

A rapid and cheap protocol for preparation of PCR templates in peanut

Chuan Tang Wang

Ocean University of China
Qingdao 266003, P R China

Xiu Zhen Wang

Shandong Peanut Research Institute
Qingdao 266100, PR China

Yue Yi Tang

Shandong Peanut Research Institute
Qingdao 266100, PR China

Jian Cheng Zhang

Shandong Peanut Research Institute
Qingdao 266100, PR China

Shan Lin Yu

Shandong Peanut Research Institute
Qingdao 266100, PR China

Jian Zhi Xu

Shandong Peanut Research Institute
Qingdao 266100, PR China

Zhen Min Bao*

Ocean University of China
Qingdao 266003, PR China
Tel: 86 532 8203196
E-mail: zmbao@ouc.edu.cn

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Keywords: DNA extraction, groundnut, PCR, peanut.

Abbreviations: GXAS: Gaungxi academy of agricultural sciences

ITS: internal transcribed spacer

MAS: marker-assisted selection

PCR: polymerase chain reaction

PVP: polyvinylpyrrolidone

SCAR: sequence-characterized region

SSR: simple sequence repeat

This paper describes a simple, low cost and reliable DNA template preparation protocol for polymerase chain reaction (PCR) using immature leaves from peanut seeds or leaves from field-grown plants. The technique may find wide utility in studies involving PCR-based molecular markers, rapid screening for transformants and gene cloning.

Conventional DNA extraction protocols usually involve many steps; for plants species with abundant secondary metabolites, a lengthy procedure of over 10 steps is generally needed (Weising et al. 2005; Sarwat et al. 2006). The cultivated peanut and its wild relatives in the genus *Arachis* are species with carbohydrates and poly-phenols. Several DNA extraction and purification protocols for

*Corresponding author

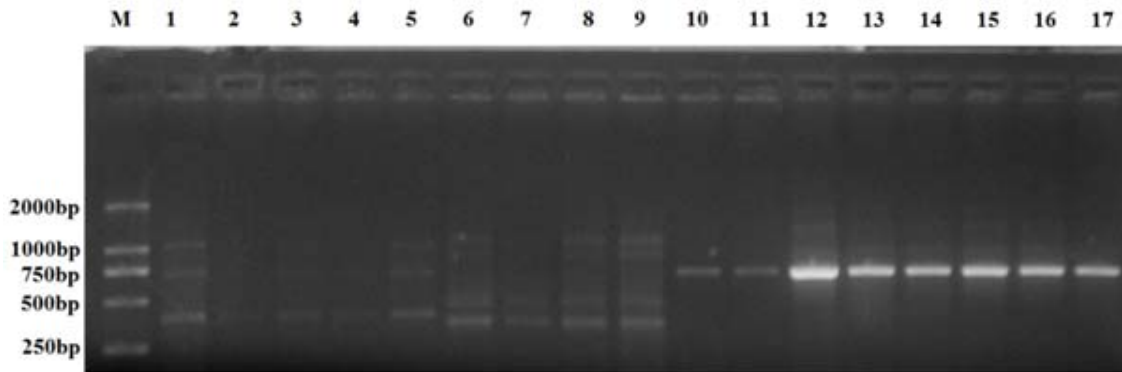


Figure 1. PCR products resolved on a 1.0% agarose gel. M: Tiangen D2000 DNA marker. The numbers used in the figure were the same as in the first column of Table 1. Genotypes, source of leaflets, primer pairs and treatments were listed in Table 1.

peanut have been published and proved competent in restriction digestion and Southern hybridization (Kochert et al. 1991; Choi et al. 1999; Burow et al. 2001; Wang et al. 2002; Chen et al. 2008). However, it is still difficult, within a short period of time, to deal with large number of samples even with sophisticated stainless steel beads and a grinding machine. This inevitably impedes the wide application of marker-based selection and fast screening for transformants in peanut.

Here we described a rapid, simple and cost-effective method for preparation of polymerase chain reaction (PCR) templates for peanut, which may facilitate marker-assisted selection (MAS) and gene mapping using simple sequence repeat (SSR) or sequence-characterized region (SCAR), screening of transgenic peanut plants and homology-based cloning as well.

MATERIALS AND METHODS

Materials

For primary evaluation of the protocol, totally 7 peanut genotypes were utilized. These included 3 peanut cultivars (I8B4, Luhua14 and L-1), 2 interspecific derivatives [6-33 (Silihong x *Arachis rigonii*) and L7-1 (Silihong x *A. glabrata*)] and 1 chemical mutant of L7-1 (m5) (Table 1).

