Application of SSR Markers for Purity Testing of Commercial Hybrid Soybean (Glycine max L.)

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ABSTRACT

Exploitation of the full potential of any hybrid requires the possessing of genetically high-purity seeds. Commercial soybean hybrids have been developed using a cytoplasmic male sterility (CMS) system. In order to avoid reduction in yield caused by using low-purity seeds, development of a simple, rapid, and accurate method for hybrid purity assessment is of great essence and significance. Therefore, the parental lines of HybSoy 1 to 5 were screened using 160 Simple Sequence Repeat (SSR) makers, of which 8 markers exhibited polymorphism. A PCR-based assay with these markers detected both alleles of the parental lines in pure hybrids, proving their heterozygosity, whereas impurities were identified by the presence of only one parental allele. The confirmation of hybrid purity indicated that a single polymorphic marker was sufficient for detection of contaminations of these hybrids from their parents. It was also found that if a hybrid seed lot was contaminated by another hybrid or its parental lines, two or more appropriate markers could be used to easily detect such contamination. This method could accurately and effectively identify the hybrid purity in a predetermined sample of soybean hybrids constituted by deliberately mixing seeds of parental lines. This is the first report that demonstrates the utility of SSR markers for assessment of genetic purity of soybean hybrids.

Keywords: Cytoplasmic male sterility, Genetic purity, Molecular marker, Contamination, Polymorphism.

INTRODUCTION

Soybean is one of the most important oil crops in the world. However, the yield is less than one third of corn. Exploitation of heterosis can significantly improve the yield of soybean (Palmer et al., 2010). A soybean CMS system had been developed and a method for producing soybean hybrid was invented by our team (Sun et al., 1994 and 2001). Then, the world’s first commercial soybean hybrid, HybSoy 1, was bred and released in China. The yield of HybSoy 1 was 20.9% higher than that of the CK (Jilin 30) (Zhao et al., 2004). Subsequently, seven soybean hybrids, designated as HybSoy 2, HybSoy 3, HybSoy 4, HybSoy 5, Zayoudou 1, Zayoudou 2 and Fuzajiaodou 1, respectively, have been developed and released for commercial production in China. Good promotion and application of any hybrid require high-quality seeds. Exploitation of the full potential of the high purity hybrid can improve farmers’ enthusiasm for growing soybean hybrids, which, in return, increases the overall yield. In order to avoid reduction in yields caused by using low-purity soybean hybrid seeds, a simple, reliable and efficient method is developed for assessment of the genetic purity of hybrids. Currently, a morphology-based identification method is used to assess the genetic purity of seeds.
soybean hybrids (unpublished). The method relies on seeds or plants possessing different phenotypic traits to identify the individual, which is intuitive and simple. However, direct observation of agronomic traits is often difficult. For instance, some reproductive traits must be observed within a specific period in order to detect phenotypic differences, and some traits are environmentally labile, which makes it particularly difficult to differentiate individuals that have a close genetic relationship. Color traits are only useful for identification of soybean hybrid purity when the parents possess a different color phenotype. If the parents possess the same stem, flower, and pubescence color phenotype, the purity of the hybrids cannot be identified on the basis of those traits. In addition, the morphological identification of rogue genotypes from differences in seed traits and growth form of individual plants is applied to avoid wastage of land, labor resources, and environmental resources (e.g., soil nutrients and water) by cultivating less-productive genotypes. In recent years, Marker Assisted selection (MAS) not only have been used for the analysis of genetic diversity (Naghavi et al., 2009), but also used extensively to test hybrid purity to overcome the shortcomings of morphology-based methods (Varshney et al., 2009). A variety of marker types, such as Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPD), Sequence-related Amplified Polymorphism (SRAP), Inter-simple Sequence Repeat (ISSR), EST-SSR and SSR markers, have been used in hybrid purity test (Grzebelus et al., 2001; Ilbi 2003; Jang et al., 2004; Dongre and Parkhi 2005; Liu et al., 2007a; Asif et al., 2009; Naresh et al., 2009; Dongre et al., 2011). Given that SSRs are locus-specific and co-dominant markers, they have been used widely to assess hybrid purity in maize (Daniel et al., 2012), rice (Sundaram et al., 2008), sunflower (Iqbal et al., 2010), cabbage (Liu et al., 2007b), bunching onion (Tsukazaki et al., 2006), cauliflower (Zhao, et al., 2012) and other crops. However, the utilization of SSR markers for testing of seed genetic purity of soybean hybrids has not been reported previously.

