Characterization of strawberry (\textit{Fragaria \times ananassa} Duch.) cultivars and hybrid clones using SSR and AFLP markers

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Abstract

Simple sequence repeat (SSR) and amplified fragment length polymorphism (AFLP) markers are commonly used in genetics and breeding studies due to their multi-allelic nature, high abundance, reproducibility, transferability over genotypes and extensive genome coverage. The genetic characterization of 44 strawberry (\textit{Fragaria \times ananassa} Duch.) genotypes using SSR and AFLP markers is presented in the study. The genetic diversity of strawberry cultivars and hybrid clones developed mostly at the Institute of Horticulture of Lithuanian Research Centre for Agriculture and Forestry’s breeding programme was evaluated using 11 previously published SSR primer pairs and 6 AFLP primer combinations. Nine to 21 alleles per primer pair were identified in the SSR multiplex analysis. The number of differentiated genotypes varied between 12 and 38. The microsatellite primer pairs ARSFL-009, CFACT152 and EMFv104 were the most informative. The number of polymorphic fragments in the AFLP study varied between 44 and 197. The rate of polymorphism varied from 39\% (primer combination EcoRI-AGG/MseI-CAA) to 88\% (EcoRI-ACC/MseI-CAC). The results in this study demonstrated that the chosen previously published SSR primer pairs and the selected AFLP primer combinations after pre-screening procedure were suitable for the genotyping of strawberry accessions. For the cluster analysis fragments of both marker systems were used to get a more comprehensive description of the genetic relationships of the evaluated strawberry accessions. The cluster analysis revealed two main groups consisting of 10 and 34 strawberry cultivars and clones, respectively.

Key words: amplified fragment length polymorphism, genetic diversity, genotyping, hybrids, simple sequence repeat, strawberry.

Introduction

Commercially important strawberries (\textit{Fragaria \times ananassa} Duch.) belong to the family \textit{Rosaceae} and the genus \textit{Fragaria}, which comprises 23 species (Rousseau-Gueutin et al., 2009). With its high nutritional value, the strawberry is one of the most popular berry fruits in the world. The cultivated strawberry, \textit{F. \times ananassa}, is an octoploid (2n = 8x = 56). Cultivated strawberry arises from a narrow genetic base of approximately 50 founding clones (Dale, Sjulin, 1990). Because of this, it is difficult to effectively breed new varieties with differing genetic characteristics. Marker-assisted selection, with the help of polymorphic markers may be of benefit (Yoon et al., 2012). It allows clarifying the level of genetic divergence among strawberry genotypes.

Many biochemical and molecular marker systems have been used for strawberry cultivar identification, including isozymes (Bell, Simpson, 1994), randomly amplified polymorphic DNA (RAPD) (Milella et al., 2006), amplified fragment length polymorphism (AFLP) (Degani et al., 2001), inter simple sequence repeat (ISSR) (Arnau et al., 2002) and simple sequence repeat (SSR) markers (Lewers et al., 2005; Gil-Ariza et al., 2006; Govan et al., 2008; Sargent et al., 2008). Each of these systems has their own technical limitations. While microsatellites exhibit co-dominant inheritance, RAPD and AFLP markers are usually dominant (Brunings et al., 2010).

SSR markers have been employed extensively in strawberry because of their reproducibility and ability to sensitively detect subtle polymorphisms. Application of this technology to strawberry is particularly difficult because strawberries are octoploid, with eight copies of each gene, and because inbreeding can lead to cultivars with multiple copies of the same allele at a single locus. Dangl et al. (2007) described an SSR marker system that can distinguish closely related strawberry cultivars. This
system uses published markers to reduce development time, and scores the amplified fragments as dominant markers. Because primer binding is highly specific, this system is both highly accurate and reproducible by other laboratories.

