Differences in seedling emergence, plant morphology, soil moisture removal by cropping, yield and quality components and allelism of several Betzes barley (Hordeum vulgare L.) brachytic isotypes
by Matthew Norman Ries

A thesis submitted in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE in Agronomy
Montana State University

Abstract:
To assist in breeding a lodging resistant, more efficient short barley with high yield and quality, I studied the characteristics of eight brachytic and one erectoides isotype. Isogenic analysis provided close evaluation of mutant alleles in the background variety, Betzes.

An early May planted dryland nursery in Amsterdam Silty clay loam of single row plots of derived and mutant isotypes of Aks,uz/4*Bz and ms3,Gwy,br l/2*Titan//4*Bz, and an early June dryland planting in the same soil type of 4-row yield plots of Hly,br 1/4*Bz which has an early maturing derived normal, Cpn,br 1/4*Bz, Hnh,br 1/4*Bz, ms3,Gwy,br 1/ Vtg//4*Bz, Shl,br 2/4*Bz, Beebe,br,,/7*Bz and Bz Double Ert (Ert I and Ert II) were evaluated.

Isogenic analysis allowed evaluation of brachytic genes. The isotypes were developed through backcross breeding with Betzes as the recurrent parent. Bz Double Ert is the result of crossing two different spontaneous mutants. Diallele analysis determined br 1, br 2, uz, and a new br,, gene were involved. Coleoptiles grown in a dark, moist, germinator at 22°C showed all reduced height types had significantly shorter coleoptiles than derived normals. No significant difference for seedling emergence was detected when isotypes were planted in sandy loam at 25 and 50 mm deeper than each mean isotype coleoptile length. Plant height, awn length and rachis internode length of main culm spikes of brachytic isotypes were significantly shorter than derived normals, except for awn length of Bz Double Ert. Soil moisture removal percent by weight, was significantly less at the 120-150 cm depth for all brachytics except Hly,br l/4*Bz. Soil moisture samples were not taken for Aks,uz/4*Bz and ms3,Gwy,br 1/2*Titan//4*Bz.

Brachytic yields ranged from 56% - 96% of their derived normal. Yield reductions of brachytic types were due to fewer tillers for Cpn,br 1/ 4*Bz, Beebe/br,,/7*Bz and Bz Double Ert, while lower kernel weight accounted for the reduction in all other entries. No protein or lysine difference was detected between isotypes by use of Neotec GQA and microbiological assay.

STATEMENT OF PERMISSION TO COPY

In presenting this thesis in partial fulfillment of the requirements for an advanced degree at Montana State University, I agree that the Library shall make it freely available for inspection. I further agree that permission for extensive copying of this thesis for scholarly purposes may be granted by my major professor, or, in his absence, by the Director of Libraries. It is understood that any copying or publication of this thesis for financial gain shall not be allowed without my written permission

Signature Matthew N. Ries

Date August 23, 1977

DIFFERENCES IN SEEDLING EMERGENCE, PLANT MORPHOLOGY, SOIL MOISTURE REMOVAL BY CROPPING, YIELD AND QUALITY COMPONENTS AND ALLELISM OF SEVERAL BETZES BARLEY (*Hordeum vulgare* L.) "BRACHYTIC" ISOTYPES

by

MATTHEW NORMAN RIES

A thesis submitted in partial fulfillment
of the requirements for the degree

of

MASTER OF SCIENCE

in

Agronomy

Approved:

Robert L. Eslick
Chairperson, Graduate Committee

Kurt C Feltner
Head, Major Department

Henry L Parsons
Graduate Dean

MONTANA STATE UNIVERSITY
Bozeman, Montana

August, 1977

ACKNOWLEDGMENT

I wish to acknowledge and express my thanks for the contributions of the following people:

Professor R. F. Eslick for serving as my major professor. I also wish to thank Professor Eslick for offering me the chance to gain professional training and work experience under his supervision, by working as his Research Assistant.

Drs. E. A. Hockett, R. L. Ditterline, L. E. Wiesner, and K. C. Feltner, Department Head, for serving as committee members.

My fellow barley graduate students for assisting me with the work needed to compile my data and for their friendship and support.

A very special and close friend, Miss Jody L. Bellach, for her endless encouragement, support and many hours of help in the greenhouse and laboratory which meant personal sacrifice by her.

To my sisters, Cynthia and Sylvia, my brothers, Brian, Edwin, Jerome and Norbert, for their personal support and encouragement, which made this one time remote accomplishment become a reality for me.

To my parents, Sylvester A. and Marie K. Ries, for their unending friendship, support, encouragement and prayers, to whom I dedicate this thesis. I love you, Mom and Dad.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

ABSTRACT

To assist in breeding a lodging resistant, more efficient short barley with high yield and quality, I studied the characteristics of eight brachytic and one erectoides isotype. Isogenic analysis provided close evaluation of mutant alleles in the background variety, Betzes. An early May planted dryland nursery in Amsterdam Silty clay loam of single row plots of derived and mutant isotypes of Aks,uz/4*Bz and ms3,Gwy,br 1/2*Titan//4*Bz, and an early June dryland planting in the same soil type of 4-row yield plots of Hly,br 1/4*Bz which has an early maturing derived normal, Cpn,br 1/4*Bz, Hnh,br 1/4*Bz, ms3,Gwy,br 1/ Vtg//4*Bz, Shl,br 2/4*Bz, Beebe,br,,/7*Bz and Bz Double Ert (Ert I and Ert II) were evaluated.

Isogenic analysis allowed evaluation of brachytic genes. The isotypes were developed through backcross breeding with Betzes as the recurrent parent. Bz Double Ert is the result of crossing two different spontaneous mutants. Diallele analysis determined br 1, br 2, uz, and a new br,, gene were involved. Coleoptiles grown in a dark, moist, germinator at 22°C showed all reduced height types had significantly shorter coleoptiles than derived normals. No significant difference for seedling emergence was detected when isotypes were planted in sandy loam at 25 and 50 mm deeper than each mean isotype coleoptile length. Plant height, awn length and rachis internode length of main culm spikes of brachytic isotypes were significantly shorter than derived normals, except for awn length of Bz Double Ert. Soil moisture removal percent by weight, was significantly less at the 120-150 cm depth for all brachytics except Hly,br 1/4*Bz. Soil moisture samples were not taken for Aks,uz/4*Bz and ms3,Gwy,br 1/2*Titan//4*Bz. Brachytic yields ranged from 56% - 96% of their derived normal. Yield reductions of brachytic types were due to fewer tillers for Cpn,br 1/ 4*Bz, Beebe/br,,/7*Bz and Bz Double Ert, while lower kernel weight accounted for the reduction in all other entries. No protein or lysine difference was detected between isotypes by use of Neotec GQA and microbiological assay.

INTRODUCTION

Many factors such as plant height, seed size, kernel weight, tiller number, rachis internode number, and water use efficiency limit the yield of short statured barley (*Hordeum* spp.), but some are more limiting than others. Identification of the most limiting factor or factors for a given environment would assist in directing future research emphasis.

Commercial production of a short statured barley could prove useful under several cropping systems and practices. The shorter plant type may reduce trash and facilitate planting under continuous cropping systems. They have improved lodging resistance in high rainfall areas and under irrigation. The short types may also be used to obtain taller winter types, but still maintaining much of the straw strength. The short types are also easily recognized and can be utilized as genetic markers in research programs.

Isotype analysis offers a reasonably effective means of evaluating a particular allele in a given genetic background. Nine Betzes reduced height isotypes were studied to: 1) determine the allelism of the height reducing genes; 2) evaluate isotype differences for plant height, awn length, rachis internode length, spike length, culm internode length, coleoptile length; 3) determine root system extent and soil water removal differences; and 4) determine yield and quality differences between isotypes.

LITERATURE REVIEW

Semi-brachytic and/or brachytic barley types have been described by many researchers. Three genes br 1 (brachytic), br 2 (brachytic), and uz (semi-brachytic) have been located and described.

The br 1 mutant plant type is described as brachytic or semi-dwarf with short leaves, short awns, short internodes, can be readily classified and is equal in viability to the normal (5,13,18). The br 1 gene is a monofactorial recessive located on chromosome 1. It was found as a spontaneous mutant in the cultivar Himalaya (5,13,18).

The br 2 mutant plant type is described as being shorter in height and having shorter stems, leaves, spikes, awns, kernels, glumes and glume awns, rachillas and coleoptiles than the normal. The auricles are well developed and are larger than normal (5). The br 2 gene is a monofactorial recessive located on chromosome 4. It was found as an X-ray induced mutant in the cultivar Svanhals (5).

The uz mutant plant type has shorter coleoptile length, leaves, spikes, awns, culms, empty glumes, axis of rachilla, and grain, than normal barley. There is to be no influence on the kernel weight or heading date (5). The coleoptile possesses a hook near the apex and often has a V-shaped notch on the opposite side of the hook, thus causing a double notch at the apex. The uz gene is a monofactorial recessive located on chromosome 3. It was a spontaneous mutant found in many Japanese cultivars (5,19,20,22).

The plants in barley populations segregating simultaneously for both the br 1 and uz gene were reported to be lethal or semi-lethal (8). Another experiment reported the double recessives to have an additive diminutive effect (8).

The uzu type barley is common to the warmer regions of Korea and Japan. It occupies 80% of Japan's barley acreage (22). Currently, nearly all Korean varieties are winter habit and uzu.

Plant Morphology (Coleoptile)

The coleoptile length of barley varies with growing conditions. The mean coleoptile length of a variety grown under specified conditions is stable and regarded as a heritable character peculiar to a variety (19,20).

The F_1 coleoptile lengths of uzu(uz)-lax(L) X normal (Uz)-dense (ℓ) and (Uz-L) X (uz-ℓ) crosses equal or exceed the length of the normal type parents (19,20). The frequency distribution of coleoptile lengths grown from seed haravested from F_1 plants is bimodal. In his study, coleoptiles less than 20 mm in length were uzu type, while those greater than 21 mm in length were normal type (20).

