	40.10	4.00	46.25
949	BC/29/15	8.00	303.00	39.53	3.75	39.75
950	BC/29/16	7.25	229.00	41.08	3.25	40.25
951	BC/29/18	7.00	264.50	34.50	2.75	36.33
952	BC/29/19	7.75	312.25	18.92	3.75	37.50
953	BC/29/20	7.00	284.00	41.33	3.25	38.25
954	BC/29/21	8.00	284.25	44.35	3.25	36.75
955	BC/29/22	7.25	299.75	41.38	3.75	39.75
956	BC/29/23	6.50	296.25	41.88	3.00	40.50
957	BC/29/25	7.00	290.00	61.32	3.75	39.00
958	BC/29/26	6.25	238.25	41.10	3.50	36.00
959	BC/29/27	5.25	221.00	16.60	1.50	39.25
960	BC/29/28	7.50	239.75	42.98	3.25	36.75

Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
		0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
		PGI	GOT	SOD
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	0	1
0	0	0	0	1
0	0	0	1	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	1	0
0	0	0	0	1
0	0	0	0	1
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	1	0
0	0	0	1	0
0	0	0	0	0
0	0	0	1	0
0	0	0	1	0
0	0	0	1	1
0	0	0	1	1
0	0	0	1	0
0	0	0	1	0
0	0	0	0	1
0	0	0	0	0
0	0	0	1	0
0	0	1	0	1
0	0	0	0	1

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn 1=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									0=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
961	BC/29/29	8.75	299.50	50.55	3.50	37.75	0	0	0	1	0
962	BC/29/32	7.25	243.25	41.25	2.25	38.00	0	0	1	0	1
963	BC/29/33	6.33	292.67	37.70	3.00	41.33	0	0	0	1	1
964	BC/29/34	6.00	194.00	29.48	2.75	38.00	0	0	0	0	0
965	BC/29/35	6.25	256.25	42.33	2.25	37.00	0	0	0	1	0
966	BC/29/36	8.25	282.25	46.18	3.75	45.25	0	0	0	0	0
967	BC/29/38	7.00	248.00	48.53	2.50	36.50	0	0	0	1	0
975	BC/30/3	7.00	315.75	3.33	5.00	75.50	0	0	0	0	0
976	BC/30/4	8.50	357.25	24.80	3.75	65.75	0	0	0	0	0
977	BC/30/11	9.50	319.00	34.10	4.75	56.25	0	0	0	0	0
978	BC/30/15	9.00	266.75	10.20	3.75	54.75	0	0	0	0	1
979	BC/30/16	10.00	337.50	29.10	3.75	48.50	0	0	0	0	0
980	BC/30/19	10.75	278.25	31.75	4.80	41.50	0	0	1	0	1
981	BC/30/21	7.75	369.50	21.20	4.25	54.50	0	0	1	1	0
982	BC/30/25	9.25	286.50	27.70	4.00	65.00	0	0	0	0	0
983	BC/30/30	7.50	344.25	8.60	5.00	77.67	0	0	0	0	0
984	BC/30/32	9.00	308.00	36.53	3.75	47.75	0	0	1	0	0
985	BC/31/3	8.50	370.75	9.57	4.25	67.25	0	0	0	0	0
986	BC/31/6	8.50	315.00	47.85	3.25	54.00	0	0	1	0	0
987	BC/32/1	7.50	363.50	12.20	3.50	57.75	0	0	1	0	0
988	BC/32/2	8.50	331.75	18.43	3.75	75.67	0	0	1	0	0
989	BC/32/5	7.75	352.75	0.00	4.75	58.00	0	0	1	0	0
990	BC/32/6	8.00	390.25	0.00	2.25	49.67	0	0	1	0	0
991	BC/32/7	9.50	412.00	8.70	3.25	55.50	0	0	1	0	0
992	BC/33/1	9.50	352.50	31.45	4.50	51.00	0	0	0	0	0
993	BC/33/2	9.00	310.50	42.85	3.25	47.00	0	0	1	0	0
994	BC/33/6	7.25	284.25	30.38	4.50	58.33	0	0	0	0	0
995	BC/33/10	8.50	312.25	30.90	3.50	52.00	0	0	0	1	0
996	BC/33/11	6.75	287.50	16.83	3.75	46.25	0	0	0	0	1
997	BC/33/13	8.00	337.25	15.63	3.50	52.32	0	0	1	0	0

TABLE 2 (continued)

Clone number	Identity of clones	Mean leaf width (mm)	Mean leaf length (mm)	Mean per cent stem (angles)	Mean regrowth score	Mean ear emergence days	Mean awn l=Presence 0=Absence	Mean red base 0=Green 1=Red	Isozymes		
									O=Absence of alleles from F5P8 1=Presence of alleles from F5P8		
									PGI	GOT	SOD
968	F5/P8 ^{††}	4.00	173.50	0.00	3.00	73.50	1	1	*	*	*
998	F5/P8 ^{††}	4.00	250.75	0.00	3.00	70.67	1	1	*	*	*
969	F5/4P [†]	7.50	272.75	25.67	4.50	44.00	0	0	*	*	*
970	F5/5P [†]	7.25	340.25	22.95	4.50	48.50	0	0	*	*	*
971	F/7P [†]	6.50	330.50	26.17	4.50	59.00	0	0	*	*	*
972	F5/6P [†]	7.00	349.75	15.10	4.25	68.50	0	0	*	*	*
973	F5/P3 [†]	8.00	341.50	30.15	4.50	68.35	0	0	*	*	*
974	F5/44P [†]	7.50	268.75	32.40	4.00	43.50	0	0	*	*	*
999	F5/4P [†]	7.00	251.75	31.43	4.00	51.00	0	0	*	*	*
1000	F5/44P [†]	6.50	272.75	39.70	4.00	47.00	0	0	*	*	*
Overall mean		7.82	321.15	24.74	3.74	48.00					
Mean of perennial Parent		4.00	212.13	0.00	3.00	72.10					
Mean of Italian Parent		7.16	303.30	27.95	4.28	53.70					
P		<0.001	<0.001	<0.001	<0.001	<0.001					
SED		0.642	24.946	6.013	0.410	4.006					
CV %		11.62	11.00	34.50	15.50	11.80					

†† = Perennial ryegrass parents

† = Italian ryegrass parents

‡

Red leaf base

Table 2 shows the presence or absence of red leaf base, which was consistent over replicates. The frequency of red leaf base plants is shown in Table 3. Assuming that red leaf base is controlled by genes showing complementary dominance at loci R and C we can have several different outcomes depending on the genotype of the parents. For red leaf base to be present both R and C are required together. Three possibilities must be considered.

(1) The original parental genotypes were homozygous at both loci.

Thus -

Diploid genotypes

RR

CC

Tetraploid genotypes

r r r r

c c c c

Triploid genotypes X

rrR

ccC

Diploid Italian ryegrass genotypes

r r

c c

Chance of haploid gametes

having R = $\frac{1}{3}$

having C = $\frac{1}{3}$

having both C and R = $\frac{1}{9}$

All gametes

r

c

all green

Therefore the progeny should be 1 red to 8 green.

