VARIABILITY AND HERITABILITY OF FLORAL DEVELOPMENT IN APPLE FULL-SIB OFFSPRINGS

Ayşe Nilgün ATAY, Şerif ÖZONGUN, Turgay SEYMEN, Alamettin BAYAV, *Ersin ATAY

TAGEM, Fruit Research Institute,32500 Eğirdir, Isparta, Turkey


The timing of blooming in spring is highly crucial for temperate zone tree fruit production. In this study, we aimed to investigate floral development using the all parents and full-sib offsprings of two different crossing combinations (‘Kaşel 37’ × ‘Delbarestivale’ and ‘Kaşel 41’ × ‘Williams’ Pride’). Assessments of variability in floral development have been done according to a numerical assessment scheme defined by ten stages (stage 0–9). The assessments were conducted three different dates, early (21 04), intermediate (28 04), and late (05 05). The results showed significant variations for floral development among the 273 genotypes. In particular, the genotypes 326, 340, 369, 88 and 146 were found as superiors for floral development. The broad sense heritability ($h^2$) for floral development was reliable on the first assessment date, with no reliability on the other assessment dates. Our results would be useful to geneticists and breeders.

Key words: Amasya, breeding, F1, Malus slyvestris, new cultivar, progeny, spring frost.

INTRODUCTION

The practitioners have seen a rapid acceleration of new apple cultivars coming from both public and private breeding programs across the world (BROWN and MALONEY, 2013). The one of the most important objectives of modern breeding programs is to increase profitability in the orchard. The blooming time is crucial on the economic success of an orchard, and, therefore, it is usually taken into account in an apple breeding program. Flowering is a complicated developmental process of physiological and morphological functions affected by both external and internal factors (HANKE et al., 2007).

From the horticultural viewpoint, characterization of flowering phenology in apple trees has great importance for the control of spring frost and pollination. There are severe risks of frost

* Corresponding author: Ersin Atay, TAGEM, Fruit Research Institute,32500 Eğirdir, Isparta, Turkey, atayersin@yahoo.com
during blossoming and early fruitlet stages in many regions of the world (WERTHEIM and SCHMIDT, 2005). Fruit buds are usually hardy when they are dormant, but their sensitivity increases as they develop towards full blooming due to increasing water content in plant. Whereas there are variations in the susceptibility of blossom to spring frost among cultivars, almost 50% of apple flowers are generally damaged when the temperature dropped to -10°C at bud burst, -4°C at tight cluster and -2.8°C at the first bloom (RICHARDSON et al., 1976). Generally, an early flowering cultivar has more susceptibility to spring frost than the late flowering ones. A delay in blooming time may contribute to spring frost avoidance. Therefore, fruit tree breeders do not wish to select early flowering genotypes, and they generally prefer late flowering genotypes (WERTHEIM and SCHMIDT, 2005).

The native forms of ‘Amasya’ (Malus sylvestris subsp. orientalis var. microphylla Browicz) have existed in the Amasya city of Turkey and cultivated for over thousands of years in the temperate fruit regions of Turkey (DAVIS, 1972). Numerous strains of ‘Amasya’ apple such as ‘Kaşel 37’ and ‘Kaşel 41’ exist, varying in the proportion of red skin colour and fruit size that are crucial for marketability of apples (ATAY et al., 2010). Because of the excellent eating quality, ‘Amasya’ is the most important local apple of Turkish germplasm (ATAY and ATAY, 2011; ZIYA MOTALEBIPOUR et al., 2015), indicated considerable diversity (GULSEN et al., 2010). Though its very high preferences in the markets by Turkish consumers, the situation for growers is not brilliant because of the some special problems of this cultivar including the biennial bearing, low productivity and limited postharvest life. To solve the major problems of ‘Amasya’, we have conducted a breeding programme in Turkey. Blooming time is a critical trait for our breeding programme because ‘Amasya’ has a susceptibility to frost risk in many regions due to early blooming in spring. An understanding of floral development in the full-sib offsprings of an apple cultivar breeding programme is crucial for the efficient selection of genotypes that can have a natural adaptation to different climatic conditions. In this study, we evaluated four parent cultivars and 269 full-sib offsprings derived from ‘Kaşel 37’ × ‘Delbarestivale’ and ‘Kaşel 41’ × ‘Williams’ Pride’ crossing combinations with the experimental objectives of (1) documenting variations in floral development and (2) selection of superior genotypes that show late blooming. Besides, we calculated h² with a confidence interval (CI) on different assessment dates to explore the proportion of total variation between genotypes studied for floral development.