Dominance of the Uz or L genes over their recessive is not complete. Genotypes singly or double heterozygous for Uz and/or L have shorter coleoptiles than homozygous dominant genotypes (19,20).

A plant designated Dxx, an X-ray mutant from the cultivar Domen, was shown to be allelic to br 1 and the coleoptiles of Dxx were significantly shorter than those of Domen (7).

Plant Morphology (Roots)

The importance of the root system for maintenance of water balance in the plant, and as a characteristic of drought hardy varieties has been emphasized repeatedly (15). Most researchers who have investigated cereal crops have found that the greater the depth of adequate moisture in the soil, the greater the root penetration. It was also found that drying of the upper soil layer increases growth of roots at deeper depths (15).

Experiments on barley plants that were grown in large pots indicated that maximum root development, as regards to weight of roots, is reached at the time of pollination (27). Nitrate fertilizer at any rate lessens root penetration but greatly increases root branching, whereas potassium salts and phosphates greatly promote root penetration (27). Depending upon environmental and soil conditions, barley roots penetrate to as little as 10 cm, to depths beyond 205 cm (27). Root hair elongation varies with temperature and temperature duration around the roots and also with water absorption rate of the roots (12). The development of secondary roots of barley is similar to that of wheat and oats (27).

There was no significant difference between two wheat genotypes, a single gene dwarf, Sonalike RR-21, and a three gene dwarf, Up 301, in respect to either the total water extracted or the extraction rate per unit root volume for the 12 day duration of the experiment, or in root volume (17). However, the dry weight of roots per unit root volume increased significantly with increasing soil water tension of 0.3-0.8, 2.0-2.5, and 4.0-4.5 bars, for both genotypes (17). Longer finer roots developed under drier soil conditions which gave more root surface area in a fixed soil volume.

Plant Morphology (Leaves)

Leaves from both normal and br 1 Himalaya barley contained longer, narrower terminal cells and shorter, wider basal cells, with middle region cells intermediate in length and width. Older leaves had longer, narrower cells than younger leaves for both types (18).

A less extensive study of leaf morphology compared an equal number of tall and uz short types. The short type seedling was thick-set with deeper green leaves, positioned at an acute angle to the culm. These leaves also have projections on both surfaces, a V-shaped notch at the leaf apex, and a counter-clockwise twist at the middle (19,25). The tall type seedlings were slender, and had paler green leaves that were devoid of the short type peculiarities. Leaf sheath length was 19-37 mm for the tall type and 9-10 mm for the short type.

The leaf shape index, width/length, for the tall and short types was 45-105 and 105-170, respectively. Data taken on length and width of upper most leaves of mature plants suggested a similar pattern (19,25).

Plant Morphology (Culm)

In 1929 a spontaneous dwarf barley mutant found in the cultivar Himalaya was described as "A shortened plant with short leaves, short awns and short internodes, something like brachytic corn, but far less extreme." It is easily distinguished, and is equally as viable as the normal (18). Normal and mutant Himalaya mean culm epidermal cell lengths were 118 μ and 115 μ, respectively, with mean culm parenchyma cell length 173 μ and 163 μ, respectively. A reduced number of cells contributed to the reduced brachytic height (18). This mutant gene was labeled br 1 (13).

A marked reduction in plant height is noted for the uzu type compared to the normal (19,21).

Kumar et al. (10) broadly classified height induced mutants into three groups: 1) shortening of ear bearing internode is the major path of height reduction; 2) length of each successive internode is reduced in proportion to their contribution to total culm length in the control; and 3) the length of all middle internodes are reduced to the same length irrespective of their relative lengths in the control. Class two is the typical brachytic type.

Plant Morphology (Spike)

Rachis internode number and length determine total spike length. Uzu type spike length is primarily determined by the Uz alleles, the L alleles, or a combined effect of both genes (20), although quantitative characters also affect spike length (6).

Takahashi (20) evaluated the relationship of spike length and rachis internode length to spike type and found them closely related. The normal-lax spike is the longest and the uzu-dense spike is the shortest. The normal-dense and uzu-lax ears are intermediate. The effects of the dominant alleles Uz and L on ear length and rachis internode length were almost equal. Ear length increased by a factor of approximately 1.5 when homozygous dominant genes, Uz or L, were present (20).

Barthakur and Poehlman (2) and Hoskins and Poehlman (9) were unable to distinguish between uzu-lax and uzu-dense.

Hayes (6) summarized information on barley rachis internode length: 1) it is an environmentally stable character; 2) segregation occurs in the F_2 generation where homozygous dense types are found; 3) in some crosses, densities differeing from their parents cannot be isolated, while in other cases, lines of non parental densities may be isolated; and 4) unexplained minor factors result in homozygous intermediate densities with continuous variation between parent means.

Yield

Takahashi et al. (21) compared yield data for 24 lines isogenic for the uz gene. Isogenic pairs showed marked differences for stem length, grain yield, 1000 kernal weight, and number of spikes per plant. Grain yield and 1000 kernel weight for normal lines exceeded that of the uz lines in most instances. Differential interaction of Uz and uz of these isogenic pairs originated from their differing genetic background, especially in the alleles L and l.

Barthakur and Poehlman (2) compared a normal Minnesota winter barley variety, Mo. B-475, and a uzu type winter barley variety, C.I. 7439, in yield trials. Three fertilizer rates were applied to solid and space planted rows. The Mo. B-475 produced higher grain yield as a result of more spike-bearing tillers and heavier kernels. The uzu type had more kernels per spike. No significance was found for the fertilizer by variety interaction (2).

Pleiotropy and Associated Genes

Leonard et al. (11) reported a second uzu gene (uz 2). Garza-Falcon (4) reported a third uzu gene (uz 3). Plant height was the only determining criterion used in these studies. Tsuchiya (23, 24,25) determined that improper classification was the reason uz 2 and uz 3 were reported and argues that only one uz gene is known to exist.

The expression of some characters, particularly culm length, are affected by the Lk 2 lk 2 gene for awn length, the L l gene for rachis internode length and other quantitative factors (19,20). Spring and winter growth habit affects culm length under some greenhouse conditions (25).

GENERAL MATERIALS AND METHODS

Eight brachytic Betzes isotypes and one erectoides Betzes isotype were evaluated (Table 1). Physiological, morphological, and agronomic traits as well as components of the quality were evaluated (Table 2).

The data reported are from both field planted and greenhouse planted experiments. The field data are from two dryland plantings fallowed the previous year. Isotypes Aks,uz/4*Bz and ms3,Gwy/2*Titan//4*Bz were early planted in single rows of 50 seed per 3 m row. The other entries were planted as a yield trial in a split plot design with replicated four row plots 3 m long, 30 cm spacing between rows and with one gm of seed planted per 30 cm of row. The soil was an Amsterdam silty clay loam which receives an average annual precipitation of 38.73 cm (Appendix Tables 1 and 2). The greenhouse was temperature controlled with a sandy loam soil in the benches. A soluble fertilizer of 14.39% ammonical nitrogen (NH_4^+), 5.61% nitrate nitrogen (NO_3), 20% phosphoric acid (P_2O_5) and 20% potash (K_2O) is added to the greenhouse water.

Each mutant isotype was compared to its normal derived Betzes by means of the F-test. When applicable, the analysis of variance and individual degree of freedom F-test was utilized (Appendix Tables 3 through 9).

Table 1. Pedigrees of Betzes isotypes evaluated.

Pedigree[#]	Seed Source		Mutant Phenotype
	Derived Normal	Mutant	
Hly,br 1/4*Bz,[†](5)	76BBIN 193	76BBIN 195	br
Shl,br 2/4*Bz,(5)	75BBIN 344	75BBIN 309	br
ms3,Gwy/2*Titan//4*Bz,[†](br 1)	77BBIN 66	77BBIN 81	br
ms3,Gwy/Vtg//4*Bz,[†](br 1)	75BBIN 392	75BBIN 375	br
Cpn/4*Bz,[†](br 1)	75BBIN 709	75BBIN 746	br
Hnh/4*Bz,[†](br 1)	75BBIN 420	75BBIN 464	br
Aks,uz/4*Bz (5)	77BBIN 1	77BBIN 14	uzu
Beebe/7*Bz	MT4483	MT44814	br
Bz Double Ert,(ert I/ert II)	CI6398	MT87148	ert

[†]Allelic height reducing genes, (Table 3).

[#]Variety abbreviations are as follows: Himalaya (Hly), Betzes (Bz), Svanhals (Shl), Gateway (Gwy), Vantage (Vtg), Compana (Cpn), Hannchen (Hnh), Akasiniriki (Aks), Beebe and Titan are not abbreviated (3). Gene symbols are as follows: brachytic (br), semi-brachytic (uz), and erectoides (ert), adapted from Craddock (3). After 4 and 7 backcrosses the mutant types are theoretically 93.75% and 99.21% isogenic respectively for the chromosomes not containing the mutant gene being backcrossed into the recurrent parent.

Table 2. Components of yield and other quality and agronomic traits measured.

	Characteristics
1.	coleoptile length, (mm)
2.	coleoptile reaction to Gibberellic acid
3.	seedling emergence depth, (%)
4.	number of roots originating from crown, (no.)
5.	removal of soil moisture by depths, (%)
6.	plant height, (cm)
7.	culm internode length by internode number, (mm)
8.	tiller number, (no.)
9.	awn length, (mm)
10.	spike length, (mm)
11.	rachis internode length, (mm per 10 internodes)
12.	seed per spike (no.)
13.	kernel weight, (mg per kernel)
14.	sieve size assortment (on 2.381×19.05 mm and thru 2.182×19.05 mm slotted sieves)
15.	yield, (quintals per hectare)
16.	protein, (%)
17.	lysine in grain, (%)

ALLELE TEST

Materials and Methods

Single, space planted rows 3 m in length, 30 cm apart were field planted under dryland conditions, using segregating male sterile seed for each brachytic isotype (Table 1). The ms3,Gwy/2*Titan//4*Bz isotype was not included in this planting. The male sterility was introduced earlier for the development of the isotypes. All the brachytic isotypes were inter-crossed by hand pollination, and the crossed seed and one selfed spike of each brachytic isotype harvested.