(2) The original diploid perennial ryegrass was heterozygous in one or both loci and the tetraploid was homozygous in both loci.

Thus -

TABLE 3. The frequencies and ratios of Redbase/no red base, Awn/no awns, Isozymes (PGI, GOT, SOD)/no isozymes as they occurred in various families including expected ratios and χ^2 tests for isozymes

Family	BC/18 ^a	BC/19 ^X	BC/20 ^X	BC/21 ^a	BC/22 ^X	BC/23 ^X	BC/24 ^X	BC/25 ^X	BC/26 ^X	BC/27 ^a	BC/28 ^X	BC/29 ^X	BC/30 ^a	BC/31 ^a	BC/32 ^X	BC/33 ^X	Total	
Number of clones	49	95	26	79	55	144	267	92	91	21	18	30	10	2	5	6	990	
Red base	4	2	2	1	3	5	8	8	6	0	0	0	0	0	0	0	0	39
Green	45	93	24	78	52	139	259	84	85	21	18	30	10	2	5	6	951	
Red/Green	1:11	1:46	1:12	1:78	1:17	1:28	1:32	1:10	1:14	-	-	-	-	-	-	-	1:24	
χ^2	0.43	7.81 ^{**}	0.30	7.75 ^{**}	1.78	8.51 ^{**}	17.81 ^{**}	0.54	1.88	2.62	2.25	3.75	1.25	0.25	0.63	0.75	58.31 ^{**}	
No awns	2	5	0	4	1	10	4	1	2	0	0	0	0	0	0	0	29	
Awned	47	90	26	75	54	134	263	91	89	21	18	30	10	2	5	6	961	
No awns/awned	1:24	1:14	-	1:19	1:54	1:13	1:66	1:91	1:45	-	-	-	-	-	-	-	1:33	
χ^2	5.60 [*]	8.89 ^{**}	5.20 [*]	7.66 ^{**}	8.74 ^{**}	9.80 ^{**}	44.22 ^{**}	16.08 ^{**}	13.72 ^{**}	4.20 [*]	3.60	6.00 [*]	2.01	0.40	1.00	1.19	138.31 ^{**}	
PGI	10	16	0	9	4	15	44	6	5	4	2	2	3	1	0	2	123	
No PGI	39	79	26	70	51	129	223	86	86	17	16	28	7	1	5	4	867	
PGI/No PGI	1:4	1:5	-	1:8	1:13	1:9	1:5	1:14	1:17	1:4	1:8	1:14	1:2	1:1	-	1:2	1:70	
Expected ratio	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	
χ^2	3.68	10.99 ^{**}	13.01 ^{**}	17.11 ^{**}	16.79 ^{**}	34.03 ^{**}	34.13 ^{**}	29.75 ^{**}	31.73 ^{**}	1.92	3.99 [*]	9.60 ^{**}	0.05	0.24	2.51	0.01	209.55 ^{**}	
GOT	7	30	13	9	22	45	69	32	42	4	4	14	1	0	5	1	298	
No GOT	42	65	13	70	33	99	198	60	49	17	14	16	9	2	0	5	692	
GOT/No GOT	1:6	1:2	1:1	1:8	1:1.5	1:2	1:3	1:2	1:1	1:4	1:3	1:1	1:9	-	-	1:5	1:2.3	
Expected ratio	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	
χ^2	7.99 ^{**}	0.13	3.24	17.11 ^{**}	1.11	0.28	6.74 ^{**}	0.09	6.73 ^{**}	1.93	1.00	2.41	2.44	1.01	9.97 ^{**}	0.75	62.93 ^{**}	
SOD	17	15	5	35	10	25	45	55	15	11	5	10	2	0	0	1	251	
No SOD	32	80	21	44	45	119	222	37	76	10	13	20	8	2	5	5	739	
SOD/No SOD	1:2	1:5	1:4	1:1.3	1:4.5	1:5	1:5	1:0.7	1:5	1:1	1:3	1:2	1:4	-	-	1:5	1:2.9	
Expected ratio	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	1:2	
χ^2	0.03	13.16 ^{**}	2.33	4.29 [*]	5.68 [*]	16.53 ^{**}	32.63 ^{**}	28.95 ^{**}	11.62 ^{**}	3.44	0.24	0.0001	0.80	1.01	2.51	0.75	124.07 ^{**}	

*** Significant at P = 0.001; ** Significant at P = 0.01; * Significant at P = 0.05.

• = Crosses with P122/5 triploid parent.

X = Crosses with P122/6 triploid parent.

Diploid genotypes

Rr or RR or Rr
Cc Cc CC

Tetraploid genotypes

r r r r
c c c c

Triploid genotypes

Rrr or rrr or rrr or Rrr
Ccc ccc Ccc ccc

Diploid Italian
ryegrass genotypes

r r
c c

Chance of: No chance of both

$R = 1/3$ R and C in hybrids

$C = 1/3$ with diploid

C and R =

$$1/3 \times 1/3 = 1/9$$

in the hybrids
with diploid

(3) The diploid Italian ryegrass parents were heterozygous, at the R or C locus which would give a higher frequency of red base plants than expected on the basis of (2).

There was no significant heterogeneity among the families in the proportion of plants with red base, suggesting that both triploid parents had the genotype Rrr Ccc and that a 1:8 ratio can be expected. However, a 1:24 ratio was obtained which deviated significantly from a 1:8 ratio (Table 3).

