## CONCLUSIONS

M-6/4 had significantly higher values of GCA for plant height and leaf number than the other lines.

Additive and nonadditive component were equally important in the inheritance of plant height. In the inheritance of leaf number, the latter component, including dominance and epistasis, was more important.

The analysis of the components of genetic variance and regression analysis (VrWr and WrW') indicated the presence of superdominance in the inheritance of plant height and leaf number.

Dominant genes (u) were more frequent than the recessive (v) for plant height. The picture was reverse for leaf number. Accordingly, the value of $K_D/K_R$ for plant height was larger than one, for leaf number smaller than one.

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T1982GEN12

# INHERITANCE OF TRICHOME CHARACTERISTICS IN SUNFLOWER, *HELIANTHUS*, SPP.


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## ABSTRACT

**Trichome characteristics of length, density, stiffness, and coarseness of *Helianthus annuus* L., cultivar HA 89, *H. argophyllus* Torrey and Grey, a wild species, and their $F_1$, $F_2$, and backcrossed progenies were examined using laboratory and field methods of evalution.**

**The date obtained using the laboratory method of evaluation showed an $F_2$ segregation ratio of 1:2:1, short:medium:long, for stem trichome length and 3:1, sparse:dense, for trichome density. The data obtained using the field method of evaluation showed an $F_2$ segregation ratio of 3:1 for trichome length (short:long) and trichome stiffness (erect:appressed), a 9:7 segregation ratio for trichome coarseness (coarse:fine), and a 15:1 segregation ratio for trichome density (sparse:dense). These data indicate that trichome characteristics are simply inherited and controlled by one or two genes, and that additive genetic variance accounted for a major portion of the genetic variation for these traits.**

**The laboratory method provided more defined data; however, these data agreed sufficiently with those of the field. Therefore, the latter method could be used to select lines with desirable trichome characteristics in a breeding program. The presence of additive genetic variance indicates that selection could be made with relative ease.**


## INTRODUCTION

Investigation on the genetics of pubescence has been initiated by many scientists on different crops (Maxwell and Jennings, 1980; Painter, 1951; Sprange and Dahms, 1972; Webster, 1975). Leisle (1974) has found that pubescence in durum wheat (*Triticum turgidum* L.) is controlled by three genes, and these genes may be acting in an additive manner to determine length of trichomes. Since this character is relatively simply interherited, Leisle contends that a backcross program can be used to transfer this characteristic to commercial cultivars.

Ringlund and Everson (1968) indicated that in wheat the pubescent character is quantitatively inherited with gene action primarily additive. They also indicated that pubescent density is partially dominant with heritability approximately 50%. Bernard and Weiss (1973) reported that seven genes have been identified that control different trichome characteristics in soybean (*Glycine max* L.). These characteristics were reported to be simply inherited and controlled by either one or two genes. These reports indicate that the pubescent characteristics, independent of crop species, are simply inherited and relatively easily transferred.

## MATERIALS AND METHODS

Interspecific hybridization of *H. annuus* L. cultivar HA 89, a cultivated inbred sunflower line was made with a number of plants from a population of *H. argophyllus.* Later, backcrosses of the $F_1$ to both parents were also made.

Seeds of HA 89, $F_1$, $F_2$, and backcrosses to both parents were planted at Fargo, ND at a depth of approximately 20 mm in 1.6 m rows spaced 0.9 m apart with approximately 30 cm between plants within rows. The plants of the *H. argophyllus* parent were transplanted from the greenhouse into the field at the fifth true leaf stage.

Stem and leaf samples were collected when the ray flowers on the main head developed yellow petals. Two thin sections of the epidermal layer of the stem, each approximately

10 mm by 20 mm by 1 mm were collected from the section of the plant immediately below the head (Section I) and from the lower one-half section of the plant (Section II). Leaf disc samples, approximately 8 mm in diameter, were collected from the top leaf and from leaves that were closest to the central section of the plant.

These samples were placed in 20 ml liquid scintillation vials containing approximately 10 ml of 50% ETOH. The scintillation vials containing the stem and leaf samples were refrigerated at approximately 5°C until the samples were evaluated for trichome characteristics.