A greenhouse planting followed the field harvest. A border row of the variety Betzes was planted first in each bench 5 cm from the edge and 15 cm between plants. Each experimental row in the bench began with two derived normal seed, followed by as many as 10 F_1 seed and ending with two brachytic seed. Rows were 15 cm apart with seed 5 cm apart within the row planted at a depth of 2.5 cm. A constant 22°C temperature was maintained throughout germination and seedling establishment. Alternating 13°C day and 8°C night temperatures were maintained for one month for tillering purposes. After the tillering period, temperatures were alternated 22°C during the day and 13°C during the night. No supplemental lighting was provided. Plant type was recorded, and all plants were harvested.

A field planting using the same row length and spacing followed the greenhouse harvest. A single row of derived normal, a row of F_1,

two rows of F_2 and a single row of brachytic were planted. Each isotype was planted in the same manner. Plant type was recorded for each row and plant counts were made within segregating F_2 rows and recorded.

Results and Discussion

The expected F_1 plant type is brachytic for the allelic mutants (genes) and normal for the independent mutants. The Hly,br 1/4*Bz, ms3,Gwy/Vtg//4*Bz, Hnh/4*Bz and Cpn/4*Bz were allelic (Table 3). The ms3,Gwy/2*Titan//4*Bz originated from the same initial cross as ms3,Gwy/Vtg//4*Bz and is assumed to be allelic to the above group. Crosses with br 1 are planned to verify this assumption. The expected F_2 ratio of the independent mutants is 3 normal:1 brachytic, and 0 normal:1 brachytic for the allelic mutants (Table 4).

The Beebe/7*Bz brachytic was not allelic to br 1 or br 2. It might well be a new brachytic gene. Until it is allele tested with the newly designated brachytic genes, br 3 through br 7 (24), this is unknown.

Table 3. Results of inter-crossing Betzes brachytic isotypes to determine alleles.

Female Pedigree	Male Pedigree: Hly,br 1/ 4*Bz	Shl,br 2/ 4*Bz	Aks,uz/ 4*Bz	Beebe/ 7*Bz	ms3,Gwy/ Vtg// 4*Bz	Hnh/ 4*Bz	Cpn/ 4*Bz
	Number of plants and F_1 phenotypes†						
Hly,br 1/4*Bz #	10,br						
Shl,br 2/4*Bz	5,N	10,br					
Aks,uz/4*Bz	12,N	10,N	10,br				
Beebe/7*Bz	11,N	20,N	12,N	10,br			
ms3,Gwy/Vtg//4*Bz #	--	12,N	12,N	12,N	12,br		
Hnh/4*Bz #	6,br	12,N	12,N	10,N	12,br	10,br	
Cpn/4*Bz #	10,br	7,N	12,N	10,N	22,br	12,br	10,br

† br = brachytic, N = normal.

Determined to be allelic.

Table 4. Results of inter-crossing Betzes brachytic isotypes to determine alleles.

Female Pedigree	Male Pedigree: Hly,br 1/ 4*Bz	Shl,br 2/ 4*Bz	Aks,uz/ 4*Bz	Beebe/ 7*Bz	ms3,Gwy/ Vtg// 4*Bz	Hnh/ 4*Bz	Cpn/ 4*Bz
	Number of plants, F_2 ratio N:br[†]						
Hly,br 1/4*Bz[#]	br						
Shl,br 2/4*Bz	28:25	br					
Aks,uz/4*Bz	28:22	25:30	br				
Beebe/7*Bz	10:13	25:31	18:14	br			
ms3,Gwy/Vtg//4*Bz[#]	br	34:24	30:10	40:17	br		
Hnh/4*Bz[#]	br	31:20	--	--	br	br	
Cpn/4*Bz[#]		29:21	22:27	27:23	br	br	

[†] br = brachytic . uz = semi brachytic, expected ratio for non-allelic genes is 9 normal:7 brachytic. By goodness of fit X^2 test, all ratios will fit a 9:7 ratio at P .01.

[#] Determined to be allelic.

COLEOPTILE LENGTH AND SEEDLING EMERGENCE COMPARISONS BETWEEN ISOTYPES

Materials and Methods

The nine plant height isotypes (Table 1), Hulless Compana (Sermo/7*Cpn,C.I. 16185) and Hulless Compana (Stamm/7*Cpn,C.I. 16183), were included in a coleoptile length and a seedling emergence experiment. The Sermo/7*Cpn mutant isotype has a normal gibberellic acid level in the seed (1) and has a normal coleoptile length (16). The Stamm/7*Cpn mutant isotype has a higher gibberellic acid level in the seed than the derived normal (1), and a shorter than normal coleoptile length (16).

Twenty seeds of each isotype were placed, embryo end down, between two pieces of 4 × 15 cm moist blotter paper. The seed apexes were at the top edge of the blotter paper. The two pieces of blotter paper were then fastened together with paper clips at the bottom edge while firmly pressing the top edge, indenting the blotter to help hold the seed in place. The blotters with seeds at the top were placed vertically into slotted racks, submerging the bottom edge of the blotter 15 mm into distilled water. The isotypes were paired, arranged in a randomized complete block design with four replications, and germinated in a moist dark germination chamber at 22°C. After seven days, coleoptile length (mm) was measured from the seed apex to the tip of the coleoptile.

A coleoptile length pilot experiment using a distilled water check and 200, 400, and 600 ppm gibberellic acid solution for growing the seedlings was set up in the same manner as above, but using only one replication.

Two planting depths, 25 and 50 mm deeper than the mean coleoptile lengths for each isotype were selected for a greenhouse depth of emergence experiment. Four replications of 25 seed per replication for each isotype were planted at their calculated depths spaced 5 cm between seed within rows and 15 cm between the rows in greenhouse benches filled with sandy loam. The isotypes were paired and planted in a randomized complete block design. The temperature was maintained at 22°C with no supplemental lighting for the entire experiment. Total emergence was recorded after 14 days and adjusted by dividing the total percent emerged by the germination percent, as determined by official germination tests.

Results and Discussion

The brachytic types have shorter coleoptiles than their derived normals (Table 5). This reduction in coleoptile length is associated with the reduced plant height of the brachytics (Table 7). The Bz Double Ert and Beebe/7*Bz brachytic type appear to have the longest coleoptiles of the reduced height types (Table 5), which may give them

Table 5. Mean coleoptile lengths and differences between ten Betzes isotypes after being grown in the dark for 7 days

Pedigree	Coleoptile length (mm)		difference
	Derived Normal	Mutant	Derived - Mutant
Aks,uz/4*Bz	63	33	30 **
Hnh/4*Bz#	69	42	27 **
Shl,br 2/4*Bz	65	41	24 **
Hly,br 1/4*Bz#	63	40	23 **
ms3,Gwy/Vtg//4*Bz#	65	42	23 **
ms3,Gwy/2*Titan//4*Bz#	64	43	21 **
Cpn/4*Bz#	61	40	21 **
Beebe/7*Bz	60	48	18 **
Bz Double Ert	66	53	13 **
Hulless Cpn†	57	58	-1 NS
Mean	63	44	19 **

†Normal = Sermo donor for hulless, mutant = Stamm donor for hulless.

**Significant at P .01 level.

#Determined to be allelic.

an emergence advantage in heavy textured dry soils where deep planting is necessary to place the seed in contact with moisture for germination.

The coleoptile length pilot experiment showed no response of coleoptiles to the gibberellic acid treatment. These findings are not in agreement with Schneiter (16) where the Hulless Compana (Stamm/7*Cpn) isotype had a shortened coleoptile when treated with indolacetic acid. Barr's analysis (1) of gibberellic acid levels in the seed indicates that the Hulless Compana (Stamm/7*Cpn) has a higher gibberellic acid level. The higher gibberellic acid level may be restricting cell elongation, thus giving the shortened coleoptile observed by Schneiter. The lack of response to gibberellic acid by both isotypes in this experiment indicates further investigation of the gibberellic acid levels of the seed is necessary, along with testing a wider range of gibberellic acid solutions.

Significant differences for percent emergence were detected among genotypes for both planting depths, but significance was not detected between isotypes within genotypes (Table 6 and Appendix Table 3). The shorter, wider, possibly stronger plumule of the brachytics was hypothesized to give a greater percent emergence over their derived normal at the deeper depths. This was determined to be a false assumption, when all brachytic isotypes were compared collectively with their respective normal isotypes.

Table 6. Adjusted percent emergence[††] from planting depths 25 mm and 50 mm deeper than each isotype's mean coleoptile length, and isotype differences.

Pedigree	Percent Emergence					
	25 mm deeper			50 mm deeper		
	Derived Normal	Mutant	Difference Normal-Mutant	Derived Normal	Mutant	Difference Normal-Mutant
Cpn/4*Bz[#]	84	72	12	72	50	22
Shl,br 2/4*Bz	79	67	12	57	43	14
ms3,Gwy/Vtg//4*Bz[#]	80	74	6	75	63	12
ms3,Gwy/2*Titan//4*Bz[#]	68	63	5	57	48	9
Beebe/7*Bz	68	63	5	61	61	0
Aks,uz/4*Bz	89	86	3	84	69	15
Hly,br 1/4*Bz[#]	80	78	2	64	49	15
Bz Double Ert	77	76	1	83	67	16
Hnh/4*Bz[#]	73	78	-5	65	61	4
Cpn Hulless	46	51	-5	26	34	-8
Mean	74	71	3	64	54	10

[†]Normal = Sermo donor for hulless, mutant = Stamm donor for hulless.
[††]Percent emergence/germination percent × 100.
[#]Determined to be allelic.

