

A Simple and reliable extraction of genomic DNA for microsatellite analysis in wheat: an easy approach

Ram Chandra Choudhary¹, NK Sharma, Kumara Swamy R.V.², Rajeev Kumar³ and Mithilesh Kumar⁴

¹Department of Agricultural Biotechnology and Molecular Biology, Faculty of Basic Science and Humanities, Rajendra Agricultural University, Pusa 848125, India ²Department of Molecular Biology and Biotechnology, MPUAT, Udaipur, Rajasthan-313001 ³Corresponding author's email: ramchandra026@gmail.com

Received: November 2014; Revised: December 2015; Accepted: January 2015)

Abstract

For study of molecular biology applications such as microsatellite (SSR), rapid amplified polymorphic DNA (RAPD), restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), southern blotting and construction of genomic and c-DNA libraries in crops are based on high efficiency of purified DNA samples. In this study a simple, rapid, low cost and efficient method for leaf DNA extraction was optimized for microsatellite analysis in wheat with significant modification in Doyle and Doyle (1987) and Shahzadi and Shah (2010) DNA extraction method. The results showed that appropriate dilution of extracted DNA may be used directly as template DNA in PCR or PCR based techniques. Stored DNA from several months (5-6) has been successfully produced amplification with wheat microsatellite markers that show suitability of this extraction method after long-term storage of DNA.

Key word: Microsatellite (SSR), RAPD, RFLP, AFLP, genomic and c-DNA, PCR

Introduction

In recent years, molecular markers have been used for a variety of applications including examination of genetic relationships among individuals, mapping of useful genes, marker assisted selections and phylogenetic studies. Among the available molecular markers, microsatellites or SSRs are PCR based marker that are tandem repeats of 2-6bp long DNA motifs, have gained considerable importance in genetics and breeding of plant owing to many desirable genetic attributes including highly polymorphic, multiallelic nature, codominant inheritance, reproducibility, highly abundant and random distribution, extensive genome coverage and chromosome specific location. The variability in SSR length may be demonstrated by polymerase chain reaction with primers designed from the conserved flanking region. In crop species, the successful amplification requires good quality and ample amount of isolated template DNA with reproducible result. Many DNA extraction methods are known for isolation of genomic DNA from various plant sources including Cetyl Trimethyl Ammonium Bromide (CTAB) method (Doyle and Doyle, 1987) and its modifications (Ahmed *et al.*, 2009

and Huang *et al.*, 2000) were widely used in many laboratories but also have associated limitations, such as these methods are time consuming.

Other conventional methods (Jobes *et al.*, 1995 and Cheng *et al.*, 2003) for DNA extraction requires large quantities of sample to be ground are not efficient because they require long time for plant growth. Some other protocol uses small quantities of sample but with certain limitation like specialized apparatus like the matrix mill (Hill-Ambroze *et al.*, 2002). Extractions of high quality DNA from plant materials are considered the most difficult because the key is properly prepare the sample tissue. Some method (Sharma *et al.*, 2002) involves the use of liquid nitrogen flash freezing followed by grinding of sample tissues with a mortar and pestle which is difficult to handle and is not considered to be safe in open laboratory environment such as classroom. Today, many commercial DNA isolation kits are available, the advantage of DNA kit over crude method, is they are fast, minimal handling, that do not use hazardous reagents such as chloroform or phenol have these ideal properties; however which have high cost per sample ratio (Kang and Yang, 2004 and Ahmed *et al.*, 2009). We were uniformly unsuccessful in our attempts to amplify wheat genomic DNA by PCR using earlier reported methods (Dellaporta *et al.*, 1985; Doyle and Doyle, 1987; Wang *et al.*, 1993 and Davis *et al.*, 1995).

Corresponding authors- e-mail: ramchandra026@gmail.com

Published by the Indian Society of Genetics, Biotechnology Research and Development
Biotech Bhawan 5 E Nikhil Estate, DPS Road, Shastripuram, Agra 282007
Online management by www.isgbrd.co.in

Therefore, we found it necessary to devise an efficient plant DNA extraction protocol which use fresh sample is crucial when hundreds of samples need to be analysed rapidly, for many purposes in molecular biology and plant genetics analysis. In the present study, a method used for the simple, relatively quick and inexpensive extraction of genomic DNA from small amounts of plant leaf material was modified for the purpose of specially microsatellite analysis in wheat. This modified protocol may be applicable to a variety of plant species, requiring small amount of leaf sample with optimal amount of DNA and it is fast and complete DNA extraction can be achieved within 3-4 h. Samples (leaves) for microsatellite analysis were collected about 0.20g, from germinated 5-7 days old plant and put into a sterile 1.5 ml microfuge tube. Macerate the leaf tissue for 20-30 s at room temperature, using a sterile tip as grinder, without any buffer, and then add preheated freshly prepared 300 µl of extraction buffer (1M Tris-HCl, 5 M NaCl, .5M EDTA and 20% CTAB) into the tube and mixed for 10 s. Put the tube in water bath at 65°C for 30-45 min with gentle inversion 4-5 times. Subsequently, 250 µl of chloroform: isoamyl alcohol (25:1, v/v) was added and centrifuge at 13000 rpm for 15 min. Transfer the supernatant (contains DNA only) in a new microfuge tube to which, an equal volume of absolute ice-cold isopropanol was added, mixed and centrifuge the tube at 13,000 rpm for 10 min. Discard the supernatant and wash the pellet with 70% (v/v) ethanol.