MATERIAL AND METHODS

Study area and plant material. This research was conducted at Fruit Research Institute, Eğirdir, Isparta, Turkey (37°48′52.16″ N, 30°52′39.66″ E, altitude 920 m). We studied on two different crossing combinations. The first F1 population was derived from a cross between ‘Kaşel 37’ and ‘Delbarestivale’ as described by ATAY et al. (2014). It comprised 170 genotypes. The second F1 population was derived from a cross between ‘Kaşel 41’ and ‘Williams’ Pride’. This population was composed of 99 genotypes. All genotypes were grafted onto M.9 rootstock replicated twice. The trees were planted in January 2010. The planting distances were 1 m between trees and 4 m between rows. Orchard management practices were maintained as recommended for commercial orchards in the region. Temperature data were taken from the weather station of Eğirdir located 7 km from the trial orchard. Any spring frost did not occur in the trial plot in 2015 (Figure 1).
Floral development. Assessments of variations in floral development have been done according to a numerical assessment scheme defined by ten stages (stage 0–9) (GOTTSCHALK and NOCKER, 2013). Floral development is partially different from traditional phenological scales like BBCH (Biologische Bundesanstalt, Bundessortenamt and CHemical industry) (CHAPMAN and CATLIN, 1976; MEIER et al., 1994; ATAY, 2013). Briefly, at the earliest stage (stage 0), plants had just broken dormancy. At stage 1, the inflorescence was visible without dissection. By stage 2, individual flowers were apparent, and petals were showed on most flowers within the inflorescence in stage 3. By stage 4, petals were apparent in all flowers and petals became dominant over sepals in the bud in stage 5. In stage 6, petals of one or more flowers failed to enclose bud. One flower was fully open at stage 7, and all flowers were open at stage 8. By stage 9, nearly all flowers had shed petals. Assessment of genotypes for floral development was performed on three dates – 21 April 2015 (first assessment date), 28 April 2015 (second) and 5 May 2015 (third) by early, intermediate and late flowering time of the population.

Statistical analysis. Data were analyzed using the software SAS-JMP, version 7.0 (SAS Institute Inc., Cary, North Carolina, USA) in the following three steps. Firstly, we compared the floral development of all genotypes using analysis of variance (ANOVA). When the F-test was significant, means between genotypes were separated using least significant difference (LSD) multiple comparison test ($P \leq 0.05$). Means are reported with the standard deviation (s.d.) in the tables. Secondly, to expose the principal component groups, we subjected the data to a factor analysis, and mean values were separated using LSD test at $P \leq 0.05$. Then, we created dendrograms using cluster analyses to show similarity or dissimilarity between genotypes for floral development. Thirdly, the $h^2$ was calculated using F-value in ANOVA as $1 - (1 / F)$ (GALLAIS, 1990). The CI was calculated according to Knapp et al. (1985) with the lower and upper limits equal to $[1 - 1 / (F_{obs} \times F_{0.975})]$ and $[1 - 1 / (F_{obs} \times F_{0.025})]$, respectively (LAURI et al., 2011).
RESULTS AND DISCUSSION

Variability in floral development among studied apple genotypes showed distinct variations (Figure 2). The mean values for evaluated genotypes derived from the cross between ‘Kaşel 41’ and ‘Williams’ Pride’ were comprised between 4.25 ± 0.50 and 7.50 ± 0.58 on the first assessment date (21 04). On this date, floral development of many genotypes including 330, 343, 309, 338 and 393 was bigger than 6. However, the some of the genotypes – 305, 332, 333, 342, 352, 401, 320, 341, 293, 326, 340 and 294, were evaluated as promising genotypes that had 4.75 ± 0.50 or lower values for floral development on the first assessment date. On this date, the floral development of the parents was determined as 6.00 ± 0.82 (Table 1).