In the present study, we tested the utilization of SSR markers for detecting the genetic purity of five commercial soybean hybrid varieties released in China. The procedure of one or two SSR markers for assessment of genetic purity of the hybrids is demonstrated.

MATERIALS AND METHODS

Plant Material

Five commercial soybean hybrids together with their parental lines were used in the study (Table 1). For each hybrid, 10 seedlings of each parental line and 60 seedlings of hybrid were grown in pots under artificial light (12 h photoperiod at 26 °C) and irrigated with water. Two-week-old plants were collected, immediately immersed in liquid N₂, and stored at −70 °C until extraction of genomic DNA for assessments of parental polymorphism and hybrid purity.

SSR Marker Polymorphism

A total of 160 SSR markers (based on data in the Soybase; http://www.soybase.org) were used for a survey of polymorphism in bulks of DNA extracted from the 10 seedlings of each female and male parent of five hybrids, respectively. Polymorphism between each parental line and hybrid was detected for a total of eight SSR markers. The polymorphism of these markers was further confirmed using DNA from individuals of the parental lines. For hybrid purity assessments, the identified markers were amplified from DNA extractions of the five hybrids and their parental lines. The PCR procedure was performed with 20 ng of template genomic DNA in 0.2 ml PCR tubes, 10 pmol of each primer, 10 mM each dNTP, 1 U of Taq polymerase, 10× Taq polymerase buffer, and double-distilled H₂O in a total

Table 1. Descriptions of the plant materials used in the study.

<table>
<thead>
<tr>
<th>Hybrids</th>
<th>Cytoplasmic male sterile lines</th>
<th>Restorer lines</th>
</tr>
</thead>
<tbody>
<tr>
<td>HybSoy 1</td>
<td>JLCMS9A</td>
<td>JLR1</td>
</tr>
<tr>
<td>HybSoy 2</td>
<td>JLCMS47A</td>
<td>JLR2</td>
</tr>
<tr>
<td>HybSoy 3</td>
<td>JLCMS8A</td>
<td>JLR9</td>
</tr>
<tr>
<td>HybSoy 4</td>
<td>JLCMS47A</td>
<td>JLR83</td>
</tr>
<tr>
<td>HybSoy 5</td>
<td>JLCMS84A</td>
<td>JLR1</td>
</tr>
</tbody>
</table>
volume of 25 µL with the following conditions: denaturation at 94 °C for 4 min, followed by 35 cycles of 94 °C for 30 s, 50 °C for 30 s, and 72 °C for 1 min, and a final extension at 72 °C for 8 min. All PCR products were separated by electrophoresis in a 6% denaturing acrylamide gel, and stained with silver nitrate solution.