Isozymes

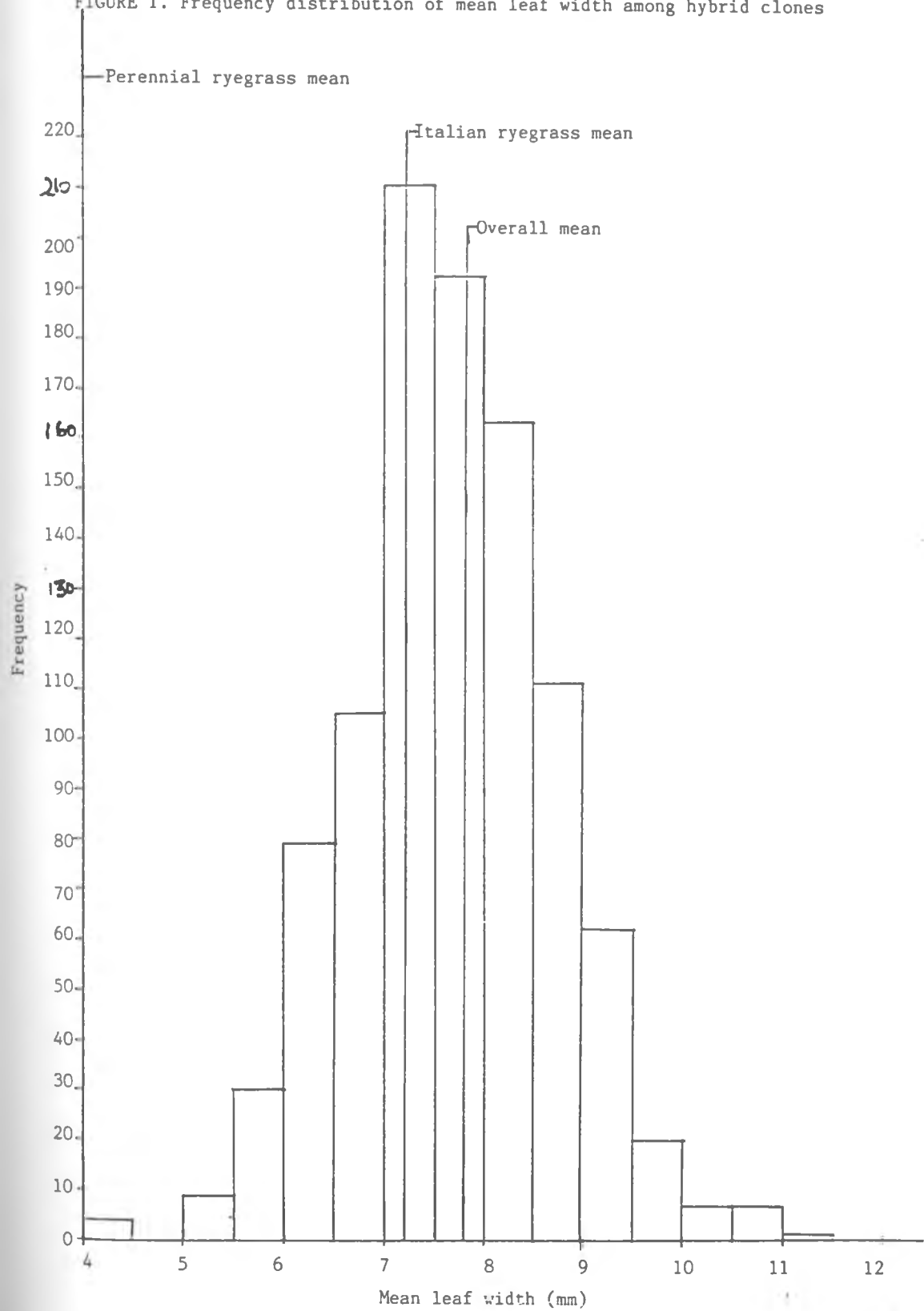
Assuming mendelian segregation, the chance of any hybrid having an allele of the perennial ryegrass origin at the loci PGI/2, GOT/1 and SOD was 1 in 3 (1:2 ratio). Overall families,

there was a large deficiency of the perennial ryegrass allele at PGI/2 and a smaller deficiency at SOD but no deficiency at GOT (Table 3). Since these loci are unlinked these results suggest loss of some chromosomes but not others. At the GOT/1 and SOD loci there was significant heterogeneity among families, but not at the PGI locus. The reason for the apparent heterogeneity among the families at these two loci is unclear.

Leaf width

The mean leaf width of the hybrids between Italian ryegrass and perennial ryegrass and of the parents; a single perennial ryegrass clone and six Italian ryegrass clones are presented in Table 2. The perennial ryegrass was tillered twice giving two mean values. Of the six Italian ryegrass parents two were tillered twice and the other four only once, giving a total of eight mean values. Differences among clone means were significant ($P < 0.001$). The mean leaf width of the perennial ryegrass parent was 4.00 mm. The mean leaf width of the six Italian ryegrass parents ranged from 6.50 mm to 8.00 mm with a mean of 7.20 mm. The mean leaf width of the hybrid clones was 7.81 mm. The mean value of the hybrid clones differed significantly from that of the perennial ryegrass parent, but the mean value of the hybrids and the six Italian parents did not differ significantly at $P = 0.05$. As the mean of Italian ryegrass parents and the hybrids are very close, it can be concluded that most hybrid clones inherited the leaf width character from the Italian ryegrass parents. Figure 1 shows the frequency distribution of the mean leaf width of the one

FIGURE 1. Frequency distribution of mean leaf width among hybrid clones



thousand clones. The majority (57%) of the clones had mean leaf width between 7.00 mm and 8.50 mm (Fig.1). Both the mean leaf width of the hybrid clones and that of the Italian ryegrass fell within this range and did not differ significantly. However, a few hybrid clones had very narrow leaves, similar in width to the perennial ryegrass parent and significantly narrower than all the Italian ryegrass parents, suggesting inclusion of genes from the perennial ryegrass parent.

Leaf length

The one thousand clones varied significantly in mean leaf length ($P < 0.001$). The mean leaf length ranged from 170.75 mm to 426.75 mm with a mean of 321.15 for the hybrids and 212.13 mm for the perennial ryegrass and 303.30 mm for the Italian ryegrass parents. The mean leaf length of the hybrids did not differ significantly from that of the Italian ryegrass parents but differed significantly from that of the perennial ryegrass parent. Thus the hybrid clones were more like the Italian ryegrass than the perennial ryegrass parent in leaf length. Figure 2 shows the frequency distribution of the mean leaf length of the hybrid clones. Over sixty per cent of the clones had a mean leaf length of between 290.00 mm and 350.00 mm, but a small proportion of hybrid clones had significantly shorter leaves than any of the Italian ryegrass parents, although none were significantly shorter than the perennial ryegrass parent at $P = 0.05$.