AFLP are highly reproducible dominant markers (Agarwal et al., 2008) and the large number of fragments gives them high statistical power (Meudt, Clarke, 2007). Therefore, AFLP markers are well suited for distinguishing between closely related genotypes. Both marker systems have pros and cons. On the one hand, SSR markers are highly specific, due to their development from already known DNA sequences. Their usefulness was shown in our previous works on other Rosaceae family plants – Prunus avium (Stanys et al., 2012) and Pyrus communis (Rugienius et al., 2013), but the number of markers (fragments) is limited and they cover mostly just the non-coding DNA regions. On the other hand, AFLP markers do not require the primary knowledge about the DNA sequences, the high number of fragments is generated with one primer combination and they cover whole genome, but they need the pre-screening option for the selection of highly polymorphic primer combinations for the object to be examined (Frercks et al., 2013; 2014).

The breeding program of strawberry in Lithuania started in the middle of the last century. New cultivars, resistant to cold and fungal diseases, with varying season of ripening and high productivity were introduced (Rugienius et al., 2004; Baniulis et al., 2012) and they cover whole genome, but they need the pre-screening option for the selection of highly polymorphic primer combinations for the object to be examined (Frercks et al., 2013; 2014).

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Results and discussion

SSR analysis. A total of 181 polymorphic alleles were identified for 44 *Fragaria* accessions using 11 SSR primer pairs. The results from the 11 SSR primer pairs are summarized in Table 2. The allele size ranged from 71 bp (EMFv-104) to 288 bp (ARSFL-011). The number of alleles per primer pair varied from 9 (CFACT-103) to 21 (EMFv-104), with an average of 16.5 alleles per SSR primer pair. The highest number of alleles (21) was obtained with the EMFv-104 primer pair. This primer pair was also the most informative by Honjo et al. (2011). According to the number of alleles in this study, the primer pairs ARSFL-009 (20), ARSFL-010 (16) and ARSFL-011 (17) were highly informative also and the number of obtained alleles was higher as compared to the studies of Dangl et al. (2007) and Brunings et al. (2010), where 26 and 45 genotypes were investigated.