Similarly, genotypes derived from the cross between ‘Kaşel 37’ and ‘Delbarestivale’ displayed visible differences for floral development. Floral development was between 6.50 ± 0.58 and 6.75 ± 0.50 in some genotypes – 198, 31, 107, 156, 164, 272, 23 and 236. The female parent (‘Kaşel 37’) showed 6.00 ± 0.82 for floral development, and this value was 5.25 ± 0.96 for the male parent (‘Delbarestivale’). Many genotypes gave 4.25 ± 0.50 or lower values for floral development in this crossing combination (Table 1).

In fruit trees, internal as well as external factors are involved in flower-bud development that is not triggered by just one factor (TROMP, 2005). Blooming time in deciduous fruits is influenced primarily by genotype (STEPULAITIENE et al., 2013). Large differences occur between cultivars and within the same cultivar between years for floral development. Furthermore, flower-bud development does not start equally throughout the tree (SZALAY, 2006). Flower buds on spurs may open earlier than lateral buds on one-year-old shoots (ATAY and KOYUNCU, 2012). Thus, here, we studied floral development on spurs.

The difference in floral development was quite distinct on the first assessment date (21 04). The second (28 04) and especially third assessment date (05 05) showed a slightly lower variability for floral development than the first assessment date (Figure 2). Floral development was
slower in middle April than in subsequent dates. In any case, when the cold period is over, the process of the floral development accelerates (TROMP, 2005). The temperature, especially in the preceding blooming period, has an overriding influence on the timing of blooming (WALTER, 2003; TROMP, 2005). The temperature was comparatively higher on the second and third assessment dates in the study that accelerated floral development. Thus, the differences in floral development were estimated to be less on these dates (28 04 and 05 05). Warm weather shortens the length of the flowering period, and cold weather does the opposite (WERTHEIM and SCHMIDT, 2005).

Table 1. Floral development (±SD) of some early and late blooming genotypes on the first assessment date (21 04 2015)

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Floral development</th>
<th>Genotypes</th>
<th>Floral development</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early blooming genotypes</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>'Kaşel 41' × 'Williams' Pride'</td>
<td>7.50±0.58 a</td>
<td>'Kaşel 37' × 'Delbarestivale'</td>
<td>6.75±0.50 a</td>
</tr>
<tr>
<td>'Kaşel 37' × 'Delbarestivale'</td>
<td>7.25±0.96 ab</td>
<td></td>
<td>6.75±0.50 a</td>
</tr>
<tr>
<td>309</td>
<td>7.25±0.95 ab</td>
<td>107</td>
<td>6.50±0.58 ab</td>
</tr>
<tr>
<td>338</td>
<td>7.00±0.82 abc</td>
<td>156</td>
<td>6.50±0.58 ab</td>
</tr>
<tr>
<td>393</td>
<td>7.00±0.82 abc</td>
<td>164</td>
<td>6.50±0.58 ab</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>272</td>
<td>6.50±0.58 ab</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>23</td>
<td>6.50±0.58 ab</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>236</td>
<td>6.50±0.58 ab</td>
</tr>
<tr>
<td>Female parent</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male parent</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>'Kaşel 41'</td>
<td>6.00±0.82 efg</td>
<td>'Kaşel 37'</td>
<td>5.25±0.96 fg</td>
</tr>
<tr>
<td>'Williams' Pride'</td>
<td>6.00±0.82 efg</td>
<td>'Delbarestivale'</td>
<td>6.00±0.82 cd</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Late blooming genotypes</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>305</td>
<td>4.75±0.50 jkl</td>
<td>140</td>
<td>4.25±0.50 jk</td>
</tr>
<tr>
<td>332</td>
<td>4.75±0.50 jkl</td>
<td>151</td>
<td>4.25±0.50 jk</td>
</tr>
<tr>
<td>333</td>
<td>4.75±0.50 jkl</td>
<td>162</td>
<td>4.25±0.50 jk</td>
</tr>
<tr>
<td>342</td>
<td>4.75±0.50 jkl</td>
<td>163</td>
<td>4.25±0.50 jk</td>
</tr>
<tr>
<td>352</td>
<td>4.75±0.50 jkl</td>
<td>223</td>
<td>4.25±0.50 jk</td>
</tr>
<tr>
<td>401</td>
<td>4.75±0.50 jkl</td>
<td>280</td>
<td>4.00±0.00 k</td>
</tr>
<tr>
<td>320</td>
<td>4.50±0.58 kl</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>341</td>
<td>4.50±0.58 kl</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>293</td>
<td>4.25±0.50 l</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>326</td>
<td>4.25±0.50 l</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>340</td>
<td>4.25±0.50 l</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>294</td>
<td>4.25±0.50 l</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

Within columns, different letters indicate significant differences according to LSD multiple comparison test at P ≤ 0.05.