FIGURE 2. Frequency distribution of mean leaf length among hybrid clones

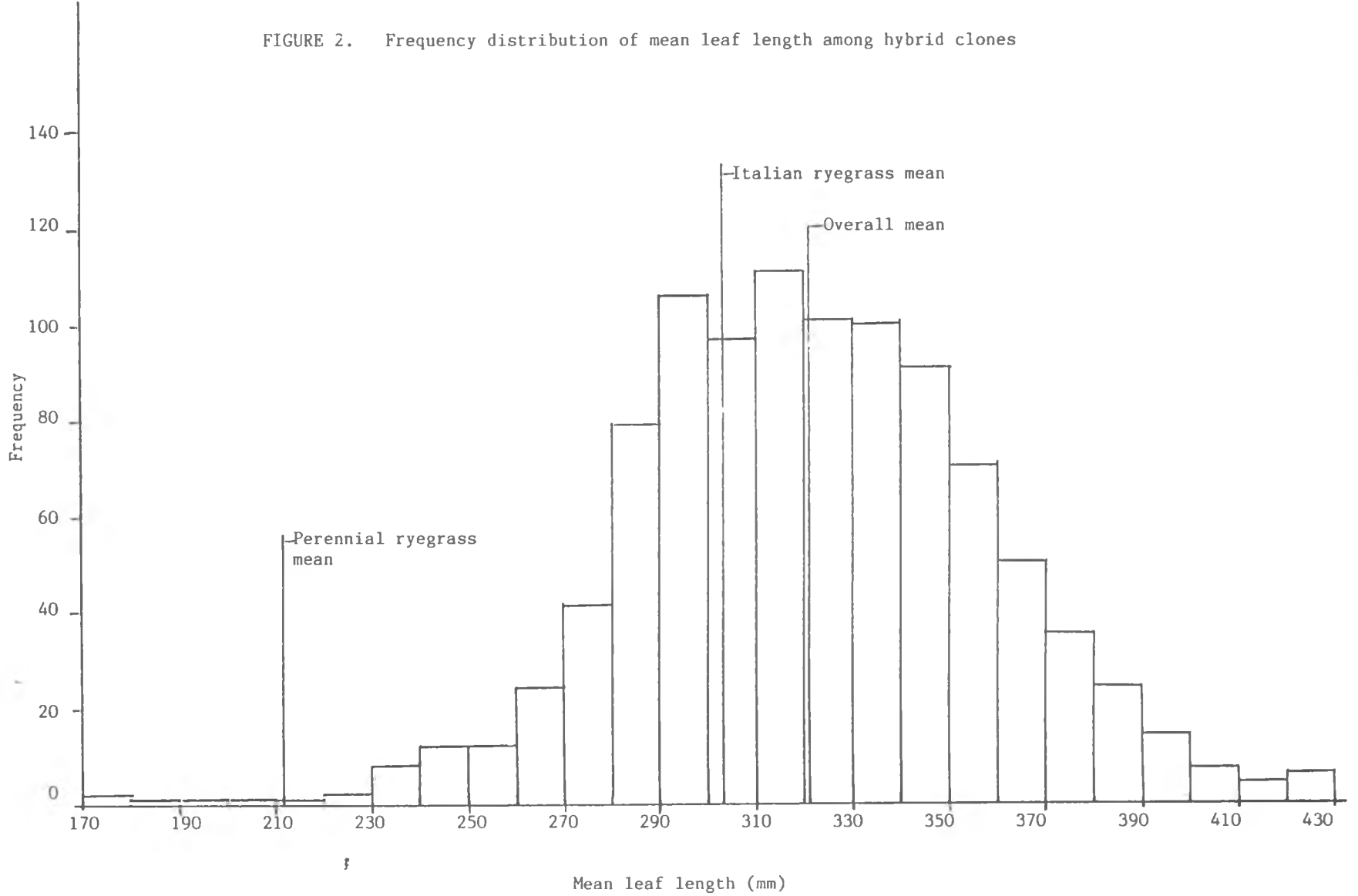
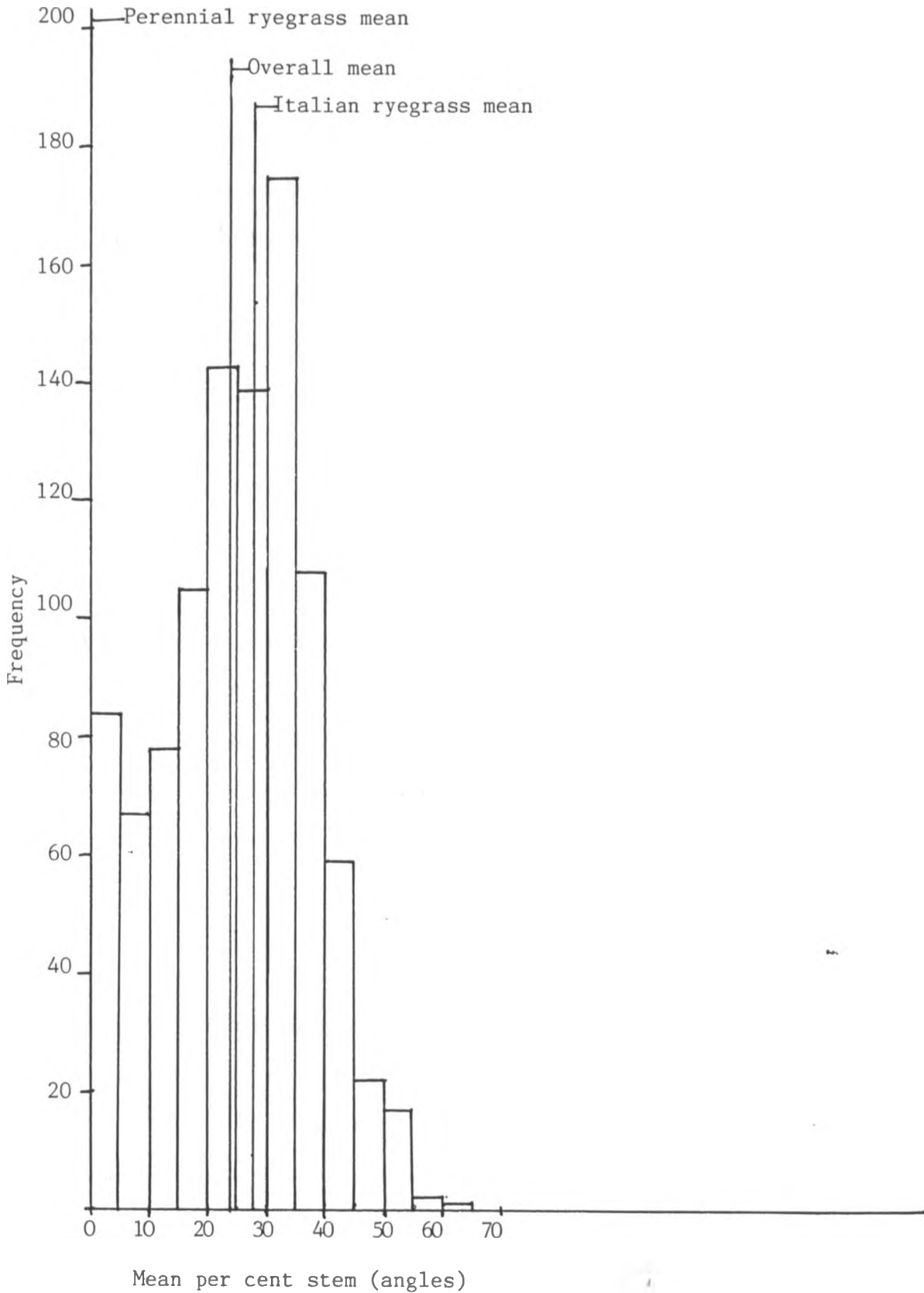


FIGURE 3. Frequency distribution of mean per cent stem among the hybrid clones



Percent Stem

Clones differed significantly ($P < 0.001$) in mean percent stem transformed to angles to bring the distribution closer to normal (Table 2). The highest percent stem was 58.38 and the lowest was zero. The majority of the hybrids had some stem in the regrowth. The Italian ryegrass parents mean values ranged from 15.10 to 39.70 with a mean of 27.95. The mean for the hybrids was 34.50 and that of the perennial ryegrass was zero. Figure 3 shows the frequency distribution of the mean percent stem. The majority of the hybrid clones had a mean value of between 20 and 40, comprising of over sixty per cent. The mean values of the hybrids and the Italian ryegrass fell within this range. This is to say that again the hybrids were closer to the Italian ryegrass than they were to the perennial ryegrass. But a substantial number of hybrid plants had no stem in the regrowth, a feature of the perennial ryegrass parent, suggesting simple genetic control of this trait.