PLANT HEIGHT, CULM INTERNODE LENGTH AND DISTRIBUTION AMONG INTERNODES, RACHIS INTERNODE LENGTH, SPIKE LENGTH AND AWN LENGTH

Materials and Methods

Data reported are for all isotypes from the two field plantings described in the General Materials and Methods section. Sixteen plant height measurements for each isotype were made after the seed reached the hard dough stage of maturity. Plant height was recorded as the distance from the ground to the apex of the uppermost kernel of the spikes in a handful of culms.

Sixteen mature dry main culms for each isotype were measured for internode length and number. The first culm headed was considered the main culm. The spike bearing internode or peduncle was designated as internode n and each consecutive internode below it as n-1, n-2, n-3, and n-4. Culm internode length of n is the distance from the base of the spike to the bottom of the first culm node. Internode length of n-1 is the distance from the bottom of the first culm node to the bottom of the second culm node and each consecutive internode is measured in the same manner.

Rachis internode length was measured for each isotype for 16 main and 16 random culm spikes as the length of rachis internodes 6 through 15, beginning the count at the spike base. The first several rachis internodes are considered too variable for a meaningful measurement. Dividing this length by 10 gives the mean rachis internode

lengths. Spike length was calculated by multiplying mean rachis internode length by rachis internode number.

Awn length of 16 main culm and 16 random culm spikes were measured as the distance from the apex of the uppermost kernel of the spike, vertically to the tip of the longest awn (7).

Results and Discussion

Plant height, culm internode length, rachis internode length, spike length, and awn length for the brachytic isotypes are significantly shorter than their derived normal isotypes except for awn length and peduncle length of Bz Double Ert, n-4 culm internode length of Aks,uz/4*Bz and spike length of Hly,br l/4*Bz (Tables 7, 8, and 9 and Appendix Tables 4 and 5).

The n-4 culm internode of Aks,uz/4*Bz is significantly longer than its normal isotype (Table 8 and Figure 1). The tendency for less reduction is also evident for the n-3 internode. There is a marked tendency for the uz genotype to result in culm internodes of approximately equal length, which is not observable for other genotypes (Figure 1). The allelic isotypes are remarkably similar for all plant parts (Figure 1).

Main culm measurements are more reliable for detecting genetic differences because they are the first to develop and are less subject

Table 7. Mean plant height (cm) and differences between isotypes.

Pedigree	Plant height (cm)		
	Derived Normal	Mutant	difference Normal-Mutant
Sh1, br 2/4*Bz	68.3	42.5	25.8 **
Aks,uz/4*Bz†	83.7	59.7	24.0 **
ms3,Gwy/2*Titan//4*Bz†#	80.3	59.0	21.3 **
Cpn/4*Bz#	71.7	50.9	20.8 **
Hnh/4*Bz #	71.0	53.2	17.8 **
Bz Double Ert	69.1	51.9	17.2 **
ms3,Gwy/Vtg//4*Bz#	70.8	55.1	15.7 **
Hly,br 1/4*Bz#	67.1	52.2	14.9 **
Beebe/7*Bz	70.3	56.7	13.6 **

**Significant at P .01 level.

†Entries not grown in same nursery as others.

#Determined to be allelic.

Table 8. Mean culm internode length (mm) for internodes n, n-1, n-2, n-3, and n-4, and differences between isotypes.

Pedigree	Internode, n			Internode, n-1			Internode, n-2		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Aks,uz/4*Bz	258	113	145 **	176	82	94 **	126	98	28 **
Shl,br 2/4*Bz	194	84	110 **	148	74	74 **	109	74	35 **
ms3,Gwy/2*Titan//4*Bz #	266	166	100 **	180	126	54 **	130	102	28 **
Cpn/4*Bz #	176	99	77 **	146	103	43 **	116	87	29 **
Hly,br 1/4*Bz #	184	113	71 **	157	99	58 **	99	75	24 **
ms3,Gwy/Vtg//4*Bz #	178	118	60 **	144	99	45 **	102	75	27 **
Hnh/4*Bz #	181	122	59 **	141	100	41 **	112	77	35 **
Beebe/7*Bz	170	118	52 **	138	110	28 **	107	80	27 **
Bz Double Ert	164	156	8	140	108	32 **	100	77	23 **

Pedigree	Internode, n-3			Internode, n-4		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Aks,uz/4*Bz	100	89	11 *	43	88	-45 **
Shl,br 2/4*Bz	88	52	36 **	42	30	12 **
ms3,Gwy/2*Titan//4*Bz #	99	70	29 **	43	37	6 *
Cpn/4*Bz #	83	60	23 **	54	40	14 **
Hly,br 1/4*Bz #	75	51	24 **	46	34	12 *
ms3,Gwy/Vtg//4*Bz #	95	57	38 **	52	34	18 **
Hnh/4*Bz #	94	53	41 **	54	35	19 **
Beebe/7*Bz	94	73	21 **	63	50	13 *
Bz Double Ert	92	58	34 **	60	28	32 **

*, **Significant at P .05 and P .01 level, respectively.

#Determined to be allelic.

Table 9. Mean rachis internode length, spike length and awn length of main and random culms and differences between isotypes.

Pedigree	Main Culm Spike								
	Rachis internode length (mm)			Spike length (mm)			Awn length (mm)		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Bz Double Ert	3.487	1.862	1.625 **	94	47	47 *	114	108	6
Aks,uz/4*Bz	3.569	2.081	1.488 **	100	63	37 *	96	27	69 **
Shl,br 2/4*Bz	3.494	3.287	.207 **	94	83	11 *	112	32	80 **
Beebe/7*Bz	3.462	2.900	.562 **	90	73	17 *	117	84	33 **
ms3,Gwy/2*Titan//4*Bz#	3.150	2.662	.488 **	93	81	12 *	110	43	67 **
ms3,Gwy/Vtg//4*Bz#	3.569	3.144	.425 **	92	83	9 *	118	55	63 **
Hly,br 1/4*Bz#	3.637	3.256	.381 **	73	82	-9 *	111	50	61 **
Hnh/4*Bz#	3.525	3.262	.263 **	94	83	11 *	116	55	61 **
Cpn/4*Bz#	3.481	3.275	.206 **	93	79	14 *	106	53	53 **
	Random Culm Spike								
	Rachis internode length (mm)			Spike length (mm)			Awn length (mm)		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Bz Double Ert	3.400	1.819	1.581 **	85	44	41 *	111	107	4
Aks,uz/4*Bz	3.400	2.037	1.363 **	95	60	35 *	95	28	67 **
Shl,br 2/4*Bz	3.425	3.219	.206 **	84	74	10 *	118	32	86 **
Beebe/7*Bz	3.444	2.850	.594 **	86	68	18 *	122	83	39 **
ms3,Gwy/2*Titan//4*Bz#	3.481	3.044	.437 **	92	81	11 *	111	46	65 **
ms3,Gwy/Vtg//4*Bz#	3.381	3.094	.287 **	80	76	4	116	52	64 **
Hly,br 1/4*Bz#	3.681	3.312	.369 **	72	78	-6 *	110	48	62 **
Hnh/4*Bz#	3.494	3.181	.313 **	88	74	14 *	120	55	65 **
Cpn/4*Bz#	3.519	3.419	.100	91	72	19 *	104	54	50 **

*, **Significant at P .05 and P .01, respectively.
#Determined to be allelic.

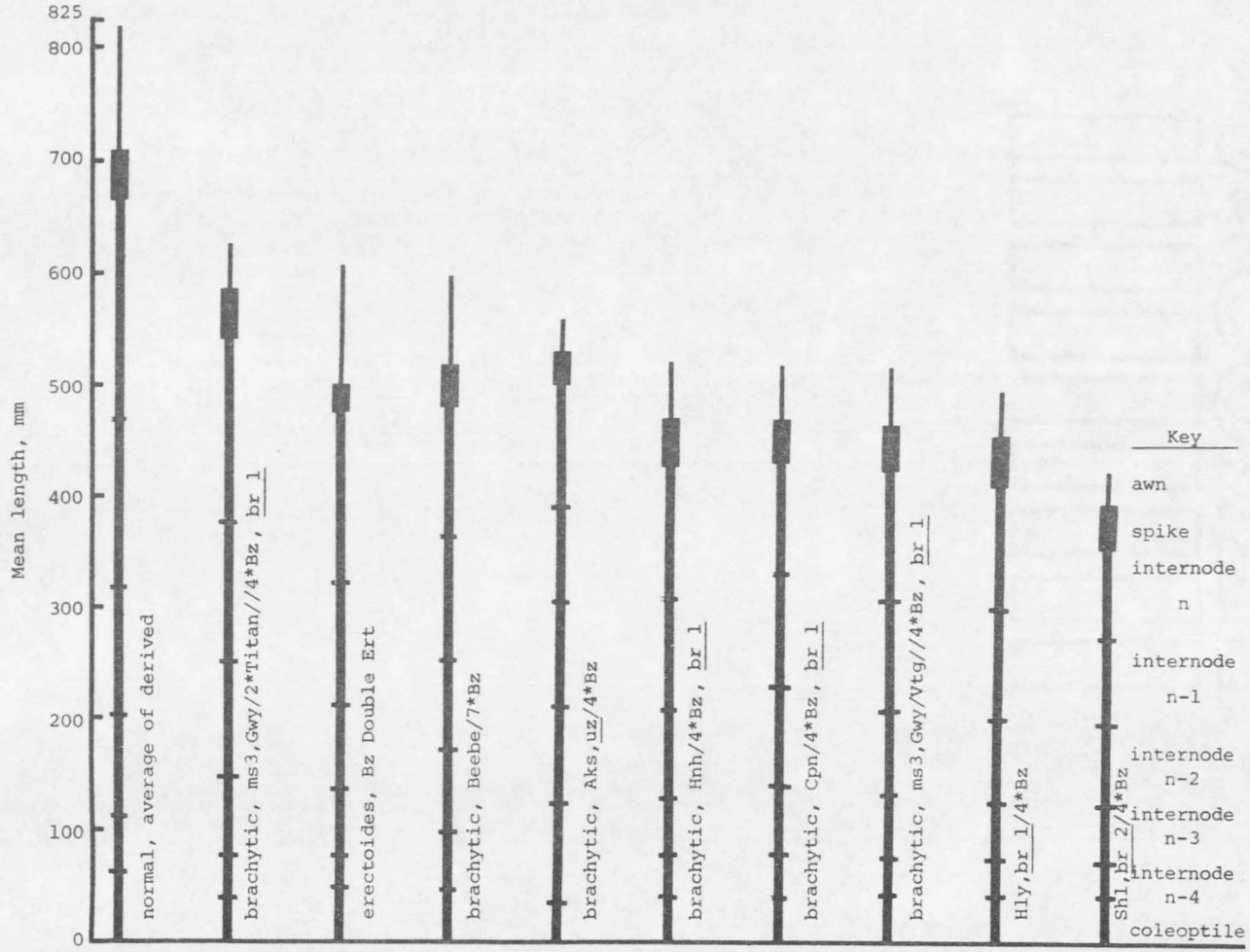

Figure 1. Schematic representation of Betzes brachytics and mutant isotypes compared to average of derived normals.

to environmental stress and are more apt to be of maximum size and length (Table 9).