Floral development is defined by ten stages (stage 0–9). The 0 is used for the earliest stage of floral development in which plants had just broken dormancy, and 9 is used for the last stage of floral development in which nearly all flowers had shed petals. The hyphens (–) represent the other genotypes employed in the study.
We identified some late blooming genotypes on the last two assessment dates (28 04 and 05 05) (Table 2). The genotypes 320, 326, 340, 333 and 294 from the cross between ‘Kaşel 41’ × ‘Williams’ Pride’ gave promising results for late blooming (<6.00 ± 0.82) on the second assessment date. The other genotypes from this crossing combination were substantially similar to the parents for floral development. On the last assessment date (05 05), most of the genotypes reached the stage 8. Only the genotypes 316, 326, 340 and 369 gave lower values than 8 for floral development. It was interesting that the genotypes 316 and 369, evaluated as promising genotypes on the third assessment date, were not promising genotypes on the second assessment date.

Table 2. Floral development (±SD) of late blooming genotypes on the second (28 04) and third (05 05) assessment dates in 2015

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Floral development</th>
<th>Genotypes</th>
<th>Floral development</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>320</td>
<td>6.00±0.82 gh</td>
<td>239</td>
</tr>
<tr>
<td></td>
<td>326</td>
<td>6.00±0.82 gh</td>
<td>39</td>
</tr>
<tr>
<td></td>
<td>340</td>
<td>6.00±0.82 gh</td>
<td>163</td>
</tr>
<tr>
<td></td>
<td>333</td>
<td>5.75±0.50 h</td>
<td>40</td>
</tr>
<tr>
<td></td>
<td>294</td>
<td>5.50±0.58 h</td>
<td>140</td>
</tr>
<tr>
<td>‘Kaşel 41’</td>
<td>7.75±0.50 ab</td>
<td>‘Kaşel 37’</td>
<td>7.75±0.50 a</td>
</tr>
<tr>
<td>‘Williams’ Pride’</td>
<td>7.50±0.58 abc</td>
<td>‘Delbarestivale’</td>
<td>6.50±0.58 def</td>
</tr>
</tbody>
</table>

We observed a similar range in the full-sib offsprings of ‘Kaşel 37’ × ‘Delbarestivale’ crossing combination as for another cross (Table 2). The promising genotypes were 239, 39, 163, 40 and 140 on the second assessment date. The genotypes 89, 88 and 146 were determined as promising genotypes on the last assessment date (05 05).
Since apple trees are more sensitive to spring frost when they are in full blooming, late-flowering selections often avoid frost damages (MEHLENBACHER and VOORDECKERS, 1991). Open flowers are more vulnerable to cold damage, and severe damage can be caused by just a few hours at a temperature of −2°C. (WEBSTER, 2005). In this study, all flowers of the parents and most genotypes entranced in stage 8 on the last assessment date (05 05). However, floral development was lower than 8 in the genotypes 326, 340, 369, 88 and 146 during the last assessment date and only one or two flowers were fully opened. A few days delaying in flowering time can reduce the risk of frost damage.

We used a hierarchical cluster analysis to do an assessment of similarity or dissimilarity in studied apple genotypes by floral development over three assessment dates. A dendrogram including six clusters was created for ‘Kaşel 41’ × ‘Williams’ Pride’ crossing combination (Figure 3). The number of genotypes in a cluster varied from 3 (Cluster F) to 24 (Cluster B). Cluster C with the highest floral development value in all assessment dates consisted of 23 genotypes. Cluster F composed of the three genotypes 326, 340 and 369 with the lowest mean values for floral development was characterized by late flowering habit (Table 3).