Regrowth

Rapid regrowth is a characteristic of the Italian ryegrass parents (both diploid and tetraploid) which are of Po Valley origin (Bb1276). Clones varied significantly in the amount of regrowth when assessed visually on a scale of 0-5 (Table 2). The highest mean regrowth was 5.00 and the lowest was 1.00. With some clones only two or three replicates regrew but all the clones made some regrowth. The perennial ryegrass control had a mean regrowth

FIGURE 4. Frequency distribution of mean regrowth score among hybrid clones

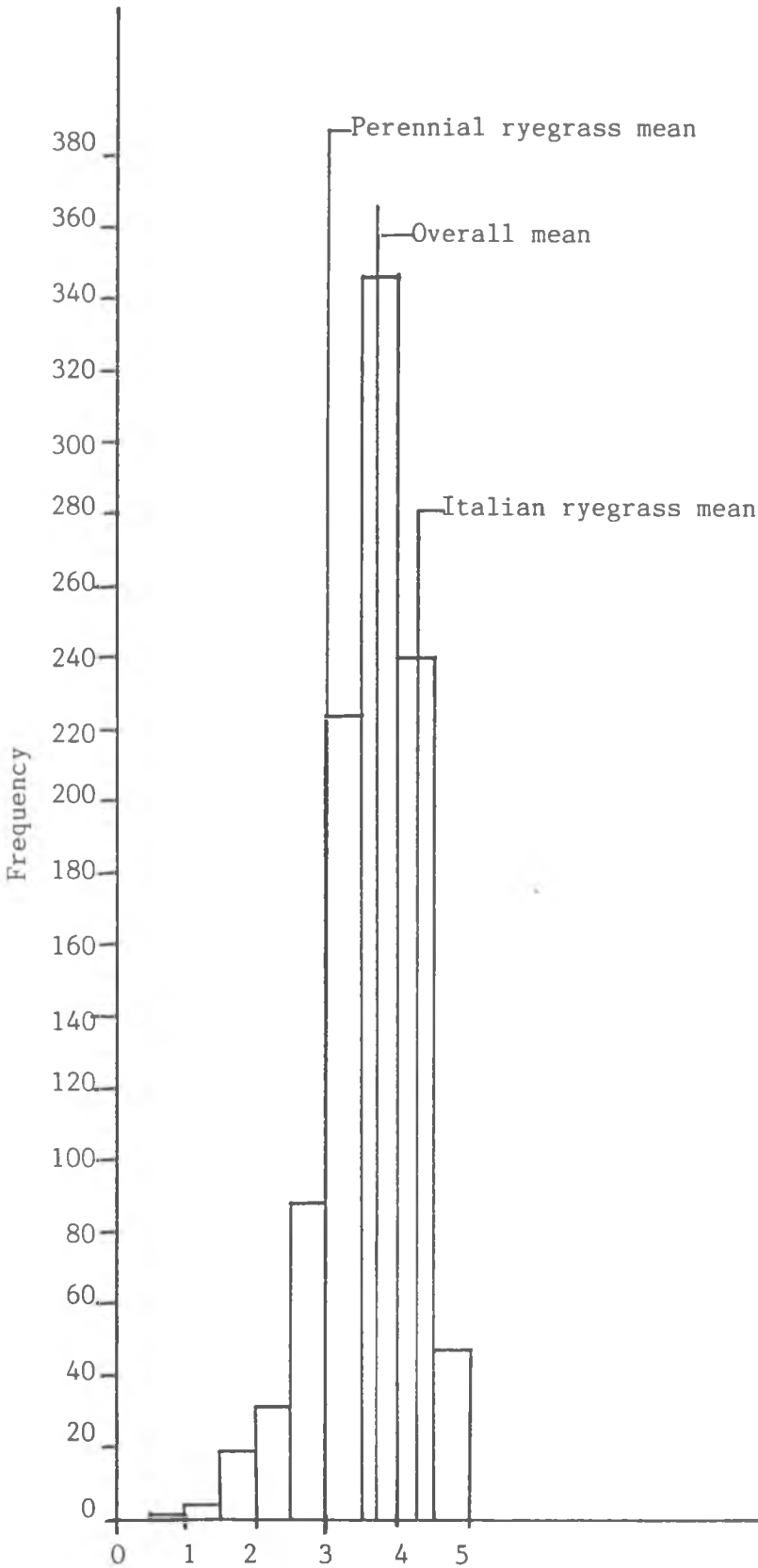
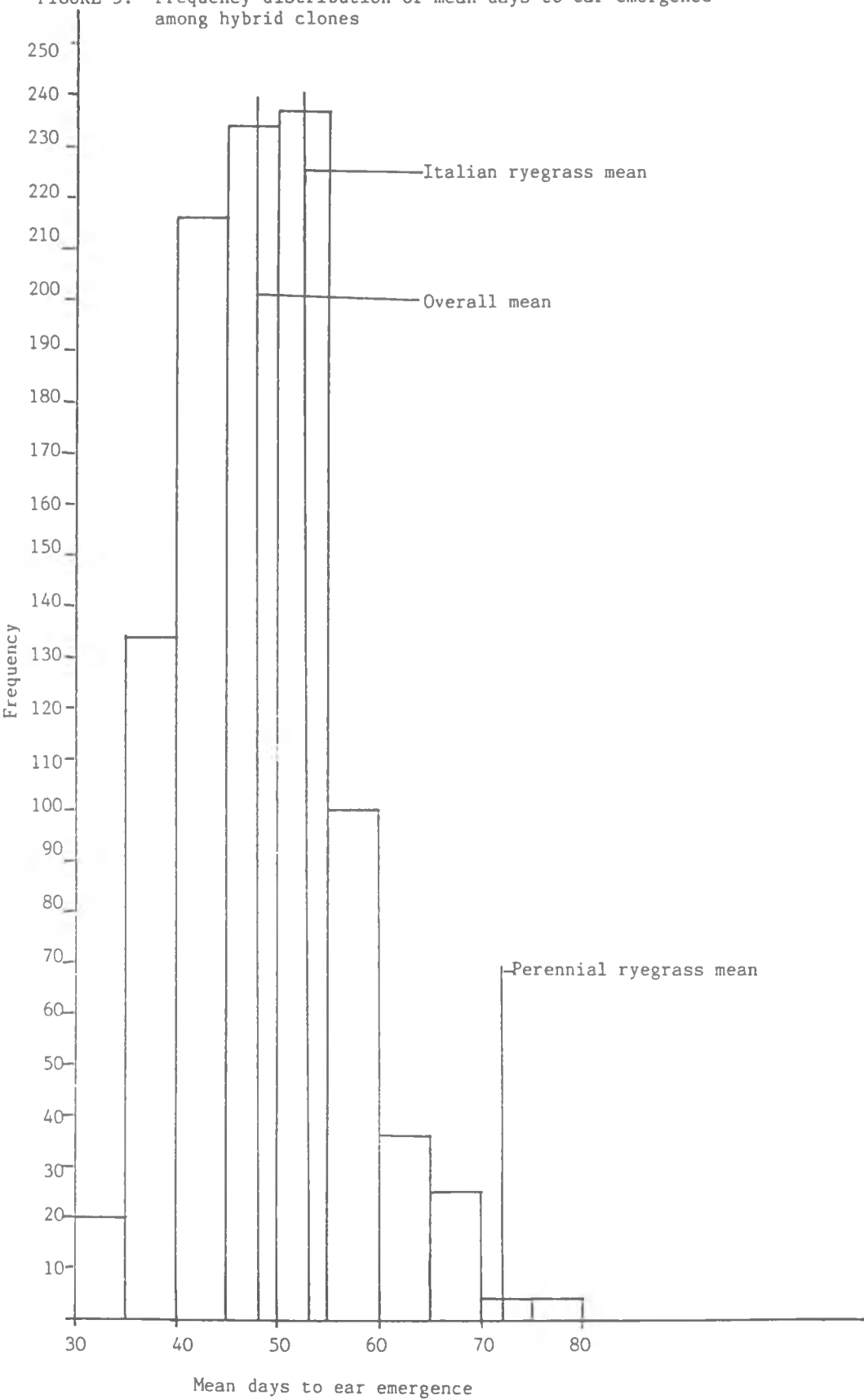


