A Study on Normal and Nubbin Productivity of Some Mango Trees in Relation to Quantification of Expressed Gene Levels
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ABSTRACT
The present investigation was carried out during 2015 and 2016 seasons on three Egyptian mango cultivars (Mangifera indica L.) named Ewais (normal & nubbin), Sedeq and Zebda grown at a private orchard in Idko region under Beheira governorate conditions. The trees were selected to study normal and nubbin fruits of some mango trees productivity and quantification of expressed gene levels as well as trying to make better understanding of embryo abortion phenomenon in mango. Real-time qPCR was used to detect the relative amounts of mRNA of four different genes. Fruit physical characteristics of Ewais (nubbin) cultivar, i e fruit length, width and pulp, stone and peel weights, as well as yield were lower significantly than normal fruits, while its pulp/ stone ratio gave the highest values, in both seasons. The chemical characteristics of Ewais (nubbin), i e TSS, TSS/ acidity, reducing sugars, total sugars and pectin methyl esterase were significantly higher than normal fruits, while acidity, vitamin C and peroxidase were the lowest values. Results showed that the four selected ESTs were differentially expressed in the tissues of normal, aborted embryos and leaves, however, the 4 ESTs (MaAGA, MaAP2, MaERF, and MaMADS) were upregulated in normal embryo tissues compared to aborted embryos of “Ewais”. Also the expression levels in the leaves tissues were upregulated in Sedeq and Zebda varieties compared to Ewais leaves. The results of total protein (SDS-PAGE) explained that Sedeq and Sedeq cultivars, which had normal fruits gave the highest several bands in both embryos and leaves tissues than Ewais cultivar which had nubbin fruits.

Keyword: Mango, Mangifera indica, Real-time qPCR, Total protein (SDS-PAGE), Productivity.
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INTRODUCTION
Mango (Mangifera indica L.) is a globally important fruit crop of the tropics and subtropics, particularly in Egypt, where it is considered the ‘king of fruits’ due to its delicate, sweet flavor and nutritional value. The total fruiting area of mango trees was about 88510 hectare that produced about 88510 ton at the year of 2014 (Arab Agricultural Statistics Yearbook, 2015). Only perfect (hermaphrodite) flowers are able to set fruit, however, the number of perfect flowers per inflorescence varies between cultivars or is variable from year to year, depending on the location of the inflorescence in the tree (Singh and Arora, 1965 and Singh, 2005).

Embryo abortion, which hinders normal fruit development, seems to play an important role in induction of the abscission process at early stages of fruit development (Mukherjee, 1953). Earlier studies and observations had focused on the physiological and anatomical aspects of mango embryo abortion, and the molecular basis of this disorder is unknown. In this regard, according to Bustin (2002), Real-time PCR differs from classical PCR by the measurement of the amplified PCR product at each cycle throughout the PCR reaction. In practice, a video camera records the light emitted by a fluorochrome incorporated into the newly synthesized PCR product. Thus, real-time PCR allows the amplification to be followed in real-time during the exponential phase of the run and thus allows the amount of starting material to be determined precisely.

It is necessary to identify the genes that are differentially expressed in aborted tissue to explore the molecular basis of embryo abortion in mango. Furthermore, He et al. (2012) used a PCR-based subtractive hybridization technique to isolate differentially expressed genes from normal and aborted embryo tissues to characterize the molecular aspects that probably play role in embryo abortion events. However, Choudhury et al. (2012) employed (SDS-PAGE 10%) markers to make an assay to systematically investigate the role of an AGAMOUS MADS-box transcription factor in regulation of fruit ripening and floral reproductive organ development in banana giant governor. They reported that single distinct protein band with an approximate molecular mass near 27-kDa was obtained in the elution fractions from both flower and fruit specific DNA-protein complexes.

The aims of the present study are to determine normal and nubbin productivity of some mango trees in relation to quantification of expressed gene levels. In addition to understand better embryo abortion phenomenon in some mango trees through obtaining the role of some ESTs genes that implicated in embryo abortion using RT-qPCR technique.

