



Shrunken endosperm mutants from barley, *Hordeum vulgare* L.  
by Alvin John Jarvi

A thesis submitted to the Graduate Faculty in partial fulfillment of the requirements for the degree by  
DOCTOR OF PHILOSOPHY in Genetics  
Montana State University  
© Copyright by Alvin John Jarvi (1970)

**Abstract:**

Six spontaneous shrunken endosperm barley mutants were identified and described. All mutants were inherited as single recessive genes and assigned the symbols *se* through *se6*. Five of the mutants do not express xenia. The mutants varied in fertility, seed weight, and sieve size assortment. Cytological studies indicated that the greatest frequency of dividing endosperm nuclei were found in samples of the third to the seventh floret from the base of the spike from collections made 5-7 days after pollination at 1-3 p.m. One multiploid sporocyte plant was found and no mitotic abnormalities in endosperm tissue were observed. Four mutants were located on chromosome 1, one on chromosome 3, and one on chromosome 6.

Double crossovers in the interstitial segments of translocations is offered as an explanation of some ratios observed. The mutants may have potential as males or pre-flowering selective genes in hybrid barley systems.

SHRUNKEN ENDOSPERM MUTANTS IN BARLEY, HORDEUM VULGARE L.

by

ALVIN JOHN JARVI

A thesis submitted to the Graduate Faculty in partial fulfillment of the requirements for the degree

by

DOCTOR OF PHILOSOPHY

in

Genetics

Approved:

PDSkaan

Head, Major Department

Robert G. Elick

Co-Chairman, Examining Committee

G. Allan Taylor

Co-Chairman, Examining Committee

J. Goering

Dean, Graduate Division

MONTANA STATE UNIVERSITY  
Bozeman, Montana

June, 1970

## ACKNOWLEDGEMENTS

The author wishes to acknowledge the assistance, encouragement and constructive criticism of Professor R. F. Eslick and Dr. E. A. Hockett during the course of this study. Appreciation is expressed to Dr. R. T. Ramage, University of Arizona, for assistance and suggestions. The author wishes to thank Lewis Lehmann for growing the F<sub>2</sub> populations of the se5 crosses in Rambar's greenhouse at Tucson, Arizona.

An acknowledgement is due to the Plant and Soil Science Department for use of their facilities.

A special acknowledgement to my wife, Maxine, and to my sons for their patience and consideration throughout the course of this study.

## TABLE OF CONTENTS

	<u>Page</u>
VITA . . . . .	ii
ACKNOWLEDGMENT . . . . .	iii
TABLE OF CONTENTS. . . . .	iv
LIST OF TABLES . . . . .	vi
LIST OF FIGURES. . . . .	vii
LIST OF PLATES . . . . .	viii
ABSTRACT . . . . .	ix
INTRODUCTION . . . . .	1
REVIEW OF LITERATURE . . . . .	2
DESCRIPTION OF MUTANT LINES: . . . . .	8
Materials and Methods . . . . .	8
Results and Discussion. . . . .	8
General Comments . . . . .	8
Betzes <u>se</u> . . . . .	9
Betzes <u>se2</u> . . . . .	9
Compana <u>se3</u> . . . . .	10
Compana <u>se4</u> . . . . .	10
Sermo X: Glacier <sup>7</sup> <u>se5</u> . . . . .	10
Compana <u>se6</u> . . . . .	11
Betzes <u>se-x</u> . . . . .	11

	<u>Page</u>
CYTOLOGY . . . . .	18
Materials and Methods . . . . .	18
Results and Discussions . . . . .	20
Endosperm Mitosis. . . . .	20
Pollen Mother Cell Meiosis . . . . .	32
LOCATION OF SHRUNKEN ENDOSPERM GENES ON BARLEY GENETIC MAPS. . . . .	42
Materials and Methods . . . . .	42
Results and Discussion. . . . .	44
Location of <u>se</u> . . . . .	44
Location of <u>se2</u> . . . . .	48
Location of <u>se3</u> . . . . .	48
Location of <u>se4</u> . . . . .	49
Location of <u>se5</u> . . . . .	49
Location of <u>se6</u> . . . . .	50
ALLELISM . . . . .	59
Materials and Methods . . . . .	59
Results and Discussion. . . . .	59
GENERAL DISCUSSION . . . . .	62
SUMMARY AND CONCLUSIONS. . . . .	64
LITERATURE CITED . . . . .	66