The derived normal of the Hly,br 1/4*Bz cross appears to be deficient in plant height and spike length when compared to the other derived normal isotypes which may well be from earlier heading and maturing of the normal isotype. The earliness is not evident in the mutant isotype. The earliness is assumed to have been introduced from a backcross using Erbet (early Betzes) pollen rather than Betzes pollen.

SOIL MOISTURE REMOVAL BY CROPPING AND NUMBER OF ROOTS ORIGINATING AT THE CROWN

Materials and Methods

In mid-October, after harvest and after receiving approximately 9 cm of pre- and post-harvest rain (Appendix Table 2), one soil sample from each 30 cm increment to 180 cm were taken near the center of each yield trial plot. Planting and other details are described in the General Materials and Methods section. Percent moisture for each sample was calculated from wet weight minus oven dry weight divided by oven dry weight

The number of roots originating from the crown was determined for all height reducing isotypes (Table 1) and for Hulless Compana (Sermo/7*Cpn) and Hulless Compana (Stamm/7*Cpn) in a greenhouse experiment. To facilitate root extraction and cleaning, seeds were planted in 30 cm lengths of dialysis tubing that were closed at one end and moistened with a distilled water and chlorox solution. Two seeds of the same isotype, washed in a distilled water and chlorox solution, were positioned embryo end down, 15 mm into the open end of each moist tube. The tubes were paired by isotypes and buried vertically into autoclaved vermiculite in a four replication randomized complete block design, with the open end 5 mm below the surface, then watered with nutrient solution. After 14 days, the seedlings were removed and the number of roots originating from the crown were counted and recorded.

The original intent of the experiment was to confine the roots within the tubing and determine root weight and length, but the dialysis tubing decomposed in 14 days. Further investigation of the technique is needed.

Results and Discussion

Soil moisture data for the first two 30-cm increments were influenced by pre- and post-harvest rains before sampling. Considering the amount of rain received and the field capacity per 30 cm increment of soil (Appendix Table 1), the first two increments were not used for drawing conclusions. The rain had not penetrated below the second increment.

Considering the reduced coleoptile lengths and plant heights of the brachytic isotypes (Tables 5 and 7), a hypothesis that the brachytics may remove less soil water at deeper depths than derived normals was supported especially at the 120-150 cm increment (Table 10 and Appendix Table 6).

Comparing the allelic isotypes, the Hly,br 1/4*Bz pair shows a more uniform water removal at deeper depths than the other alleles (Figure 2 and Table 10). This greater uniformity may be accounted for by the previously explained earlier maturing derived normal to which it is compared.

Table 10. Mean percent soil moisture remaining after harvest by 30 cm increments, to a depth of 180 cm and differences between isotypes.

Pedigree	0-30 cm			30-60 cm			60-90 cm		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Sh1,br 2/4*Bz	21.8	20.7	1.1	11.6	11.8	-0.2	8.7	8.9	-0.2
Cpn/4*Bz #	21.1	21.4	-0.3	10.2	11.1	-0.9	8.4	8.7	-0.3
Hly,br 1/4*Bz #	20.9	20.9	0.0	10.5	10.8	-0.3	8.5	8.8	-0.3
Beebe/7*Bz	21.3	20.6	0.7	10.1	9.9	0.2	8.4	8.5	-0.1
ms3,Gwy/Vtg//4*Bz #	21.5	21.7	-0.2	11.3	11.4	-0.1	8.7	8.9	-0.2
Bz Double Ert	20.6	21.1	-0.5	10.6	10.9	-0.3	8.5	8.7	-0.2
Hnh/4*Bz #	20.8	21.2	-0.4	10.6	10.5	0.1	8.5	8.8	-0.3
	90-120 cm			120-150 cm			150-180 cm		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Sh1,br 2/4*Bz	8.8	10.4	-1.6 **	10.3	12.7	-2.4 **	13.6	15.2	-1.6 **
Cpn/4*Bz #	8.0	9.1	-1.1 *	10.5	12.2	-1.7 **	14.1	14.0	0.1
Hly,br 1/4*Bz #	10.0	10.5	-0.5	12.7	13.1	-0.4	14.2	14.1	0.1
Beebe/7*Bz	8.6	8.8	-0.2	11.0	12.3	-1.3 *	14.6	14.6	0.0
ms3,Gwy/Vtg//4*Bz #	8.8	8.9	-0.1	10.3	11.6	-1.3 *	13.0	14.0	-1.0
Bz Double Ert	8.3	8.9	-0.6	9.9	11.3	-1.4 *	13.3	13.8	-0.5
Hnh/4*Bz #	8.4	9.7	-1.3	10.8	12.2	-1.4 *	13.4	14.7	-1.3 *

*, **Significant at P .05 and P .01 level, respectively.
#Determined to be allelic.

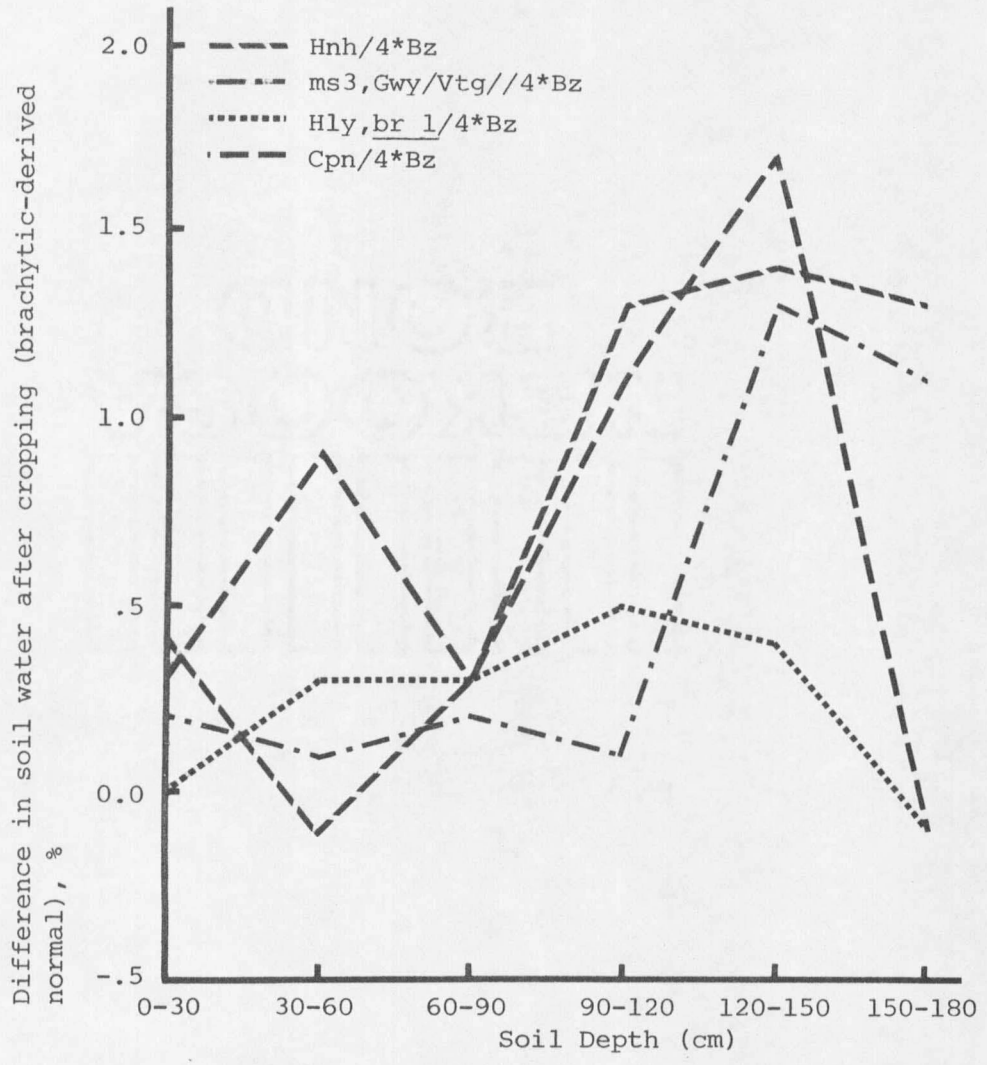

Figure 2. Mean water use differences (brachytic-derived normal), percent, sampled by 30 cm increments to a depth of 180 cm for the allelic isotypes.

