

Detection of Bt gene and seed purity in maize

Mısırdaki Bt geninin ve tohum saflığının tayini

Research Article

Shuang Yang*, Muhammad Irfan, Xue Li, Yan Bin Liu, Xing Jia Sun

Biotechnology Research Laboratory, Shenyang Academy of Agricultural Science, Shenyang Liaoning P. R. China.

ABSTRACT

In this study we have described the detection of Bt gene and seed purity in maize by using PCR based method. Fifty four maize varieties were used for the detection of Bt gene by using BT1 and 35S primer having size of 195bp and 301bp respectively. Of these, fifteen varieties contained Bt gene which means that these varieties can not be used for further breeding. Ninety six seeds of maize were used for purity check by bnlg 161 SSR primer. Results showed that these seeds were 95% pure with 5% impurity. So these results showed that PCR based markers were very helpful in cultivar identification which leads to the improvement in maize breeding programs.

Key Words

Bt gene, seed purity, PCR, maize

ÖZET

Sunulan bu çalışmada, mısırdaki Bt geninin ve tohum saflığının PCR temelli yöntemle tayini sunulmuştur. Elli dört farklı mısır türü, 1950 baz çifti ve 301 baz çifti boyutuna sahip BT1 ve 35S primerleri kullanılarak Bt geninin tayini gerçekleştirilmiştir. Örnekler arasındaki onbeş örnek Bt geni içermektedir. Bt geni içermesi daha sonraki üreme işlemlerinde kullanılamayacağı anlamına gelmektedir. Doksanaltı mısır tohumu, bnlg 161 SSR primeri ile saflık kontrolü için kullanılmıştır. Sonuçlar, bu tohumların % 5 safsızlık ile % 95 saflıkta olduğunu göstermiştir. Ayrıca, bu sonuçlar PCR temelli işaretçilerin kültür tanımlanmasında çok faydalı olduğunu ve mısır yetiştirme programlarında iyileştirmeye olanak sağlayacağını göstermektedir.

Anahtar Kelimeler

Bt geni, tohum saflığı, PCR, mısır.

Article History: Received: Sep 12, 2013; Revised: Nov 18, 2013; Accepted: Dec 9, 2013; Available Online: Dec 31, 2103.

Correspondence to: Biotechnology Research Laboratory, Shenyang Academy of Agricultural Science, Shenyang Liaoning P. R. China.

Tel and Fax: +86 24 865 02316

E-Mail: yangshuangsaas@gmail.com, yangshuang8002@126.com

INTRODUCTION

Genetically modified organisms (GMO) are those which contains some foreign genes which express new characters improved nutritional value, resistance to virus, insect, herbicide tolerance [1,2]. In 2011, globally 160 million hectares were cultivated with soybean, maize, cotton and canola as genetically modified crops [3,4] and Bt maize covered about 11.2 million ha representing 14% of global transgenic area. Bt maize contained some proteins from *Bacillus thuringiensis* which are produced during the sporulation of the bacterium which were effective against wide variety of insects and even nematodes. Among these proteins, Cry 1Ab and Cry 1Ba genes encode that proteins which were very effective against coleopteran and lepidopteran larvae [5,6]. These genes were detected by PCR based DNA specific sequence present in all kinds of food [7,8].

In crops, species identification is problem which was done by using different criteria like morphological, biochemical and molecular methods. Identification by morphological characters was poor and time consuming process. The use of modern techniques for identification began from late 1980s and scientists used electrophoresis [9,10] and reversed-phase high performance liquid chromatography (RP-HPLC) [11, 12] was used for the detection of seed storage proteins. With the laps of time, genomic era starts and this provide a well established DNA based molecular markers for identification with high resolution power [13]. Now a day different types of molecular markers such as simple sequence repeats (SSR), random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphisms (AFLPs) were being used for identification of clones [14], somaclonal variations [15], hybrids and breeding lines [16], cultivars [17], genetic diversity assessment [18-20] and in QTL mapping [21] of various crops like maize [22,23]. All these markers were PCR based and require very small amount of DNA which can be extracted from a single kernel.

MATERIALS AND METHODS

Extraction of Genomic DNA

One hundred and Fifty four maize genomic DNA were extracted by method as described earlier [24] and these varieties were obtained from Biotechnology Research Laboratory, Shenyang Academy of Agricultural Science, Shenyang Liaoning P. R. China, which were used for the detection of Bt gene and seed purity.

