Abstract – The objective of this work was to evaluate the effects of the mutant alleles alcobaça (norA), ripening inhibitor (rin), and old gold crimson (ogc), in heterozygosity or homozygosity, on the expression of color and on the postharvest quality of fruit of experimental tomato hybrids. Fourteen hybrids with contrasting genotypic constitutions in the norA, rin, and ogc loci were evaluated in a randomized complete block design with four replicates. The following fruit postharvest quality traits were evaluated: firmness in the breaker stage, color, and soluble solids content. The rin+/rin and nor+/norA genotypes increased firmness of tomato fruit at harvest (breaker stage). The rin+/rin genotypes displayed the worst internal fruit color. There was a positive effect of ogc+/ogc in improving the internal color of rin+/rin and nor+/norA fruit, making the color similar to that of the normal genotypes. The combination of the ogc/ogc rin+/rin nor+/norA genes is effective to improve tomato fruit firmness, besides maintaining or improving internal color.

Index terms: Solanum lycopersicum, alcobaça, nonripening, old gold crimson, plant breeding, ripening inhibitor.

Introduction

Tomato (Solanum lycopersicum L.) is one of the most highly consumed vegetable crops in the world. Brazil ranks eighth in the worldwide ranking for tomato production (FAO, 2013). Tomato fruit is highly perishable, with losses of up to 21% after harvest (Rinaldi et al., 2011); it has high-water content, about 90 to 95%, which makes it fragile (Rocha et al., 2009). In tomato breeding programs, the main studied aspects are yield increase, pest and disease resistance, and the improvement of fruit quality. One of the factors associated with this last aspect is the greater natural conservation of the fruit postharvest, and this conservation may be achieved by the production of F1-hybrid fruit that is firmer and has better color (Andrade Júnior et al, 2001).

An alternative to extend the shelf life of tomato fruit has been to affect the natural maturation process of Solanum lycopersicum lines by the incorporation...
of mutant genes, such as *rin* (ripening inhibitor), *nor* (nonripening), *Nr* (never ripe), and *nor*† (alcobaça) (Barry & Giovannoni, 2006). These genes block and retard the maturation process, which lends a longer life to fruit. Currently, most post-harvest long-life tomato hybrids are heterozygous for the genes *rin*, *nor*, or *nor*†, which may lead to reduced quality because of the pleiotropic effects on other metabolic pathways involved in promoting fruit color, flavor, aroma, and texture (Kovács et al., 2009). However, alleles such as *high pigment* (hp) and *old gold crimson* (og)† increase lycopene production in the fruit, which improves color, and they can be used simultaneously with mutant maturation alleles (Andrade Júnior et al., 2005).

Araújo et al. (2002) have shown that the *alcobaça* allele in heterozygosity (*nor*/nor†) prolongs the post-harvest shelf life by the reduction of weight loss and the increase of firmness, and reduces the lycopene and beta-carotene concentrations, besides increasing the Brix/acidity ratio, mainly in association with the genotypes *hp*/hp and *hp*†/hp or with *og*/og; however, its external color limits its commercial use. Câ et al. (2006) in the evaluation of the viability of simultaneous use of mutant genes, for maturity and for color in tomato hybrids, in the loci *nor*†, *rin*, *og*†, or *hp*, found that these genotypes exhibited better post-harvest shelf life than the normal genotypes, and concluded that the genotypic constitutions *nor*/nor† og*/og†, together with *nor*/nor† og*/og*† *hp*/hp, were considered most promising, both for improving post-harvest conservation and for maintaining or improving the internal color of tomato fruit.

Faria et al. (2006) showed that the use of the mutants *og*† or *hp*, in heterozygosity, improves the color and increases the concentrations of beta-carotene and lycopene of fruit in *rin*/rin and *rin*/rin nor*/nor† long shelf life hybrids. Andrade et al. (2015) concluded that the best combination of *high beta-carotene* (B) in heterozygosity for the hue angle and chroma depends on the mutant gene *og*† in heterozygosity; they also showed that the *og*† homozygous genotypes in the absence of *high beta-carotene* had a significant shift in the red direction in the placenta and in the columella, which confirms their effect on improving the internal color of fruit.