For further evaluation, 8 accessions of peanut wild relatives (field-grown plants), 2 peanut landraces (Yingkousilihong and Xingchengdahuasheng) and an interspecific derivative 1-4 (Silihong x *Arachis glabrata*) (immature leaflets from seeds) were used (Table 2).

PREPARATION OF PCR TEMPLATES

When a seed is available, the immature leaflets (embryonic tissue from a non-germinated seed, 2.2 ~3.2 mg) may be used as the starting material. The leaflets were collected and placed into a 1.5 ml Eppendorf tube, and 20, 40 or 60 μ l of 0.25 mol/L sodium hydroxide (NaOH) was added.

The leaflets were then smashed using a thin-walled PCR tube mounted with a 1 ml pipette tip as a pestle. The mixture was boiled for 30 sec. Then 80, 160 or 240 μ l of Tris-HCl (pH 7.6) with 5 mg/ml of polyvinylpyrrolidone (PVP) (4 times the volume of NaOH added) was added followed by boiling for 2 min. After centrifugation at 10,000 RPM for 5 min, the supernatant was collected and stored at 4°C for use within a week, or stored at -20°C for several months.

Leaves from peanut plants grown in glasshouse or field may also be used, but the unexpanded or freshly expanded leaflets on the apex of branches/stems are most preferable. The unused end (without a tip) of a ball point pen refill was utilized as a hole puncher. The leaf disc (6.5 mm²) thus prepared may be handled using the alkali-lysis protocol, just as immature leaflets from a seed, which was described above.

PCR

To amplify the internal transcribed spacer (ITS) of peanut, 2 μ l DNA template was used in a 25 μ l reaction using Tiangen 2 x Taq PCR MasterMix (Tiangen Biotech) and the primer a and primer b as recommended by Wang et al. (1999). The PCR profile consisted of a pre-denaturation of 94°C for 3 min, 35 cycles of 94°C for 50 sec, 55°C for 1 min, and 72°C for 1.5 min, and a final extension of 7 min.

To amplify the β -tubulin gene-derived DNA regions, Tiangen 2 x Taq PCR MasterMix and primer pairs TBPfex1/TBPprex1 and TBPfin2/TBPfin2 were used. The primer pairs and PCR profile were the same as Breviaro et al. (2007).

Agarose gel electrophoresis of PCR products

After amplification was complete, 3 μ l of liquid from the PCR tube were run on a 1.0% agarose gel (1 x TBE) for 40 min at 100 V, and the gel was subsequently stained using