Table 1. Pedigree of strawberry cultivars and hybrid clones

<table>
<thead>
<tr>
<th>No.</th>
<th>Cultivar or hybrid clone</th>
<th>Pedigree</th>
<th>Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>‘Antea’</td>
<td>FB6L-3 × ‘Onebor’</td>
<td>Italy</td>
</tr>
<tr>
<td>2.</td>
<td>‘Ariel’</td>
<td>Unknown</td>
<td>Italy</td>
</tr>
<tr>
<td>3.</td>
<td>‘Asia’</td>
<td>Unknown</td>
<td>Italy</td>
</tr>
<tr>
<td>4.</td>
<td>‘Chelsea Pensioner’</td>
<td>UK and Italian selections</td>
<td>United Kingdom</td>
</tr>
<tr>
<td>5.</td>
<td>‘Darsselect’</td>
<td>‘Parker’ × ‘Elsanta’</td>
<td>France</td>
</tr>
<tr>
<td>6.</td>
<td>‘Elegance’</td>
<td>EM834 × EM1033</td>
<td>United Kingdom</td>
</tr>
<tr>
<td>7.</td>
<td>‘Elkat’</td>
<td>‘Elsanta’ × ‘Dukat’</td>
<td>Poland</td>
</tr>
<tr>
<td>8.</td>
<td>‘Figaro’</td>
<td>‘Elsanta’ × ‘Pajaro’</td>
<td>Netherlands</td>
</tr>
<tr>
<td>9.</td>
<td>‘Gava’</td>
<td>Unknown</td>
<td>Italy</td>
</tr>
<tr>
<td>10.</td>
<td>‘Lucy’</td>
<td>‘Honeoyce’, ‘Selva’, ‘Rapella’</td>
<td>United Kingdom</td>
</tr>
<tr>
<td>11.</td>
<td>‘Orleans’</td>
<td>‘L’Acadie’ × ‘Joliette’</td>
<td>Canada</td>
</tr>
<tr>
<td>12.</td>
<td>‘Rubinovyy kulon’</td>
<td>‘Senga Sengana’ × ‘Fairfax’</td>
<td>Russia</td>
</tr>
<tr>
<td>13.</td>
<td>‘Sara’</td>
<td>‘Senga Sengana’, <em>Fragaria vesca</em></td>
<td>Sweden</td>
</tr>
<tr>
<td>14.</td>
<td>‘Saulene’</td>
<td>‘Senga Sengana’ × ‘Shuksan’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>15.</td>
<td>‘Valotar’</td>
<td>‘Jewell’ × ‘Senga Sengana’</td>
<td>Finland</td>
</tr>
<tr>
<td>16.</td>
<td>‘Venta’</td>
<td>‘Senga Sengana’ × ‘Festivalnaja’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>17.</td>
<td>‘Venta Rvk’</td>
<td>‘Venta’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>18.</td>
<td>‘Zumba’</td>
<td>Unknown</td>
<td>Netherlands</td>
</tr>
<tr>
<td>19.</td>
<td>L-181</td>
<td>Unknown</td>
<td>Italy</td>
</tr>
<tr>
<td>20.</td>
<td>3973856</td>
<td>K88-4 × ‘Mohawk’</td>
<td>Canada</td>
</tr>
<tr>
<td>21.</td>
<td>940101</td>
<td>‘Guardian’ × ‘Pegasus’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>22.</td>
<td>051901</td>
<td>‘Sophia’ × ‘Aroa’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>23.</td>
<td>000206</td>
<td>‘Anapolis’ × ‘Polka’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>24.</td>
<td>080801</td>
<td>‘Venta’ × ‘Irma’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>25.</td>
<td>080901</td>
<td>‘Venta’ × ‘Ariel’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>26.</td>
<td>080903</td>
<td>‘Venta’ × ‘Ariel’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>27.</td>
<td>080904</td>
<td>‘Venta’ × ‘Ariel’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>28.</td>
<td>082901</td>
<td>‘Irma’ × ‘Salut’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>29.</td>
<td>083101</td>
<td>‘Marmolada’ × ‘Pink Panda’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>30.</td>
<td>084308</td>
<td>‘Venta’ × ‘Roxana’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>31.</td>
<td>084309</td>
<td>‘Venta’ × ‘Roxana’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>32.</td>
<td>102101</td>
<td>‘Ariel’ × ‘Jonsok’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>33.</td>
<td>102201</td>
<td>‘Fenella’ × ‘Festivalnaja’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>34.</td>
<td>102401</td>
<td>‘Fenella’ × ‘Orleans’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>35.</td>
<td>102601</td>
<td>‘Sonata’ × ‘Festivalnaja’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>36.</td>
<td>103001</td>
<td>‘Elegance’ × ‘Rubinovyy kulon’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>37.</td>
<td>103301</td>
<td>‘Lucy’ × ‘Festivalnaja’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>38.</td>
<td>103701</td>
<td>98.167.1 × ‘Jonsok’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>39.</td>
<td>103801</td>
<td>L-181 × ‘Jonsok’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>40.</td>
<td>104001</td>
<td>‘Asia’ × ‘Desnianka’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>41.</td>
<td>104002</td>
<td>‘Asia’ × ‘Desnianka’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>42.</td>
<td>104601</td>
<td>‘Salut’ × ‘Elsanta’</td>
<td>Lithuania</td>
</tr>
<tr>
<td>43.</td>
<td>104701</td>
<td>‘Darsselect’ open pollinated</td>
<td>Lithuania</td>
</tr>
<tr>
<td>44.</td>
<td>005042</td>
<td>‘Selen’ × 952020 (‘Tribute’ × <em>F. chiloensis</em>)</td>
<td>Lithuania</td>
</tr>
</tbody>
</table>
respectively. Primer pair CFACT-110 was also one of the most informative ones according to one of the highest number of alleles in our study and the study of Yoon et al. (2012) as well.

