

# Inheritance Of Shape And Kernel Color In Sweet Corn Using JM2 And JM4 Populations

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## Abstract

Corn kernel is one of the most important characters that correlate with corn yield and quality. Sweet corn kernels can be distinguished by its color which is either yellow and white or pale yellow. Sweet corn breeding by crossing genotypes with different kernel colors will affect the inheritance pattern of kernel color. The aims of this research were to understand the inheritance pattern in sweet corn kernel color by crossing yellow and pale yellow color with red and purple corn kernels using qualitative and quantitative approaches. Genetic materials consisted of P1 (JM2 and JM4) and P2 (Red and Purple) and F1, F2, F3, and F1 reciprocals. P1 consists of JM2 and JM4 with flint shape with yellow and pale yellow color; P2 consists of Red and purple with non-yellow colored kernel and flint shape. The results showed maternal effect influenced the kernel color, but did not affect the kernel shape. Epistatic effects were found in kernel shape but it was co-dominant on kernel color inheritance. Broad-sense heritability values were high for all quantitative variables.

Keywords : color, heritability, pale yellow, purple, red, shape

## Introduction

Inheritance is one of the most important aspects in plant breeding; it determines gene action, inheritance patterns, and heritability values, and this information can be used in the process of breeding for both self and cross-pollinated crops. In addition, information about the direction of formation of varieties such as hybrids or open pollinated or synthetic varieties can also be used (Tracy, 2002).

The phenotype of an organism is determined not only by the environment it experiences and its genotype, but also by the environment and genotype of its

mother. The female gamete provides the cytoplasm for the developing embryo. There are factors that were released by the nuclear genes of the female and those factors may have specific effects upon the developing embryo. The phenotypes that are controlled by nuclear factors found in the cytoplasm of the female are said to have a maternal effect. The phenotypes that are controlled by organelle genes exhibit maternal inheritance.

Pattern of inheritance in sweet corn includes yield and agronomic characters. The yield of sweet corn is a quantitative character, whereas kernel shape and seed color are qualitative characters. Qualitative characters in sweet corn include seed shape and seed color (Haggard et al., 2018). The seed shape in sweet corn affects the weight of cobs and yield per plant at harvest. Corn seed shape can be divided into two categories, wrinkly and flint.

There are four corn kernel colors; yellow, red, purple and white (Figure 1). Yellow, red and purple color are produced by pigments synthesized from one of two metabolic pathways, the carotenoid or yellow pigments or the anthocyanin or red and purple pigment pathway. White kernel color results from the lack of pigments produced from either pathway (Ford, 2000). The synthesis of each pigment requires numerous genes (Ford, 2000).

Quantitative observation of the shape and color of kernel is a new perspective in the breeding of sweet corn. Quantitative observation of kernels includes kernel length, kernel width, kernel area, and kernel weight. These variables are observed to distinguish the shape of the kernel among observed genotypes. Quantitative color variables could be determined using several seed color models viz. RGB (Red, Green, and Blue), HSB (Hue, Saturation, Brightness), CMYK (Cyan, Magenta, Yellow, Key) (Liang et al., 2016). The color model can explain the coloring intensity, color brightness, and color accuracy (Liang et al., 2016).

The accuracy of the inheritance study can be improved using quantitative and qualitative approaches. The quantitative measurements of kernel shapes and colors can confirm the action of genes, number of genes, and other patterns of inheritance. This study was conducted to determine the genetic inheritance of kernel shape and color of the progenies from the crosses between red and purple flint using qualitative and quantitative approaches.

## Materials and Methods

The plant materials in this research consisted of a female parent (P1) JM4 and JM2 (yellow, white and wrinkly) and a male parent (P2) consisted of Red and Purple (non-yellow and flint) (Figure 1). This research was conducted at the Alam Sinar Sari experimental field, Dramaga, Bogor, Indonesia.

F1, F1R, F2, and F3 cobs were harvested when crops were physiologically mature, i.e. at 120 days after planting. The F1 planting materials consisted of 121 kernels (JM2 X Red), 112 kernels (JM2 X Purple), 210 kernels (JM4 X Red), and 114 kernels (JM4 X Purple). F2 consisted of 1250 kernels (JM2 X Red), 203 kernels (JM2 X Purple), 530 kernels (JM4 X Red), and 430 kernels (JM4 X Purple). F3 consisted of 1639 kernels (JM2 X Red), 2107 kernels (JM2 X Purple), 1576 kernels (JM4 X Red), and 1697 kernels (JM4 X Purple).