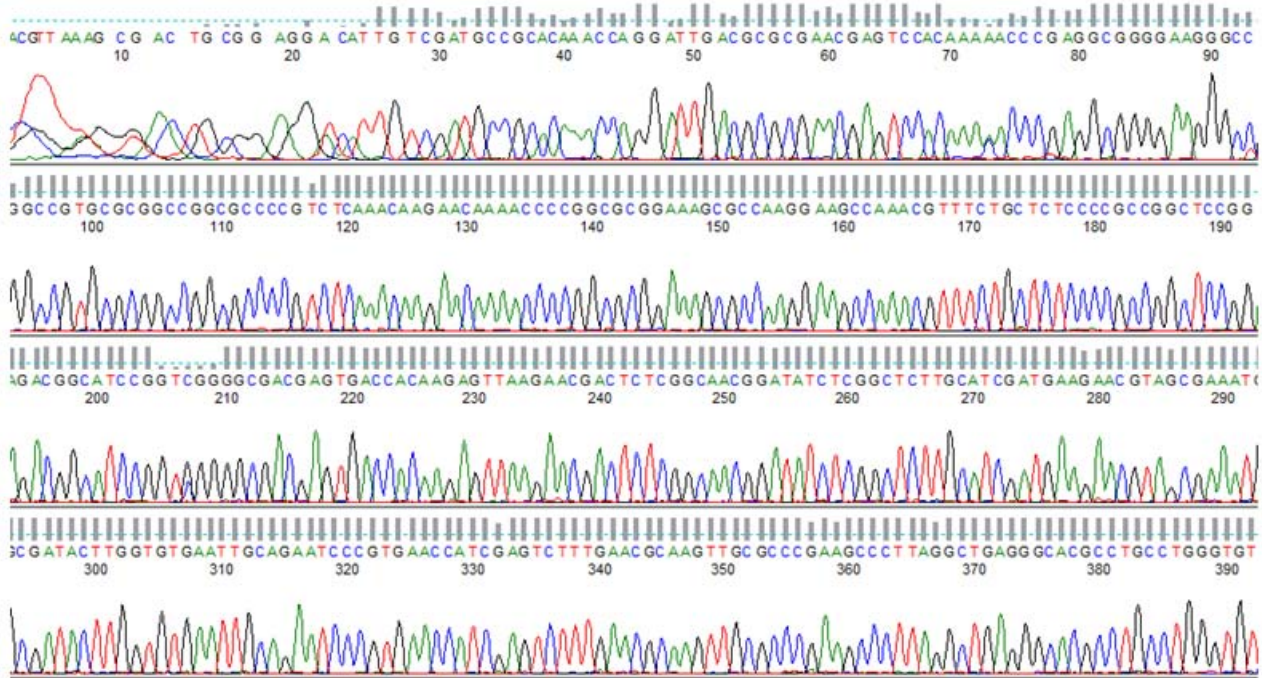


Figure 2. ITS of *A. duranensis* PI263133 (A19).

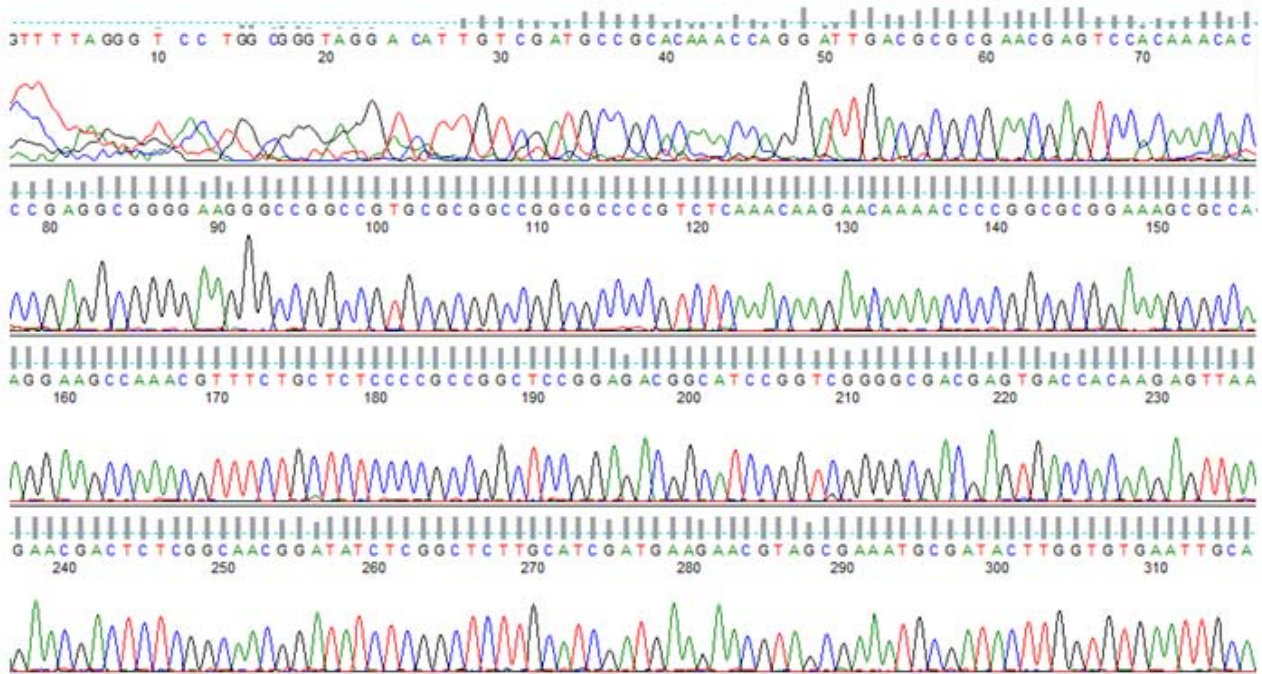


Figure 3. ITS of *A. pusilla* PI289628 (A10).

ethidium bromide and visualized under UV light to check for the presence of PCR products.

DNA sequencing

The PCR products of primer pairs a/b were recovered using the E.Z.N.A. Cycle Pure Kit, and DNA sequencing was performed on an ABI 3730XL sequencer using the primer a or b.

RESULTS AND DISCUSSION

Primary evaluation of the protocol

All of the materials/treatments produced distinct bands of expected size on agarose gel (Figure 1). The PCR products resulting from 20, 40 or 60 μ l NaOH treatment were all acceptable; therefore, in subsequent studies only the 60 μ l NaOH treatment was used. The concentration of the PCR templates prepared using 60 μ l NaOH was around 3 ng/ μ l.