The objective of this work was to evaluate the effects of the mutant alleles *alcobaça* (nor†), *ripening inhibitor* (rin), and *old gold crimson* (og†), in heterozygosity or homozygosity, on the expression of color and on the postharvest quality of fruit of experimental tomato hybrids.

**Materials and Methods**

The study was carried out in a greenhouse and in the field, at the experimental station of HortiAgro Sementes S.A., in the Palmítal farm (21°14′16″S, 45°08′00″W, at 920 m altitude), Ijaci, Minas Gerais state, Brazil, as well as in the Departamento de Agricultura, of Universidade Federal de Lavras (Ufla), and in the laboratory of vegetable crop post-harvest, of Departamento de Ciências dos Alimentos of Ufla.

The experiment in the greenhouse was carried out in a randomized complete block design, with 14 treatments, and four replicates. Heterozygous lines for the genes *rin*, *nor*, and *og*, from the germplasm bank of HortiAgro Sementes S.A., were used as parent lines for different combinations in the loci *rin*, *nor†*, and *og†*, and the following hybrids were obtained: TEX-432=F1(TOM-667 x TOM-756), TEX-433=F1(TOM-591 x TOM-756), TEX-434=F1(TOM-714 x TOM-756), TEX-435=F1(TOM-756 x TOM-761), TEX-436=F1(TOM-713 x TOM-761), TEX-437=F1(TOM-591 x TOM-761), TEX-438=F1(TOM-756 x TOM-762), TEX-439=F1(TOM-713 x TOM-762), TEX-440=F1(TOM-591 x TOM-762), TEX-441=F1(TOM-763 x TOM-713), TEX-442=F1(TOM-757 x TOM-713), and TEX-443=F1(TOM-758 x TOM-713).

These hybrids, all with determinate growth habit, together with two commercial hybrids as controls ('Giselle' and 'Colono', also of determinate growth habit), constituted 14 treatments that were placed in five different categories, in relation to their genotypic constitutions in the loci *rin*, *nor†*, and *og†* (Table 1).

The plots consisted of a single row of 10 plants. The 14 genotypes were sown on 04/27/2015, and seedlings were produced in 128-cell expanded polystyrene trays that contained the commercial substrate Topstrato. Plants were thinned to one seedling per cell, at 15 days after sowing. Seedlings were transplanted in the field at 30 days after sowing. The experiment was conducted in the field according to the commercial growing recommendations for tomato under field conditions (Alvarenga, 2013), with a 0.5 m spacing between plants and 1.5 m between rows. The plants were tied on a half-length stake and the experiment was irrigated by drip.
The plants were pruned up to the height of the first flowering shoot, and from that point on, they were not pruned. Fertilization at planting and topdressing, and plant health control treatments were also performed, according to the specific recommendations for the tomato cropping.

The soluble solids content (°Brix) was evaluated through direct reading in a refractometer. Post-harvest conservation of fruit was evaluated (N m⁻²) by fruit firmness collected at the beginning of the maturity stage, which is characterized by change of the fruit green color to the appearance of slightly red spots in the region of the stem scar – “breaker stage”) using the applanation technique described by Calbo & Nery (1995).

The same samples harvested at the beginning of the maturity stage for the firmness evaluation were used for color evaluation. Fruit were stored at 15°C and 60% relative humidity until reaching full maturity. Color readings were made at 4 parts of the fruit – epidermis, pericarp, placenta, and columella – with the Minolta CR-400 colorimeter in the CIE mode L*, a*, and b*, in which L* (lightness) is the coordinate of brightness (z axis), which ranges from -100 (black) to +100 (white), in which the higher values indicate brighter colors; a* is the hue coordinate (x axis), which ranges from +60 (red) to -60 (green); b* is the hue coordinate (y axis), which ranges from +60 (yellow) to -60 (blue). From the a* and b* values, the hue angle [defined as arc tg (b/a)] and chroma or saturation [the square root of (a²+b²)] were obtained. The hue angle is considered from the ‘a’ axis and is expressed in degrees: 0° is defined as +a (red); 90°, as +b (yellow); 180° as -a (green), and 270° as -b (blue). Mature tomato fruit in general range from 0° (red) to 90° (yellow); the nearer the values to zero (0°), the redder the fruit; and the nearer to 90°, the yellower the fruit (Konica Minolta, 2014).