Estimates of trichome length and density were obtained from samples collected from sections I and II of the plant, respectively. The samples were removed from the ETOH, blotted to remove the excess liquid, and placed between two microscope slides. Photomicrographs of the stem and leaf samples were taken at settings of 25 and 50X with a steromicroscope, adapted with a 35 mm camera body. The negative film was cut, placed in 35 mm plastic slide mounts, and projected on a viewing table. The projections were enlarged 10 times. Measurements of trichome length were made directly from the projected image on the viewing table. Density determinations were made by counting the number of trichomes projected on the viewing table in a 50 $mm^2$ area.

Estimates of trichome length and density of the parents and progenies were also obtained by visual examination in the field. Obvious differences of trichome length, density, stiffness (erect or appressed), and coarseness (relative thickness of trichome) among individuals of the $F_2$ generation were recorded.

The *H. annuus* L. cultivar HA 89 trichome characteristics, short, sparse, erect, and coarse, contrasted with those of *H. argophyllus*, long, dense, appressed, and fine. Also associated with the *H. argophyllus* agronomic characteristics were anthocyanic pigmentation, slow growth habit, and darker green coloration of the leaves. All of the above characteristics were considered in classifying individuals of the $F_2$ generation into one of two classes which resembled the general characteristics of either one of the parents.

## RESULTS

### Laboratory Evaluation of Trichome Characteristics.

Heritability estimates were determined by using the variances of all of the parents and progenies. Broad sense heritability estimates for stem trichome length of 56% was lower than the narrow sense heritability estimate of 69%. The data of the $F_2$ generation for stem trichome characteristics were observed to fall into three classes (Table 1). Stem trichome length ranged from 2.2 to 3.6 mm with a mean of 2.6 mm for class 1 (TsTs), from 3.7 to 5.3 mm with a mean of 4.5 mm for class 2 (Tsts), and from 6.1 to 6.9 mm with a mean of 6.5 mm for class 3 (tsts). The observed segregation ratio was tested for goodness of fit to a 1:2:1, short:medium: long, ratio using the Chi-square analysis. The observed segregation ratio fit the expected ratio ($0.25 < P < 0.50$).

**Table 1. Chi-square analysis of goodness of fit of various genetic ratios of segregation for stem and leaf trichome characteristics observed in the $F_2$ generation resulting from the interspecific hybridization of *H. annuus* cultivar HA 89 and *H. argophyllus*.**

| Trichome Loc. | Sampled Section | Trichome Characteristic Range | Mean Length | Number of Plants Genotype† TsTs | Tsts | tsts | Test Ratio | n | $x^2$ | P Value |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Length (mm) | | | | | | | | |
| Stem | I | 2.2 — 6.9 | 4.4 | 29 | 61 | 38 | 1:2:1 | 128 | 1.55 | $(0.25 < P < 0.50)$ |
| Leaf — Adaxial | I | 0.6 — 13.1 | 7.6 | 112 | | 16 | 3:1 | 128 | 2.00 | $(0.10 < P < 0.25)$ |
| Leaf — Abaxial | I | 0.5 — 3.5 | 1.2 | 105 | | 26 | 3:1 | 131 | 1.91 | $(0.10 < P < 0.25)$ |
| | | Density (no./5 $mm^2$) | | Density Td— | | tdtd | | | | |
| Stem | II | 2.0 — 24.0 | 6.9 | 105 | | 26 | 3:1 | 131 | 1.85 | $(0.10 < P < 0.25)$ |
| Leaf — Adaxial | II | 2.2 — 14.2 | 5.1 | 90 | | 40 | 3:1 | 130 | 2.31 | $(0.10 < P < 0.25)$ |
| Leaf — Abaxial | II | 3.0 — 19.8 | 7.9 | 94 | | 37 | 3:1 | 131 | 0.74 | $(1.25 < P < 0.50)$ |

† Trichome characteristic genotype: TsTs = short, Tsts = medium, tsts = long; Td— = sparse, tdtd = dense.

The broad sense heritability estimate of 28% for trichome length of the adaxial side of the leaf was lower than the narrow sense heritability estimate of 74%. Two classes were observed for the trichome length on the adaxial side of the leaf. The leaf trichome length for class I ranged from 2.7 to 13.1 mm with a mean of 5.6 mm. The observed $F_2$ ratio was tested for goodness of fit to a 3:1, short:long, ratio. The observed data fit the expected ratio ($0.10 < P < 0.25$).

