

USE OF SSR MARKERS IN IDENTIFICATION OF SUNFLOWER ISOGENIC LINES IN LATE GENERATIONS OF BACKCROSSING

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SUMMARY

In the present study, thirteen SSRs (Simple Sequence Repeats) were employed for screening the level of similarity between sunflower parental lines and progeny obtained in final stages of selection. Another aim of the study was to compare the success of making isogenic lines through selection. Line P (donor line) was used as a donor of downy mildew gene *Pl₆* and backcrossed with four commercial inbred lines (A, B, C and D) susceptible to downy mildew. HAP3, a DNA-specific primer, was used to test the success of transfer of *Pl₆* gene from the donor line to the progeny lines in the F₆ and F₇ generations. It was found that all progeny lines were resistant to downy mildew. Results obtained by using thirteen primers showed that progeny lines were similar to their respective recipient parent, but further studies have to be conducted using a larger number of primers and a larger number of genotypes.

Key words: sunflower, *Helianthus annuus* L., isogenic line, backcross, SSR, downy mildew

INTRODUCTION

Molecular markers offer specific advantages in assessment of genetic diversity and in trait-specific crop improvement, but are also used for cultivar identification, as well as for the study of polymorphism and genetic similarity in major crops such as maize (Carvalho *et al.*, 2004), soybean (Narvel *et al.*, 2000), potato (Solano Solis *et al.*, 2007), common bean (Duarte *et al.*, 1999), sorghum (Smith *et al.*, 2000), coconut (Perera *et al.*, 1998) and others.

Classical backcrossing is a time-consuming process, due to the number of backcrosses needed to achieve desired results. Selection based on phenotypic char-

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acteristics can be unreliable because of the environmental effects and measurement errors. By using molecular markers, required number of backcrosses can be significantly decreased, which makes their use a cost-efficient method (Knapp, 1998). Molecular markers provide an insight in the variability of the progeny at the molecular level in each generation (Moose and Mumm, 2008). The efficiency of the marker-assisted backcrossing depends on experimental design, especially on the marker density and position, population size and selection strategy (Frisch and Melchinger, 2005).

The level of polymorphism and genetic relationship have been studied by means of different molecular markers such as RAPDs (Random Amplified Polymorphic DNA), RFLPs (Restriction Fragment Length Polymorphisms), AFLPs (Amplified Fragment Length Polymorphisms) and, more recently, SSRs (Wünsch and Hormaza, 2002). Because of their multiallelic and highly polymorphic nature, microsatellite markers or SSRs are currently becoming the preferred technique for the molecular breeding in plant species. In sunflower (*Helianthus annuus* L.), microsatellites have been particularly useful in the studies of phylogenetic relationships, genotype identification and calculation of genetic relationship between inbred lines (Smith *et al.*, 2000; Paniego *et al.*, 2002; Solodenko *et al.*, 2005; Antonova *et al.*, 2006; Hvarleva *et al.*, 2007).

In the present study, thirteen SSRs were employed for screening the level of similarity between parental lines and their progeny obtained by selection. Line P (donor line) was used as a donor of *Pl₆* gene (downy mildew resistance gene) and crossed with four commercial lines (A, B, C and D), which are susceptible to downy mildew. The aim of this study was to check the success of backcrossing and to determine the degree of similarity of backcross progenies to both parents using SSR markers, as well as to determine if chosen SSR primers could be used for this purpose. HAP3, a DNA-specific marker, was used to determine whether *Pl₆* gene has been successfully transferred from the donor line to the progeny plants.

MATERIALS AND METHODS

Leaf samples were taken from original inbred lines: donor line P and four recipient lines: A, B, C, D, and their backcross progeny A₁₋₁₀, B₁₋₁₀, C₁₋₁₀ and D₁₋₁₀, respectively. Modified CTAB protocol (Permingeat *et al.*, 1998) was used for DNA extraction.