## LIST OF TABLES

<u>TABLE</u>	<u>Page</u>
I. Physical data on mutant lines. . . . .	13
II. ANOVA for weight/100 seeds and fertility . . . . .	13
III. F <sub>2</sub> plant segregation ratios for shrunken endosperm genes. . . . .	17
IV. Distribution of endosperm mitotic stages in Compana at various days after pollination. . . . .	22
V. Distribution of endosperm mitotic stages in samples from Betzes at various hours of the day. . . . .	25
VI. Distribution of endosperm mitotic stages at various positions along the spike of Betzes. . . . .	28
VII. Distribution of endosperm mitotic stages within the variety Betzes based on one head samples . . . . .	31
VIII. Distribution of endosperm mitotic stage in the shrunken endosperm lines, Compana and Betzes . . . . .	33
IX. F <sub>2</sub> genetic linkage data. . . . .	52
X. F <sub>3</sub> mutant X translocation data . . . . .	53
XI. F <sub>2</sub> genetic linkage data. . . . .	55
XII. F <sub>2</sub> mutant X translocation data . . . . .	56
XIII. Allelism data for seven shrunken endosperm mutants. . . . .	61

## LIST OF FIGURES

<u>FIGURE</u>		<u>Page</u>
1.	Sieve size distribution of Betzes and Betzes shrunken endosperm mutants. . . . .	14
2.	Sieve size distribution of Betzes and Betzes shrunken endosperm mutants. . . . .	15
3.	Sieve size distribution of Glacier and Sermo X Glacier <sup>7</sup> <u>se5</u> . . . . .	16
4.	Percentage of endosperm cells in prophase in Compana at various days after pollination . . . . .	23
5.	Percentage of endosperm cells in Betzes at various hours of the day. . . . .	26
6.	Percentage of endosperm cells in prophase at various positions of the spike of Betzes. . . . .	29

## LIST OF PLATES

<u>PLATE</u>		<u>Page</u>
1.	Early prophase of endosperm mitosis in <u>se5</u> 1300x. . . . .	34
2.	Prophase of endosperm mitosis in Betzes 4000x. . .	35
3.	Prophase of endosperm mitosis in <u>se3</u> 4000x . . . .	36
4.	Late prophase of endosperm mitosis in <u>se6</u> 5000x. .	37
5.	Metaphase of endosperm mitosis in <u>se</u> 4000x . . . .	38
6.	Unusual metaphase spread of endosperm mitosis in <u>se2</u> 2000x. . . . .	39
7.	Anaphase I in the <u>se5</u> multiploid sporocyte illustrating more than 14 univalents 1000X . . . .	40
8.	Anaphase I in the <u>se5</u> multiploid sporocyte illustrating variations in ploidy levels .250X . .	41

## ABSTRACT

Six spontaneous shrunken endosperm barley mutants were identified and described. All mutants were inherited as single recessive genes and assigned the symbols se through se6. Five of the mutants do not express xenia. The mutants varied in fertility, seed weight, and sieve size assortment. Cytological studies indicated that the greatest frequency of dividing endosperm nuclei were found in samples of the third to the seventh floret from the base of the spike from collections made 5-7 days after pollination at 1-3 p.m. One multiploid sporocyte plant was found and no mitotic abnormalities in endosperm tissue were observed. Four mutants were located on chromosome 1, one on chromosome 3, and one on chromosome 6. Double crossovers in the interstitial segments of translocations is offered as an explanation of some ratios observed. The mutants may have potential as males or pre-flowering selective genes in hybrid barley systems.

## INTRODUCTION

Very few qualitative factors affecting the endosperm have been described in barley (Hordeum vulgare L.). It is unusual that more of these factors have not been identified and studied in barley because of the ease with which endosperm characteristics expressing xenia can be handled. Endosperm mutants have played an important role in the basic studies of maize genetics. The characteristics most studied have been those which express xenia. In these cases  $F_2$  segregation ratios can be obtained directly from the seed on  $F_1$  ears.

The possible use of pre-flowering selective genes in hybrid barley systems suggested this study of six mutants influencing endosperm development. Gene action and linkage relationships are of prime importance in hybrid barley systems presently proposed.