For saturation or chroma, the values range from 0 to 60. Values equal to zero correspond to the origin center of the coordinates; values near zero indicate less saturated colors, and the value of 60 indicates the maximum saturation (Konica Minolta, 2014).

Data were subjected to the analysis of variance, and means were compared by the Tukey test’s, at 5% probability, by the SAS statistical application (SAS Institute, Inc., Cary, NC, USA). Experimental precision was checked by the estimate of selection accuracy (Resende & Duarte, 2007). Contrasts of interest were also calculated for comparisons between genotypes with different genotypic constitutions in the loci rin, ogc, and norA.

### Results and Discussion

In the evaluated fruit quality characteristics – firmness, soluble solids content, and fruit color –, significant differences were observed between treatments, and all the quality traits showed accuracy higher than 70% (Table 2). Experimental precision was, therefore, considered high, according to Resende & Duarte (2007). The content of soluble solids, in the evaluated genotypes, varied from 3.72 °Brix, for ‘Colono’, to 4.72 °Brix for TEX-435 and TEX-441, respectively (Table 2). Only the differences between these extreme values were significant. The other genotypes, with intermediate °Brix values, did not differ from either of the two extreme values; this indicates that all the hybrids used were satisfactory for soluble solids content, and similar to the controls.

### Table 1. Description of the treatments.

| Treatment | Characteristics |
|-----------|-----------------|
| Giselle   | Normal (rin/rin nor/nor ogc/ogc) |
| Colono    | rin heterozygote (rin/rin) |
| TEX-432   | rin heterozygote (rin/rin) |
| (TOM-667 x TOM-756) | nor heterozygote |
| TEX-433   | nor heterozygote; ogc heterozygote (nor/nor ogc/ogc) |
| TEX-434   | Normal (rin/rin nor/nor ogc/ogc) |
| (TOM-714 x TOM-756) | rin heterozygote; |
| TEX-435   | rin heterozygote; |
| (TOM-756 x TOM-761) | ogc heterozygote (rin/rin ogc/ogc) |
| TEX-436   | nor heterozygote; rin heterozygote; |
| (TOM-713 x TOM-761) | nor heterozygote (rin/rin ogc/ogc) |
| TEX-437   | nor heterozygote; |
| (TOM-591 x TOM-761) | ogc homozygote (nor/nor rin/rin ogc/ogc) |
| TEX-438   | rin heterozygote; |
| (TOM-591 x TOM-761) | ogc heterozygote (rin/rin ogc/ogc) |
| TEX-439   | rin heterozygote; |
| (TOM-756 x TOM-762) | rin heterozygote; |
| TEX-440   | nor heterozygote; rin heterozygote; |
| (TOM-713 x TOM-762) | ogc heterozygote (rin/rin ogc/ogc) |
| TEX-444   | Normal (rin/rin nor/nor ogc/ogc) |
| (TOM-763 x TOM-713) | Normal (rin/rin nor/nor ogc/ogc) |
| TEX-442   | Normal (rin/rin nor/nor ogc/ogc) |
| (TOM-757 x TOM-713) | Normal (rin/rin nor/nor ogc/ogc) |
| TEX-443   | Normal (rin/rin nor/nor ogc/ogc) |
| (TOM-758 x TOM-713) | Normal (rin/rin nor/nor ogc/ogc) |
'Giselle' or 'Colono'. Fruit firmness was affected by both the genotypic constitution in the loci (rin, nor⁴, and og)⁶ and the genetic base (Table 2). The normal genotypes proved to be less firm at the beginning of the maturity stage than the heterozygous genotypes rin (C1, Table 3), og⁶ and nor⁴ (C3), and the genotypes og⁶/og⁶ rin⁺/rin⁻ nor⁺/nor⁻ (C4); besides, they did not differ significantly from the genotypes og⁺/og⁺ rin⁺/rin⁻ (C2). These results confirmed reports on rin⁺/rin⁻ and nor⁺/nor⁻ as responsible for the shelf life increase of the fruit (Araújo et al., 2002; Faria et al., 2003; Santos Júnior et al., 2005; Cá et al., 2006). These reports also showed that the genetic base also plays an important role in fruit firmness, when considering, for instance, the amplitude of the firmness values found among the normal genotypes 'Giselle', TEX-434, TEX-441, TEX-442, and TEX-443, among the heterozygous genotypes rin ('Colono', TEX-432), and among the genotypes og⁺/og⁺ rin⁺/rin⁻ (TEX-435, TEX-436, TEX-438, TEX-439). The og allele in heterozygosity seems not to have a direct effect on firmness, since the heterozygous hybrids og⁺ and rin were less firm than the heterozygous genotypes rin alone (C5, Table 3). Heterozygous genotypes og⁺ and nor⁻ were firmer than the heterozygous rin (C6). However, simultaneous heterozygosity in the loci rin and nor⁻ seems to be the most effective combination for increasing firmness in relation to the presence of only one of these heterozygotes, when the magnitude and significance of the contrasts C7, C8, and C9 and of the negative signal (though nonsignificant) of the C10 contrast are considered.