PCR mix of 15 μ l contained 1 \times buffer, 3 mM MgCl₂, 0.2 mM dNTP, 0.3 μ l mixed primer, 1 U enzyme, 25 μ g BSA, and 40 ng DNA. The primers used for PCR amplification were: ORS 7, ORS 78, ORS 307, ORS 316, ORS 349, ORS 509, ORS 561, ORS 610, ORS 613, ORS 1079, ORS 1114, ORS 1144, ORS 1209 and HAP3. In PCR reaction with ORS primers DNA was amplified at 95°C for 2 min, 1 cycle of 94°C of 30 sec, 64°C for 30 sec, 65°C for 45 sec, followed by 6 cycles in which temperature was decreased by 1°C per cycle, followed by 32 cycles of 94°C for 30 sec, 58°C for 30 sec, and 65°C for 45 sec. Final extension was at 65°C for 20 min. For HAP3, PCR reaction described by Panković *et al.* (2007) was used. All PCR products were separated on 2% MetaPhor agarose gel.

PCR profiles obtained from ORS 509 and ORS 1209 showed that progeny lines B_{1-10} and D_{1-10} in the F_6 generation were not completely identical with their respective recipient parent. ORS 509 and ORS 1209 amplified some non-specific bands, in most of the progeny plants of back crosses with the line B (B_{1-10}) and the line D (D_{1-10}). In the F_7 generation in all progeny lines of line D, ORS 509 amplified the same bands as in recipient line (D). In the progenies of line B the same primer amplified some, bands originating from donor line (P). Non-specific bands were not amplified. ORS 1209 amplified four bands of the same size in all parental and progeny lines. Although ORS 610 amplified three bands in the work of Hvarleva *et al.* (2007), in our study this primer amplified four bands in all parental lines and F_6 progeny lines, so there was no need to use this primer in the analysis of the next generation.

Primers ORS 307, ORS 1079, ORS 1114, and ORS 1144 were also highly informative in our study, amplifying three bands. In the work of Tang and Knapp (2003) and Zhang *et al.* (2005) the same number of bands in elite inbred lines was amplified by using ORS 307, while in the work of Hvarleva *et al.* (2007) this primer amplified two bands. ORS 1144 amplified seven bands in wild and domesticated sunflower species and two in inbred lines (Solodenko and Sivolap, 2005).

In progeny lines B_{1-10} and D_{1-10} in the F_6 generation, bands that belonged to both parental lines were amplified by ORS 1079 (Figure 1), therefore, this primer was used to test the degree of similarity of progeny lines with their maternal line in the next generation of selection.

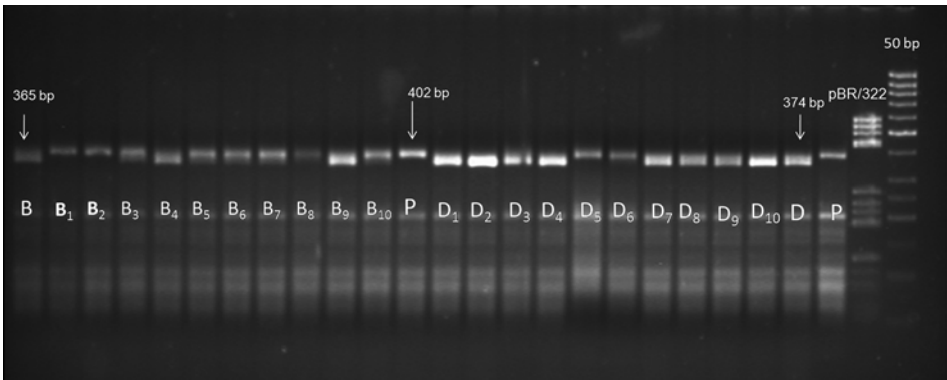


Figure 1: PCR amplification profile of parental lines (B and D) and their respective progeny lines from crosses with line P (B_{1-10} and D_{1-10}) (the F_6 generation) obtained with ORS 1079 primer.