PCR for Detection of Bt gene

Detection of the Bt gene was done by using specific primers (35S and BT1) obtained from SBS gene biotech Co. China and amplification reaction was done in 10 µl reaction volume containing 5 µl PCR master mix (SBS gene biotech Co. China), 2 µl 25 µM primer, 2 µl distilled water and 1 µl DNA. The reaction was programmed (Eppendorf thermal cycler) at initial denaturation at 94°C for 5 min followed by 34 cycles of 94°C 30s, 50°C 30s, 72°C 45s and final extension at 72°C for 5 min. After PCR reaction, the amplified products were resolved on 1.8% agarose.

PCR for Seed purity

Seed purity was checked by using specific primer (bnlg161) obtained from SBS gene biotech co and amplification reaction was done in 10 µl reaction volume containing 5 µl PCR master mix (SBS gene biotech Co. China), 2 µl 25 µM primer, 2 µl distilled water and 1 µl DNA. The reaction was programmed (Eppendorf thermal cycler) at initial denaturation at 94°C for 5 min followed by 30 cycles of 94°C 40s, 60°C 35s, 72°C 45s and final extension at 72°C for 5 min. After PCR reaction, the amplified products were resolved on 8% PAGE followed by silver staining.

RESULTS AND DISCUSSION

In this investigation fifty four different maize varieties were used for the detection of Bt genes. Genomic DNA from these fifty four maize varieties was amplified by using specific primers. Among these fifty four varieties, fifteen contains Bt genes which are named as transgenic lines and rest of the thirty nine lines did not contain Bt gene as shown in Figure 1. These fifteen transgenic

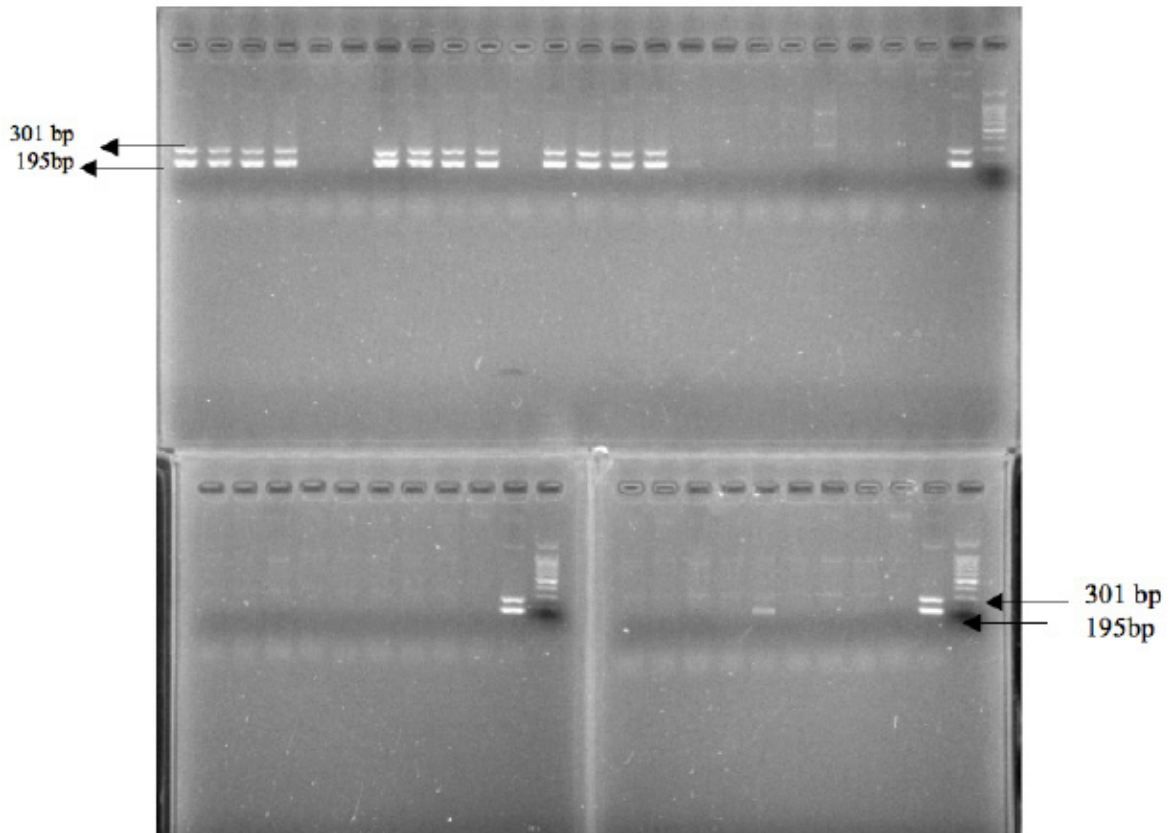


Figure 1. Detection of Bt gene in maize.

lines contained some genes from *Bacillus thuringiensis* which can produce some proteins effective against insects. So these fifteen lines were insecticide resistant while the other thirty nine lines were non-insecticide resistant lines. Many studies reported the detection of Bt genes in maize and maize processed food products and all these reports used PCR based methods for detection [25-27].