Among the experimental hybrids, TEX-440 had the firmest fruit, and the fact that it has the genotypic constitution og⁺/og⁺ rin⁺/rin⁻ nor⁺/nor⁻ confirms the effectiveness of obtaining firm hybrids through the homozygous genotype og⁺ and heterozygous genotypes for both rin and nor⁻.

As to fruit color, differences were observed among the treatments for all the evaluated characteristics (epidermis, pericarp, placenta, and columella) for both hue angle and chroma values (Table 4). The hue angle was affected both by the presence of the mutants rin, nor⁻, and/or og⁺ and by the genotypic background.

Table 2. Mean values of firmness in the breaker stage and of soluble solids in tomato (Solanum lycopersicum) fruit.

| Treatment | Firmness (10⁴ N m⁻²) | Soluble solids (°Brix) |
|-----------|----------------------|-----------------------|
| Giselle   | 2.40bcd              | 4.35ab                |
| Colono    | 3.50a                | 3.72b                 |
| TEX-432 (TOM-667 x TOM-756) | 2.02d | 4.01ab |
| TEX-433 (TOM-591 x TOM-756) | 3.06abcd | 3.98ab |
| TEX-434 (TOM-714 x TOM-756) | 2.03d | 3.97ab |
| TEX-435 (TOM-756 x TOM-761) | 2.70abcd | 4.72a |
| TEX-436 (TOM-773 x TOM-761) | 2.12d | 4.44ab |
| TEX-437 (TOM-591 x TOM-761) | 3.31abc | 4.15ab |
| TEX-438 (TOM-756 x TOM-762) | 2.33bcd | 4.29ab |
| TEX-439 (TOM-773 x TOM-762) | 2.35bcd | 4.42ab |
| TEX-440 (TOM-591 x TOM-762) | 3.44ab | 4.13ab |
| TEX-441 (TOM-763 x TOM-713) | 2.21cd | 4.72a |
| TEX-442 (TOM-757 x TOM-713) | 2.52abcd | 4.62ab |
| TEX-443 (TOM-758 x TOM-713) | 2.30bcd | 4.25ab |

Accuracy (%) 92.97 76.60

¹Mean values followed by equal letters, in the columns, do not differ by the Tukey’s test, at 5% probability.

Table 3. Estimates of contrasts of interest for firmness (2x10⁴ N m⁻²) in tomato (Solanum lycopersicum) fruit.

| Contrast | Description | Firmness estimate (N m⁻²) |
|----------|-------------|----------------------------|
| C1       | Normal genotypes vs heterozygous genotypes rin | -0.47*                      |
| C2       | Normal genotypes vs heterozygous genotypes og⁺ and rin | -0.08w                      |
| C3       | Normal genotypes vs heterozygous genotype og⁺ and nor⁻ | -0.77**                     |
| C4       | Normal genotypes vs homozygous genotypes og⁺ and heterozygous rin and nor⁻ | -1.08**                     |
| C5       | Heterozygous genotypes rin vs heterozygous genotypes og⁺ and rin | 0.39*                       |
| C6       | Heterozygous genotypes rin vs heterozygous genotype og⁺ and nor⁻ | -0.30w                      |
| C7       | Heterozygous genotypes rin vs homozygous genotypes og⁺ and heterozygous rin and nor⁻ | -0.61**                     |
| C8       | Heterozygous genotypes og⁺ and rin vs heterozygous genotype og⁺ and nor⁻ | -0.68**                     |
| C9       | Heterozygous genotypes og⁺ and rin vs homozygous genotypes og⁺ and heterozygous genotypes rin and nor⁻ | -1.00**                     |
| C10      | Heterozygous genotype og⁺ and nor⁻ vs homozygous genotypes og⁺ and heterozygous genotypes rin and nor⁻ | -0.31**                     |