ORS 1079 showed that progeny of line D (D_{1-10} , the F_7 generation) was genetically identical to this line, while only one progeny plant, B_5 , was genetically identical with its recipient line B, two progeny plants, B_2 and B_7 , were identical with the donor line (P) and the rest of the progeny plants had bands from both parents (Figure 2).

In our experiment, ORS 316 and ORS 561 amplified two allele combinations. These primers amplified three and five alleles in sunflower elite inbred lines, respectively (Tang and Knapp, 2003). ORS 561 amplified some non-specific bands or bands that originated from both parental lines, B and P, in F₆ and F₇ progeny genotypes of B₁₋₁₀.

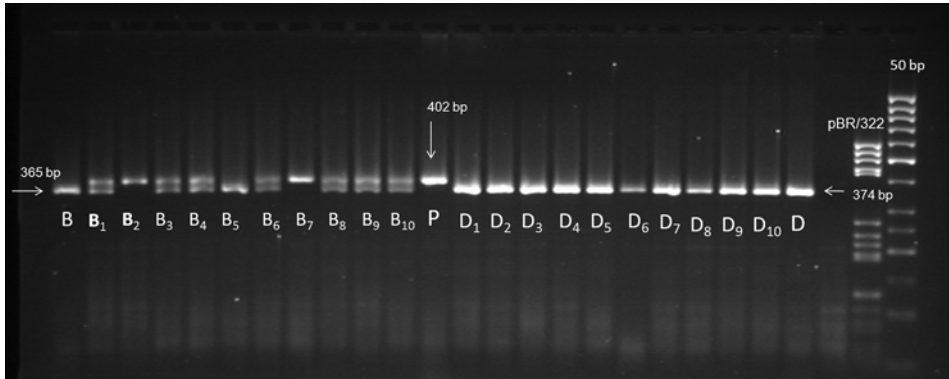


Figure 2: PCR amplification profile of parental lines (B and D) and their respective progeny lines from crosses with line P (B₁₋₁₀ and D₁₋₁₀) (the F₇ generation) obtained with ORS 1079 primer.

ORS 7 and ORS 78 amplified only one band in the tested inbred lines and their progenies. This is not in agreement with the results of Haverleva *et al.* (2007) and Solodenko and Sivolap (2005) who found these markers to be polymorphic, amplifying two and three bands, respectively. ORS 78 amplified a band of the same size as in the work of Solodenko and Sivolap (2005). Beside ORS 7 and ORS 78, ORS 349 and ORS 613 also did not appear to be reliable markers for further research because of their monomorphic nature. Tang and Knapp (2003) found ORS 349 to be monomorphic for elite inbred lines, but polymorphic for exotic domesticated and wild sunflower populations.

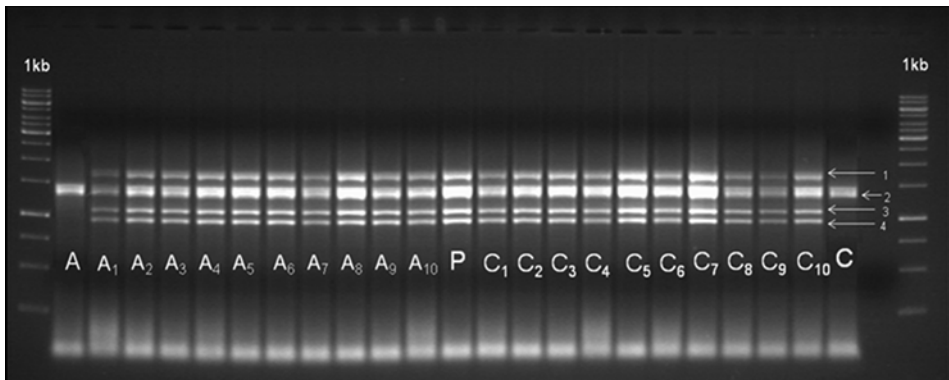


Figure 3: HAP3 primer amplified 4 bands (1. 1720 bp, 2. 1330 bp, 3. 1060 bp, 4. 940 bp) in resistant P and all progeny plants A₁₋₁₀ and C₁₋₁₀ (the F₇ generation), and one band in susceptible recipient lines A and C.