Currently maize cultivated globally and is basic food source for human beings in many countries. It is essential to check whether it is transgenic or

normal, because transgenic crops may be harmful for human consumption. Some transgenic maize such as Bt-11, MON810 and Bt-176 contain genes from *Bacillus thuringiensis* and the plant is resistant against certain lepidopteron insects such as European Corn Borer (ECB) and European Union approved these as a food or feed [28].

To check the seed purity, DNA from ninety six seeds were extracted and amplified by specific primer. Results (Figure 2) indicated that among these ninety six seeds, five seeds belong to different parents, while rest of the ninety one seeds was same

Table 1. List of Primers used for Bt gene and seed purity.

Primer	Sequence (5'-3')	T _m (°C)	GC (%)
35S-1	GCTCCTACAAATGCCATCA	56.0	47.4
35S-2	GATAGTGGGATTGTGCGTCA	57.3	50.0
BT1, R	CGATCAGCCTAGTAAGGTCGT	49.2	52.4
BT1, F	GGGCCCCTGAATCCAAC	49.7	66.7
Bnlg 161 F	GCTTTCGTCATACACACATTCA	59.3	41.7
Bnlg 161 R	ATGGAGCATGAGCTTGCCATATTT	57.1	39.1

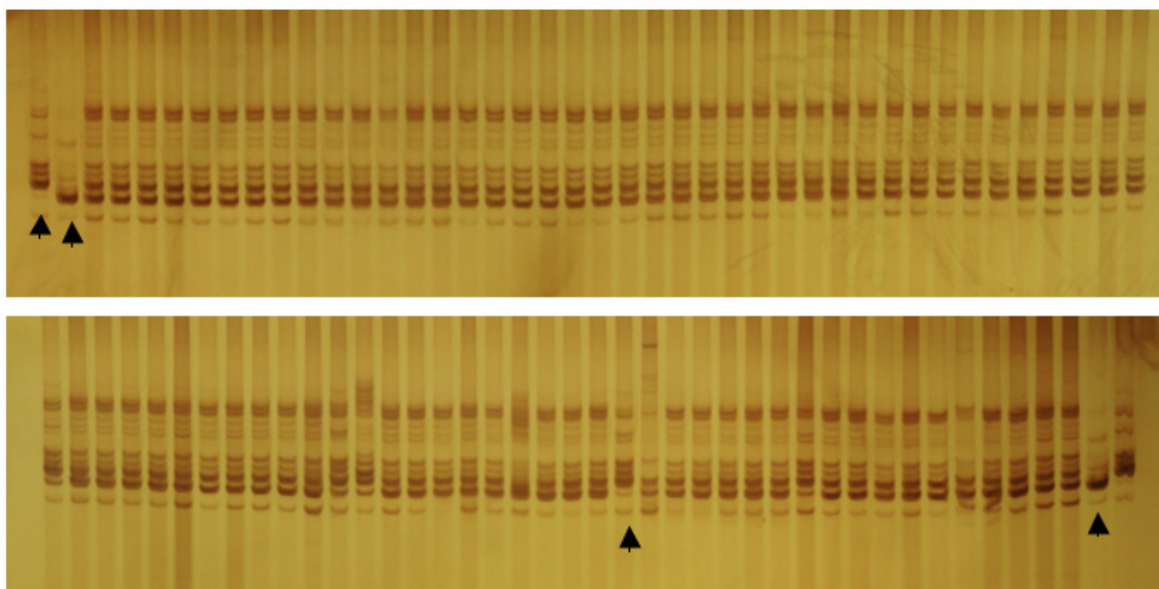


Figure 2. Purity check of maize seeds (arrows indicate the different seeds).

indicating these were pure. So the purity level in this selected panel was 95% with 5% impurity. Seed purification is very important to get the crops with better yield and if the seeds were not pure this will affect the product yield. The main cause of seed impurity was cross pollination which could be done through wind or insects. Wu et al [29] used isozymes and SSR markers for seed purity and identification, their results showed that SSR markers were reliable method for assessing the purity of the maize seeds. RAPD technique was also used for the purification of the maize hybrids [30,31]. Some researchers used both biochemical (isoenzymatic pattern) and molecular markers (microsatellite) for seed genetic purity determination revealing that microsatellite technique was fast and precise as compared to biochemical [32].