MATERIALS AND METHODS
The present investigation was carried out during two successive seasons 2015 and 2016 on three Egyptian mango cultivars (Mangifera indica L.) named Ewais (normal & nubbin), Sedeq and Zebda grown in a private orchard in Idko region under Beheira governorate conditions. The experimental trees were about eight years old, budded on Sukkari rootstock, planted on sandy soil at 3 X 5 m For the present study, twenty trees were selected as uniform as possible in vigor (i e 4 accessions x 5 replicates = 20 trees) and under regular horticultural practices including: fertilization, pruning as well as pest and disease control. Flooding system was used for irrigation.

1. Trees productivity
In order to determine mango trees productivity, number of normal and nubbin fruits/ tree was counted and the yield in Kg was calculated by multiplying...
number of fruits per tree X the average of fruit weight. Additionally, fruit physical and chemical characteristics were determined in samples collected randomly from each replicate (5 fruits) at the harvest date in 30 August for Ewais, 20 August for Sedeq and 25 July for Zebda each replicate (5 fruits) at the harvest date in 30 August were determined in samples collected randomly from

A. Fruit physical characteristics

Average fruit length and diameter (cm) were measured for each individual fruit using a Vernier caliper and fruit length /diameter ratio was calculated. Fruit, pulp and peel weight (g) were determined for each cultivar. Also, pulp / stone ratio was estimated in the fruit samples by weighing the stone and pulp then the fruit pulp / stone ratios were calculated.

B. Fruit chemical characteristics

In another sample of five fruits, juice from each replicate was used to determine the percentage of TSS by hand refractometer. Vitamin C was determined in 1 ml fruit juice by titration with 2,6-dichlorophenolindophenol blue dye as mg ascorbic acid/100 ml juice according to the AOAC (1995). Five ml from the obtained juice were used to determine the titratable acidity as g citric acid/100 ml juice according to the method described by Chen and Mellenthin (1981). The total reducing sugars % was determined according to the method of Malik and Singh (1980). The reducing sugars were determined by the Nelson arsenate-molybdate colorimetric method (Dubois et al., 1956).

The peroxidase activity in fruits pulp was estimated using the method of Thomas et al. (1981). According to Matsuno and Uritani (1972) and Carvalho et al. (2015), enzyme activity was reported as enzymatic units (U) and is defined as the amount of enzyme that produces a change in absorbance of 1.0/min under the assay conditions at 25°C. Extraction of pectin methyl esterase (PME) was as described by Lazan et al. (1989). Pectin esterase activity was assayed using a modification of the method of Lazan et al. (1995). The assay mixture (25.5 ml) comprising Ca 1% (w/v) pectin containing 2.5 mmol CaCl2 and enzyme extract (0.5 ml) was titrated (25°C) with 0.01 M NaOH at pH 7.5 for 15 min.

RESULTS AND DISCUSSION

1. Trees productivity

A. Fruit physical characteristics

The data presented in Table 2 cleared that Zebda cultivar had significantly higher yield per tree than the other cultivars, while Ewais (nubbin) cultivar had lowest yield in both seasons. Additionally, Sedeq cultivar had significantly heavier fruit, pulp, stone and peel weight than the other cultivars in both seasons. Meanwhile, Ewais (nubbin) cultivar had lowest values in both seasons. In addition, Ewais (nubbin) recorded