FIGURE 5. Frequency distribution of mean days to ear emergence among hybrid clones



score of 3.00 and the Italian ryegrass parent had a mean regrowth score of 4.28, and the hybrids of 3.74. Most hybrids were closer to the Italian ryegrass than to the perennial ryegrass in regrowth. Figure 3 shows the frequency distribution of the mean regrowth of all the hybrid clones. Over eighty per cent of the clones had a regrowth mean of 3.00 and above, but a few clones had mean values significantly lower than the Italian ryegrass control at $P < 0.05$.

Ear emergence date

Clones varied significantly in mean days to ear emergence (Table 2). The earliest clone emerged after 33.50 days and the latest after 77.25 days. All the clones except one flowered. The perennial ryegrass was among the latest to flower with a mean ear emergence date of 72.10 days, the Italian ryegrass had a mean ear emergence date of 53.70 days and the hybrids had a mean ear emergence date of 48.00 days.

The mean values of the hybrids did not differ significantly at $P = 0.05$ from that of the Italian ryegrass. Figure 5 presents the frequency distribution of mean ear emergence dates of the hybrid clones, 841 having mean ear emergence date of 55 days or less. This shows that at least eighty per cent of the clones flowered earlier or nearly at the same time as the Italian ryegrasses and less than 20% were as late flowering as the perennial ryegrass parent.

Awn length

Plants were categorised into two groups, long awns and short awns. In many cases all the four plants were in the same category of either long or short awned. However, for quite a number of clones the awn length was not consistent over replicates. In some cases one of the four plants was recorded as long awned and the other three as short awned or vice versa. In other cases two of the plants were in one category and the other two in the other.

Awn length therefore does not seem to be a qualitative character and was not used as one of the traits in the present assessment of the hybrids.

Association Between Traits

Association between qualitative traits

Chi-square tests showed that the observed frequencies of plants with PGI, GOT and SOD alleles from the perennial ryegrass did not differ significantly from the hybrid population mean frequency at $P = 0.05$ (Table 4). There was no association between any of the traits; no awns, red base, PGI, GOT and SOD. However, it should be pointed out that the number of plants with awns or red base were small, so only strong linkage would show.

TABLE 4. Chi-square values for association between qualitative traits. Expected frequency equals frequency in hybrid population as a whole

	No awns	Red base	PGI	GOT	SOD
No awns	0.0	1.09	2.166	1.811	2.811
Red base	1.09	0.0	0.366	1.671	0.0
PGI	2.166	0.366	0.0	0.171	0.062
GOT	1.811	1.671	0.171	0.0	0.508
SOD	2.811	0.0	0.062	0.58	0.00

$P > 0.05$ in all cases. Therefore no significant difference from the expected frequency

TABLE 5. Table of F-test to test for association between qualitative and quantitative traits.

$$n_1 = 1; \quad n_2 = 988$$

	Qualitative characters				
	No awns	Red base	PGI	GOT	SOD
Quantitative characters:					
Leaf width	1.205	1.484	1.510	1.036	1.136
Leaf length	1.33	7.605**	15.247***	14.018***	1.168
Percent stem	1.085	1.540	1.023	1.023	1.019
Regrowth	1.371	1.722	1.069	1.065	2.009
Ear emerge days	1.603	1.586	1.265	1.042	1.446

** Significant at $P = 0.01$; *** Significant at $P = 0.001$

F-test for association of qualitative and quantitative traits

Table 5 shows the F-tests for the association of qualitative and quantitative traits. They test whether plants with a particular qualitative character differ from the population mean in the quantitative characters. There were significant associations between leaf length and red leaf base, PGI and GOT, suggesting that leaf length is linked to red leaf base, PGI and GOT. All the other traits were not significantly associated and therefore not strongly linked. Since both red leaf base loci, PGI and GOT probably are unlinked, this shows that genes for leaf length occur at three (or more) different loci.

Genetic and environmental correlation among quantitative traits

Table 6 shows genetic and environmental correlations between quantitative traits. There were significant positive genetic and environmental correlations between leaf length and leaf width, longer leaves being wider and shorter leaves narrower. In terms of proportions this should be the expectation since both leaf width and length depend on cell size and number. There was also a strong positive genetic correlation between ear emergence date and leaf length, the later flowering clones tending to have longer leaves. This result also must have a physiological origin, since genetic linkage would produce a negative correlation. There was a substantial correlation between ear emergence date and percent stem,

TABLE 6. Genetic and environmental correlations between quantitative traits (df = 2681)

	Width	Length	Ear emergence date	Regrowth	Per cent stem
<u>Genetic correlation</u>					
Width	1.0000				
Length	0.3920***	1.0000			
Ear emergence date	-0.0223	0.4128***	1.0000		
Regrowth	0.0476	0.1882	0.1151	1.0000	
Per cent stem	0.0673	-0.2615	-0.4956***	-0.0047	1.0000
<u>Environmental correlation</u>					
Width	1.0000				
Length	0.3179***	1.0000			
Ear emergence date	-0.0474	0.0812	1.0000		
Regrowth	0.0082	-0.0217	0.0288	1.0000	
Per cent stem	0.0172	0.0072	-0.0206	0.0847	1.0000

*** Significant at P = 0.001.

the earlier-flowering clones tending to be more stemmy. This correlation could have been due to genetic linkage as the Italian ryegrass parents were both earlier-flowering and more stemmy than the perennial parent.