CONCLUSION

Results of this study revealed that controlling the quality of crops before breeding is very essential in yield improvement and making the pure lines. Because so many crops containing Bt genes are not declared as a safe of human and animal feed. SSR markers were widely used for the identification of crops and there are about 2300 SSR primers are available in maize database (maizegdb) which are being used for identification of variety of hybrids. So seed selling companies

must check the seed purity prior to marketing with farmers.

ACKNOWLEDGEMENT

This study was supported by Shenyang Science & Technology Bureau Project 2011 entitled "Construction of detection system of Bt-maize using MPCR".

References

1. M. Querci, M. Jeremini, V. G. den Eede. The analysis of food samples for the presence of genetically modified organisms. User Manual. JRC. Available from: URL: <http://gmotraining.jrc.it/>. (2006)
2. Z. Sieradzki, M. Mazur, K. Kwiatek. Validation of procedures based on PCR reactions for detection and identification of genetically modified maize & soybean. Bull. Vet. Inst. Pula., 52 (2008) 611-614.
3. C. Tengel, P. Schusler, E. Setzke, J. Balles, M. Sprenges-Hausels. PCR- based detection of genetically modified soy bean & maize in raw & highly processed food stuffs. Biotechnology 31(2001) 426-429.
4. ISAAA 2011. International Service for the Acquisition of Agri- biotech Application. Available from: URL: <http://www.isaaa.org>.