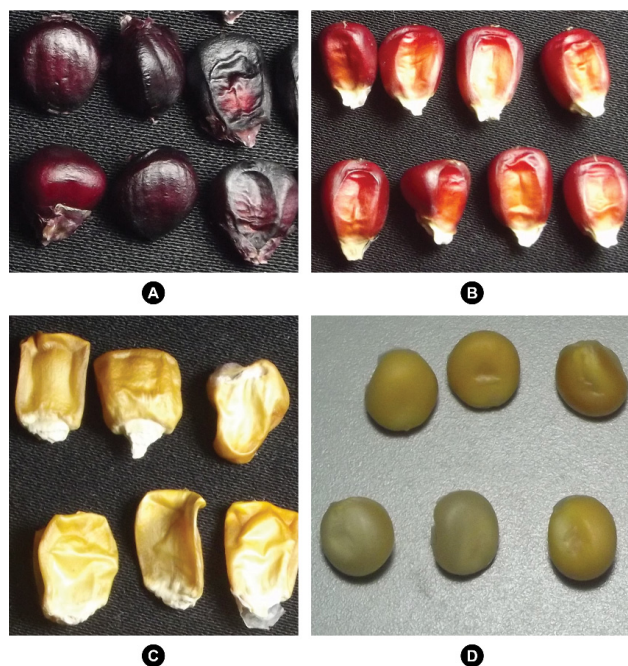


Figure 1. Parent corn kernels: purple (A), red (B), JM2 (C) and JM4 (D).

Qualitative observation was conducted using the

method employed by Harakotr et al. (2016) and Jha et al. (2016) by separating kernel shapes (wrinkly and flint) and kernels colors (yellow, red, purple and others colors). The quantitative variables of kernels consisted of areas, weights RGB, Red (R), Green (G), and Blue (B) (Miller et al. 2017). Tools were used for observation and scoring include a Fujifilm S2980 camera, mini studio, two 9-watt LED lamps, two photo frames, a ruler, an analytical balance, 18 gray-colored fabrics and a camera tripod assembled as a mini studio. Vertical distance of capture was 20 cm using a fix camera exposure (aperture 8.0, F 40 and ISO 100) and 30 x 30 cm field of view.

Chi-square analysis was used to analyze the qualitative characters of kernels shape and colors. Kernels shape used ratios of 3:1 and 11:5 as expected ratio of flint to wrinkly shape, whereas the color of kernels used ratios of 1:2:1 (yellow : bronze : red), 9:3:4 (purple: red: yellow), 12:3:1 (red: yellow: white) and 9:3:3:1 (purple: red: yellow: white). Maternal effects were recorded by visual observation on the shapes and colors of the kernels. Broad-sense heritability ( $h^2_{bs}$ ) was calculated using variance components of F1, P1, P2 and F2 populations. The quantitative analysis used R software with Agricolae package, and ImageJ to measure the area of kernel and RGB, R, G, B of kernel color (Liang et al., 2016).

## Result and Discussion

### Maternal Effects

Maternal effects were found in the kernel color inheritance pattern. Kernel color in JM2 X Red and JM2 X Purple genotypes showed the yellow color in the F1 while the F1R showed red and purple colors according to each crosses of each parent. The kernel color in JM4 X Red and JM4 X Purple had white color whereas the F1R had red and purple color according to the crosses of each parent. Maternal effects were caused by the genes in the cytoplasm, therefore the inheritance will be influenced by female parent (Ron-Parra et al., 2016). The maternal effect in kernel shape was not found, which shows the similarity in shape of the F1 and the F1R. This character is not affected by the maternal effect but by the epistasis effect of the *sh2* gene in the dominant condition of each parent. The dominant *sh2* gene comes from flint parents (Doodson, 2013; Philips and Evans, 2011).

### Qualitative Analysis

The chi-square test results showed that JM2 X Red and JM4 X Red had genetic proportions of 1: 2: 1 (red: gold: yellow) and 12: 3: 1 (red: yellow: white) (Figure

1). The observed ratio used for those populations were 397: 856: 386 (red: gold: yellow) and 1235: 322: 121 (red: yellow: white) (Table 1).

condition. *pr1* was controlled by the red and purple pigment in the aleuron layer (Ford, 2000). Gold color was formed by gene *c* in heterozygous conditions in the JM2 X Red population (Figure 2).