<table>
<thead>
<tr>
<th>Primers</th>
<th>Accession No.</th>
<th>Nucleotide sequence 5' to 3' (F=Forward, R=Reverse)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>MaAGA</td>
<td>JK513220</td>
<td>F:AGAGATGGGGAGAGGAAAAATT&lt;br&gt;R:CGGTCTGGAGAAATAGG&lt;br&gt;F:GGGGTTTGTCTTCTCTTT&lt;br&gt;R:CAACCTGGACACCGTTG&lt;br&gt;F:GGGGTTTGTCTTCTCTCT&lt;br&gt;R:CCCGCTGCCTATCCTCGTA&lt;br&gt;F:GGCCCATCGGAGATAAGC&lt;br&gt;R:CCATAAATCACGCGAGTAACAGT</td>
<td>He et al. (2012)</td>
</tr>
<tr>
<td>MaMADS</td>
<td>JK513393</td>
<td>F:AGAGTGGGGAGAGGAAAAATT&lt;br&gt;R:CGGTCTGGAGAAATAGG&lt;br&gt;F:GGGGTTTGTCTTCTCTTT&lt;br&gt;R:CAACCTGGACACCGTTG&lt;br&gt;F:GGGGTTTGTCTTCTCTCT&lt;br&gt;R:CCCGCTGCCTATCCTCGTA&lt;br&gt;F:GGCCCATCGGAGATAAGC&lt;br&gt;R:CCATAAATCACGCGAGTAACAGT</td>
<td>He et al. (2012)</td>
</tr>
<tr>
<td>MaAP2</td>
<td>JK513603</td>
<td>F:AGAGATGGGGAGAGGAAAAATT&lt;br&gt;R:CGGTCTGGAGAAATAGG&lt;br&gt;F:GGGGTTTGTCTTCTCTTT&lt;br&gt;R:CAACCTGGACACCGTTG&lt;br&gt;F:GGGGTTTGTCTTCTCTCT&lt;br&gt;R:CCCGCTGCCTATCCTCGTA&lt;br&gt;F:GGCCCATCGGAGATAAGC&lt;br&gt;R:CCATAAATCACGCGAGTAACAGT</td>
<td>He et al. (2012)</td>
</tr>
<tr>
<td>MaERF</td>
<td>JK513364</td>
<td>F:AGAGATGGGGAGAGGAAAAATT&lt;br&gt;R:CGGTCTGGAGAAATAGG&lt;br&gt;F:GGGGTTTGTCTTCTCTTT&lt;br&gt;R:CAACCTGGACACCGTTG&lt;br&gt;F:GGGGTTTGTCTTCTCTCT&lt;br&gt;R:CCCGCTGCCTATCCTCGTA&lt;br&gt;F:GGCCCATCGGAGATAAGC&lt;br&gt;R:CCATAAATCACGCGAGTAACAGT</td>
<td>He et al. (2012)</td>
</tr>
</tbody>
</table>
the highest significant pulp/stone ratio as compared to the other cultivars, while Zebda had the lowest total pulp/stone ratio. In both seasons, Sedeq cultivar had significantly longer fruits length than the other cultivars in both seasons, while Ewais (nubbin) cultivar had the lowest fruit length and width. No significant difference was found between Zebda and Sedeq cultivars in fruit width in the first season, while Sedeq cultivar had higher fruit width than Zebda.

It was noted that the variations in fruit physical characteristics (normal or nubbin) and among the studied cultivars could be due to the variability in the genetic structures. The observed data concurred with those mentioned by Shaban and Ibrahim (2009) whereas, trees of all evaluated cultivars produced higher significant yield of normal fruit than nubbin fruit. Also, Shaban (2005), Boshra (2009), El-Khawaga and Maklad (2013) and Elsheshetawy et al. (2016), who measured the physical properties of six cultivars from Sharkia and Ismailia region and Ibrahim et al. (2016), who studied genetic diversity on some polyembryonic & monoembryonic mango genotypes using morphological and molecular markers.

B. Fruit chemical characteristics

The results in Table 3 indicated that nubbin and normal Ewais had significantly higher juice reducing and total sugars and TSS percentage TSS/acidity ratio as compared to the other cultivars in both seasons, while the remained cultivars had the lowest ones. In addition, Zebda and Sedeq cultivars had significantly higher juice acidity as compared to the other cultivars in both seasons. Sedeq cultivar had significantly higher juice vitamin C, while Ewais (nubbin) cultivar the lowest ones. Zebda cultivar had the significantly higher peroxidase activity (POD) than the other cultivars, while Ewais (nubbin) cultivar the lowest one. On contrary, Ewais (nubbin) cultivar had the significantly higher pectin methyl esterase (PME) than the other cultivars, while Zebda had cultivar the lowest one.