RESULTS AND DISCUSSION

SSR Polymorphism in the Parental Lines

In a previous study, the restorer gene (Rf), which gametophytically restores soybean cytoplasm, was located on linkage group J (LG J) (Wang et al., 2010). It can be used for identifying SSR markers linked to Rf gene of soybean to distinguish hybrid soybean and parental lines. On this basis, a total of 160 SSR markers from LG J were selected and used for the survey of polymorphism among the parental lines of the five commercial soybean hybrids, using bulks of DNA extracted from the 10 seedlings of each female and male parent of five hybrids, respectively. Eight of these markers (Table 2) were polymorphic for the parental lines and they were screened. Among these markers, Satt547, Sctt_011 and BARC16_1102 showed polymorphism between the parental lines of three hybrids, BARC16_1124 showed polymorphism between the parents of two hybrids, and Satt529, BARC16_1095, BARC16_1097 and BARC16_1123 showed polymorphism between the parents of only one hybrid (Figure 1). Interestingly, BARC16_1102 and BARC16_1124 markers showed polymorphism between the parents of HybSoy 1 and HybSoy 3; Satt547 and Sctt_011 markers showed polymorphism between the parents of both HybSoy 2 and HybSoy 4, and Sett_011 and BARC16_1124 markers showed polymorphism between the parents of both HybSoy 1 and HybSoy 4. The polymorphism patterns of the eight markers were confirmed using DNA extracted from 10 individual plants of the parental lines. These polymorphic SSRs were then assessed using DNA bulks of both hybrids and parents. For all these markers, a single allele was detected in the parents, whereas both parental alleles were detected in the hybrids, thus, indicating the heterozygosity of the hybrids (Figure 1). The markers were further tested with DNA extracted from individual hybrid plants to assess their utility for assessment of hybrid purity. For all individual hybrid plants, both alleles specific to the parents were detected, which confirmed the utility of these markers for genetic purity assessment of the hybrids (Figure 2).

Genetic Purity Testing of Soybean Hybrids

Soybean hybrids can be produced by the use of hand crosses, gametocytes, and male-sterility. Because of being labor-intensive and time consuming, the hand crosses are used only for research purpose. Gametocytes have been used for producing hybrid seeds successfully in other crops such as wheat; however, there have been no adequate and effective gametocytes available to kill pollen grains completely in soybean. Currently, several nuclear male-sterile mutants have been found in soybean. Owing to the difficulty in removing 50% of the fertile plants in female parent, they cannot be used in hybrid seeds production in large scale. CMS male-sterile system is the only choice to avoid self-pollination in female parent in hybrid soybean production. The

Table 2. Descriptions of the polymorphic SSR markers used in the study.

<table>
<thead>
<tr>
<th>Marker</th>
<th>Forward primer sequence (5'–3')</th>
<th>Reverse primer sequence (5'–3')</th>
</tr>
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<tbody>
<tr>
<td>Satt529</td>
<td>GCGCATTAAGGCATAAAAAGGATA</td>
<td>GCACAAAGCAACACATACAA</td>
</tr>
<tr>
<td>Satt547</td>
<td>GCGCTATCCGATCCATATGTG</td>
<td>TGGTCTCTCACGTAGTAAAAATCA</td>
</tr>
<tr>
<td>Sctt011</td>
<td>CTCCGGTTGTGAT</td>
<td>TAAAGCTGAATTAGTAAGAA</td>
</tr>
<tr>
<td>BARC16_1095</td>
<td>CACCAATTTAAAAAGTTGATGGTC</td>
<td>TCCACACTTATTGTTTTCA</td>
</tr>
<tr>
<td>BARC16_1097</td>
<td>GTTGCAATTGTGCACTATGCT</td>
<td>GAGTCGTTAAACAAGGAAA</td>
</tr>
<tr>
<td>BARC16_1102</td>
<td>TTGTCTTGTGACTGAGAAAA</td>
<td>CTGGTTAGCATGACTGTTCA</td>
</tr>
<tr>
<td>BARC16_1123</td>
<td>AGAAAAGAATATATATCCAGATAA</td>
<td>ACAATTTGAAGCAGCTACATTATACAA</td>
</tr>
<tr>
<td>BARC16_1124</td>
<td>TGGAGTTATGTTAACAGTGATGCT</td>
<td>CATGGTTACTTGTTGCTAGTA</td>
</tr>
</tbody>
</table>
Figure 1. SSR markers polymorphic between an individual hybrid and its parental lines for five hybrids. PCR amplifications were performed with SSR markers Sctt_011, BARC16_1102 and BARC16_1124 for HybSoy 1 (H1), female parent (1F) and male parent (1M); SSR markers Satt547, Sctt_011 and BARC16_1123 for HybSoy 2 (H2), female parent (2F) and male parent (2M); SSR markers Satt529, BARC16_1102 and BARC16_1124 for HybSoy 3 (H3), female parent (3F) and male parent (3M); SSR markers Satt547, Sctt_011 and BARC16_1102 for HybSoy 4 (H4), female parent (4F) and male parent (4M); SSR markers Satt547, BARC16_1095 and BARC16_1097 for HybSoy 5 (H5), female parent (5F) and male parent (5M). Marker: 100 bp DNA ladder.