When normal and mutant isotype differences are used as a means of comparison, the non-allelic isotypes, Bz Double Ert and Beebe/7*Bz brachytic type show a greater percent of water removed at the 120-150 cm depth than Sh1,br 2/4*Bz (Figure 3). The Sh1,br 2/4*Bz brachytic type may have a reduced root system beginning after 90 cm, indicated by the big difference at this depth through 150 cm. The Bz Double Ert and Beebe/7*Bz brachytic type appear to have very similar water removal difference from 60 cm through 150 cm in depth.

A Heterogeneity X^2 test showed the number of roots originating from the crown did not vary significantly between isotypes and across all genotypes (Table 11). This would lead one to believe that rooting depth in association with other plant parts such as total leaf area and stomata size and number are responsible for the difference in soil moisture removal.

The coleoptile length and/or plant height may be good indicators of the depth of the root system. A correlation of root length after n number of days to coleoptile length would help verify or disprove this hypothesis.

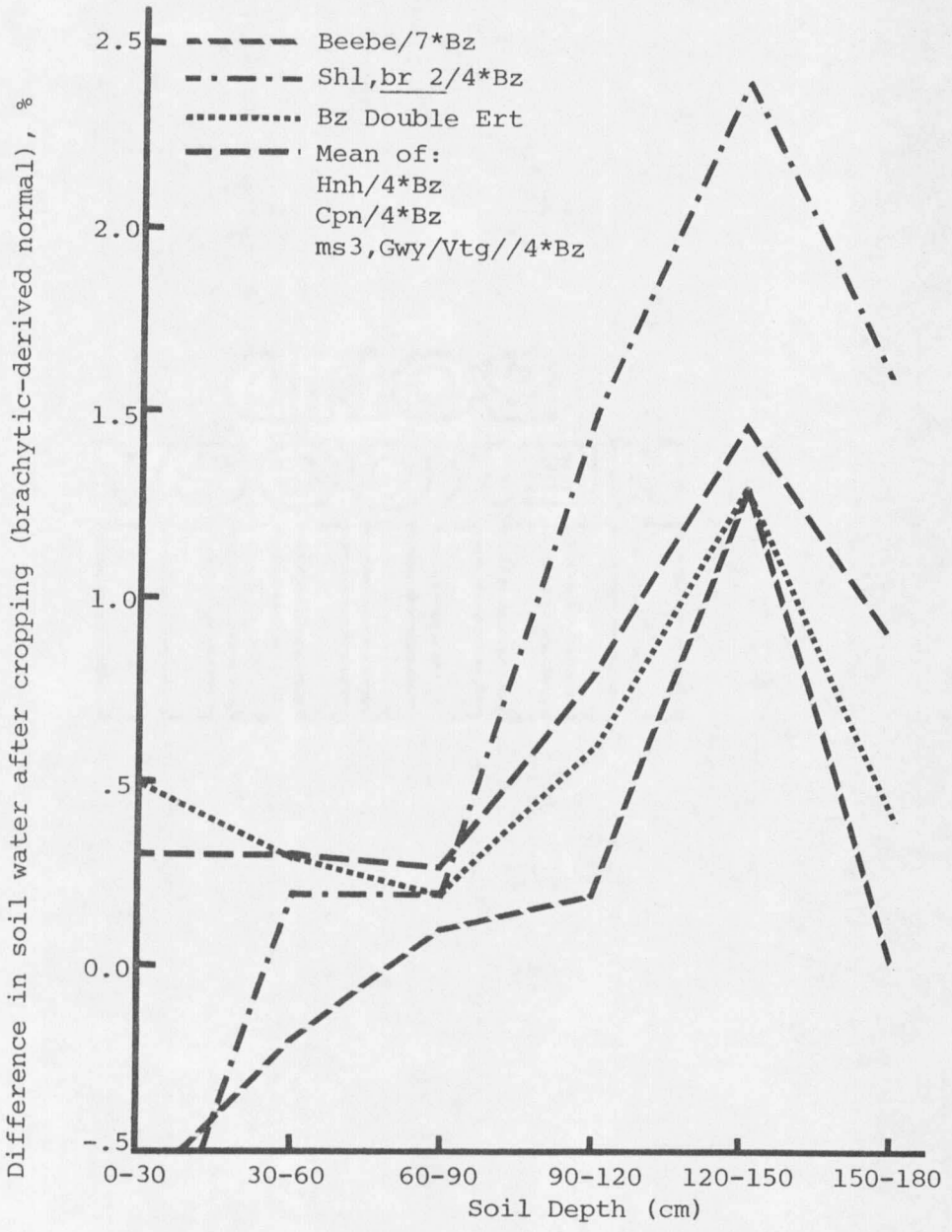

Figure 3. Mean water use differences (brachytic-derived normal), percent, sampled by 30 cm increments to a depth of 180 cm for the non-allelic isotypes.

Table 11. Mean number of roots originating from the crown and isotype differences

Pedigree	Derived Normal	Mutant	difference Normal-Mutant
Shl,br 2/4*Bz	5.50	5.75	-.25
Cpn/4*Bz[#]	6.00	5.75	.25
Hly,br 1/4*Bz[#]	5.75	6.00	.75
Beebe/7*Bz	5.50	5.75	-.25
ms3,Gwy/Vtg//4*Bz[#]	6.00	6.00	0.0
Bz Double Ert	5.75	5.50	.25
Hnh/4*Bz[#]	5.75	5.50	.25
Aks,uz/4*Bz	5.50	5.50	0.0
ms3,Gwy/2*Titan//4*Bz[#]	5.25	6.25	1.0
Cpn Hulless (Stamm vs Sermo)	5.75	6.75	-1.0

[#]Determined to be allelic.

YIELD COMPONENTS

Materials and Methods

Yield component measurements, tiller number, kernel weight and seed/spike, were made for all height isotypes (Table 1) grown under the conditions described in the General Materials and Methods.

Total tiller number and spiked tiller number were recorded for 16 random plants for each isotype. Plants were taken from the border rows of the yield plots and from rows that appeared to have the most uniform plant distribution within the rows of the single row planted material. Tiller number was counted after the seed had reached the hard dough stage of maturity. Non-spiked tillers were compared by use of heterogeniety X^2.

Seed per spike and kernel weight measurements were made on 16 main culm spikes and 16 random culm spikes for each isotype from the same rows as tiller number above, except the plants were harvest ripe. Yield determinations were made from a 1.5 square meter area of the center two rows of each yield plot.

Theoretical plant yields were calculated by using the means of the 16 samples measured for each isotype and named component. Four methods of calculating the theoretical yield were used. In the first method it was assumed that a theoretical plant would produce a mean main culm kernel weight and seed/spike for all spikes produced for a means of all tillers produced. The means are multiplied

together for the three components, kernel weight, seed/spike and tiller number for each isotype for its theoretical yield under the specific condition. In method II only the tiller number is changed, from mean total tillers to mean spiked tillers. In method III, mean total tillers is used with random culm kernel weight and seed/spike. In method IV only the tiller number is changed from mean total tillers to mean spiked tillers.

Results and Discussion

All of the reduced height isotypes had fewer total and spiked tillers and lower kernel weight except for spiked tiller number for ms3,Gwy/Vtg//4*Bz (Tables 12 and 13, and Appendix Table 7). Main culm and random culm seed/spike were significantly higher for the brachytic isotypes for ms3,Gwy/Vtg//4*Bz, Aks,uz/4*Bz and Hly,br 1/4*Bz and only the random culm seed/spike was higher for brachytic ms3,Gwy/2*Titan//4*Bz (Table 14 and Appendix Table 8).

Heterogeneity X^2 indicated that the ratio of non-spiked tillers for the mutant and normal isotypes is the same across all genotypes. The ratio seen between isotypes is the same ratio for all genotypes and the totals are not different from each other, they fit a 1:1 ratio at P .01.

Table 12. Mean total, spiked, and non-spiked tiller number[+] and difference between isotypes.

Pedigree	Total Tiller Number			Spiked Tiller Number			Non-Spiked Tiller Number		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Cpn/4*Bz[#]	7.31	4.81	2.50 **	6.31	4.19	2.12 **	1.00	.62	.38
Beebe/7*Bz	4.94	3.37	1.56 **	3.62	2.81	.81 **	1.31	.56	.75
Aks,uz/4*Bz	11.75	8.37	3.38 **	9.69	7.19	2.50 **	2.06	1.19	.87
Hly,br 1/4*Bz[#]	5.75	4.37	1.38 *	5.12	4.06	1.06 *	.62	.31	.31
Shl,br 2/4*Bz	6.06	4.69	1.37 *	5.00	4.00	1.00	1.06	.69	.37
Bz Double Ert	4.81	4.25	.56	4.19	3.56	.63	.62	.69	-.07
ms3,Gwy/Vtg//4*Bz[#]	5.44	4.87	.57	3.75	3.94	-.19	1.69	.94	.75
Hnh/4*Bz[#]	5.62	5.19	.43	4.75	4.31	.44	.87	.87	0.0
ms3,Gwy/2*Titan//4*Bz[#]	11.94	11.37	.57	10.12	10.12	0.00	1.81	1.25	.56

*, **Significant at P .05 and P .01 level, respectively.

[+]Tiller number based on 16 random plants in the row.

[#]Determined to be allelic.

Table 13. Mean kernel weights, mg per kernel, of main culm spikes and random culm spikes and differences between isotypes.