Further evaluation of the protocol

All of the 11 peanut accessions (Table 2) gave good results, regardless of the starting materials. Clear bands were visualized on agarose gel, even with some wild accessions whose leaflets coated with thick cuticle. The bands were recovered and directly sequenced. Two of the trace files (partial) were shown in Figure 2 and Figure 3. The

sequencing results verified that the PCR template preparation protocol was successful.

CONCLUDING REMARKS

To the best of our knowledge, this is the first report on high through-put preparation of PCR template in peanut. The present protocol was developed on the basis of the alkali-lysis method as proposed by Wang et al. (1993) with some modifications. The boiling steps and the PVP component were included to ensure better and repeatable results.

Chenault et al. (2007) reported a non-destructive seed sampling method for PCR-based analysis with potential in marker assisted selection and transgene screening in peanut, where as little as 20 mg of peanut seed sample was enough for PCR template preparation; however, 20 steps are still needed. Using the present protocol, peanut DNA can be extracted in a relatively short period of time whenever a

Table 1. Peanut materials used for primary evaluation of the protocol.

No.	Genotype	Leaflet	Primer pair	Treatment
1	I8B4	immature	TBPfex1, TBPex1	40 μ l NaOH
2	L-1	immature	TBPfex1, TBPex1	40 μ l NaOH
3	Luhua 14	immature	TBPfex1, TBPex1	40 μ l NaOH
4	6-33	immature	TBPfex1, TBPex1	40 μ l NaOH
5	m5	immature	TBPfex1, TBPex1	40 μ l NaOH
6	I8B4	immature	TBPfin2, TBPrin2	40 μ l NaOH
7	L-1	immature	TBPfin2, TBPrin2	40 μ l NaOH
8	Luhua14	immature	TBPfin2, TBPrin2	40 μ l NaOH
9	6-33D3	immature	TBPfin2, TBPrin2	40 μ l NaOH
10	L7-1	immature	a, b	40 μ l NaOH
11	m5	immature	a, b	40 μ l NaOH
12	L7-1	field-grown	a, b	20 μ l NaOH
13	L7-1	field-grown	a, b	40 μ l NaOH
14	L7-1	field-grown	a, b	60 μ l NaOH
15	m5	field-grown	a, b	20 μ l NaOH
16	m5	field-grown	a, b	40 μ l NaOH
17	m5	field-grown	a, b	60 μ l NaOH

Note: The numbers used in the first column were the same as in Figure 1.

Table 2. Peanut materials used for further evaluation of the protocol. (Primer pairs: a/b, treatment: 60 µl NaOH).

Identity	Plant Introduction No.	Species	Section	Botanical type
GXAS* No. A 19	263133	<i>A. duranensis</i>	<i>Arachis</i>	
GXAS No. A2	338280	<i>A. stenosperma</i>	<i>Arachis</i>	
GXAS No. A14	331192	<i>A. correntina</i>	<i>Arachis</i>	
GXAS No. A8	210555	<i>A. villosa</i>	<i>Arachis</i>	
GXAS No. A7	219824	<i>A. monticola</i>	<i>Arachis</i>	
GXAS No. A10	289628	<i>A. pusilla</i>	<i>Heterantheae</i>	
GXAS No. A6	289639	<i>A. sp</i>	<i>Uncertain affinity</i>	
GXAS No. A13	289637	<i>A. sp</i>	<i>Uncertain affinity</i>	
Yingkousilihong (Landrace)	-	-	-	<i>fastigiata</i>
Xingchengdahuasheng (Landrace)	-	-	-	<i>hypogaea</i>
1-4 (Silohong x <i>A. glabrata</i>)	-	-	-	-

*GXAS: Gaungxi academy of agricultural sciences.

seed or a leaflet is available. It should be noted that although the ITS amplified in this report has high a copy number in plant genomes, this does not mean that the protocol is only suitable for DNA segments with high copy number. In fact, we have successfully cloned and sequenced partial *fad 2* and conglutin genes using similar protocols (Wang et al. 2001; Wang et al. 2004).

In conclusion, we have developed a short protocol, suitable for high through-put preparation of PCR templates in peanut, with no genotypes proved recalcitrant thus far. Neither nitrogen treatment nor organic solvent is needed. It should not only save time and money, but also reduce the possibility of contamination. This protocol may find wide utility in PCR-based applications in peanut.

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