Primer pairs used in this study were able to distinguish between 12 and 38 of 44 strawberry genotypes (Table 2). According to the number of differentiated genotypes, the most informative primer pairs were ARSFL-009 and CFACT-152. Dangl et al. (2007) suggested using the primer ARSFL-009, followed by primers ARSFL-010 and ARSFL-011 for cultivar identification according to their highest number of alleles and unique peak profiles. The primer pair EMFv-104 distinguished 36 genotypes in this study and was most informative in the study of Brunings et al. (2010) as well with the ability to distinguish 24 genotypes. The least informative primer pairs in this study were EMFax-381827 and EMFv-125 as both were able to distinguish only 12 genotypes.

Table 2. Characteristics of SSR (simple sequence repeat) loci

<table>
<thead>
<tr>
<th>No.</th>
<th>SSR primer pair</th>
<th>Allele size range in bp</th>
<th>Number of alleles</th>
<th>Number of differentiated genotypes</th>
<th>Genetic diversity</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>ARSFL-009</td>
<td>200–236</td>
<td>20</td>
<td>38</td>
<td>0.37</td>
</tr>
<tr>
<td>2.</td>
<td>ARSFL-010</td>
<td>214–268</td>
<td>16</td>
<td>28</td>
<td>0.69</td>
</tr>
<tr>
<td>3.</td>
<td>ARSFL-011</td>
<td>247–288</td>
<td>17</td>
<td>31</td>
<td>0.42</td>
</tr>
<tr>
<td>4.</td>
<td>EMFax-380097</td>
<td>146–183</td>
<td>20</td>
<td>34</td>
<td>0.30</td>
</tr>
<tr>
<td>5.</td>
<td>EMFax-381827</td>
<td>138–186</td>
<td>12</td>
<td>12</td>
<td>0.35</td>
</tr>
<tr>
<td>6.</td>
<td>EMFv-125</td>
<td>207–234</td>
<td>10</td>
<td>12</td>
<td>0.33</td>
</tr>
<tr>
<td>7.</td>
<td>EMFv-104</td>
<td>71–128</td>
<td>21</td>
<td>36</td>
<td>0.25</td>
</tr>
<tr>
<td>8.</td>
<td>CAFCT-084</td>
<td>105–147</td>
<td>20</td>
<td>30</td>
<td>0.19</td>
</tr>
<tr>
<td>9.</td>
<td>CAFCT-110</td>
<td>136–182</td>
<td>20</td>
<td>32</td>
<td>0.26</td>
</tr>
<tr>
<td>10.</td>
<td>CAFCT-103</td>
<td>117–151</td>
<td>9</td>
<td>28</td>
<td>0.36</td>
</tr>
<tr>
<td>11.</td>
<td>CAFCT-152</td>
<td>105–147</td>
<td>16</td>
<td>38</td>
<td>0.19</td>
</tr>
<tr>
<td>Mean</td>
<td></td>
<td></td>
<td>16.5</td>
<td>29</td>
<td>0.34</td>
</tr>
</tbody>
</table>

The genetic diversity among primer pairs varied from 0.19 (CAFCT-084 and CFACT-152) to 0.69 (ARSFL-010), with an average of 0.34. This indicates the conservativeness of non-coding regions in strawberry genome. According to the results obtained in this study, we agree with Dangl et al. (2007) suggestion to use the primer pairs ARSFL-009, ARSFL-010 and ARSFL-011 for cultivar identification.

AFLP analysis. A total of 1178 fragments were identified in 44 strawberry accessions using six AFLP primer combinations, of which 927 (78.7%) were polymorphic. The fragment number generated with each AFLP primer combination varied between 112 and 237, with an average of 196 (Table 3).