Table 1. Chi-square test of kernel color

Population	Observed kernel color ratio	Expected kernel color ratio	Gene segregation	X <sup>2</sup> value / P-value
JM2 X Red	397 : 856 : 386 (red : gold : yellow)	1:2:1 (red : gold : yellow)	<i>c</i>	3.40/0.18
JM2 X Purple	932 : 322 : 443 (purple : red :yellow)	9:3:4 (purple : red :yellow)	<i>pr1</i> and <i>c</i>	1.41/0.50
JM4 X Red	1235 : 322 : 121 (red : yellow :white)	12:3:1 (red : yellow :white)	<i>c</i> and <i>y1</i>	3.09/0.21
JM4 X Purple	1034 :322:335:128 (purple :red: yellow: white)	9 :3:3:1 (purple :red: yellow: white)	<i>pr1</i> , <i>c</i> and <i>y1</i>	3.09/0.38

Note: X<sup>2</sup> and P values of > 0.05 indicate that the observed ratio fits the expected ratio according to chi-square goodness of fit test

The chi-square test results showed that JM2 X Purple and JM4 X Purple had genetic proportions of 9: 3: 4 (purple: red: yellow) and 9: 3: 3: 1 (purple: red: yellow: white)

The purple color in the JM2 X Purple and JM4 X Purple population was formed due to the presence of the *c* gene in the dominant condition followed by the *pr1* gene in the dominant condition (Figure 3).

(Figure 3 and 4). The observed ratio of the populations were 932: 322: 443 (purple: red: yellow) and 1034: 322: 335: 128 (purple: red: yellow: white). The P-values of the population were not significantly different, indicating that the observed proportions correspond well to the expected proportions.

Yellow and white corn kernel color are expressed when gene *c* in homozygous recessive. Gen *c* in homozygous recessive must be followed by the *y1* gene in dominant for yellow color while homozygous recessive for white color. Gene *c* and *pr1* simultaneously controlled the formation of color in the aleurone (Ford 2000; Harakotr et al., 2014). Gene *c* in a recessive homozygous caused the color not to form in the aleurone layer so that the color of the endosperm was exposed. Yellow and white kernel colors are controlled by the *y1* gene (Figure 4).

Gene segregation in color inheritance patterns was found in the genes *pr1*, *c*, and *y1*. The red color was formed by gene *c* in a homozygous dominant condition followed by the *pr1* gene in a homozygous recessive