og⁺, presence of the old gold crimson allele; rin, ripening inhibitor allele; nor⁻, alcobaca allele. ** and *Significant by the Tukey’s test, at 1 and 5%, respectively. *Nonsignificant. Normal genotypes: rin⁺/rin⁻, nor⁺/nor⁻ og⁺/og⁺.
Evidence of the effect of the genotypic background can be observed in the difference between the normal genotypes – 'Giselle' had a significantly greater hue angle (therefore, lower tendency to red) – in the placenta than the other normal hybrids: TEX-434, TEX-441, TEX-442, and TEX-443.

Differences were detected in the external color (epidermis) and internal color (pericarp, placenta, columella) of the fruit due to the presence of the loci rin, nor, and ogc (Table 5). The heterozygosity in the locus rin increased the hue angle in relation to the normal genotypes (C1), in both the external and internal parts of the fruit, which shows the detrimental effect of rin'/rin on color. The detrimental effects of rin'/rin on internal color of the fruit were however reversed by the presence of ogc in heterozygosity (C2 and C5).

In the present study, it was not possible to measure the effect of the genotype nor'/norA, separately, on the internal and external colors, due to the absence of a heterozygous genotype norA in the absence of ogc. However, it is clear that this detrimental effect, if it exists, is counterbalanced by the presence of ogc.

Table 4. Mean values of hue angle (in degrees) for epidermis, pericarp, placenta, and columella of tomato (Solanum lycopersicum) fruit.

| Treatment                  | Epidermis | Pericarp | Placenta | Columella |
|----------------------------|-----------|----------|----------|-----------|
| Giselle                    | 38.77ab   | 38.90abcd| 58.63a   | 39.11ab   |
| Colono                     | 38.34abcd | 39.76ab  | 59.08a   | 34.81bc   |
| TEX-432 (TOM-667 x TOM-756)| 38.58abc | 41.02a   | 52.99bc  | 39.09ab   |
| TEX-433 (TOM-591 x TOM-756)| 33.84e   | 35.10d   | 51.31bc  | 34.73bc   |
| TEX-434 (TOM-714 x TOM-756)| 35.32de  | 36.79bcd | 50.05c   | 35.03bc   |
| TEX-435 (TOM-756 x TOM-761)| 37.89abcd| 36.78bcd | 50.56c   | 49.06a    |
| TEX-436 (TOM-713 x TOM-761)| 38.92a   | 38.65abcd| 55.36ab  | 40.66a    |
| TEX-437 (TOM-591 x TOM-761)| 35.81bcde| 36.06bcd | 49.27c   | 39.13ab   |
| TEX-438 (TOM-756 x TOM-762)| 38.47abe | 38.17abcd| 52.38bc  | 32.66c    |
| TEX-439 (TOM-713 x TOM-762)| 38.33abc | 39.73abc | 55.57ab  | 37.87abc  |
| TEX-440 (TOM-591 x TOM-762)| 37.20abc | 37.13abcd| 48.89c   | 39.79abc  |
| TEX-441 (TOM-763 x TOM-713)| 35.53cde | 35.93bcd | 51.06bc  | 36.64abc  |
| TEX-442 (TOM-757 x TOM-713)| 36.85abcde| 37.55abcd| 51.91bc  | 40.62a    |
| TEX-443 (TOM-758 x TOM-713)| 36.68abcde| 37.82abcd| 52.71bc  | 38.52ab   |
| Accuracy (%)               | 89.53     | 85.03    | 95.41    | 85.47     |

(1) Mean values followed by equal letters, in the columns, do not differ by the Tukey’s test, at 5% probability.