The possible role of endosperm mutant types in barley hybrid systems was the objective of this study. Areas of investigation included the inheritance of the mutant genes, location of mutants on the barley genetic maps and the endosperm cytology of the mutant lines.

## REVIEW OF LITERATURE

Weijer (1952) catalogued the existing genetic studies in maize and included the following endosperm characteristics: brittle endosperm, bt; defective endosperm, de; floury endosperm, fl; soft starch, n; mealy endosperm, me; opaque endosperm, o; reduced endosperm, re; shrunken endosperm, sh; sugary endosperm, su; and waxy endosperm, wx. All of the above mutant types are recessive and express xenia.

One plant characteristic influencing the endosperm phenotype in maize was reported by Mangelsdorf (1926). In a study of several xenia expressing defective endosperm types, Mangelsdorf included one plant character defective endosperm, depl. Xenia was not expressed by depl which gave 3 normal : 1 defective endosperm plant segregations. Pollination of mutant plants with normal pollen resulted in defective endosperm F<sub>1</sub> seed and reciprocal crosses yielded normal F<sub>1</sub> seed. He concluded that the characteristic was dependent on the genotype of the mother plant, not of the developing seed.

A typical example of the xenia expressing endosperm characters in maize is the reduced endosperm genes rel and re2 reported by Esther (1931). Both genes were single recessives and pollination of homozygous recessive plants with normal pollen and the reciprocal crosses resulted in normal F<sub>1</sub> seed. The F<sub>2</sub> seed, on the F<sub>1</sub> plant ear, segregated 3 normal : 1 reduced endosperm seed. There was a direct effect of the pollen on the trait being studied.

Harlan (1914) reported that the blue aleurone character in barley was due to an anthocyanin pigment. This is one of the few characters in barley which expresses xenia. Myler and Stanford (1942) demonstrated that two dominant complementary genes were involved in the expression of this character. For the blue aleurone to be expressed there must be at least one dominant allele present at each of the two loci. They found one gene to be in the linkage group that is now designated as part of chromosome 1 and the other on what is now designated as chromosome 4, Ramage, Burnham, and Hagberg (1961).

Two genes which influence the chemical composition of the starchy endosperm have been reported in barley. Nilan (1964) summarized the studies on the waxy endosperm character. One of the genes, wx, is a simply inherited recessive and expresses xenia for the trait. The mutant gene, wx, alters the composition of the starch by decreasing the amylose content from about 20% to nearly zero. Another gene, reported by Walker and Merritt (1969), approximately doubled the amylose content in the endosperm of the variety 'Glacier'. The mutant has been designated as ac38 and was inherited as a simple recessive. There was a dosage effect of the mutant gene and with increasing doses of the mutant gene there was a logarithmical increase in the amylose content. From the dosage effect it appears that this mutant gene expresses xenia.

Reid and Wiebe (1968) referred to a kernel type in barley in which the starch was replaced by a sugary liquid. As the seed matured it collapsed and the collapsed seed failed to germinate. Stocks of this mutant could be maintained as heterozygotes which expressed xenia. Harlan (1957) referred to a similar or possibly the same mutant type. Harlan and Pope (1925) discussed a similar nonheritable situation of "watery kernels" in which the seeds contained a sugary liquid. These seeds had a normal seed coat and embryo but no aleurone layer or starchy endosperm. The authors proposed that these may be cases of single fertilization in which only the embryo was fertilized. Another case of liquid endosperm was reported by Brown (1955) in Limnodea arkansana, which differs from the cases mentioned in barley. This type of endosperm remains as a liquid even under dry storage conditions where it contained about 26% water. Dore (1956), following Brown's observations, reported on an additional 17 genera in four species of grass having a similar liquid endosperm.

Robertson (1932) described a simply inherited recessive albino mutant (at<sub>2</sub>), which also influenced endosperm development in the barley variety 'Canada Thorpe'. Seed containing the mutant gene in the homozygous condition expressed an altered endosperm phenotype. The altered endosperm facilitated an accurate separation of the homozygous mutant seed prior to germination. Upon germination the

mutant seeds had a watery appearance compared to the white starchy appearance of normal seeds. The mutant seeds weighed 2.34 grams/100 compared to 4.65 grams/100 for the normal.