Not all the genetic variation in the quantitative traits arose from the perennial ryegrass parent since the Italian ryegrass parents were not homozygous. Nevertheless, these results do suggest that levels of linkage between these quantitative traits are generally low, the main exception being linkage between early-flowering and stemminess in the regrowth.

Selection of Hybrid Clones With Single Ryegrass Traits

The hybrid clones with a single perennial ryegrass trait which were selected for further experimentation are shown in Table 7. The clones selected had the following single perennial traits: late flowering, red leaf base, no awns, and leafy regrowth.

Late flowering clones. Four clones were selected for late flowering. The days to ear emergence for the four clones were 65.25, 66.00, 65.75 and 65.00. These clones did not differ significantly from the mean ear emergence date of the perennial ryegrass (72.10).

Red leaf base. Four clones with red leaf as the only perennial ryegrass trait were selected from among the hybrids.

TABLE 7. Clones selected for having a single perennial ryegrass trait

Clone number	Identity	Mean leaf width	Mean leaf length	Mean per cent stem	Mean regrowth	Mean ear emergence days	1 = Awns 0 = No awns	1 = Red base 0 = Green	PGI	GOT	SOD
<u>Late-flowering clones</u>											
46	BC/18/51	7.75	315.75	29.97	4.25	67.25	0	0	0	0	0
577	BC/24/160	8.75	369.75	2.88	4.00	66.00	0	0	0	0	0
976	BC/30/4	8.50	357.25	24.80	3.75	65.75	0	0	0	0	0
982	BC/32/25	9.25	286.50	27.7	4.00	65.00	0	0	0	0	0
<u>Red base</u>											
122	BC/19/62	7.75	314.50	33.75	3.75	48.00	0	0	0	0	0
600	BC/24/190	8.50	352.00	19.73	4.00	55.50	0	0	0	0	0
810	BC/26/3	9.25	346.50	32.42	4.25	44.33	0	0	0	0	0
819	BC/26/16	8.75	290.75	37.97	3.50	53.00	0	0	0	0	0
<u>No awns</u>											
119	BC/19/58	8.50	358.75	32.75	3.75	55.33	0	0	0	0	0
390	BC/23/107	8.25	295.75	31.18	3.25	37.00	0	0	0	0	0
752	BC/25/53	9.00	316.00	34.38	3.25	46.00	0	0	0	0	0
<u>Leafy regrowth</u>											
233	BC/21/89	9.25	320.50	0.00	3.50	40.75	0	0	0	0	0
554	BC/24/130	8.75	352.75	0.00	4.00	54.50	0	0	0	0	0
755	BC/25/57	8.75	344.50	0.00	3.75	51.00	0	0	0	0	0
797	BC/25/108	8.0	371.50	0.00	3.50	50.75	0	0	0	0	0
<u>Controls</u>											
	Perennial ryegrass	4.00	212.13	0.00	3.00	72.10	0	0	-	-	-
	Italian ryegrass	7.16	303.3	27.95	4.28	53.70	0	0	-	-	-
	Hybrid mean	7.82	321.15	24.74	3.74	48.00					
<u>No flowering at all</u>											
833	BC/26/35	7.00	303.75	25.43	3.33	*	*	0	0	0	0
<u>Very narrow leaves</u>											
205	BC/21/50	4.00	200.75	13.75	3.25	55.75	0	0	1	0	0
SED		0.642	24.946	6.013	0.410	4.006					

No awns. Three clones were selected with no awns as the single perennial ryegrass trait. All the other traits were characteristically Italian ryegrass.

Leafy regrowth. Four clones without any stems in the regrowth were selected. Two other hybrid clones were kept for their exceptional differences from the other hybrids. Clone number 833 did not flower at all while clone number 205 had very many narrow leaved tillers. The mean leaf width was 4.00 mm like the perennial ryegrass. The non-flowering clone had poor regrowth but was otherwise similar to Italian ryegrass while the very narrow-leaved clone had short leaves, was less stemmy in the regrowth, had poor regrowth vigour and had a perennial ryegrass allele at the PGI locus.

DISCUSSION

Objectives

This experiment was carried out primarily to evaluate the effectiveness of the breeding technique developed by Thomas et al. (1986) in reducing the time taken to selectively transfer genes between Lolium species by cutting down the number of generations of backcrossing required. There were two further objectives; to identify individuals that might be used in further breeding, and to provide information on linkage relationships in Lolium.

Summary of the technique

Triploid hybrids were produced by hybridizing diploid perennial ryegrass with tetraploid Italian ryegrass, and the embryos rescued by in vitro culture. The resultant triploid plants were hybridized with diploid Italian ryegrass. Eighty-five per cent of the progeny were euploid with 14 chromosomes; the haploid pollen apparently having a marked selective advantage over aneuploid gametes so forming a sieve to eliminate aneuploid gametes.

Value of the technique for breeding

Assuming normal mendelian inheritance a triploid backcrossing would result in progeny with an average $\frac{1}{6}$ or 17% of genes originating from the recipient species. Two generations of ordinary

backcrossing which could be carried out in the same time would result in progeny with $\frac{1}{4}$ or 25% of genes originating from the recipient species. A disadvantage of the triploid technique is that the choice of recipient parental genotype is limited by the availability of isogenic or near-isogenic diploid and tetraploid plants or populations. Consequently, there is little to choose between the two methods of backcrossing if normal mendelian segregation occurs in the triploid x diploid cross. But if there is strong preferential pairing at meiosis between chromosomes of the recipient species at meiosis in the triploid, resulting in loss of chromosomes from the donor species, the potential value of triploid backcrossing is greatly enhanced.

The clearest evidence for this chromosome loss was the marked deficiency of plants with an allele of perennial ryegrass origin at the PGI locus, the expected ratio being 1 perennial ryegrass to 2 Italian ryegrasses while the obtained ratio was 1:7. The number of plants with red base also was much less than that expected, the expected ratio being 1:8 and the obtained ratio 1:24. Since the inheritance of the red base character has been studied in detail (Jenkins, 1930; Hill, 1942) the expectation of 1:8 ratio is reasonable and this suggests marked loss of perennial ryegrass genes at an additional locus. The number of hybrid plants with awns also was less than that expected. In this case, however, the expected 1:5 ratio, based on the assumption of control by a single locus, may well have been incorrect. In interspecific tetraploid hybrids between perennial and Italian ryegrass, the frequency of awnless plants was lower than would

have been expected on the assumption of single locus control (Ahloowalia, 1977). Jenkin (1959) concluded that in Italian ryegrass the presence of awns was controlled by more than one pair of genes but the details were not elucidated. None of the quantitative traits showed clear evidence of loss of perennial ryegrass chromosomes, the frequency distribution being broadly in line with what would be expected assuming 17% of the genes to be of perennial ryegrass origin. The similarity of the hybrid and Italian ryegrass leaf width means and leaf length means could perhaps have been a consequence of the greater age and reduced vigour of the older Italian ryegrass clones.