Table 5. Estimates of contrasts of interest for hue angle of the epidermis (EP), pericarp (PE), placenta (PL), and columella (CO) of tomato (Solanum lycopersicum) fruit.

| Contrast                      | Description                                           | EP  | PE  | PL  | CO  |
|-------------------------------|-------------------------------------------------------|-----|-----|-----|-----|
| C1                            | Normal genotypes vs heterozygous genotypes rin         | -1.83**| -2.99**| -4.02**| 3.30**|
| C2                            | Normal genotypes vs heterozygous genotypes ogc and rin | -1.77**| -0.93**| -0.22**| 1.77**|
| C3                            | Normal genotypes vs heterozygous genotypes ogc and norA| 2.79**| 2.30**| 0.13**| -1.6**|
| C4                            | Normal genotypes vs homozygous genotypes ogc and heterozygous genotypes rin and norA | 0.12**| 0.80**| 4.04**| -0.63**|
| C5                            | Heterozygous genotypes rin vs heterozygous genotypes ogc and rin | 0.06**| 2.05**| 3.80**| -1.93**|
| C6                            | Heterozygous genotypes rin vs heterozygous genotypes ogc and norA | 4.62**| 5.29**| 4.15**| -4.47**|
| C7                            | Heterozygous genotypes (HG) rin vs homozygous genotypes ogc and HG rin and norA | 1.95**| 3.79**| 8.07**| -3.94**|
| C8                            | Heterozygous genotypes ogc and rin vs heterozygous genotypes ogc and norA | 4.56**| 3.23**| 0.35**| -2.54**|
| C9                            | Heterozygous genotypes (HG) ogc and rin vs homozygous genotypes ogc and HG rin and norA | 1.90**| 1.74*| 4.26**| -2.00**|
| C10                           | Heterozygous genotypes (HG) ogc and norA vs homozygous genotypes ogc and HG rin and norA | -2.67**| -1.50**| 3.92**| 0.53**|

ogc, presence of the old gold crimson allele; rin, ripening inhibitor allele; norA, alcobaça allele. ** and *Significant by the Tukey’s test at 1 and 5% probability, respectively. ns Nonsignificant. Normal genotypes: rin'/rin, nor'/nor, ogc+/ogc.
in heterozygosity because the combination og\(^{+}\)/og\(^{-}\) nor\(^{+}\)/nor\(^{-}\) improved the epicarp and placenta colors in comparison to the normal genotypes (C3, Table 5). The possible detrimental effect of nor\(^{-}\)/nor\(^{-}\), if it exists, appears to be less than that brought about by rin\(^{-}\)/rin because the beneficial effects of ogc\(^{+}\)/ogc\(^{-}\) are more accentuated in the first case (C6) than in the second one (C5).

The simultaneous presence of heterozygosity in rin and nor\(^{-}\) besides homozygosity in og\(^{-}\)/og\(^{-}\) provided not only a red color comparable to that of normal genotypes in the epidermis, pericarp, and columella, but also improved it in the placenta (C4, Table 5). Andrade et al. (2015) found that homozygous genotypes og\(^{-}\) did not differ from the normal genotypes for the hue angles in the epidermis and pericarp, but had a significant shift in the red direction in the placenta and columella.

As to the genotype rin\(^{-}\)/rin alone, the combination og\(^{-}\)/og\(^{-}\) rin\(^{+}\)/rin nor\(^{+}\)/nor\(^{-}\) exhibited color closer to red in all the measured points (C7, Table 5), and the same happened in the combination og\(^{+}\)/og\(^{-}\) rin\(^{-}\)/rin (C9). In relation to the genotype og\(^{-}\)/og\(^{-}\) nor\(^{+}\)/nor\(^{-}\), the genotypic combination og\(^{-}\)/og\(^{-}\) rin\(^{+}\)/rin nor\(^{+}\)/nor\(^{-}\) brought about the best color in the placenta and the worst color in the epidermis (C10). Araújo et al. (2002) reported that the mutants og\(^{-}\) and hp, with a genotypic background 'Floradade', isolated or in combination, in both homozygosity and in heterozygosity, brought about significant increases in internal and external colors.

From these results it can be inferred that the allele og\(^{-}\), both in homozygosity and in heterozygosity, is able to counterbalance the negative effects of the heterozygotes rin\(^{-}\)/rin or nor\(^{-}\)/nor\(^{-}\) in fruit color, mainly in internal color. Similar effects on fruit color were found by Faria et al. (2003) and Cá et al. (2006). In fact, the three smallest chromaticity angles (nearest to red) among the studied genotypes were TEX-435 of the genotype og\(^{-}\)/og\(^{-}\) rin\(^{-}\)/rin, and TEX-437 and TEX-440 of the genotype og\(^{-}\)/og\(^{-}\) rin\(^{-}\)/rin nor\(^{+}\)/nor\(^{-}\).