### Table 3. The number of genotypes of ‘Kaşel 41’ × ‘Williams’ Pride’ and ‘Kaşel 37’ × ‘Delharestivale’ crossing combinations in each cluster (n) and mean (±SD) Floral development values of clusters on three assessment dates (first, second and third)

<table>
<thead>
<tr>
<th>Cross</th>
<th>Cluster</th>
<th>n</th>
<th>First (21 04)</th>
<th>Second (28 04)</th>
<th>Third (05 05)</th>
</tr>
</thead>
<tbody>
<tr>
<td>‘Kaşel 41’ × ‘Williams’ Pride’</td>
<td>A</td>
<td>19</td>
<td>5.37±0.59 d</td>
<td>7.17±0.62 c</td>
<td>8.43±0.50 b</td>
</tr>
<tr>
<td></td>
<td>B</td>
<td>24</td>
<td>6.25±0.83 b</td>
<td>7.38±0.67 b</td>
<td>8.44±0.50 b</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>23</td>
<td>6.60±0.63 a</td>
<td>7.58±0.62 a</td>
<td>8.86±0.35 a</td>
</tr>
<tr>
<td></td>
<td>D</td>
<td>21</td>
<td>5.71±0.67 c</td>
<td>7.30±0.64 bc</td>
<td>8.82±0.39 a</td>
</tr>
<tr>
<td></td>
<td>E</td>
<td>11</td>
<td>4.68±0.56 f</td>
<td>6.32±0.71 d</td>
<td>8.55±0.50 b</td>
</tr>
<tr>
<td></td>
<td>F</td>
<td>3</td>
<td>4.67±0.78 f</td>
<td>6.25±0.75 d</td>
<td>7.58±0.67 c</td>
</tr>
<tr>
<td><strong>F ratio</strong></td>
<td></td>
<td></td>
<td>149.6518</td>
<td>62.2324</td>
<td>51.8055</td>
</tr>
<tr>
<td><strong>P value</strong></td>
<td></td>
<td></td>
<td>0.0001</td>
<td>0.0001</td>
<td>0.0001</td>
</tr>
<tr>
<td>‘Kaşel 37’ × ‘Delharestivale’</td>
<td>A</td>
<td>48</td>
<td>5.81±0.69 b</td>
<td>7.28±0.65 b</td>
<td>8.83±0.37 ab</td>
</tr>
<tr>
<td></td>
<td>B</td>
<td>14</td>
<td>6.25±0.51 a</td>
<td>7.73±0.45 a</td>
<td>8.88±0.33 a</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>21</td>
<td>5.30±0.51 d</td>
<td>6.76±0.51 d</td>
<td>8.76±0.43 b</td>
</tr>
<tr>
<td></td>
<td>D</td>
<td>27</td>
<td>5.32±0.59 d</td>
<td>6.56±0.57 e</td>
<td>8.42±0.51 e</td>
</tr>
<tr>
<td></td>
<td>E</td>
<td>24</td>
<td>5.65±0.60 c</td>
<td>7.02±0.60 c</td>
<td>8.53±0.50 d</td>
</tr>
<tr>
<td></td>
<td>F</td>
<td>11</td>
<td>6.30±0.63 a</td>
<td>7.41±0.62 b</td>
<td>8.50±0.51 de</td>
</tr>
<tr>
<td></td>
<td>G</td>
<td>11</td>
<td>4.48±0.51 e</td>
<td>6.25±0.69 f</td>
<td>8.25±0.44 f</td>
</tr>
<tr>
<td></td>
<td>H</td>
<td>14</td>
<td>4.61±0.53 e</td>
<td>6.20±0.67 f</td>
<td>8.64±0.48 c</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>2</td>
<td>4.75±0.46 e</td>
<td>6.00±0.76 f</td>
<td>7.25±0.71 g</td>
</tr>
<tr>
<td><strong>F ratio</strong></td>
<td></td>
<td></td>
<td>142.5838</td>
<td>109.7445</td>
<td>58.8449</td>
</tr>
<tr>
<td><strong>P value</strong></td>
<td></td>
<td></td>
<td>0.0001</td>
<td>0.0001</td>
<td>0.0001</td>
</tr>
</tbody>
</table>