Harvey, Reinbergs, and Somaroo (1968) described a simply inherited recessive gene for female sterility derived from a colchicine-treated barley population. The character was a simply inherited recessive gene. Seed set on the female sterile plants ranged from 14-22% in a rough-awn, hairy-stigma genotype. The authors stated that the seed obtained on the sterile plants was small and could be removed mechanically from a mixture. They indicated the line may have potential as a pollen parent in hybrid barley in which the female sterile line could be mixed directly with the female parent. Nilan (1964) summarized quantitatively inherited factors influencing kernel weight.

Hakansson (1953) reported on endosperm development in 2x X 4x barley crosses and the reciprocal crosses. In the 2x X 4x crosses endosperm mitotic irregularities were common, especially the formation of giant endosperm nuclei. Small amounts of starch were deposited very late in development. In the reciprocal crosses, 4x X 2x, mitotic irregularities were rare and starch deposition began early. Brink and Cooper (1947) reviewed many studies similar to the one of Hakansson's. This review covered many species crosses and demonstrated

results similar to Hakansson's study. They indicated that the high chromosome number female X low chromosome number male crosses were more nearly in balance, with respect to ploidy level, between the endosperm, the embryo, and the maternal tissue, than were the reciprocal crosses. The high chromosome number female X low chromosome number male crosses generally resulted in fewer and plumper seeds than the reciprocals. The reciprocal seeds were badly shriveled and germinated poorly. The seed produced from the crosses between different ploidy levels and/or between species was generally smaller than normal. Ramage and Day (1960) reported that the frequency of trisomics produced from translocation heterozygotes is higher in the lighter seed portion. They pointed out that the frequency of the trisomics could be increased by the use of an aspirator or seed blower to separate the lighter seed.

The post fertilization period of 15 hours of barley was described by Pope (1937). The first endosperm division was within 6 hours after pollination and at 15 hours there were eight endosperm cells. Randolph (1936) followed the endosperm development in maize. At 3 days there were free endosperm nuclei with a definite tendency for the divisions to occur in unison. This tendency continued even after the endosperm was almost completely cellular. At first cell division activity was prevalent throughout the endosperm and later became localized in the

perpheral regions.

Clark and Copeland (1940) and Duncan and Ross (1950) used similar and quite simple techniques for fixing and preparing smear preparations of the dividing endosperm cells of maize. The fixing was accomplished with 3 parts 100% ethanol : 1 part acetic acid. The endosperm was smeared in a small drop of aceto-carmin and heated after the cover slip was in place. Clark and Copeland used the above method for studying abnormal endosperm division which gave rise to high rates of mosaic formations. Punnett (1953), using similar methods for fixing and staining, observed hexaploid endosperm cells in maize. It was postulated that these  $6N=60$  cells arose from two duplications during interphase followed by a single normal mitosis.

## DESCRIPTION OF MUTANT LINES

### Materials and Methods

The mutants involved in this study are characterized by a "thin" or "shrunken endosperm" phenotype. These mutants are designated as shrunken endosperm mutants and have been given the gene symbol "se".<sup>1</sup> All are natural occurring mutants in spring barley cultivars, Hordeum vulgare L. The mutants include 'Betzes' se and se2; 'Compana' se3, se4, and se6; and 'Sermo' x 'Glacier'<sup>7</sup> se5 which were collected and seed provided for this study by R. F. Eslick. A possible shrunken endosperm mutant in Betzes (se-x) was collected by the author.

### Results and Discussion

General Comments. All of the numbered mutants are fairly easy to classify compared to the normal phenotypes. Comparisons of all mutant types, Betzes and Compana are presented in Table I. The mutants se, se2, se3 and se6 have normal fertility whereas se4 and se5 have significantly lower levels of fertility (Table I). Considerable variation exists in seed weight (Table I) and sieve size distribution (Figures 1, 2 and 3) among the various lines. When se, se2, se3, se4 and se5 were used as females, the F<sub>1</sub> seed (hybrid seed) was shrunken, but when these lines were used as a pollen source in crosses with normal types, the F<sub>1</sub> seed was normal. The F<sub>1</sub> plants and F<sub>2</sub> seed (seed produced on a F<sub>1</sub>

---

<sup>1</sup>Correspondence with T. Tsachiya, Colorado State University, Fort Collins, Colorado. Dates January 26, 1970.

