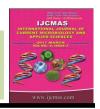


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#### **Original Research Article**

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### **Exploring Rapid and Efficient Protocol for Isolation of Fungal DNA**

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#### ABSTRACT

#### Keywords

Deoxyribonucleic acid (DNA), Rapid and efficient, Extraction protocol, Fungi.

#### **Article Info**

Accepted: 18 February 2017 Available Online: 10 March 2017 A simple, rapid, safe and cost effective DNA extraction method is an all time need for efficient molecular screening of fungus using polymerase chain reaction (PCR). A number of protocols are now available to suit recovery of DNA from different fungi. But, only a few are universally used for all fungal origin. In this pursuit, the authors presented a detailed review of the status of fungal DNA isolation using different methods.

#### Introduction

Rapid and reliable detection of pathogenic organisms is a basic requirement for diagnosis of food-borne illness and diseases. The detection of fungal pathogens in clinical and plant samples by PCR requires an efficient method of DNA extraction. A variety of extraction protocol is available for isolation of DNA. No single extraction method seems to be optimal for all organisms (Bolano et al., 2001). Fungus may form mycellial growth (filamentous) or spores on the media depending upon the strain used. The fungus is freeze dried or lyophilized before isolation. Fungal nucleases and high polysaccharide content (mannan, β-glucans and chitin) in rigid cell wall (Chaffin et al., 1998) add to the difficulties in isolating DNA from filamentous

fungi (Muller et al., 1998; Fredricks et al., 2005). Therefore, additional lysis steps, such as mechanical disruption or sonication, enzymatic digestion or use of toxic chemicals are required (Alaey et al., 2005). The CTAB extraction method was originally developed by Doyle and Doyle in 1987 for plant tissue extraction. It was considered superior for removing carbohydrates but it is timeconsuming and labor-intensive and does not result DNA yields satisfactorily from all biological samples including fungal mycelia and spores. A variety of modified CTAB methods are now available (Saghai-Maroof et al., 1984) for extraction and purification of fungal DNA using organic solvents (Blin and Stafford, 1976). Besides, several DNA

extraction methods have been designed that include use of liquid nitrogen combined with lysis buffer, enzymatic lysis method, use of SDS or proteinase K, lysozyme (Flamm et al. 1984a,b; Wilson, 1990), high speed cell disruption (Muller et al., 1998) and beadvortexing with SDS lysis (Sambrook and Russel, 2001). Additionally, although some methods do not involve maceration in liquid nitrogen, they are still time consuming and require special columns (Noor Adila et al., 2007). Other factors for modification often adopted to minimize the time, avoid the use of expensive and hazardous chemicals, maximize the DNA yield and amenability for use in various downstream enzymatic applications, such as PCR amplification, restriction digestion, southern blotting and DNA sequencing. This may be achieved by agitating the fungal samples using sonication (ultrasound disruption: >20-30kHz) microwave thermal shock (heat shock: 600-700watt).

Plating methods are aminable for detection of fungi. Now-a-days, such age-old methods have been replaced by more rapid and sensitive techniques, such as Fluorescence In-Situ Hybridization (FISH) (Chattopadhyay et al., 2013), Enzyme Linked Immuno-Sorbent Assays (ELISA) (Naravaneni and Jamil, 2005), Polymerase Chain Reaction (PCR) (Jaykus, 2003), and Real-Time PCR (RT-PCR) (Wolffs et al., 2004). However, the polymerase chain reaction (PCR) increasingly being used for identification (nucleic acid detection) and characterization microbial communities of in various environmental samples including air, soils, landfills, waters etc. PCR-based molecular marker techniques made it possible to elucidate the principles or factors underlying molecular evolution, population genetics, plant fungus interactions, or pathogen evolution at molecular level (Milgroom and Fry, 1997).

## Role of chemicals used for fungal DNA extraction

Extraction of DNA requires homogenization of the fungi (mycelium/conidia/spores) and separation of DNA from rest of the biomolecules. Different chemicals used for the purpose are-

TRIS (hydroxymethyl aminomethane, Mol. wt.121.14g): It is a very strong base and also available complexes with HCl to form Tris-HCl (Mol. wt. 157.56g). Tris binds with lipopolysaccharides (in the cell outer membrane). Thereby it helps to permealize the membrane and maintains a constant pH in the solution.