major steps for hybrid seeds production include: (a) F1 seeds production by planting female parent CMS A-line and male parent R-line alternatively in isolation plots, harvesting F1 seeds from female parent for farmer planting; (b) Seed increase of CMS A-line by planting female parent CMS-A line and B-line alternatively in isolation plots, harvesting male-sterile seeds from female parent for F1 seeds production the next year (insect pollinators must be used in step a and b); and (c) Seed increase of R-line in isolation plots if needed, harvesting seeds for F1 seeds production the next year. The seeds contamination mainly come from step a and b. One possible way is the mechanical mixture of male and female parents during planting, harvesting, and seed processing. Another possible way is the biological contamination. In case the A-line mixed with B-line in the A-line seed increase field, some female parent may be pollinated by B-line instead of R-line in F1 seed production field and certain amount of male-sterile plants will appear in farmer’s production field. This is the number one problem and the serious situation we are facing now as far as seed purity is concerned. SSR markers have been used for purity testing of many crop hybrids, and national and local standards for hybrid purity testing methods using SSR markers are being established.

Some seed companies also appreciate the advantages of the method, and actively develop SSR polymorphic primers to control the seed genetic purity at the parental line and hybrid seed production stage. Over the past 10 years, major advances in soybean hybrid research have been achieved. Currently, we have released five commercial soybean hybrids, which have promoted hybrid soybean cultivation in the major soybean-producing areas of northeastern China. In order to ensure the hybrid purity of seeds available to farmers, and to demonstrate the utility of the eight polymorphic SSR markers for hybrid purity testing, a predetermined mixture of the hybrids HybSoy 1 to 5 were created by mixing 3 or 5 seeds of each parental line to make a sample of 50 seeds, approximately. The markers BARC16_1102, BARC16_1123, BARC16_1124, Sctt_011 and BARC16_1097, which are polymorphic between the hybrids’ respective parents, were used to amplify the genomic DNA of HybSoy 1 to 5 seedlings by PCR. After separation of the amplified fragments by SDS-PAGE electrophoresis, impurities among these seedlings were clearly identified on the basis of fragment sizes (Figure 2). The impurities were identified on the basis of DNA marker-based genotyping, which corresponded with the proportion of parental-line seeds in the mixture. This result
Identification of genetic impurity owing to hybridization with two or more genotypes can also be detected by SSR markers. For example, the SSR marker Satt529 only detected polymorphism in HybSoy 2 and its parents, thus, it can be used to detect whether a mixture contains other hybrids or parents other than those of HybSoy 2. Therefore, with the appropriate markers, such contamination can be easily detected. In the present study, the markers Satt547, Sctt_011, BARC16_1102, and BARC16_1124 amplified a similar band in multiple hybrids, which may be the reason that some hybrids derived from the same parent had similar genetic backgrounds. Under these conditions, such markers cannot be used to distinguish hybrids. However, by screening a large number of SSR markers, it is possible to identify one marker that can distinguish more than two hybrids at the same time. Because the current hybrid seeds production of soybean are produced in arid areas where commercial soybean production is seldom practiced. The contamination mainly comes from only parents of hybrid within one isolation area or other isolation area nearby. We know exactly the parents of every hybrid. Therefore, the method of this study can be
used to identify the commercial hybrids, rather than developing more SSR makers. SSR markers exhibit a high degree of polymorphism, co-dominant inheritance, are reproducible and provide accurate results, and thus are far preferable to RFLP, RAPD, and AFLP molecular markers. SSR marker technology requires only small volumes of DNA samples and does not have stringent DNA purity requirements, which allows shortening of the detection time. Although it is expensive and requires experience to screen SSR primers, many primer sequences for SSR loci are available in public databases for a variety of crops, including soybean. In addition, SSR markers for seed purity identification have potential for broad application. However, this method can only test the mixture of the studied hybrids with each other or with their parental lines. If the sample is contaminated with another unknown genotype carrying the same alleles this method would not be able to detect. Thus, more than one PCR is needed for detection of contaminations from other unknown genotypes, and the more the number of markers, the better will be the judgment about purity.