Within columns, different letters indicate significant differences according to LSD multiple comparison test at $P \leq 0.05$. Floral development is defined by ten stages (stage 0–9). The 0 is used for the earliest stage of floral development in which plants had just broken dormancy, and 9 is used for the last stage of floral development in which nearly all flowers had shed petals.
Figure 3. Dendrogram of floral development for ‘Kaşel 41’ × ‘Williams’ Pride’ cross
Hierarchical cluster analysis grouped full-sib offsprings of the ‘Kaşel 37’ × ‘Delbarestivale’ crossing combination into nine clusters based on floral development (Figure 4). The mean values of clusters on each assessment date were presented in Table 3. Cluster B with 14 genotypes had quite high values for floral development on all assessment dates. Similarly, cluster F with 11 genotypes had high values for floral development as for Cluster B. The clusters G, H and I gave lower mean values for floral development in comparison to the other clusters for the
first and second assessment dates. In the last assessment, Cluster I, composed of the genotypes 88 and 146, had the lowest floral development value (7.25 ± 0.71).

In our full-sib offsprings based on two different crossing combinations, early blooming genotypes had a considerable number in the total population, whereas, the number of late flowering genotypes was a few. The female parents of our crossing combinations, (‘Kaşel 37’ and ‘Kaşel 41’), opened their flowers in an early period in our growing conditions. We observed that the offsprings of parents showed mostly an early flowering as for their parents. The timing of flowering in apples is a polygenic trait with high $h^2_b (>0.7)$ (Currie, 2000; Liebhard et al., 2003; Hancock et al., 2008). Our results for $h^2_b$ verify literature when assessment date is comparatively early. Thus, we calculated $h^2_b$ as >0.7 in the genotypes of both crossing combinations on a comparatively early date (21 04) (Table 4). However, $h^2_b$ values for the offsprings of both crosses sharply decreased when the days passed (28 04 and 05 05). We can say that at a comparatively later date, $h^2_b$ for the time of flowering would not be practical because of a possible interaction between a high ambient temperature and floral development in field condition.

Table 4. Broad sense heritability ($h^2_b$) and confidence interval (CI at 95%) of Floral development on three assessment dates (first, second and third) for the full-sib offspring populations of ‘Kaşel 37’ × ‘Delbarestivale’ and ‘Kaşel 41’ × ‘Williams’ Pride’

<table>
<thead>
<tr>
<th></th>
<th>‘Kaşel 37’ × ‘Delbarestivale’</th>
<th>‘Kaşel 41’ × ‘Williams’ Pride’</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$h^2_b$ CI (95%)</td>
<td>$h^2_b$ CI (95%)</td>
</tr>
<tr>
<td>First (21 04)</td>
<td>0.71 0.63–0.77</td>
<td>0.78 0.72–0.83</td>
</tr>
<tr>
<td>Second (28 04)</td>
<td>0.64 0.53–0.71</td>
<td>0.50 0.35–0.60</td>
</tr>
<tr>
<td>Third (05 05)</td>
<td>0.13 (−0.12)–0.31</td>
<td>0.33 0.14–0.47</td>
</tr>
</tbody>
</table>

To conclude, there was considerable genetic variation in floral development among the genotypes derived from two different crossing combinations. On the last assessment date (05 5), the genotypes 326, 340, 369, 88 and 146 were found as superiors for the floral development trait. On May 5, the other genotypes were fully opened their flowers while these superior genotypes had only a few opened flowers. These outputs are highly critical of our breeding programme. Besides, as a scientific result, we can say that the $h^2_b$ for the floral development of genotypes is quite reliable when the temperature is mild in spring.

ACKNOWLEDGEMENTS

We thank Dr. Pierre Eric Lauri (INRA, France) for helpful discussions on heritability.

Received January 28th, 2016
Accepted April 11th, 2016

REFERENCES


VARIJABILNOST I NASLEDNOST RAZVOJA CVETA JABUKE U POTOMSTVA PUNIH SRODNIKA

Ayşe Ilgın ATAY, Şerif ÖZONGUN, Turgay SEYMEN, Alamettin BAYAV, *Ersin ATAY

TAGEM, Fruit Research Institute 32500 Eğirdir, Isparta, Turkey

Izvod


Odobreno 11. IV. 2016.