These outcomes were in harmony with those of Hamdard et al. (2004) and Anjum et al. (2014), who evaluated chemical contents of eight mango cultivars. It was clearly obtained that the variations in the chemical characteristics like total sugars, reducing sugars, TSS, acidity, the ratio between TSS/acidity, vitamin C, peroxidase activity and pectin methyl esterase of fruit (normal or nubbin) and among the studied cultivars could be due to the variability in the genetic structures.

<table>
<thead>
<tr>
<th>Cultivars (accessions)</th>
<th>Yield (Kg/tree)</th>
<th>Fruit weight(g)</th>
<th>Pulp weight (g)</th>
<th>Stone weight (g)</th>
<th>Peel weight (g)</th>
<th>Pulp/ Stone ratio</th>
<th>Fruit length(cm)</th>
<th>Fruit width(cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ewais (Normal)</td>
<td>61.62</td>
<td>56.64</td>
<td>251.58</td>
<td>247.40</td>
<td>184.02</td>
<td>12.58</td>
<td>11.94</td>
<td>28.36</td>
</tr>
<tr>
<td>*Ewais (Nubbin)</td>
<td>2.73</td>
<td>2.78</td>
<td>78.42</td>
<td>76.92</td>
<td>55.84</td>
<td>5.68</td>
<td>5.30</td>
<td>16.92</td>
</tr>
<tr>
<td>Sedeq</td>
<td>51.18</td>
<td>54.40</td>
<td>334.94</td>
<td>337.66</td>
<td>241.78</td>
<td>54.24</td>
<td>52.94</td>
<td>66.36</td>
</tr>
<tr>
<td>Zebda</td>
<td>89.70</td>
<td>83.86</td>
<td>380.20</td>
<td>373.24</td>
<td>273.24</td>
<td>51.32</td>
<td>49.18</td>
<td>60.84</td>
</tr>
<tr>
<td>LSD_0.05</td>
<td>6.11</td>
<td>4.77</td>
<td>22.26</td>
<td>19.52</td>
<td>21.319</td>
<td>19.32</td>
<td>3.57</td>
<td>4.86</td>
</tr>
</tbody>
</table>

*: Normal fruits of Ewais (Nubbin) was excluded from the yield

Table 3. Fruit chemical characteristics of three mango cultivars Ewais (normal and nubbin), Sedeq and Zebda during 2015 and 2016 seasons.

<table>
<thead>
<tr>
<th>Cultivars (accessions)</th>
<th>Total sugars (%)</th>
<th>Reducing sugars (%)</th>
<th>TSS (%)</th>
<th>Acidity (%)</th>
<th>TSS/ acidity ratio</th>
<th>Vitamin C (mg/100 ml juice)</th>
<th>POD (U/gm)</th>
<th>PME (U/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ewais (Normal)</td>
<td>11.94</td>
<td>13.46</td>
<td>6.66</td>
<td>7.10</td>
<td>19.00</td>
<td>20.20</td>
<td>0.69</td>
<td>133.72</td>
</tr>
<tr>
<td>Ewais (Nubbin)</td>
<td>12.58</td>
<td>13.90</td>
<td>7.36</td>
<td>7.06</td>
<td>20.50</td>
<td>22.00</td>
<td>0.60</td>
<td>133.22</td>
</tr>
<tr>
<td>Sedeq</td>
<td>9.92</td>
<td>9.40</td>
<td>5.02</td>
<td>5.32</td>
<td>15.80</td>
<td>15.00</td>
<td>0.75</td>
<td>98.52</td>
</tr>
<tr>
<td>Zebda</td>
<td>7.98</td>
<td>10.10</td>
<td>5.14</td>
<td>5.14</td>
<td>14.18</td>
<td>15.50</td>
<td>0.77</td>
<td>77.80</td>
</tr>
<tr>
<td>LSD_0.05</td>
<td>1.19</td>
<td>0.88</td>
<td>0.63</td>
<td>0.90</td>
<td>2.10</td>
<td>2.21</td>
<td>0.13</td>
<td>3.25</td>
</tr>
</tbody>
</table>