The number of polymorphic fragments varied from 44 to 197 (154.5 on average). The highest number of polymorphic fragments (197) was generated using the EcoRI-AGG/MseI-CAC primer combination. The least polymorphic was the primer combination EcoRI-AGG/MseI-CAA with 44 polymorphic fragments. The polymorphism rate among the six AFLP primer combinations varied between 39% and 88% (75.2% on average). For strawberry accessions used in this study, the most informative was the EcoRI-ACC/MseI-CAC primer combination. The number of polymorphic fragments for primer combinations EcoRI-ACC/MseI-CAC and

<table>
<thead>
<tr>
<th>No.</th>
<th>Primer combination</th>
<th>Number of fragments</th>
<th>Number of polymorphic fragments</th>
<th>Polymorphism %</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>EcoRI</td>
<td>MseI</td>
<td>ACT</td>
<td>172</td>
</tr>
<tr>
<td>2.</td>
<td>AGG</td>
<td>CAA</td>
<td>112</td>
<td>44</td>
</tr>
<tr>
<td>3.</td>
<td>ACC</td>
<td>CAT</td>
<td>237</td>
<td>191</td>
</tr>
<tr>
<td>4.</td>
<td>ACC</td>
<td>CTA</td>
<td>224</td>
<td>191</td>
</tr>
<tr>
<td>5.</td>
<td>ACC</td>
<td>CAC</td>
<td>223</td>
<td>197</td>
</tr>
<tr>
<td>6.</td>
<td>ACC</td>
<td>CAG</td>
<td>210</td>
<td>175</td>
</tr>
<tr>
<td>Mean</td>
<td></td>
<td></td>
<td>196.3</td>
<td>154.5</td>
</tr>
</tbody>
</table>

Table 3. Number of fragments, number of polymorphic fragments and degree of polymorphism in our AFLP study of 44 strawberry cultivars and hybrid clones
EcoRI-ACC/MseI-CAG was notably larger than in the previous study on strawberry (Degani et al., 2001). This may be due to the use of capillary electrophoresis in this study, which is a more sensitive method than gel electrophoresis.

**Cluster analysis.** For the investigation of genetic relationships among 44 strawberry genotypes, the common dendrogram using AFLP and SSR markers was constructed, due to the fact that the different DNA marker systems cover the different (sequence specific-tagged and nonspecific) DNA segments of genome and enables a more comprehensive characterization of the genome as compared to the use of different marker systems separately. The assessed strawberry genotypes were clustered into two groups in the dendrogram (Fig.).

![Dendrogram of 44 strawberry accessions based on combined analysis of SSR (simple sequence repeat) and AFLP (amplified fragment length polymorphism) molecular markers](image)

The first group contained 34 accessions of strawberry. The cv. ‘Chelsea Pensioner’ was separated from remaining accessions in this group (bootstrap value 74%). Some of associations in this group could be explained according to the pedigree: the seedling clone 103301 is an offspring of cv. ‘Lucy’, the seedling clone 103801 is an offspring of L-181 and ‘Venta Rvk’ is the somaclonal variant of ‘Venta’. The remaining associations (with the bootstrap value ≥50%) were not related to pedigree in this group. It indicates the dependence of the analysis results on the type of markers and as well as of the number of markers used for the analysis. The second group of the dendrogram consisted of ten accessions, mostly of bred clones. Two separations in this group were indicated with high bootstrap values (96–100%): the seedlings 080903

**Notes.** The numbers above the nodes of dendrogram indicate the bootstrap values of equal or greater than 50%. The scale above the dendrogram indicates the distance level between accessions.

**Figure.** Cluster analysis of 44 strawberry accessions based on combined analysis of SSR (simple sequence repeat) and AFLP (amplified fragment length polymorphism) molecular markers
and 080904 were separated together due to the same cross combination of common parents ‘Venta’ × ‘Ariel’ and two seedlings 080801 and 082901 – due to the common parent ‘Irma’.

Genetic diversity of cultivated strawberry is quite low (Dale, Sjulin, 1990) and genetic affinities among hybrid clones are not unexpected. Although strawberries have complicated ploidy levels and different parentages, most of the alleles are shared among the cultivated strawberries (Yoon et al., 2012). The level of genetic diversity in strawberry germplasm is a critical consideration for the breeding of new cultivars. Inbreeding in cultivated strawberry leads to rapid loss of vigour, yield and fruit size. The gene pool of strawberry cultivars is narrow due to the intense selection for certain traits and the use of relative small number of parental forms. Determining the amount of genetic diversity available in germplasm has typically been estimated through pedigree analysis. However, inaccurate pedigree records, absence of pedigree records, or misnamed and/or renamed cultivars can confound the accuracy of such estimation (Degani et al., 2001). Cultivars often express remarkably similar phenotypes, especially in the vegetative stage. Moreover, discerning phenotypic descriptors may vary greatly with environmental conditions and cultural practices (Brunings et al., 2010). As molecular methods greatly with environmental conditions and cultural practices (Brunings et al., 2010). As molecular methods are not influenced by environment and therefore stable in any development stage, they provide information, which can be useful for increasing effectiveness of breeding and for performing purposeful plant genetic studies.