The chroma saturation seems to have been less affected than the hue angle among the studied genotypes (Table 6), particularly in the epidermis, pericarp, and placenta, whereas the normal genotype control 'Giselle' had the lowest numerical chromas among the treatments, and the hybrid TEX-441, which is also of normal genotype, had some of the highest chromas at these points.

The most significant differences in the chromas occurred in the columella (Table 7). The genotypes rin\(^{-}\)/rin had significantly lower chromas than the normal genotypes (C1), but due to the magnitude of variation among the normal genotypes themselves, it is possible that this difference arises mainly from the effect of different genotypic backgrounds, and not from the allele rin only. Nevertheless, the effect of the allele og\(^{-}\) in heterozygosity is clear as for the increasing of the chroma of the hybrids rin\(^{-}\)/rin, both in the external and internal part of the fruit (C5). Genotypes og\(^{-}\)/og\(^{-}\) nor\(^{+}\)/nor\(^{-}\) also showed greater internal chroma than the rin\(^{-}\)/

### Table 6. Mean values of chroma for epidermis, pericarp, placenta, and columella of tomato (Solanum lycopersicum) fruit.

| Treatment | Epidermis | Pericarp | Placenta | Columella |
|-----------|-----------|----------|----------|-----------|
| Giselle   | 28.23ab   | 27.39a   | 24.22ab  | 31.68abcd |
| Colono    | 26.72b    | 26.15a   | 21.87b   | 25.93d    |
| TEX-432 (TOM-667 x TOM-756) | 28.91ab | 28.74a | 23.51ab | 32.77abc |
| TEX-433 (TOM-591 x TOM-756) | 29.81ab | 30.13a | 26.08ab | 32.19abc |
| TEX-434 (TOM-714 x TOM-756) | 27.90ab | 31.38a | 27.40a | 35.55a |
| TEX-435 (TOM-756 x TOM-761) | 29.66ab | 30.89a | 25.46ab | 32.99abc |
| TEX-436 (TOM-713 x TOM-761) | 31.98a | 29.76a | 24.96ab | 30.95abcd |
| TEX-437 (TOM-591 x TOM-761) | 29.89ab | 31.03a | 23.86ab | 29.54bcd |
| TEX-438 (TOM-756 x TOM-762) | 28.26ab | 28.98a | 24.46ab | 31.60abcd |
| TEX-439 (TOM-713 x TOM-762) | 30.14ab | 29.76a | 23.79ab | 32.08abc |
| TEX-440 (TOM-591 x TOM-762) | 30.26ab | 29.58a | 25.15a | 29.10cd |
| TEX-441 (TOM-763 x TOM-713) | 30.32ab | 30.41a | 27.61a | 35.31ab |
| TEX-442 (TOM-757 x TOM-713) | 28.72ab | 29.12a | 27.09a | 30.48abcd |
| TEX-443 (TOM-758 x TOM-713) | 28.13ab | 27.20a | 25.24ab | 29.59bcd |

| Accuracy (%) | 75.43 | 70.53 | 75.79 | 90.32 |

(1)Mean values followed by equal letters, in the columns, do not differ by the Tukey's test, at 5% probability.

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Table 7. Estimates of contrasts of interest for chroma of the epidermis (EP), pericarp (PE), placenta (PL), and columella (CO) of tomato (*Solanum lycopersicum*) fruit.