plant) from the above crosses were of the normal phenotype and did not express xenia. The mutant se6 expresses xenia for the endosperm trait. F1 seed from crosses using se6 either as a male or female with normal types does not express the shrunken characteristic. F2 seed segregation of 375 normal seeds : 143 shrunken fit a 3 : 1 ratio at a probability of .10 - .25. This segregation was obtained from heads of se6 x normal F1 plants expressing xenia. Plant segregations of the numbered mutants except se5 fit the hypothesis that each mutant is a single recessive gene (Table III). The hypothesis that se5 is a single recessive gene was rejected by the plant segregation reported in Table III, however, supported by the good fit to the independent Chi-squares with the unlinked translocations as tabulated in Table X.

Betzes se. Betzes shrunken endosperm-1 (se) was collected from a seed increase field at Aberdeen, Idaho in 1958. Fair stands of this mutant can be obtained under field conditions, but poor stands result from adverse conditions during emergence.

Betzes se2. Betzes shrunken endosperm-2 (se2) was collected from a commercial field of Betzes near Bozeman, Montana in 1965 as a shrunken endosperm mutant. The homozygous line has never produced a plant under field conditions. Plants can be obtained from the shrunken seeds by germinating the seed on blotters with a 10% sucrose solution. About 25% of the seeds germinated produce plants after transplanting the

seedlings to soil when the coleoptile has reached an inch in length. There is little or no starch deposited in the seed that develops on a homozygous mutant plant. Due to poor germination no F<sub>1</sub> plants were obtained from the hybrid seed produced when se2 was used as the female.

Compana se3. Compana shrunken endosperm-3 (se3) was collected from a commercial field of Compana near Bozeman, Montana in 1963 as a possible male sterile. The mutant se3 is phenotypically quite similar to Betzes se. Generally good stands of this mutant can be obtained under field conditions.

Compana se4. Compana shrunken endosperm-4 (se4) was collected from a commercial field of Compana near Bozeman, Montana in 1960 as a possible male sterile. It has a mean seed set of 51.2% which is significantly less than Compana (Table I). The sterile florets appear to start seed development but abort before they reach half the length of the lemma. The mutant se4 can be grown under field conditions but poor stands are obtained when less than optimum conditions prevail during germination and emergence.

Sermo X Glacier<sup>7</sup> se5. Sermo X Glacier<sup>7</sup> shrunken endosperm-5 (se5) was obtained from one of the backcross breeding programs at Bozeman, Montana in 1965. The mutant se5 has a reduced level of fertility with a mean seed set of 16.9% which is significantly less

than all of the other lines examined (Table I). Sieve size distribution of se5 and Glacier are compared in Figure 3 which indicates that se5 has a higher proportion of thinner seeds and a greater range in size than Glacier. It is difficult to classify se5 compared to normal types on seed size alone. The caryopsis of se5 generally extends beyond the lemma and palea more than the normal types. With the difference in caryopsis length and the high degree of female sterility it is possible to classify this mutant.

Compana se6. Compana shrunken endosperm-6 (se6) was collected from a commercial field of Compana near Bozeman, Montana in 1963 as a possible unicum mutant. Compana se6 will grow equally as well as Compana under field conditions. No differences can be detected between se6 and Compana in development until the hard dough stage. At this stage; se6 develops a depression in the center of the lemma which becomes progressively more distinct with maturity. The mature endosperm of se6 appears much harder than Compana when cut with a knife but no qualitative tests were made. Segregation ratios can be separated into three classes due to the expression of xenia in the heterozygous plants (Table III).

Betzes se-x. Betzes shrunken endosperm-x (se-x) was collected as a shrunken mutant in 1969 at Tucson, Arizona. The original plant appeared to be similar to se. This line was planted at Bozeman in

1969 and did not appear to be a classifiable mutant. It was similar to Betzes in fertility and seed weight (Table I) and in-sieve size distribution (Figure 1). The F<sub>1</sub> seed, F<sub>1</sub> plants, and F<sub>2</sub> seed from crosses involving se-x did not appear to be abnormal in any way. This may be an example of material which must be screened to find heritable mutants or may be an environmentally sensitive mutant and possibly could be classified under a different environment.

TABLE I. Physical data on mutant lines.