Our results show that combination of SSR and AFLP methods is effective and useful for identification of cultivars and for assessing the level of genetic diversity in strawberry cultivars and breeding lines.

Conclusions

1. The study identified SSR (simple sequence repeat) primer pairs ARSFL-009, CFACT-152 and EMFv-104, and AFLP (amplified fragment length polymorphism) primer combinations EcoRI-ACC/MseI-CTA as the most informative among the 44 strawberry cultivars and hybrid clones.

2. Cluster analysis of 44 strawberry accessions based on combined analysis of SSR and AFLP markers revealed two main groups consisting of 10 and 34 strawberry cultivars and clones. The combined analysis of 181 SSR and 1178 AFLP markers provided improved knowledge of genetic diversity of strawberry, developed in Lithuania.

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Characterization of strawberry (Fragaria × ananassa Duch.) cultivars and hybrid clones using SSR and AFLP markers

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Daržinės braškės (Fragaria × ananassa Duch.) veislių ir hibridinių klonų apibūdinimas naudojant PPS bei PFIP molekuliniai žymeklius

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Santrauka

Atliekant genetinius ir selekcinius tyrimus, paprastų pasikartojančių sekų (PPS) ir pagausintų fragmentų ilgio polimorfizmo (PFIP) žymeklių plačiai naudojami dėl savo daugiaaleliškumo, gausumo, atsikartojamumo ir plataus genomo padengimo. Straipsnyje pateiktas daržinės braškės (Fragaria × ananassa Duch.) 44 skirtingų genotipų genetinis apibūdinimas naudojant PPS ir PFIP molekuliniaus žymeklius. Braškės veislių ir hibridinių klonų, kurių daugelis yra sukurti Lietuvos agrarinių ir miškų mokslų centro Sodininkystės ir daržininkystės institute, genetinė įvairovė įvertinta naudojant 11 anksčiau paskelbtų PPS pradmenų porų ir 6 PFIP pradmenų kombinacijas. PPS multipleksinės analizės duomenimis, kiekvienai pradmenų porai identifikuota nuo 9 iki 21 alelių. Diferencijuotų genotipų skaičius svyravo nuo 12 iki 38. PPS pradmenų poros ARSFL-009, CFACT-152 ir EMFv-104 buvo pačios informatyviausios. Tirišiant PFIP polimorfinių fragmentų skaičius variavimo nuo 44 iki 197. Polimorfinių fragmentų dažnis svyravo nuo 39 % (pradmenų kombinacija EcoR1-AGG/MseI-CAA) iki 88 % (EcoR1-ACC/MseI-CAC). Tyrimo rezultatai rodo, kad pasirinkti anksčiau publikuoti mikrosatelitiniai pradmenys ir atrinktos didelio polimorfibūkumo PFIP pradmenų kombinacijos po pirmąjį atrankos atlikta, yra tinkami genotipuoti braškės pavyzdžius. Siekiant gauti išsamų tirtų braškės genotipų įvairovės aprašymą, buvo naudojami DNR fragmentai, išskirti taikant abi žymeklių sistemų. Klasterinė analizė atskleidė dvi pagrindines genotipų grupes, kurias sudarė atitinkamai 10 ir 34 braškės veislių ir klonų.

Reikšminiai žodžiai: daržinė braškė, genetinė įvairovė, genotipavimas, hibridai, pagausintų fragmentų ilgio polimorfizmas, paprastos pasikartojančios sekos.