HAP3 was chosen for its specific use in detecting the presence of Pl_6 , a downy mildew resistance gene (Panković *et al.*, 2007). HAP3 primer amplified 4 bands (1720 bp, 1330 bp, 1060 bp and 940 bp) in donor line P and all progeny lines in the F_6 and F_7 generations, and one band (1330 bp) in recipient lines A, B, C and D, confirming that downy mildew resistance gene has been successfully transferred from line P to all progeny lines (Figure 3).

Bands generated in F_7 progenies and parental lines using all thirteen ORS primers and HAP3 primer were analyzed by assigning 1 or 0 depending on the presence or absence of each allele form. The dendrogram showed that there was a great

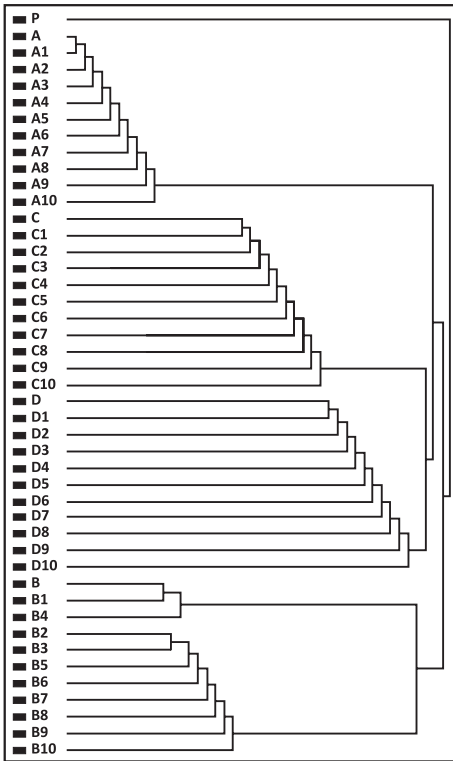


Figure 4. Dendrogram based on SSR data of parental and progeny lines

difference between parental line P (donor line) and recipient lines A, B, C and D (Figure 4).

All progeny lines showed the highest similarity to their recipient parental line (*e.g.*, A_1 to A_{10} belong to the same sub-cluster as their recipient line A, *etc.*). However, due to the presence of bands that originated from both parental lines in F_7 progeny lines B_{1-10} , there was an additional sub-cluster formed in B sub-cluster. Consequently, an additional back-cross should be carried out in order to create a population that will be genetically close (preferably identical) to its maternal line, and still be resistant to downy mildew. An improvement in the level of similarity between progeny lines D_{1-10} and line D was shown, as all progeny lines showed the same profile as their recipient line, after electrophoresis.

CONCLUSIONS

Progeny lines formed clusters with their respective recipient line, while line P

formed a separate cluster. This shows that the combination of primers used in this study is sufficiently informative. ORS 509, ORS 610 and ORS 1209 proved to be the most informative primers, because they amplified bands that differed between recipient lines and donor line P, thus clearly distinguishing these lines. Besides ORS 509 and 1209, ORS 1079 amplified bands that belonged to both parental lines in some individual plants of B_{1-10} and D_{1-10} in F_6 generation. All F_7 progeny lines D_{1-10} had the same profile as their recipient line D, but there were still some plants

in F₇ generation of B₁₋₁₀ that did not show the same profile as their recipient line B. These results showed that an additional backcross should be carried out. Downy mildew resistance gene *Pl₆* was successfully transferred to all progeny plants. The results obtained by using thirteen ORS primers showed that progeny lines are similar to their respective recipient line, but further studies are needed which would include new primers on greater number of genotypes.

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