Pedigree	Main Culm kernel weights (mg/kernel)			Random culm kernel weights (mg/kernel)		
	Derived Normal	Mutant	difference Normal-Mutant	Derived Normal	Mutant	difference Normal-Mutant
Sh1,br 2/4*Bz	44.56	30.81	13.75 **	42.32	29.25	13.07 **
ms3,Gwy/2*Titan//4*Bz #	47.50	35.31	12.19 **	48.24	35.46	12.78 **
Hnh/4*Bz #	44.19	33.56	10.63 **	42.12	32.44	9.68 **
Hly,br 1/4*Bz #	44.62	34.06	10.56 **	44.35	33.69	10.66 **
ms3,Gwy/Vtg//4*Bz #	44.69	34.31	10.38 **	41.54	32.50	9.04 **
Cpn/4*Bz #	43.87	35.56	8.31 **	43.97	34.44	9.53 **
Aks,uz/4*Bz	45.44	37.37	8.07 **	44.24	37.42	6.82 **
Bz Double Ert	42.62	36.00	6.62 **	40.72	35.30	5.42 **
Beebe/7*Bz	44.00	39.94	4.06 **	43.38	37.96	5.42 **

**Significant at P .01, F-test.

#Determined to be allelic.

Table 14. Mean seeds per spike of main culm spikes and random culm spikes and differences between isotypes.

Pedigree	Main culm seeds per spike			Random culm seeds per spike		
	Derived Normal	Mutant	difference Normal-Mutant	Derived Normal	Mutant	difference Normal-Mutant
Cpn/4*Bz #	25.69	23.31	2.38 *	24.37	19.56	4.81 **
Shl,br 2/4*Bz	25.69	24.06	1.63 *	23.44	22.00	1.44 *
Bz Double Ert	25.87	24.37	1.50 **	23.44	23.00	.44 **
Beebe/7*Bz	24.87	23.56	1.31 *	23.44	23.31	1.13
ms3,Gwy/2*Titan//4*Bz #	27.81	26.87	.94	23.00	25.00	-2.00
Hnh/4*Bz #	25.25	24.37	.88	23.81	22.50	1.31
ms3,Gwy/Vtg//4*Bz #	24.06	25.50	-1.44 *	22.31	23.37	-1.06
Aks,uz/4*Bz	26.81	29.19	-2.38 *	25.50	27.12	-1.62
Hly,br 1/4*Bz #	19.06	24.19	-5.13 **	17.81	22.25	-4.44 **

*, **Significant at P .05 and P .01, respectively, F-test.

#Determined to be allelic.

Tiller number per plant appears to be the yield component most responsible for the mutant isotype yield reduction compared to its derived normal for Cpn/4*Bz, Beebe/7*Bz and Bz Double Ert (Tables 15 and 16). Kernel weight appears to be the yield reducing factor for Sh1,br 2/4*Bz, Hnh/4*Bz, ms3,Gwy/Vtg//4*Bz and Hly,br 1/4*Bz, three of which are allelic (Tables 15 and 16). Both tiller number and kernel weight are critical factors to consider for increasing the mutant isotypes yield.

The theoretical plant yields illustrate that the main culm components produce the highest yield for both isotypes (Table 17). Several possibilities of increasing the per plant yield of the brachytic isotypes are indicated from these data. A plant with only main culms would be the best. This may mean considering uniculm or a determinate tillering plant, so all tillers have an equal opportunity to develop the same size seed. The ideal plant would be a multi-main tillered, large seeded, six-row spike typed plant. Under optimum growing conditions, this plant type should have the greatest yield potential.

Table 15. A determination of which factor, tiller number, kernel weight, or seed/spike is most reponsible for yield reduction of the mutant isotype

Pedigree	Mutant Percent of Derived Normal			
	Spiked Tiller no.	Random culm spike		Yield (Quintals/ Hectare)
		Kernel wt. (mg)	Seed/ Spike no.	
Cpn/4*Bz[#]	66[††]	80	78	65
Shl,br 2/4*Bz	80	69[††]	94	56
Beebe/7*Bz	77[††]	87	99	74
Hnh/4*Bz[#]	90	77[††]	94	69
ms3,Gwy/Vtg//4*Bz[#]	105	78[††]	104	81
Bz Double Ert	85[††]	86	98	78
Hly,br 1/4*Bz[#]	79	76[††]	125	96

[#]Determined to be allelic.

[††]Factor contributing most to the yield reduction of the mutant isotype.

Table 16. Mean yield (quintals/hectare) and differences between isotypes.

Pedigreee	Yield		difference Normal-Mutant
	Derived Normal	Mutant	
Sh1,br 2/4*Bz	36.68	20.65	16.03 **
Cpn/4*Bz #	43.06	27.99	15.07 **
Hnh/4*Bz #	42.51	29.21	13.30 **
Beebe/7*Bz	40.71	30.26	10.45 **
Bz Double Ert	43.15	33.68	9.47 **
ms3,Gwy/Vtg//4*Bz #	40.36	32.55	7.81 **
Hyl,br 1/4*Bz #	29.96	28.76	1.20

** Significant at P .01 level.

Determined to be allelic.

Table 17. Theoretical seed yields per plant[†] and differences between isotypes.

Pedigree	Main Culm: All Tillers (Method I) Derived Normal	Mutant	differ. Normal-Mutant	Main Culm: Spiked Tillers (Method II) Derived Normal	Mutant	differ. Normal-Mutant
Aks,uz/4*Bz	15.08	9.42	5.66 **	12.49	8.14	4.35 **
ms3,Gwy/2*Titan//4*Bz[#]	16.90	11.24	5.66 **	14.28	10.01	4.27 **
Cpn/4*Bz[#]	8.61	4.19	4.42 **	7.45	3.62	3.83 **
Shl,br 2/4*Bz	7.29	3.75	3.54 **	6.05	3.18	2.87 **
Beebe/7*Bz	5.76	3.43	2.33 **	4.15	2.87	1.28 **
Hnh/4*Bz[#]	6.62	4.39	2.23 **	5.61	3.67	1.94 **
ms3,Gwy/Vtg//4*Bz[#]	6.27	4.44	1.83 **	4.30	3.63	.67
Bz Double Ert[#]	5.58	3.92	1.66 **	4.86	3.28	1.58 **
Hly,br 1/4*Bz[#]	5.18	3.78	1.40 **	4.62	3.50	1.12 *
	Random Culm: All Tillers (Method III) Derived Normal	Mutant	differ. Normal-Mutant	Random Culm: Spiked Tillers (Method IV) Derived Normal	Mutant	differ. Normal-Mutant
Aks,uz/4*Bz	14.52	9.32	5.20 **	11.95	7.97	3.98 **
ms3,Gwy/2*Titan//4*Bz[#]	15.47	10.88	4.59 **	13.10	9.66	3.44 **
Cpn/4*Bz[#]	8.31	3.49	4.82 **	7.21	3.04	4.17 **
Shl,br 2/4*Bz	6.32	3.26	3.06 **	5.20	2.76	2.44 **
Beebe/7*Bz	5.34	3.06	2.28 **	3.94	2.53	1.41 **
Hnh/4*Bz[#]	6.02	3.99	2.03 **	5.08	3.30	1.78 **
ms3,Gwy/Vtg//4*Bz[#]	5.31	3.93	1.38 **	3.65	3.14	.51
Bz Double Ert	4.85	3.61	1.24 **	4.22	3.03	1.19 **
Hly,br 1/4*Bz[#]	5.02	3.52	1.50 **	4.49	3.26	1.23 *

*, **Significant at P .05 and P .01 level, respectively.

[†]Theoretical plant yields were determined by multiplying kernel weight, seed/spike and tiller number

[#]Determined to be allelic.

QUALITY COMPONENTS

Materials and Methods

Sieve size assortment data include material from all plant height isotypes (Table 1). The ms3,Gwy/2*Titan//4*Bz and Aks,uz/4*Bz isotypes were not analyzed for protein and lysine percent of the grain.

Sizing was accomplished by use of an electric shaker equipped with a 2.381 × 19.05 mm and a 2.182 × 19.05 mm slotted sieves. Seed remaining on the larger sieve are considered plump and seed passing through the smaller sieve are considered thin. Protein percent was obtained from ground samples using the Neotec Grain Quality Analyzer.

Lysine percent in the grain was obtained by a microbiological assay technique developed at Montana State University (25).

Results and Discussion

The mutant isotypes had significantly fewer plump seed and significantly more thin seed than the derived normals except for Beebe/7*Bz which was significantly higher for percent plump (Table 18 and Appendix Table 9). Both percent protein and lysine percent were not significantly different between isotypes (Table 18).

Table 18. Quality components, percent plump, percent thin, percent protein, percent lysine in the grain and isotype differences.

Pedigree	% Plump			% Thin		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Sh1,br 2/4*Bz	58.5	11.2	47.3 **	13.1	58.3	-45.2 **
Hly,br 1/4*Bz #	77.2	34.9	42.3 **	5.3	29.2	-23.9 **
ms3,Gwy/2*Titan//4*Bz #	87.5	51.9	35.6 **	2.6	14.7	-12.1 **
ms3,Gwy/Vtg//4*Bz #	58.7	28.3	30.4 **	11.5	36.6	-25.1 **
Hnh/4*Bz #	51.9	22.4	29.5 **	13.3	44.0	-30.7 **
Cpn/4*Bz #	61.5	33.5	28.0 **	10.4	33.1	-22.7 **
Bz Double Ert	52.8	30.5	22.3 **	14.1	25.2	-11.1 **
Aks,uz/4*Bz	87.4	76.6	10.8 **	1.6	4.7	-3.1 **
Beebe/7*Bz	62.7	79.9	-17.2 **	10.5	6.2	4.3
	% Lysine in grain			% Protein		
	Derived Normal	Mutant	differ. Normal-Mutant	Derived Normal	Mutant	differ. Normal-Mutant
Sh1,br 2/4*Bz	.416	.455	-.039	12.05	13.92	1.87
Hly,br 1/4*Bz #	.447	.483	-.036	13.27	13.60	-.33
ms3,Gwy/Vtg//4*Bz #	.420	.448	-.028	12.45	12.40	.05
Hnh/4*Bz #	.421	.403	.018	12.45	12.20	.25
Cpn/4*Bz #	.457	.426	.031	12.17	12.97	-.80
Bz Double Ert	.443	.411	.032	11.65	12.30	-.65
Beebe/7*Bz	.405	.436	-.031	12.37	13.17	-.80

**Significant at the P .01 level.
Determined to be allelic.

SUMMARY, CONCLUSIONS AND GENERAL DISCUSSION

Isogenic analysis allowed careful scrutiny of nine Betzes reduced height isotypes developed through backcross breeding. Diallel analysis determined four new mutants allelic with br 1 and one new allele br,, was found in Beebe br,,/7*Bz. The br 2 and uz allele were independent of all new mutants.