2. Quantification of expressed gene levels
A. Real-time quantitative PCR (RT-qPCR)

The data representing the relative expression ratio was accurately quantified as in Figures (1-4) and calculated according to the algorithm 2^(-ΔΔCt) and outcomes are listed in Table (4). The results explained that Zebda and Sedeq cultivars, which had normal fruits had the highest ratio (fold) of AGAMOUS (MaAGA), MADS box (MaMADS), AP2 domain (MaAP2) and ethylene response factor (MaERF) protein than the other cultivar (Ewais), which had a nubbin fruits (aborted) in both of embryos and leaves tissues.
by Liu and Ma plants, proving that the 17 ERFs encode the ERF family box genes can convert leaves into floral organs, according to Abdel-Sattar, M. et al. (2007). Additionally, these findings showed that the highest numerous and intensity bands were (8 bands) in Zebda cultivar followed by (7 and 5 bands) in Sedeq and Ewais (normal), respectively. While the lowest multiples were (3 bands) in Ewais (nubbin) cultivar. The bands were with an approximate molecular mass ranging from (28-kDa to 74-KDa) were obtained in the elution fractions of protein from embryos.

### Table 4. Gene expression of mango embryos from Zebda, Sedeq and Ewais (normal and nubbin) cultivars and leaves using RT-qPCR.

<table>
<thead>
<tr>
<th>Target Genes</th>
<th>Cultivars</th>
<th>Embryos 2^-\Delta\Delta Ct (fold)</th>
<th>Leaves 2^-\Delta\Delta Ct (fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MaAGA</td>
<td>Ewais</td>
<td>0.03</td>
<td>0.71</td>
</tr>
<tr>
<td></td>
<td>Sedeq</td>
<td>1.43</td>
<td>5.76</td>
</tr>
<tr>
<td></td>
<td>Zebda</td>
<td>1.82</td>
<td>22.5</td>
</tr>
<tr>
<td></td>
<td>Ewais</td>
<td>0.03</td>
<td>0.42</td>
</tr>
<tr>
<td>MaMADS</td>
<td>Sedeq</td>
<td>1.09</td>
<td>1.92</td>
</tr>
<tr>
<td></td>
<td>Zebda</td>
<td>2.04</td>
<td>20.5</td>
</tr>
<tr>
<td></td>
<td>Ewais</td>
<td>0.04</td>
<td>0.04</td>
</tr>
<tr>
<td>MaAP2</td>
<td>Sedeq</td>
<td>1.28</td>
<td>0.48</td>
</tr>
<tr>
<td></td>
<td>Zebda</td>
<td>2.55</td>
<td>0.63</td>
</tr>
<tr>
<td></td>
<td>Ewais</td>
<td>0.04</td>
<td>1.50</td>
</tr>
<tr>
<td>MaERF</td>
<td>Sedeq</td>
<td>1.42</td>
<td>2.10</td>
</tr>
<tr>
<td></td>
<td>Zebda</td>
<td>2.43</td>
<td>9.51</td>
</tr>
</tbody>
</table>

These findings referred to increasing in gene expression of AGAMOUS in the cultivars, which had normal fruit than the aborted one and illustrated the role of AGAMOUS in fruit development and floral organ identity which controlled by diverse families of homeotic transcription factors, the floral homeotic gene AGAMOUS (AG) is a group C gene and it encodes a MADS box transcription factor as explained by Yanofsky et al. (1990). These findings pointed to expanding in gene expression of MADS box in the cultivars, which had normal fruit than the aborted one and represented the role of MADS box in fruit as master regulators of flowering transition and development of flowers, fruits, and seeds as recorded by Ma et al. (2011) and Hemming and Trevaskis (2011). Also, Genome-wide studies suggest that most MADS-box genes are expressed in a variety of organs and cell types at different developmental stages as reported by Rijpkema et al. (2007). Loss-of-function mutations in multiple MADS-box genes can convert floral organs to leaf-like structures, and ectopic expression of MADS-box genes can convert leaves into floral organs, illustrating the critical role MADS-box genes play during floral development as mentioned by Trevaskis et al. (2007).