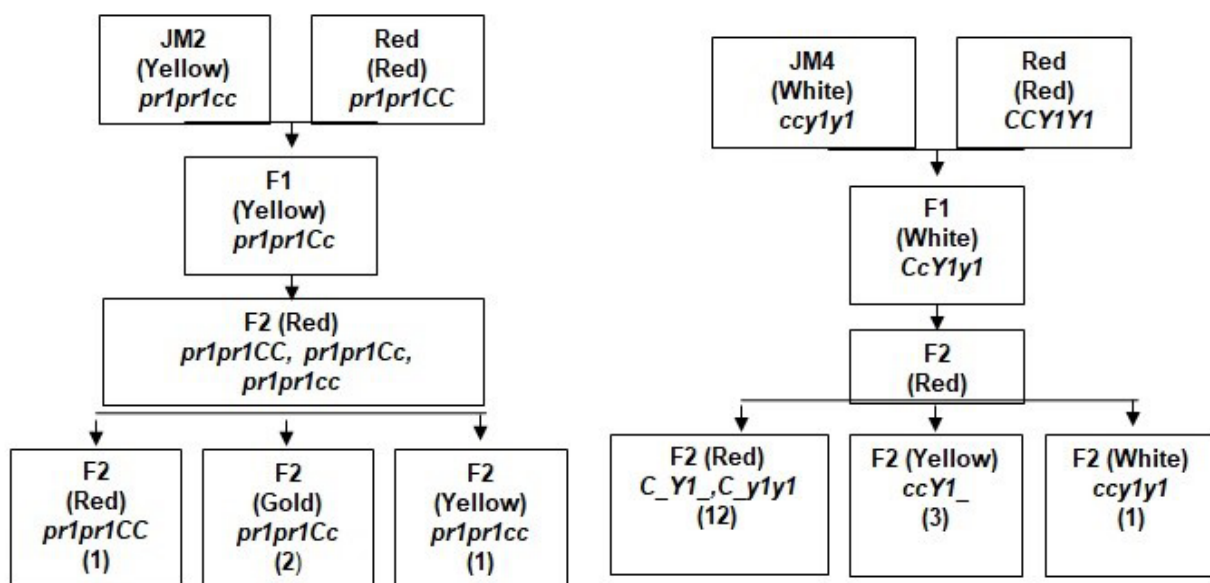


Figure 2. Inheritance scheme of kernel color of JM2 X Red and JM4 X Red

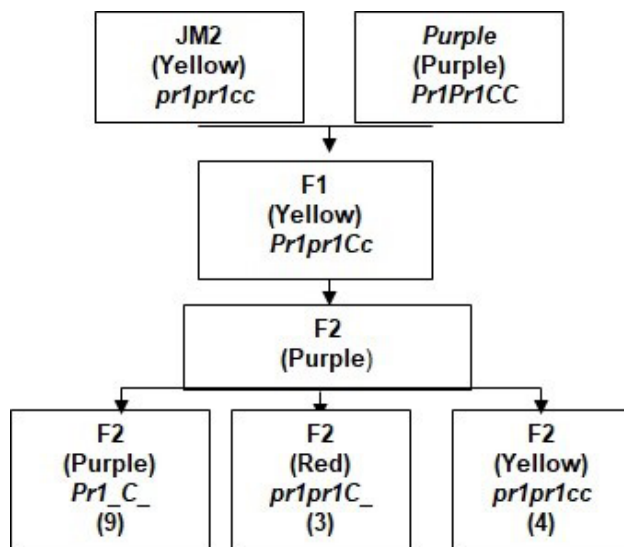


Figure 3. Inheritance scheme of kernel color of JM2 X Purple

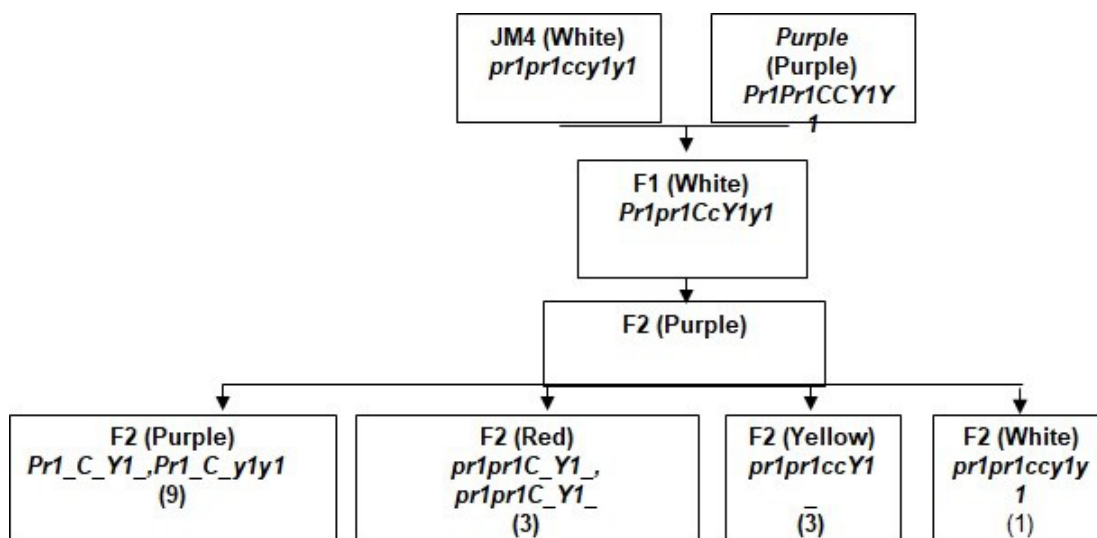


Figure 4. Inheritance scheme of kernel color of JM 4 X Purple

The results of the chi-square test in the kernel shape character showed that JM2 X Red and JM4 X Red had genetic proportion of flint to wrinkly of 13:3. The observed ratio used for those populations were 270: 84 (flint: wrinkly) and 420: 110 (flint: wrinkly). X<sup>2</sup> and P values indicated that the expected ratio used was in accordance with the observed ratio (Table 2).

The results of the chi-square test in kernel shape showed that JM2 X Purple and JM4 X Purple showed genetic proportion of 3: 1 (flint: wrinkles). The observed ratio used is 270: 84 (flint: wrinkly) and 344: 86 (flint: wrinkly). X<sup>2</sup> and P values indicated that the expected ratio used was in accordance with the observed ratio (Table 2).