The broad sense heritability estimate of 16% for trichome length of the abaxial side of the leaf was lower than the narrow sense heritability estimate of 71%. The $F_2$ data for trichome length of the abaxial side of the leaf fell into two classes. The leaf trichome length for class 1 ranged from 0.5 to 1.2 mm with a mean of 0.6 mm and in class 2, the length ranged from 1.2 to 3.5 mm with a mean of 2.1 mm. The Chi-square analysis showed that the expected segregation ratio of 3:1, short:long, ($0.10 < P < 0.25$) fit the observed data.

The broad sense heritability estimate for stem trichome density of 41% was lower than the narrow sense heritability estimate of 66%. The stem trichome density for class 1 ranged from 2.0 to 12.6 with a mean of 5.1 and that for class 2 ranged from 16.0 to 24.0 with a mean of 19.8 trichomes per 5 $mm^2$. The Chi-square analysis showed that the expected segregation ratio of 3:1, sparse:dense, ($0.10 < P < 0.25$) fit the observed data.

The broad sense heritability estimate for trichome density of the adaxial side of the leaf of 42% was lower than the narrow sense heritability estimates of 85%. The $F_2$ data for trichome density of the adaxial side of the leaf fit an expected segregation ratio of 3:1, sparse:dense, ($0.10 < P < 0.25$). Trichome density for class 1 ranged from 2.2 to 10.6 with a mean of 6.3 and that for class 2 ranged from 11.3 to 14.2 with a mean of 9.2 trichomes per 5 $mm^2$.

The broad sense heritability estimate of 38% for trichome density of the abaxial side of the leaf was lower than the narrow sense heritability estimate of 88%. The $F_2$ data for trichome density fit an expected segregation ratio of 3:1, sparse:dense, ($0.25 < P < 0.50$). Trichome density for class 1 ranged from 3.0 to 9.9 with a mean of 6.3 trichomes per 5 $mm^2$ and that for class 2 ranged from 11.6 to 19.8 with a mean of 12.3.

### Field evaluation of trichome characteristics.

Data for leaf and stem trichome length, density, stiffness, and coarseness were gathered from the $F_2$ progeny and are shown in Table 2. These data for each of the trichome characteristics were grouped into two classes and were tested using the Chi-square analysis for goodness of fit to a specified segregation ratio. The observed data for trichome length fit the expected segregation ratio of 3:1, short:long, ($0.10 < P < 0.25$). The data for trichome density fit the expected 15:1, sparse:dense, segregation ratio.

**Table 2. Chi-square tests for goodness of fit of various genetic ratios to segregation data for trichome characteristic observed in the $F_2$ generation resulting from the hybridization of *H. annuus* cultivar HA 89 and *H. argophyllus*.**

| Trichome Characteristic | Number of Plants | | Test Ratio | n | $x^2$ | P Value |
|---|---|---|---|---|---|---|
| | Trichome† Genotype | | | | | |
| | Ts— | tsts | | | | |
| Length | 90 | 39 | 3:1 | 129 | 1.88 | $(0.10 < P < 0.25)$ |
| | $Td_1$— | $td_1td_1$ | | | | |
| | $Td_2$— | $td_2td_2$ | | | | |
| Density | 121 | 11 | 15:1 | 121 | 0.70 | $(0.25 < P < 0.50)$ |
| | Te— | tete | | | | |
| Stiffness | 92 | 38 | 3:1 | 130 | 1.24 | $(0.25 < P < 0.50)$ |
| | $Tc_1$— | $Tc_1$— | | | | |
| | $Tc_2$— | $tc_2tc_2$ | | | | |
| Coarseness | 80 | 49 | 9:7 | 129 | 1.74 | $(0.10 < P < 0.25)$ |
| | HA 89 | *H. argophyllus* | | | | |
| Combined Parental Characteristic | 122 | 8 | 15:1 | 130 | 0.002 | $(0.90 < P < 0.95)$ |

† Trichome genotype characteristic: Ts— = short, tsts = long; Td— = sparse; tdtd = dense; Te— = erect; tete = appressed; tc— = coarse; tctc = fine.

When the short, sparse, erect, and coarse trichome characteristics of HA 89, and the long, dense, appressed, and fine trichome characteristics of *H. argophyllus* were compared in association with other agronomic characteristics such as anthocyanic pigmentation, growth habit, and green coloration of the leaves, the data again were divided into two classes as shown in Table 2. These observed data fit the expected 15:1, HA 89 plant type: *H. argophyllus* plant type, segregation ratio.