These outputs referred to the increasing in gene expression of AP2D domain class transcription factor (MaAP2) in the cultivars, which had normal fruit than the aborted one and represented the role of AP2D domain transcription factor in fruit development and ripening. However, the deduced amino acid sequences of ERFs comprise a conserved DNA-binding ERF/AP2 domain (ranging from 58 to 59 amino acids), which is characteristic of the plant ERF gene family as described by Liu et al. (2010). The 17 ERFs share a highly conserved ERF/AP2 domain with ERF proteins of other plants, proving that the 17 ERFs encode the ERF family TF in the mango fruit, and the cDNA sequences obtained from the RNA-seq are credible according to Hoang et al. (2015).

These outputs referred to the increasing in gene expression of ethylene response factor (MaERF) in the cultivars which had normal fruit than the aborted one and represented the role of ethylene response factor (MaERF) in fruit development and ripening. Moreover, Aharoni and O'Connell (2002) isolated a plant specific transcription activation factor associated with ethylene and abscisic acid response (ERF) from strawberry and suggested its involvement in late achene development. High expression of this gene suggested that it is one of the key transcription factors involved in multitude of activities. Also, ethylene response factor (MaERF) may play an important role in cell resistance to infections and degradation as illustrated by Hoang et al. (2015).

#### B. Total protein biochemical (SDS-PAGE) markers

**1. Embryos**

The SDS-PAGE 15% image of total protein electrophoresis in embryos for the studied mango cultivars were marked and figured in Figure (5-A). The results showed that each cultivar had several numbers of bands were arranged in a descending order: 8, 7, 5 and 3 bands for Zebda, Sedeq, Ewais (normal) and Ewais (nubbin) cultivars, respectively. These results defined that the highest numerous and intensity bands were (8 bands) in Zebda cultivar followed by (7 and 5 bands) in Sedeq and Ewais (normal), respectively. While the lowest multiples were (3 bands) in Ewais (nubbin) cultivar. The bands were with an approximate molecular mass ranging from (28-kDa to 74-KDa) were obtained in the elution fractions of protein from embryos.

**2. Leaves**

The SDS-PAGE 15% image of total protein electrophoresis in leaves for the studied mango cultivars were marked and figured in Figure (5-B). The results showed that each cultivar had several numbers of bands were arranged in a descending order: 6, 5 and 4 bands for Zebda, Sedeq, Ewais (normal) and Ewais (nubbin) cultivars, respectively. These results defined that the highest numerous and intensity bands were (6 bands) in Zebda cultivar followed by (5 bands) in Sedeq. While the lowest multiples were (4 bands) in Ewais cultivar. The bands with an approximate molecular mass ranging from (27-kDa to 73-KDa) were obtained in the elution fractions of protein from leaves.

The results explained that the Zebda and Sedeq cultivars which had normal fruits had the highest several bands than Ewais cultivar which had nubbin (aborted) fruits, these were supported to the above described results where, there were high genes expression for all the experimented ESTs primers, especially in cultivars which had the normal fruits and that is reflected on the protein electrophoresis with more bands essentially in normal fruits.

These results agreed with other investigator as He et al. (2012) who evaluated the gene expression using subtractive suppression hybridization to investigate the differentially expressed genes involved in embryo abortion of mango fruit cv. ‘Jinhuang’. Seven candidate genes from different categories were selected for semi-quantitative PCR analysis, and their possible functions in embryo abortion. They found that many transcriptionally regulated genes differentially accumulated in 2 types of mango embryo. However, 4 ESTs (MaAGA, MaAP2, MaERF, and MaMADS) were upregulated in normal embryo tissues compared to aborted embryos.
Figure 1. Amplification plot of fluorescent signal versus cycle number measured during quantitative amplification of AGAMOUS protein (MaAGA) by RT-qPCR.