**CTAB** (N-Cetyl-N, N, N-trimethyl ammonium bromide, Mol. wt. 364.46g): This is a cationic detergent that simultaneously degrades and solubilizes the plant cell wall and lipid membranes of internal organelles and denatures proteins (enzymes). Besides, it dissociates complex polysaccharides and secondary metabolites like polyphenols from DNA. CTAB is probably the only compound that can separate partial nucleic acids from polyphenols. Removal of polysaccharides is badly necessary for proper restriction digestion of DNA.

EDTA (Ethylenediamine tetraacetic acid, Mol. wt. 372.2g): It prevents DNA from degradation by chelating magnesium ions needed for enzymes that degrade DNA. Urea and EDTA (bind with Mg<sup>+2</sup>) is used to chelate Mg<sup>+2</sup> (a co-factor of DNase) and thereby restrict cellular DNase activity.

Sodium chloride (Mol. wt. 58.44g): DNA is negatively charged. Negatively charged phosphates tend to repel each other. NaCl provides Na<sup>+</sup> ions that will neutralize the negative charge of phosphates in DNA and allow the DNA molecules to come together.

B-ME ( $\beta$ -mercaptoethanol:  $\beta$ -mercaptoethanol is a strong reducing agent which can remove polyphenols in the crude fungal extract. Besides, being basically a reducing agent, it breaks the disulphide bonds in protein and hence helps to separate the protein component from DNA.

PVP (Polyvinyl pyrroledone): PVP removes phenolic contaminations by forming hydrogen bonds with them. Browning of the DNA sample is checked as addition of PVP prevents oxidation phenolic compounds.

Potassium acetate (Mol. wt. 98.14g): Potassium acetate sometimes added prior to centrifugation or even added the supernatant after centrifugation to precipitate most of the proteins and polysaccharides (if any) in form of insoluble potassium dodecyl sulphate. Incubate the contents for 20min. at 0°C in ice box for chelating. This step may be avoided if intended for proteinase K or Naacetate treatment (for removal of protein) during the purification of DNA step.

Phenol: Phenol is an effective purifier of nucleic acids owing to its non-polarity and higher density (1.07g/cm<sup>3</sup>) than water (1.0g/cm<sup>3</sup>). Phenol does not interact with DNA (polar). When phenol is added to the cell homogenate, it further breaks down superfluous cell materials that otherwise contaminate the DNA sample. Following centrifugation, water (acquous phase at top) and phenol (organic phase at bottom) remain separate in the solution owing to differential density. DNA being polar in nature, it is dissolved in water (acquous phase) and thereby separated from organic debries settled at bottom. Clear supernatant following centrifugation is indicative of low phenolics.

Chloroform: It disrupts the bonds that hold the cell membranes by dissolving proteins, lipids, and then form complexes to precipitate out of the acquous solution. Thus, it solubilizes lipids and a lot of proteins to remove them from the DNA. Chloroform and water will separate into two distinct phases. The lower phase will be Chloroform, while DNA is present in the upper acquous phase.

Isoamyl alcohol: Iso-amyl alcohol helps to reduce foaming during extraction as well as helps to separate the aqueous phase from the organic phase by forming a thin separating layer.

Isopropanol and ethanol: DNA molecules in solution are surrounded by water molecules (shell of hydration). Ethyl alcohol and isopropanol are dehydrating agents which result disruption of hydration shell and thereby precipitate the DNA. Pre-chilled isopropanol offers better precipitation of DNA than ethanol at lesser concentration. 0.6 volume of isopropanol is sufficient for the purpose as against 2 times required in case of ethanol, but the DNA yield is more in the later. Low temperature slows down enzymes that can break down DNA, thus resulting better extraction results.

Deionized water: Deionized water is used to get rid of ions which can interfere with the extraction and follow up PCR and other molecular analysis.

#### **Fungal DNA extraction methods**

Isolation of fungal DNA is a multi-step method. It includes growing the fungus in liquid or solid medium, lyophilizing the fungal samples, disrupting cell wall, removing proteins with phenol and chloroform, and precipitating DNA with ethanol or isopropanol. Several modified methods have been designed by a number of researchers. Several workers compared different methods for ease in degradation/lysis of cell wall and

organelle membranes. Liquid nitrogen is most commonly used for homogenization (Wu et al., 2001). Some researchers used dry ice (Griffin et al., 2002), SDS lysis (Syn and Swarup, 2000), high-speed cell disruption (Muller et al., 1998) and glass bead/magnetic bead-vortexing/SDS lysis (Sambrook and Russel, 2001; Faggi et al., 2005), lysozyme lysis/enzyme digestion (Flamm et al., 1984a,b; Li et al., 2002), benzyl chloride lysis (Xue et al., 2006), sonication (Sharma et al., 2007), microwave exposure (Goodwin and Lee, 1993) and combinations of different methods (Zhang et al., 2008). In each method, the major objective lies with elimination of **PCR** inhibitors (metallic cations, polysaccharide, polyphenols, and other secondary metabolites) in DNA samples which would otherwise prevent DNA amplification. Besides, any protocol to be efficient for isolation of DNA relies on the ideal ratio of biological material to chemical reagents used. The usual methods of DNA extraction from filamentous fungi are either time-consuming and require toxic chemicals or are based on expensive technologies (Cheng and Jiang, 2006).