Mutant types had significantly shorter coleoptiles when germinated in a dark moist germinator, which is supported by other researchers (4,7,8,13,19,20). Seedling emergence from 25 and 50 mm deeper than mean coleoptile lengths for each isotype were not significantly different. This evidence does not support my hypothesis that the wider, possibly stronger, plumule would have a greater emergence percentage from deeper planting depths.

Mutant plant heights, awn lengths and rachis internode length of main culm spikes were significantly shorter than derived normals except for awn length of Bz Double Ert. Swenson (18) indicates that the reduction in culm length is from a reduction in cell number, not in cell size. The length of each successive culm internode of the typical brachytic is reduced in propostion to their contribution to total culm length in the control (10). By this definition, uz and Bz Double Ert would not be brachytics.

Soil moisture removal was significantly less at the 120-150 cm depth for all mutant isotypes sampled, suggesting a reduced root

system. This may be helpful for areas of double cropping. Early maturity, in addition to reduced plant height, may further reduce water removal for double cropping, however, yield would have to be sacrificed for the sake of earlier planting of the second crop. The number of roots originating from the crown indicates root mass may not be a factor. Sharma and Ghildyal (17) report no reduction in roots per unit volume for a single and triple dwarf wheat.

Yield tests showed all mutant types were reduced in yield compared to their normals, whereas Takahashi et al. (21) found some isogenic lines of uz equal to their normals. The yield reductions were due to reduced tiller number of kernel weight of the mutants. Reduced kernel weight may provide for faster dry down of kernels after physiological maturity. This increased rate of drying may be very important where double cropping is practiced and where the seed may be harvested at 35% moisture and dried after threshing, as in Korea. This evidence suggests several approaches of increasing the mutant yields. These are: 1) maintain tiller number and increase kernel weight; 2) increase tiller number and maintain kernel number and weight per spike; 3) try different irrigation regimes, planting rates, planting dates, planting depths, row spacings, fertilization rates and combinations of these; 4) uniculm or determinant tillering large seeded six-rowed types; 5) fall planted winter types; 6) "Happy Home for Genes" concept of R. T. Ramage (14). Repeated yield trials are also

necessary to provide more reliable information. This identification of some of the weak points of the mutants will be helpful in directing further research of short statured barley.

APPENDIX

Appendix Table 1. Bulk density, field capacity (percent by weight), wilting point (percent by weight) for Amsterdam silty clay loam at Bozeman 6W (Crops and Soils Field Research Laboratory).†

Soil Depth (cm)	Bulk Density (%)	Field Capacity (%)	Wilting Point (%)
0- 7.5 cm	1.27	22.9	11.7
7.5-15	1.27	22.9	11.7
30	1.25	22.4	10.4
60	1.24	24.0	9.2
90	1.27	23.0	12.4
120	1.24	23.0	12.4
150	1.24	19.0	10.0

†Courtesy of Dr. A. H. Ferguson, Montana State University, Bozeman, Montana

Appendix Table 2. Comparison of monthly average of weather data for 1975, 1976, and 1958-1976 for Bozeman 6W (Crops and Soils Field Research Laboratory).[†]

	Air Temperature (Fahrenheit									Precipitation (cm)		
	Average 1975			Average 1976			Average 1958-1976			Actual		Average
Month	Mean	Max	Min	Mean	Max	Min	Mean	Max	Min	1975	1976	1958-1976
January	21.6	31.8	11.3	25.1	35.4	14.8	21.1	32.1	10.1	1.80	.81	1.24
February	19.5	31.4	7.6	29.8	39.7	19.8	26.7	37.7	15.7	2.13	.94	.96
March	27.9	38.6	17.2	27.9	40.2	15.6	30.7	42.5	18.8	2.16	1.40	2.34
April	32.8	43.0	22.5	43.1	55.5	30.6	40.5	52.8	28.1	3.17	7.42	3.91
May	47.3	60.0	34.6	54.0	69.0	39.0	50.7	64.8	36.6	10.34	4.01	5.79
June	56.2	70.0	42.4	57.7	72.7	42.6	58.2	72.6	43.7	6.91	8.10	6.96
July	67.5	82.8	52.2	65.8	82.2	49.4	65.1	82.0	48.1	6.40	2.51	3.22
August	60.1	75.2	45.0	62.8	79.8	45.7	63.7	80.6	46.8	3.96	1.47	3.38
September	54.1	70.5	37.7	56.4	72.4	40.3	53.7	69.0	38.3	2.62	6.15	3.50
October	43.0	55.6	30.4	44.5	58.2	30.7	44.8	58.8	30.8	8.97	2.87	3.66
November	29.1	41.5	16.6	34.0	46.2	21.8	32.1	43.5	20.6	2.54	.46	2.44
December	29.0	38.9	19.1	29.2	39.9	18.4	24.1	34.7	13.4	3.61	.18	1.32
Total	488.1	639.3	336.6	530.3	691.2	368.7	511.4	671.1	351.0	54.61	36.32	38.73
Average	40.7	53.3	28.1	44.2	57.6	30.7	42.6	55.9	29.3			

Frost-free Period

	1975	1976	1958-76 (18 years of data)
Last Freeze	June 28	June 14	June 2
First Freeze	Sept. 12	Aug. 27	Sept. 9
Freeze Free Season	75 days	74 days	100 days

[†]Courtesy of Dr. J. M. Caprio, Montana State University, Bozeman, Montana.

Appendix Table 3. Mean square values for individual degree of freedom analysis of variance tables of coleoptile length and adjusted seedling emergence depth.

Source of Variance		Coleoptile Length (mm)	Adjusted Emergence 25 mm	Adjusted Emergence 50 mm
Total	79	--	--	--
Replications	3	16.23	1301.70 **	691.8 *
Genotypes	9	90.13 **	1003.90 **	1531.7 **
Error (a)(reps×genotypes)	27	11.70	110.00	190.7
Subtotal (plots of genotypes	39	--	--	--
Hly,br 1/4*Bz#	1	1162.82 **	8.0	433.1
Shl,br 2/4*Bz	1	1001.73 **	264.5	406.1
ms3,Gwy/2*Titan//4*Bz #	1	835.18 **	55.1	136.1
ms3,Gwy/Vtg//4*Bz#	1	1083.45 **	78.0	264.5
Cpn/4*Bz#	1	915.28 **	300.1	968.0
Hnh/4*Bz#	1	1454.49 **	45.1	36.1
Aks,uz/4*Bz	1	1753.50 **	24.5	450.0
Beebe/7*Bz	1	668.32 **	60.5	.5
Bz Double Ert	1	337.74 **	351.0	220.5
Cpn Hulless (Sermo vs Stamm)	1	.769	40.5	144.5
Error (b)(derived× brachytic)	30	4.70	145.8	209.7

*,** Significant at P .05 and P .01.

Determined to be allelic.

Appendix Table 4. Mean square values from F-test of plant height and culm internode lengths for nine Betzes isotypes.

Source of Variance		Plant Height (cm)	Culm Internode Length (mm)				
			Internode n	Internode n-1	Internode n-2	Internode n-3	Internode n-4
Total	31	--	--	--	--	--	--
Hly,br 1/4*Bz[#]	1	1781.45 **	41256.22 **	26449.88 **	4728.22 **	4875.72 **	1250.00 *
Error	30	8.57	1239.22	295.16	72.40	227.83	183.38
Total	31	--	--	--	--	--	--
Sh1,br 2/4*Bz	1	5291.12 **	97460.50 **	43659.50 **	9418.22 **	10223.88 **	1224.88 **
Error	30	16.93	694.70	256.67	124.83	227.57	129.50
Total	31	--	--	--	--	--	--
ms3,Gwy/2*Titan//4*Bz[#]	1	3620.15 **	79500.50 **	23381.47 **	6555.00 **	6497.88 **	330.72
Error	30	8.76	729.97	120.17	349.10	198.81	304.00
Total	31	--	--	--	--	--	--
ms3,Gwy/Vtg//4*Bz[#]	1	1837.09 **	28800.00 **	15886.47 **	5912.47 **	11099.88 **	2520.50 **
Error	30	47.30	950.87	327.13	129.77	151.33	212.17
Total	31	--	--	--	--	--	--
Cpn/4*Bz[#]	1	3459.87 **	47431.88 **	15137.88 **	6669.88 **	4163.00 **	1638.47 **
Error	30	16.67	526.93	206.37	106.13	140.49	128.77
Total	31	--	--	--	--	--	--
Hnh/4*Bz[#]	1	2529.02 **	27552.97 **	13570.47 **	9834.47 **	13860.88 **	2944.47 **
Error	30	8.57	1126.17	260.37	73.97	140.60	257.23
Total	31	--	--	--	--	--	--
Aks,uz/4*Bz	1	4597.61 **	167475.50 **	70405.47 **	6105.00 **	1001.22 *	15293.87 **
Error	30	13.51	425.50	190.93	135.00	238.70	231.00
Total	31	--	--	--	--	--	--
Beebe/7*Bz	1	1491.12 **	21372.22 **	6132.72 **	5618.00 **	3486.00 **	1224.00 *
Error	30	12.66	1485.43	404.33	2966.00	247.10	282.26
Total	31	--	--	--	--	--	--
Bz Double Ert	1	2351.61 **	412.72	8159.72 **	4370.50 **	9078.47 **	8319.88 **
Error	30	7.39	984.20	211.40	81.03	168.23	249.93

*,** Significant at P .05 and P .01.
[#]Determined to be allelic.