Figure 2. Amplification plot of fluorescent signal versus cycle number measured during quantitative amplification of MADS box protein (MaMADS) by RT-qPCR.

Figure 3. Amplification plot of fluorescent signal versus cycle number measured during quantitative amplification of AP2D domain class transcription factor protein (MaAP2D) by RT-qPCR.

Figure 4. Amplification plot of fluorescent signal versus cycle number measured during quantitative amplification of ERF ethylene response factor protein (MaERF) by RT-qPCR.

Figure 5 A&B. SDS-PAGE of (A) total protein of mango embryos Zebda, Sedeq and Ewais (normal and nubbin) cultivars, (B) total protein of leaves from Zebda, Sedeq and Ewais (normal and nubbin) cultivars. The bands were calibrated with molecular marker ranging from 10 to 244 kDa.

CONCLUSION
This study suggests that relative quantification data provide basic ESTs and a step forward in our understanding of gene function and regulatory pathways belonged to embryo abortion in some mango cultivars.

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دراسة على إنتاجية الثمار الطبيعية والفص لبعض أشجار المانجو وعلاقتها بمستويات التعبير الجيني كمياً

محمود عادل استارا ً, عاطف إبراهيم ً, نادر عثمان ً, وعزت شمس

قسم الفلاحة ـ كلية الزراعة ـ جامعة الأسكندرية

قسم أمراض النبات ـ كلية الزراعة ـ جامعة الأسكندرية

قطاع الإرشاد ـ وزارة الزراعة واستصلاح الأرض ـ الجزيرة

أجريت الدراسة الحالية خلال موسم 2015 و 2016 على ثلاثة أصناف مانجو مصرية هي عويس (طبيعي، فص) وصديق وزيدة مزروعة في بستان خاص بمنطقة أدكو، محافظة البحر الأحمر. الأشجار تم اختيارها لدراسة إنتاجية بعض أشجار المانجو لثمار طبيعية وفص (مجهضة الجذع) و أيضاً التقدير الكمي لمستويات التعبير الجيني لفهم أفضل لظاهرة إجهاض الجذع في المانجو. استخدمت تقنية (mRNA) للوقت المحدد كمياً لتفاعلات البلمرة المتسلسل (RT-qPCR) لتتبع الكميّات النسبية للحمض النووي الريبوزي الرسول (mRNA) لعبير الجذع في الثمار الفص مثل طول الثمرة، عرضها وارتفاعها، وزن اللب، وزن البذرة، وزن الثمرة أقلي معنوي من الثمار الطبيعية، بينما كانت نسبة لب الثمرة البنية على معنوي في كل الموسمين. الصفات الكيميائية لثمار الفص مثل (المواذن الكلبية النباتية، المواذن الكلبية الحمضية، السمكاثة المختزلة، السمكاثات الكلبية) أنجم بكوك مثيل أيستر. كانت الأعلى معنوي من الثمار الطبيعية، بينما كانت الأقلي معنوي في قيم الممواذنة ذاتي ونباي (البيروكسيدين) وقد أظهرت النتائج أن الجذعات الخصبة بالأربعة بوادٍ مختلفة مختلفة في التعبير الجيني في أنجس الأغذية (الطبية، المجففة، المجففة) و الأعراص. علاوة على ذلك أظهرت الجذعات الخصبة بالأربعة بوادٍ على تعبير خفيف في الثمار الطبيعية عن الثمار الفص المصنوع بالعويس، وقد أظهرت أيضاً مستويات التعبير الجيني في أنجس الأعراص. صورة عالية للتعبير الجيني في صناعي آلات نحاسية والزريبة معنوية المصنوع بالعويس. كذلك أوضحت النتائج تحليل البروتينات الكيميائية لثمار طبيعية في أنجس الثمرة وصفوف اللب، لحيماً ثمار طبيعية كانت الأعلى في عدد الحزم المفصول أكثر من صناعي العويس الذي لديه ثمار فص وذلك في أنجس الأغذية (الطبية، الفص) والأعراص.