## DISCUSSION

The results of the Chi-square analysis for stem trichome length shown in Table 1 show that these observed data fit the 1:2:1, short:medium:long, hypothetical segregation ratio indicating that the stem trichome length characteristic is controlled by a single gene, Ts, with incomplete dominance for short length or several genes acting additively. The results of the segregation ratio of 3:1, short:long, observed for leaf trichome length suggest that this characteristic is controlled by a single dominant gene, short length being dominant.

Assuming similar genes control trichome length for both the stem and leaf, the observed differences of incomplete dominant and complete dominant gene action, respectively, may have been due to three related factors.

1. In general, the means for the leaf trichome length were observed to be shorter than that for the stem, although the means of the trichome length of the adaxial side of the leaf may be comparable to those of the stem. Because the leaf trichome length was shorter than that of the stem, it was more difficult for classification to be made, especially for the minute differences observed. More sensitive measuring methods should be designed and employed for further studies.
2. The variation of the trichome length of both the stem and leaf was observed to be continuous which indicates that multiple genetic factors may be involved in the control of trichome length. This continuous variation, particularly at the shorter spectrum, also made classification difficult.
3. The observed difference in the genetics of the trichome length characteristic may also be caused by the variability of the characteristic that is present in the parental cultivars that were used in this study. Laboratory examination of the trichome length of *Helianthus annuus* cultivar HA 89 and *H. argophyllus* revealed that a high degree of variability exists among these presumably homogeneous cultivars. HA 89 used as the parental cultivar with the short trichome characteristic, was observed to be less variable than the *H. argophyllus* parental cultivar which possessed the long trichome characteristic. This variability among the wild *H. argophyllus* cultivars seems to emanate from its past where outcrossing may have occurred with other sunflower cultivars possessing shorter trichomes. This mixture of varying characteristics of the trichome was present on the stem as well as on the leaf.

Trichome length of the stem and leaf was observed to be highly heritable. This indicates that selection progress for trichome length can be made relatively easily.

The results of the Chi-square analysis for trichome density shown in Table 1 show that these observed data fit the 3:1, sparse:dense, hypothetical segregation ratio indicating that trichome density may be controlled by a single gene, *Td*, or several genes acting additively. These data indicate that the dense or high number of trichomes per unit area characteristic is recessive.

Similar procedures were followed to estimate the genetic factors involved in the control of leaf trichome density. The results were similar to those observed for stem density (Table 1) indicating that this trichome characteristic may be controlled by similar genetic factors.

The relative degrees of variance indicate that the HA 89 cultivar was less variable than the *H. argophyllus* cultivar. The heritability estimates calculated by using the variances of the parents and progenies indicate a high degree of heritability which would presumably facilitate the selection of this character in a breeding program.

Some of the data obtained using field estimates from the $F_2$ progeny segregates were not in agreement with the data obtained in the laboratory. The apparent lack of agreement of some of these data relates to the difficulty in the classification of these traits. The field method of evaluation is seemingly less precise than the laboratory method; however, it does provide a rapid means by which selection could be made.

The results of the field evaluation on trichome length, density, stiffness, and coarsness are shown in Table 2. Stem and leaf trichome characteristics were combined and evaluated as one, since finite differences could not be readily distinguished.

There seems to be an agreement between the data of field and laboratory methods of evaluation as to the number of genes that control trichome length; however, these data do not agree completely. The field data show a segregation ratio of 3:1, short:long, (Table 2) as compared to a segregation ratio of 1:2:1, short:medium:long, for that of the laboratory. This discrepancy is the result of the inability to classify trichome length in finite detail using the field method of evaluation.

Trichome density, as evaluated in the field, seems to be controlled by at least two genes. This is in contrast to the data obtained using the laboratory method of evaluation finding that trichome density was controlled by one gene. This discrepancy between the two methods may be the result of the observation of a combination of trichome characteristics such as stiffness and coarseness which would result in a digenic segregation ratio. This digenic ratio, however, agrees with that of the density characteristics of the soybean, *Glycine max* L. Merrill, where a dominant gene, *Pd*, causes dense pubescence and another dominant gene, *Ps*, causes sparse pubescence

(Bernard and Weiss, 1973).