There was a slight deficiency of the perennial ryegrass alleles at the SOD locus but at the GOT locus the number obtained was accorded exactly with the number expected. Since the loci controlling red base, GOT, PGI and SOD are unlinked and therefore may be on different chromosomes, these results suggest that some perennial ryegrass chromosomes are being lost while others are not.

Linkage relationships

There was no evidence for linkage between the five qualitative traits in this study, involving six or more loci. The F-tests showed that there was clear linkage between leaf length and red base, PGI and GOT. The PGI locus is known to be linked with the S incompatibility locus, which in turn is linked to the Z incompatibility locus (Hayward et al., 1983; Faeron et al., 1983). Thus, a picture is emerging of a linkage group including PGI, S, Z and one or more genes

controlling leaf length. Genetic correlations are difficult to interpret as they can result from genetic linkages or from pleiotropy. The strongest correlation was between early ear emergence and stemminess in August, both characteristics of the Italian ryegrass parent. Since harvesting of plants in an advanced stage of reproductive development usually leads to fewer rather than greater numbers of inflorescences developing in the aftermath, this correlation is likely to be genetic rather than pleiotropic in origin. By contrast, the positive correlation between late flowering and long leaves must have been pleiotropic in origin since genetic linkage would have resulted in a negative correlation. Again the positive genetic and environmental correlations between leaf length and leaf width would be expected on morphological grounds. The smaller but still highly statistically significant correlation between short leaves and stemminess in the aftermath again could not be due to genetic linkage either, the perennial ryegrass parent having the opposite combination of traits.

The overall impression from this study is one of low levels of linkage, although it must be borne in mind that the number of traits examined represent only a tiny proportion of the ryegrass genome. Low levels of linkage allow good progress to be made by breeding aimed at recombination. Results of practical breeding of Lolium shows that recombination can be successful. For example, in perennial ryegrass the exceptionally high spring growth of germplasm from Northern Italy

has been combined with good late-season growth by hybridization and recurrent selection for plot yield, resulting in a 17% increase in total annual yield under simulated grazing (Wilkins, personal communication). The success of tetraploid Italian/perennial hybrids such as Augusta could be more a reflection of the large number of genes controlling differences between the two species and of the time taken to transfer them by backcrossing than a reflection of the difficulty of overcoming strong linkages. However, the results obtained here have shown considerable linkage of three loci with leaf length (an important component of vegetative yield) and this should be borne in mind when attempting genetic transfer between the two species. Linkage between early flowering and stemmy regrowth also appeared to be quite strong. There was no difficulty in identifying hybrid clones which appeared to combine red base with long leaves or leafy regrowth with early flowering, but caution is required in interpreting these results because considerable errors are attached to these quantitative traits. Leaf length had a particularly high coefficient of variation (35%).

Possible value of some hybrid clones as parents

The perennial traits measured here which are potentially of some use are red leaf base, awnlessness, late-flowering and leafy regrowth. Red leaf base could be useful in establishing the distinctiveness of new varieties. Awnlessness could be useful both for distinctiveness and to make the seed easier to handle. At

present awns usually have to be removed so that seed flows evenly through the drill. Late-flowering might also be of some use because present Italian ryegrass varieties have similar flowering date and a spread of flowering date would allow silage to be made over a greater period without undue loss in quality which occurs with increasing maturity of the inflorescence (Hides, Lovatt, and Hayward, 1983). The non-flowering clone could be particularly interesting if it fails to flower outdoors. Most likely, given normal outdoor conditions it will flower but after the other clones. Probably of most practical value is leafy regrowth. The primary reason for the popularity of Italian/perennial hybrids is their greater leafiness in late summer. Walters (1986) found that beef cattle fed on cv. Augusta gave higher live-weight gains per hectare than those fed on cv. RvP Italian ryegrass, even though the dry matter yield of cv. RvP is higher (Anon, 1986). The superiority of Augusta was greatest where stocking rates were low. In this situation, live-weight gain per unit area depends on live-weight gain per animal, which in turn depends on the amount of grass eaten. Before grass can enter the small intestine it must be broken down into particles less than 1mm, mainly by chewing, and if the grass is tough and fibrous this stage of digestion can be rate-limiting (Minson and Bray, 1986). So the large number of hybrid clones found with no stems in the regrowth is encouraging as it suggests that this trait may be transferred to suitable diploid Italian ryegrass types by backcrossing without too much difficulty. The

resultant cultivar would be superior to the tetraploid hybrids in that there would be even fewer secondary inflorescences produced and the high spring growth of Italian ryegrasses would be unaffected. Also the persistency may be better since both tetraploidy and secondary head production are known to reduce persistency.

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APPENDIX

TABLE 8. Analysis of variance of leaf width

Item	df	M.S.	VR	P
Replicates	3	8.4525		
Clones	999	4.2126	5.110***	<0.001
Clones x Replicates	2990	0.8244		

TABLE 9. Analysis of variance of leaf length

Item	df	M.S.	VR	P
Replicates	3	27241		
Clones	999	5524	4.438***	<0.001
Clones x Replicates	2989	1245		

TABLE 10. Analysis of variance of per cent stem (angles)

Item	df	M.S.	VR	P
Replicates	3	2252.29		
Clones	998	628.20	8.689***	<0.001
Clones x Replicates	2958	72.30		

TABLE 11. Analysis of variance of days to ear emergence

Item	df	M.S.	VR	P
Replicates	3	1112.19		
Clones	998	222.36	6.928***	<0.001
Replicates x Clones	2725	32.10		

TABLE 12. Analysis of variance of regrowth

Item	df	M.S.	VR	P
Replicates	3	20.8982		
Clones	999	1595.033	4.747***	<0.001
Clones x Replicates	2984	0.3363		

*** Significant at P = 0.001

TABLE 13. Heterogeneity chi square testing whether the number of plants in each family with red base, awns, and isozymes represent a sample from a single population

<u>Awns</u>		
Expected ratio awnless/awned 1:5		
Source	df	Chi-square
Total	15	138.31***
Pooled	1	134.52***
Heterogeneity	14	3.48 NS

<u>Red base</u>		
Expected ratio red base/green base 1:8		
Source	df	Chi-square
Total	15	58.31 ***
Pooled	1	36.28 ***
Heterogeneity	14	22.03 NS

<u>Isozymes</u>		
Expected ratio isozyme/no isozyme 1:2		
<u>PGI</u>	df	Chi-square
Total	15	209.55 ***
Pooled	1	194.77 ***
Heterogeneity	14	14.78 NS

<u>GOT</u>		
Source	df	Chi-square
Total	15	62.93 ***
Pooled	1	4.655 *
Heterogeneity	14	58.265 ***

<u>SOD</u>		
Source	df	Chi-square
Total	15	124.07 ***
Pooled	1	28.37 ***
Heterogeneity	14	95.7 ***

*** Significant at P = 0.001; ** Significant at P = 0.01;

* Significant at P = 0.05.

NS = Not significant