Finally allow the DNA pellet to dry (approximately 15-20 min) at room temperature, avoid the DNA to over dry or it will be hard to re-dissolve and then dissolved in 50 µl TE buffer. Add 2 µl RNase A and incubate the tube at 37°C for 30 min. Visualize the DNA on 0.8% agarose gel and use double beam UV-VIS Spectrophotometer (UV 5704SS) to measure the absorbance of isolated DNA of eighteen wheat varieties at 260 nm and 280nm of light.

The purity of extracted DNA was conformed based on A260/A280 ratio averaged >1.70 for all organism, the yield was measured according to the formula (DNA (µg) = A260 x 50 x Dilution factor); prepare appropriate dilutions as per required concentration to be used as template in PCR or for other purposes. The values of absorbance were in the range of 1.83-1.94, indicating the good quality of the isolated DNA without any impurities. Some earlier workers (Lodhiet al., 1994 and Sharma et al., 2002) who noticed that long term storage of DNA does not give reproducible results; a major problem associated it because of freezing and thawing, which is expect to damage the DNA. But with our protocol, even more than 5-6 months old DNA dilution have been successfully amplified with microsatellite primer,

showing suitability of this method for long term storage of DNA. Screening of quality of extracted DNA was done successfully through the use of different wheat simple sequence repeat marker like, xgwm, barc, xgdm, wmc and xpsp with this protocol.

This protocol possesses significant modifications of the methods suggested (Doyle and Doyle, 1987 and Shahzadi et al., 2010), including times of centrifugation, amount of sample and concentration of DNA extraction buffer. Unlike all other protocols mentioned above, our protocol is relatively fast, consistent produced sparingly suitable DNA yields from extracted fresh leaf tissue for all wheat varieties assayed. All DNA was stable and may be amplified by PCR, requiring only 0.5 ng DNA in 20 µl reactions, for long term stored DNA. This technique has potential to be an effective protocol for DNA extraction using both fresh and mature leaf tissue for wheat, rice and perhaps for other crop species in the family of *Gramineae*. By using this protocol, it was possible to isolate DNA and perform PCR-based technique on wide range of organism, for many samples efficiently in a short period at minimal cost and in laboratory lacking state-of-the-art equipment's and technology.

References

1. **Ahmed, I., M. Islam, W. Arshad, A. Mannan, W. Ahmad and B. Mirza** (2009). High-quality plant DNA extraction for PCR: an easy approach. *Theor. Appl. Genet.* **50**:105-107.
2. **Cheng, Y.J., W.W. Guo, H.L. Yi, X.M. Pang and X. Deng** (2003). An efficient protocol for genomic DNA extraction from citrus species. *Plant Mol. Biol. Rep.* **21**:177a-177g.
3. **Davis, T.M., H. Yu, K.M. Haigis and P.J. McGowan** (1995). Template mixing: A method of enhancing detection and interpretation of codominant RAPD markers. *Theor. Appl. Genet.* **91**:582-588.
4. **Dellaporta, S.L., J. Wood and J.B. Hicks** (1985). Maize DNA miniprep, p. 36-37, in *Molecular Biology of Plants*, Malberg, J. Messing and I. Sussex, eds. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.
5. **Doyle J.J. and J. L. Doyle** (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem. Bull.* **19**:11-15.
6. **Hill-Ambroz, K.L., G.L. Brown-Guedira and J.P. Fellers** (2002). Modified rapid DNA extraction protocol for high throughput microsatellite analysis

- in wheat. *Crop Sci.* **42**: 2088-2091.
7. **Huang, X., F.J. Zeller, S.L.K. Hsam, G. Wenzel and V. Mohler.** (2000). Chromosomal location of AFLP markers in common wheat, utilizing nulli-tetrasomic stocks. *Genome* **43**: 298–305.
 8. **Jobes, D.V., D.J. Hurley and L.B. Thien.** (1995). Plant DNA isolation: a method to efficiently remove polyphenolics, polysaccharides, and RNA. *Taxon* **44**: 379-386.
 9. **Kang, T.J., and M.S. Yang.** (2004). Rapid and reliable extraction of genomic DNA from various wild-type and transgenic plants. *BMC Biotechnol.* **4**:20.
 10. **Lodhi, M.A., G.N. Ye, N.F. Weeden and B.I. Reisch.** (1994). A simple and efficient method for DNA extractions from grapevine cultivars and Vitis species and Ampelopsis. *Plant Mol. Biol. Rep.* **12**:6–13.
 11. **Shahzadi, I., R. Ahmed, A. Hassan and M.M. Shah.** (2010). Optimization of DNA extraction from seeds and fresh leaf tissues of wild marigold (*Tagetes minuta*) for polymerase chain reaction analysis. *Genet. Mol. Res.* **9**(1):386-393.
 12. **Sharma, A.D., P.K. Gill and P. Singh.** (2002). DNA isolation from dry and fresh samples of polysaccharide-rich plants. *Plant Mol. Biol. Rep.* **20**:415a–415f.
 13. **Wang, H., M. Qi and A. Cutler.** (1993). A simple method of preparing plant samples for PCR. *Nucl. Acid Res.* **21**:4153-4154.