CONCLUSIONS

The present study is the first report of the application of SSR markers for detection of genetic purity in commercial soybean hybrids. The SSR markers were able to detect identifiable non-soybean hybrids, such as paternal lines and mechanical mixtures of genotypes, and by using one or more of the SSR markers, distinguishing among different parental or hybrid genotypes in genetically impure seed mixtures was possible. The developments of SSR makers specific for each parent will simplify the procedure of purity test and the method is rapid and accurate. It will be beneficial for seed companies for implementation during processing, packaging, or dispatch of shipments since assessment using SSR markers is achieved much earlier than at a post-germination stage. There is no lag between seed production and sale of the seeds, which is a problem with field-based purity assessment methods. The method will not only help to maintain quality standards by seed production companies, but also increase farmers' enthusiasm for planting hybrids. Ultimately, it will play a positive role in promoting the popularization and utilization of soybean hybrids.

ACKNOWLEDGEMENTS

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REFERENCES

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کاربرد نشانه‌های اس آر برای آزمون خلوص هیریکه تجارت سوژا

(Glycine max L.)

س. ب. زانگ، ب. پنگ، و. ل. زانگ، س. م. وانگ، ه. م. سان، ی. س. دانگ، و. ل. زاوو

چکیده

لازم به برهنگی کامل از پتانسیل هر هیریکه داشتن بذردهای یک است که خلوص زنیکی باعث داشته باشند. هیریکه های تجاری سوژا با استفاده از نر عقیمی سیتروپلاسمی (CMS) ایجاد شده‌اند. به منظور گل‌گیری از کاهش عملکرد به علت خلوص کم بذردها، ابقاع روشی مبتنی بر ارزیابی خلوص بذر اهمیت بررسی‌های خوددار است. بنابراین در سه بهبودها و دو نسلی HybSoy 1 و HybSoy 5 با استفاده از 150 نسل‌گر سا. آر که 8 ثانیه آنها چندشکلی بودند غربال شدند. پک آزمون مبتنی بر پی سی آر با این نسل‌گرها در آلیاژی سلول های و دوم به هیریکه خالص تجسس کرده و ناخالصی آنها را ثابت کرد در حالیکه ناخالصی ها با حضور فقط یک آلیاژ والد مشخص شد. تابید خلوص هیریکه چنین اشارات داشت که یک نسل‌گر چندشکلی برای تجسس آلیاژی (ن. خالصی) این هیریکه‌ها و مدل‌های کافی است. یافته دیگر این بود که چنانچه توجه از بذر یک هیریکه با هیریکه دیگری با والدش آلیاژ شد، دو نسل‌گر مناسبی با تعداد بیشتری از آنها را می‌توان به کار برد تا به سادگی چنین ناخالصی‌ها را تشخیص داد. این روش می‌تواند به طور صحیح و موثر خلوص هیریکه را در یک نمونه از هیریکه‌های سوژا که عادت‌های مخلوط بذر رگه‌ها والد از پیش نهش شده است تشخیص دهد. این اولین گزارش است که کاربرد نشانه‌های اس آر را در ارزیابی خلوص زنیکی هیریکه‌های سوژا تشخیص می‌دهد.