Table 2. Chi-square test of corn kernel shape ratio

Population	Observed flint to wrinkly ratio	Expected flint to wrinkly ratio	Gene segregation	X <sup>2</sup> value / P value
JM2 X Red	1010 : 240	13 : 3	<i>sh2</i> and <i>su1</i>	3.95/0.20
JM2 X Purple	270 : 84	3 : 1	<i>sh2</i>	2.30/0.13
JM4 X Red	420 : 110	13 : 3	<i>sh2</i> and <i>su1</i>	5.24/0.08
JM4 X Purple	344 : 86	3 : 1	<i>sh2</i>	1.05/0.30

Note: X<sup>2</sup> and P values of > 0.05 indicate that the observed ratio fits the expected ratio according to chi-square goodness of fit test

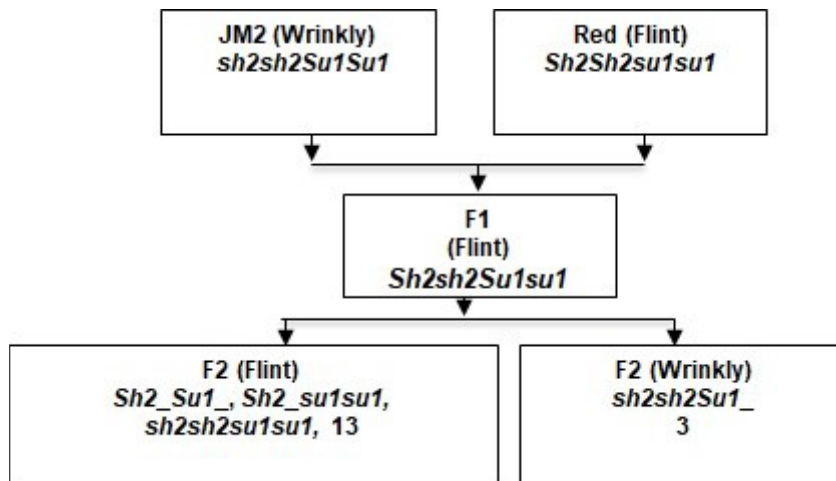


Figure 5. Inheritance scheme of kernel shape of JM2 X Red

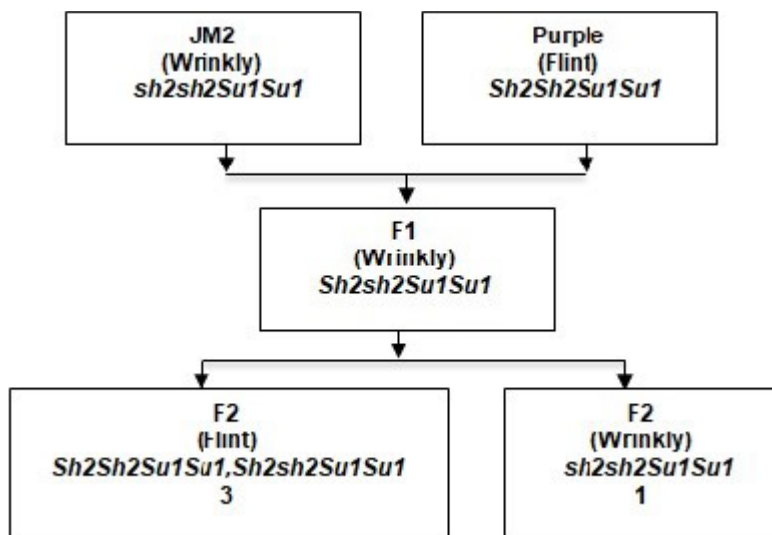


Figure 6. Inheritance scheme of kernel shape of JM2 X Purple

The *sh2* gene in a recessive homozygous condition caused a wrinkly kernel shape whereas the dominant condition caused flint shape (Tracy, 2001). The *su1* gene caused wrinkling in the homozygous recessive followed by the *sh2* gene in heterozygous conditions. The *sh2* and *su1* genes in recessive conditions caused a flint shape because of the antagonistic effects of the two classes of genes, as described in Figure 5 and 6.

#### Quantitative Analysis

High heritability values for all variables were showed for each population; the  $h^2$ s values of the RGB, R, G and B character for all populations were described in Table 3. The estimated values of the broad-sense heritability in RGB and R variables are  $68.88 \pm 7.07$  and  $65.33 \pm 7.20$ , whereas values for G and B are  $72.23 \pm 9.18$  and  $75.20 \pm 6.22$  (Table 3).