The characteristic for trichome stiffness was not evaluated in the laboratory; however, data obtained from the field evaluation suggest that this character is also simply inherited (Table 2). These data suggest a one gene factor; however, this is difficult to confirm since the field method is, at best, a cursory estimate.

The character for trichome coarseness was also not evaluated in the laboratory. Data obtained from the field evaluation suggest that this character is controlled at least by two genes (Table 2).

The observed $F_2$ segregation ratio of 15:1, HA 89 plant type: *H. argophyllus* plant type, of the combined phenotypic characteristics of trichome length, density, stiffness, coarseness as well as other agronomic characteristics mentioned previously may be an extension of the results obtained for trichome density (Table 2). The observed results indicate a digenic control of the *H. argophyllus* parental characteristics which seem to be recessive to the HA 89 parental trichome characteristics of short, sparse, erect, and coarse as well as nonanthocyanic stems and leaves, relatively rapid growth habit, and a light green coloration of the leaves. These results may also suggest linkage of some of these genes that control the various characteristics observed in this study; however, no analysis was made to determine the presence of linkage.

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T1982GEN13

# GENETIC IMPLICATIONS IN TRANSFERRING FERTILITY RESTORER GENES TO A NEW GENETIC BACKGROUND IN SUNFLOWER *(HELIANTHUS ANNUUS* L.*)*.

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## ABSTRACT

**The second generation progeny consisting of seven surviving plants of the cross between the male sterile hybrid, 2 cm 183 x E.C.68415 and the restorer line, BCZ.111 presented two types of segregation for the pollen fertile and sterile plants. Four of them gave a 3:1 ratio for the fertile and sterile fractions while the remaining three progenies fitted into a 9:7 ratio, thus suggesting two genotypes in the $F_1$ plants from the point of fertility restoration. The implications underlying this type of inheritance have been discussed and the genetic symbols of $rf_1rf_1rf_2rf_2$, $Rf_1Rf_1rf_2rf_2$ or $rf_1rf_1Rf_2Rf_2$ and $Rf_1Rf_1Rf_2Rf_2$ have been suggested for the parents 2 cm 183, E.C.68415 and BCZ.111 respectively.**

## INTRODUCTION

Sunflower has been introduced as an oilseed crop into India recently for filling the vegetable oil gap. The Russian cultivars, bearing the accession numbers, E.C.68413, E.C.68414, E.C.68415 and E.C.69874, given out for general cultivation did not make much headway because of poor yield coupled with high percentage of empty seed. During the past few years reports on the possibility of exploiting heterosis by utilising the cytoplasmic male sterility have opened new lines of work in this crop (Gundaev, 1967; Vranceanu *et al.,* 1973). The cytoplasmic male sterile line, 2 cm 183, its maintainer and the fertility restorer line, BCZ.111 were kindly made available by the French Sunflower Breeder, DR. P. Leclercq, in 1973. The restorer line was weak, stunted and was found to be unsuitable for the commercial hybrid seed production. The inheritance of fertility restoration has been investigated (Reddy and Thammi Raju, 1977) and the restorer genes have been transferred over a new genetic background of the male sterile hybrid, 2 cm 183 x E.C.68415 (Reddy *et al.,* 1976). The genetic implications underlying the transfer of restorer genes over the said genetic background are discussed in this paper.

## MATERIALS AND METHODS

The male sterile hybrid of the cross between the cytoplasmic male sterile line, 2 cm 183 and the popular cultivated variety of Russian origin, E.C.68415 was chosen for transferring the restorer genes from BCZ.111. The progeny of the three-way cross, (2 cm 183 x E.C.68415) x BCZ.111, consisted of seven surviving plants and all of them were pollen fertile, as expected. The flower heads of these plants were selfed and seeds were collected separately from each of the selfed heads. The $F_2$ generation of these seven plants was grown in two sets for want of space; the first set during October-December, 1975 and the second during February-April, 1976. the progenies were assigned the numbers $P_1$ to $P_7$. The fertile and the sterile plants were identified in the segregating progenies based on the presence or absence of pollen in the anther sacs and also its stainability in the 1% $I_2$-KI solution. The pollen fertile plants were expected to possess the restorer genes as all of them contained sterile cytoplasm of the male sterile parent, 2 cm 183.