| Contrast Description | Normal genotypes vs heterozygous genotypes rin | Normal genotypes vs heterozygous genotypes og and rin | Normal genotypes vs genotypes og/og nor/nor | Normal genotypes vs genotypes og/og rin/rin nor/nor | Heterozygous genotypes rin vs heterozygous genotypes og and rin | Heterozygous genotypes rin vs heterozygous genotypes og and nor | Heterozygous genotypes (HG) rin vs homozygous genotypes og and HG rin and nor | Heterozygous genotypes og and rin vs heterozygous genotypes og and nor | Heterozygous genotypes (HG) og and rin vs homozygous genotypes og and HG rin and nor | Heterozygous genotypes og and nor vs homozygous genotypes og and HG rin and nor |
|----------------------|-------------------------------------------------|-----------------------------------------------------|------------------------------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|
| C1                   | Normal genotypes vs heterozygous genotypes rin  | 0.84**                                              | 1.66**                                   | 3.62**                                          | 3.17**                                          | -1.35**                                         | -0.75**                                         | 1.65*                                            | 0.62**                                          | -1.42**                                         | -0.46**                                         |
| C2                   | Normal genotypes vs heterozygous genotypes og and rin | -1.15**                                         | -1.03**                                   | 0.23**                                          | 0.33**                                          | -0.26**                                         | -0.17**                                         | 0.16**                                           | 2.58**                                          | -0.26**                                         |
| C3                   | Normal genotypes vs genotypes og/og nor/nor     | -1.42**                                         | -1.20**                                   | 1.81*                                            | 3.20**                                          | -0.07**                                         | -0.46**                                         | 0.16**                                           | 2.58**                                          | -0.26**                                         |
| C4                   | Normal genotypes vs genotypes og/og rin/rin nor/nor | -1.29**                                         | -2.41**                                   | -1.98**                                          | -2.55**                                          | -0.26**                                         | -0.17**                                         | 1.58**                                           | 2.87**                                          | -0.26**                                         |
| C5                   | Heterozygous genotypes rin vs heterozygous genotypes og and rin | -2.99**                                         | -2.41**                                   | -1.98**                                          | -2.55**                                          | -2.00**                                         | -2.69**                                         | -3.39**                                          | -2.84**                                          | -0.07**                                         |
| C6                   | Heterozygous genotypes rin vs heterozygous genotype og and nor | -2.62*                                           | -2.86*                                   | -1.82**                                          | 0.03**                                          | -0.26**                                         | -0.17**                                         | 1.58**                                           | 2.87**                                          | -0.26**                                         |
| C7                   | Heterozygous genotypes (HG) rin vs homozygous genotypes og and HG rin and nor | -0.07**                                         | -0.46**                                   | 0.16**                                           | 2.58**                                          | -0.26**                                         | -0.17**                                         | 1.58**                                           | 2.87**                                          | -0.26**                                         |
| C8                   | Heterozygous genotypes og and rin vs heterozygous genotypes og and nor | 0.20**                                           | -0.28**                                   | -1.42**                                          | -0.29**                                          | -0.26**                                         | -0.17**                                         | 1.58**                                           | 2.87**                                          | -0.26**                                         |
| C9                   | Heterozygous genotypes (HG) og and rin vs homozygous genotypes og and HG rin and nor | -0.07**                                         | -0.46**                                   | 0.16**                                           | 2.58**                                          | -0.26**                                         | -0.17**                                         | 2.87**                                           | -0.26**                                         | -0.26**                                         |
| C10                  | Heterozygous genotype (HG) og and nor vs homozygous genotypes og and HG rin and nor | -0.26**                                         | -0.17**                                   | 1.58**                                           | 2.87**                                          | -0.26**                                         | -0.17**                                         | 2.87**                                           | -0.26**                                         | -0.26**                                         |

*Og*, presence of the *old gold crimson* allele; *rin*, ripening inhibitor allele; *nor*, alcobaça allele. ** and *Significant by the Tukey’s test, at 1 and 5% probability, respectively. ns*Nonsignificant. Normal genotypes: rin+/rin+ nor+/nor+ ogc+/ogc+.

rin (C6). Under the simultaneous presence of rin+/rin and nor+/nor, the allele *og* in homozygosity increased the chroma in the epidermis and in the pericarp of tomato fruit (C7).

**Conclusions**

1. The genotypic constitutions rin+/rin nor+/nor are responsible for providing greater firmness to tomato (*Solanum lycopersicum*) fruit at the time of harvest, and the allele *og* does not have a direct effect on firmness.

2. Heterozygosity in the locus rin has a detrimental effect on color of the external and internal parts of the fruit. The *og* allele is able to counterbalance the negative effects of the heterozygotes rin+/rin or nor+/nor on internal color.

3. The genotypic constitutions og/og rin+/rin nor+/nor or og+/og nor+/nor are considered the most promising ones, improving the firmness and the internal or external color of tomato fruit.

4. The simultaneous presence of heterozygous alleles rin and nor, associated with *og*/*og*, is effective in developing tomato hybrids with better post-harvest conservation.

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