The heritability values are related to the comparison

of the genotypes and the environmental variability. High heritability values indicate that the quantitative variables of kernel color had a higher genetic effect compared to environmental effect in each population, which is related to the number of genes that control the color of kernels in each population. There are three genes that interacting in all population; therefore the value of genetic influence tends to be high. The best estimate of the broad-sense heritability value was RGB with a small diversity value amongst the observed populations.

The broad-sense heritability values in the kernel weight for JM2 X Red, JM2 X Purple, JM4 X Red, JM4 X Purple were 85.42, 63.05, 82.61 and 71.85, respectively, whereas kernel area variables were 85.39, 82.63, 63.06, and 71.86, respectively (Table 4). The estimated heritability values for weight and area of kernels characters were  $75.73 \pm 10.28$  and  $75.74 \pm 10.27$ , respectively (Table 4). The broad-sense heritability of all of these variables was in a

Table 3. Broad-sense heritability values of kernel color

Populations	RGB				R			
	$\sigma^2G$	$\sigma^2E$	$\sigma^2P$	$h^2bs$	$\sigma^2G$	$\sigma^2E$	$\sigma^2P$	$h^2bs$
JM2 X Red	303.24	209.10	512.34	59.19	319.61	204.06	523.67	61.03
JM2 X Purple	245.44	97.47	342.91	71.58	276.51	89.50	366.01	75.55
JM4 X Red	275.94	124.62	400.56	68.89	252.71	171.18	423.89	59.62
JM4 X Purple	260.64	82.92	343.56	75.86	220.08	117.81	337.89	65.13
$\bar{x} \pm sd$ $h^2bs$	68.88 $\pm$ 7.07				65.33 $\pm$ 7.20			
Populations	G				B			
	$\sigma^2G$	$\sigma^2E$	$\sigma^2P$	$h^2bs$	$\sigma^2G$	$\sigma^2E$	$\sigma^2P$	$h^2bs$
JM2 X Red	346.34	204.13	550.47	62.92	453.14	127.84	580.98	78.00
JM2 X Purple	265.67	66.69	332.36	79.94	285.50	69.58	355.09	80.40
JM4 X Red	293.14	152.64	445.78	65.76	258.28	131.67	389.95	66.23
JM4 X Purple	295.36	72.53	367.89	80.28	278.61	87.28	365.89	76.15
$\bar{x} \pm sd$ $h^2bs$	72.23 $\pm$ 9.18				75.20 $\pm$ 6.22			

Note:  $\sigma^2G$  : genetic variability;  $\sigma^2E$  :environmental variability;  $\sigma^2P$  :phenotype variability;  $h^2bs$  :broad sense heritability; RGB: red, green, blue

Table 4. Broad sense heritability of kernel weight and area

Populations	Weight				Area			
	$\sigma^2G$	$\sigma^2E$	$\sigma^2P$	$h^2bs$	$\sigma^2G$	$\sigma^2E$	$\sigma^2P$	$h^2bs$
JM2 X Red	20.85	35.66	24.41	85.42	20.85	3.57	24.41	85.39
JM2 X Purple	36.74	21.52	58.27	63.05	11.40	2.40	13.80	82.63
JM4 X Red	11.40	23.97	13.80	82.61	3.67	2.15	5.83	63.06
JM4 X Purple	55.25	21.64	76.90	71.85	5.56	2.16	7.69	71.86
$\bar{x} \pm sd$ $h^2bs$	75.73 $\pm$ 10.28				75.74 $\pm$ 10.27			

Note:  $\sigma^2G$ : genetic variability;  $\sigma^2E$ : environmental variability;  $\sigma^2P$ : phenotypic variability;  $h^2bs$ : broad-sense heritability

high category, indicating that the genetic effects were more pronounced than the environmental effects.

## Conclusion

Maternal effects were found in the kernel color inheritance pattern while the effect of the *sh2* gene is dominant in the kernel shape. The qualitative approach of kernel color showed that segregation was found in genes *c*, *pr1*, and *y1*. Based on the qualitative measurement genes that segregate in the kernel shape are in *sh2* and *su1* genes. Quantitative approach shows high value of broad-sense heritability, indicating that the genetic effects were higher than the environmental effects for all characters. Quantitative and qualitative approaches could be used for future inheritance study in maize kernel color and for confirmation of the controlling genes.

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