Standard CTAB method: Doyle and Doyle (1987) were successful for DNA isolation from small quantities of fresh leaf tissue using CTAB (a detergent). Since then isolation of DNA was made possible from different biological entities including fungus. Lee et al., (1988) and Wu et al., (2001) and Zhang et al., (2010) extracted DNA from filamentous fungus using standard CTAB method. Using this protocol, cell walls of fungal mycelia are broken down by grinding with glass rods, or mortar and pestle in presence of liquid nitrogen. The CTAB extraction buffer is then added followed by incubation at 65°C, purification with phenol: chloroform: isoamyl alcohol (25: 24: 1) and precipitation with isopropanol (Ashktorab and Cohen, 1992). Finally, the DNA is dissolved in 50µl of pure water or TE buffer.

SDS method: Prabha et al., (2013) recovered DNA from water moulds using extraction buffer containing 200mM Tris-HCl, pH 7.5; 25mM EDTA and 250mM NaCl and 0.5% SDS. The protocol takes relatively less time without the need to employ mercaptoethanol, CTAB, lysozyme digestion, proteinase K treatment etc. and thereby the overall costs involved. reducing González-Mendoza et al., (2010) attempted minipreparation of DNA from a sample size of 10mg of each fungal mycelium using 0.2ml extraction buffer (3%SDS, 0.5mM EDTA, 1.0M NaCl, and 0.1mM Tris-HCl, pH 8.0 followed by addition of 0.2ml chloroformphenol mix and incubation at 65°C for 5 min. The mixture was cooled to room temperature and centrifuged at 10,000g at 4°C for 5min. The supernatant was transferred to a fresh appendorf tube, and an equal volume of cold absolute isopropanol or ethanol was added and the contents mixed thoroughly for precipitating total DNA at -20°C for 20min.

Combined CTAB and SDS method: Umesha et al., (2016) used an improved method for DNA isolation by combining CTAB with SDS method without addition of Proteinase K, RNase K and β-mercaptoethanol. This was reported to be better and rapid than CTAB, SDS and microwave method for isolation of genomic DNA from food-borne fungal pathogens. 200 mg of lyophilized mycelial powder added with 500µl extraction buffer (250mM Tris-HCl pH 8.0, 20mM EDTA pH 8.0, 200M NaCl, 10% CTAB, 0.15% SDS) was vortexed and then boiled for 10min at 50°C followed by centrifugation at 10,000rpm for 10min. The upper supernatant was pipetted out and mixed with one volume of chloroform: isoamyl alcohol (23:2) and centrifuged at 10,000rpm for 5min. The aqueous phase was recovered and mixed with one volume of ice cold isopropanol to precipitate DNA.

Urea/Chelex/SDS method: DNA isolation from *Cryptococcus neoformans* is difficult due to a thick and resistant capsule. Mseddi *et al.*, (2011) have optimized a new and rapid DNA isolation method for *C. neoformans* using a short urea treatment followed by a rapid method using a chelex resin suspension (10% Chelex 100, 0.1% SDS, 1% Nonidet P 40, and 1% Tween 80). The samples were incubated at 95°C for 30min and then on ice for 5min. DNA was removed from the supernatant after 5 min of centrifugation (10,000rpm) and stored at -20°C until used.