5. N. Bohorova, W. Zhang, P. Julstrum, S. Mclean, B. Luna, R.M. Brito, L. Diaz, M. E. Ramos, P. Estanol, M. Pacheco, M. Salgado, D. Hoisington. Production of transgenic tropical maize with cry1Ab and cry1Ac genes via microprojectile bombardment of immature embryos. *Theor. Appl. Genet.*, 99 (1999) 437-444.
6. D. Bradley, M. A. Harkey, M. K. Kim, K. D. Biever, L. S. Bauer. The insecticidal Cry IB crystal protein of *Bacillus thuringiensis ssp. thuringiensis* has dual specificity to coleopteran and lepidopteran larvae. *J Invert Path.*, 65 (1995) 162-173.
7. A. Germini, A. Zanetti, C. Salati, S. Rossi, C. Forre, S. Schmid, R. Marchelli. Development of a seven- target multiplex PCR for the simultaneous detection of transgenic soybean and maize in feeds and foods. *J Agr Food Chem.*, 52 (2004) 3275-3280.
8. M. Rabiei, M. Mehdizadeh, M. Alebouyeh, H. Rastegar. 2011. Screening of genetically modified organisms and specific detection of Bt-11 maize in foodstuffs. Proceedings of the 2nd International Congress of Food Hygiene, April 30th- May 1st, Tehran, Iran.
9. R.R. Zillman, W. Bushuk. Wheat cultivar identification by gliadin electrophore-grams. III. Catalogue of electrophoregram formulas of Canadian wheat cultivars. *Canadian J. Plant Sci.*, 59 (1979) 287-298.
10. R. Tkachuk, V.J. Mellish. Wheat cultivar identification by high voltage electrophoresis. *Annals Technol. Agr.*, 29 (1980) 207-212.
11. B.A. Marchylo, D.W. Hatcher, J.E. Kruger. Identification of wheat cultivars by reversed-phase high-performance liquid chromatography of storage proteins. *Cereal Chem.*, 65 (1988) 28-40.
12. M.G. Scanlon, H.D. Sapirstein, W. Bushuk. Computerized wheat varietal identification by high-performance liquid chromatography. *Cereal Chem.*, 66 (1989) 439-443.
13. D.J. Perry. Identification of Canadian durum wheat varieties using a single PCR. *Theor. App. Gen.* 109 (2001) 55-61.
14. R.M. Devarumath, S. Nandy, V. Rani, S. Marimuthu, N. Muraleedharan, S.N. Raina. RAPD, ISSR and RFLP fingerprints as a useful markers to evaluate genetic integrity of micropropagated plants of three diploid and tetraploid elite tea clones representing *Camellia sinensis* (China type) and *C. assamica sp. assamica* (Assam-India type). *Plant Cell Rep.*, 21 (2002) 166-173.
15. M.H. Rahman, O.P. Rajora. Microsatellite DNA somaclonal variation in micropropagated trembling aspen (*Populus tremuloides*). *Plant Cell Reports* 20 (2001) 531-536.
16. T. Bastia, N. Scotti, T. Cardi. Organelle DNA analysis of Solanum and Brassica somatic hybrids by PCR with universal primers. *Theo. Appl. Genet.*, 102 (2001) 1265-1272.
17. A. Mohanty, J.P. Martin, I. Aguinagalde. Chloroplast DNA study in wild populations and some cultivars of *Prunus avium* L. *Theo. Appl. Genet.*, 103(2001) 112-117.
18. M. Rahman, D. Hussain, Y. Zafar. Estimation of genetic divergence among elite cotton cultivars-genotypes by DNA fingerprinting technology. *Crop Science* 42 (2002) 2137-2144.
19. M. Rahman, M. Asif, I. Ullah, K.A. Malik, Y. Zafar. 2005. Overview of cotton genomic studies in Pakistan. *Plant & Animal Genome Conference XIII*. San Diego, CA. USA. PP81.
20. M. Asif, M. Rahman, Y. Zafar. DNA fingerprinting studies of some wheat (*Triticum aestivum* L.) genotypes using random amplified polymorphic DNA (RAPD) analysis. *Pak J Bot.*, 37(2005) 271-277.
21. A.H. Paterson, Y. Saranga, M. Menz, C.X. Jiang, R.J. Wright. QTL analysis of genotype x environment interactions affecting cotton fiber quality. *Theor. Appl. Genet.*, 106 (2003) 384-396.
22. R.V. Kantety, X. Zeng, J.L. Bennetzen, B. Zehr. Assessment of genetic diversity in dent and popcorn (*Zea mays* L.) inbred lines using Inter-Simple Sequence Repeat (ISSR) amplification. *Mol. Breed.*, 1(1995) 365-373.
23. T. Lubberstedt. A.E. Melchinger, C. Dussle, M. Vuylsteke, M. Kuiper. Relationships among early European maize inbreds: IV. Genetic diversity revealed with AFLP markers and comparison with RFLP, RAPD and pedigree data. *Crop Sci.*, 40 (2000) 783-791.
24. M. Irfan, T.T. Zhang, Y. Wang, C. Zhang, Q. Miao, L. Zhang, F. Lin. Modification of CTAB protocol for maize genomic DNA extraction. *Res. J. Biotechnol.*, 8 (2013) 41-45.
25. M. Rabieia, M. Mehdizadeh, H. Rastegar, H. Vahidic, M. Alebouyeh. Detection of Genetically Modified Maize in Processed Foods Sold Commercially in Iran by Qualitative PCR. *Iranian J. Pharma. Res.*, 12 (2013) 25-30.
26. J.W. Danson, M. Kimani, M. Mbogori. Detection of *Bacillus thuringiensis* genes in transgenic maize by the PCR method and FTA paper technology. *Afr. J. Biotechnol.*, 5 (2006) 2345-2349.
27. E. Margarit, M.I. Reggiardo, R.H. Vallejos, H.R. Permingeat. Detection of BT transgenic maize in foodstuffs. *Food Res. Int.*, 39 (2006) 250-255.
28. T.C. Lee, J. Zeng, M. Bailey, S. R. Sims, P. R. Sanders, R. L. Fuchs. Assessment of equivalence of insect protected corn and *E.coli* produced B.T.K. HD-1 protein. *Plant Physiol. Suppl.*, 108 (1995) 151.
29. M. Wu, X. Jia, L. Tian, B. Lv. Rapid and Reliable Purity Identification of F1 Hybrids of Maize (*Zea mays* L.) Using SSR Markers. *Mol. Plant Breed.*, 4(2006): 381-384.

30. Q. Lin, H. Yang, K. Lei, S. Zhang, F. Hao, Z. Cai, H. Wu. Genetic purity identification of ' Yunuo' serial fresh 2 table maize hybrids by RAPD technique. Southwest China J. Agr. Sci., 19(2006) 182-184.
31. M. Asif, M. Rahman, Y. Zafar. Genotyping analysis OF six maize (*Zea mays* L.) hybrids using DNA fingerprinting technology. Pak J. Bot., 38 (2006) 1425-1430.
32. K.C.P.C. Salgado, M.D.G.G.C. VIEIRA, É. V. D.V. Pinho, C.T.Guimarães, R.G. V. Pinho, L. V. Sousa. Genetic purity certificate in seeds of hybrid maize using molecular markers. Revista Brasil. de Sem., 28(2006): 169-175.