Variety	Gene symbol assigned	Previous symbol	fertility <sup>1/</sup>	100 seed weight <sup>1/</sup>	Seed size distribution	
					on 6/64 sieve	thru 5/64 sieve
			%	gms	%	%
Betzes	---	---	98.1a	4.06bc	71	1
Betzes	<u>se</u>	<u>th1</u>	96.7a	1.34f	0	98
Betzes	<u>se2</u>	<u>th2</u>	96.8a	0.60g	0	100
Betzes	<u>se-x</u>	<u>th-x</u>	96.6a	3.82c	56	5
Compana	---	---	94.2a	5.68a	94	1
Compana	<u>se3</u>	<u>th7</u>	95.0a	1.88e	0	94
Compana	<u>se4</u>	<u>th6</u>	51.2b	2.13e	2	61
Compana	<u>se6</u>	<u>th5</u>	95.0a	4.26b	26	3
Sermo X	<u>se5</u>	<u>th8</u>	16.9c	2.64d	36	17
Glacier <sup>7</sup>						

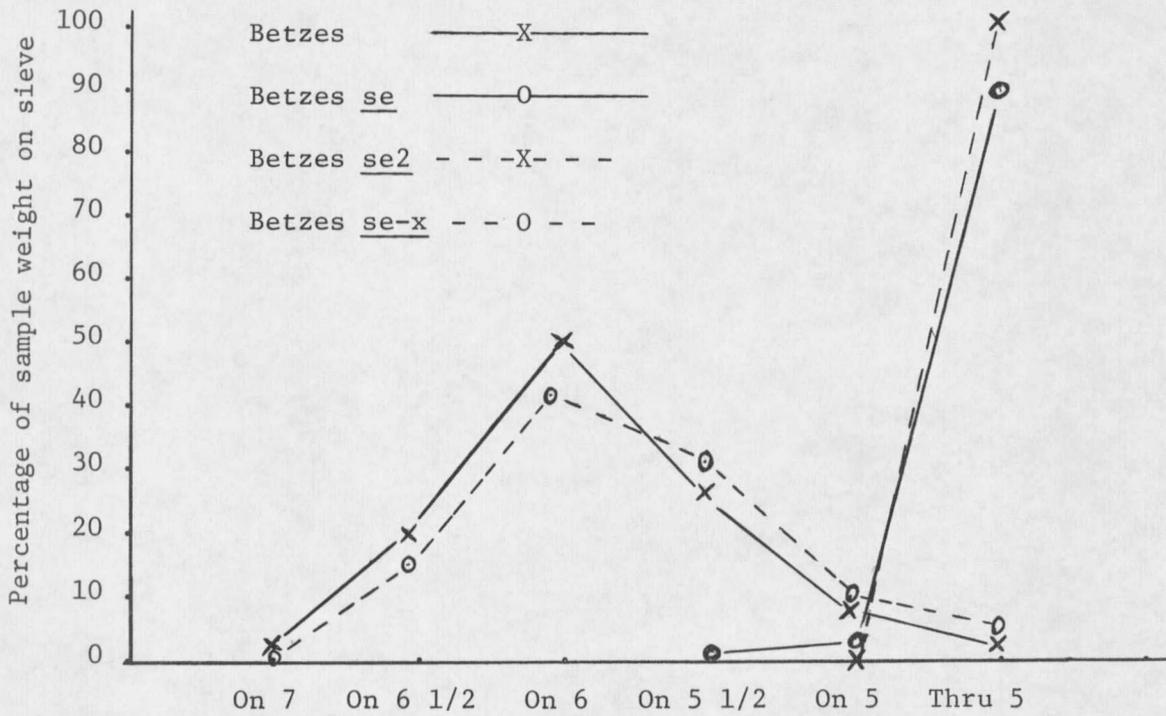
<sup>1/</sup> Means with like letters are not significantly different from each other at the 1% probability level.

-13-

TABLE II. ANOVA for weight/100 seeds and fertility.

Source	DF	Mean Squares	
		Weight/100 seeds	Fertility
Lines	8	62.11**	4132.14**
Error	36	0.08	8.69
Total	44		

\*\* Significant at the 1% probability level.



3/4 inch slotted sieve size width in 64th's of an inch

Figure 1. Sieve size distribution of Betzes and Betzes shrunken endosperm mutants.













































































