method: Glass beads Although **PCR** amplification can be performed directly on various microbial cultures, for filamentous fungi and yeast, prior isolation of DNA is often preferred. Standard methods available that eliminates many interfering substances like mineral salts, proteins, polysaccharides, and plays an important role in ensuring consistent results. But, such method is laborious, expensive and time consuming (Van Burik et al., 1998). Therefore, some workers used glass beads as a substitute to liquid nitrogen. Gontia-Mishra et al., (2014) employed glass bead method for disruption of filamentous fungal cell walls in an extraction buffer (0.1M Tris-HCl pH 8.0, 10mM EDTA pH 8.0, 2.5M NaCl, 3.5% CTAB) followed by inactivation of proteins using 150µl of 20mg/ml Proteinase K. The DNA yield from fungal isolates (Aspergillus niger, A. flavus, A. awamori, A. fumigatus, A. ficuum and A. terreus) varied from 310-1879µg/g dry mycelium and a clear intact DNA band was observed upon agarose gel electrophoresis. Aamir et al., (2015) also used glass beads for homogenizing mycelium in lysis buffer (100mM Tris-HCl pH8.0, 50mM EDTA, 3%SDS). Plaza et al., (2004) used 200-500mg fungal mycelium to add with 500ul extraction buffer solution (in a 1.5ml micro centrifuge tubes) containing: 0.1M NaCl, 0.5M Tris-HCl pH8.0 and 5% SDS.

The contents are ground 10 min. using glass beads followed by centrifugation at 11,000g for 10min., precipitation of DNA in the supernatant by isopropanol and washing of DNA pellets using 70% ethyl alcohol. The protocol can be applied to filamentous fungi from soil as well as from other environmental sources.

Lysis buffer method: Most of the methods rely on using a grinder (with or without liquid nitrogen) for homogenization. Zhang et al., (2010) developed a simple and rapid method for isolation of DNA from different fungal isolates. In this context, the fungal mycelia or yeast cells were first rinsed with pure water to remove potential PCR inhibitors followed by thermolysis at 85°C in a lysis buffer (50mM sodium phosphate at pH 7.4, 1mM EDTA and 5% glycerol) to break down cell walls and membranes. High as well as single-copy number genes were successfully amplified from the extracted DNA samples. The DNA samples obtained by this method can be stored at 20°C for over 1 year. Besides, Liu et al., (2000) used a lysis buffer containing 400mM Tris-HCl pH 8.0, 60mM EDTA pH 8.0, 150mM NaCl, 1% SDS followed by addition of 5M Potassium acetate for extraction of DNA from filamentous fungi.

Microwave method: Microwave radiation has been shown to be effective in killing *Magnaporthe grisea* (rice blast fungus). Genomic DNA may be isolated from as little as 2 mg dry biomass of such filamentous fungus by microwave radiation treatment within 30s (Tendulkar *et al.*, 2003). The Fungal biomass (2 mg) was washed and suspended in 50µl of TE (10mM Tris/HCl buffer, pH 8.0, 100mM EDTA pH 8.0) in microcentrifuge tubes followed by microwave treatment at 2450MHz frequency in a microwave oven of 230V output at 28°C for 30s. The treated biomass was incubated at 28°C for 5min and centrifuged at 10,000g for

5min. The supernatant contained genomic DNA and was used directly for PCR as well as for dot blot hybridization. This method avoids the use of hazardous chemicals like CTAB, SDS, \(\beta\)-mercaptoethanol, phenol, chloroform and isoamyl alcohol. technique has been also suitably used along with chitinase treatment in case filamentous fungi, like Aspergillus (Bir et al., 1995). The quantity of DNA was good enough for PCR analysis and Dot blot hybridization. Further, genomic DNA yield as high as 9091ng/µl can be extracted from 5mg of 3-4 day old fungal mycelium, Fusarium, Verticillium, Bipolaris oryzae, Rhizoctonia solani by combined lysis buffer-microwave treatment. The method seems to be quite simple, cost effective, rapid and efficient for PCR assay of specific gene tagging.

Sonification method: The ultra sonic waves can easily destroy the cell wall (Voget *et al.*, 2003, Sharma *et al.*, 2007). However, it is less used for extraction of DNA than other cellular components such as proteins and pigments. Sonication is a very efficient and reliable tool that allows a complete control over different parameters. This ensures a high selectivity on materials release and product purity. It is a quite versatile method suitable to all cell types and easily applicable in small and large scale (Kennedy and Marchesi, 2007). Lysis of mycelia can be achieved by sonication for 40min. at 55°C in a Bransen 2200 waterbath sonicator (Van Burik *et al.*, 1998).

Enzymetic lysis method: Lysozyme alone or in combination with SDS is *in vogue* used for lysis of fungal cell walls (Flamm *et al.*, 1984a,b). An extraction method based on enzymatic lysis produced high levels of fungal DNA with *Candida albicans* (a model filamentous fungal pathogen) but low levels of fungal DNA with *Aspergillus fumigatus* conidia or hyphae (a model yeast pathogen) as revealed from qPCR (Fredricks *et al.*, 2005).

Purohit and Singh (2009) included lysozyme in the lysis buffer for extraction of metagenomic DNA of microbes living in saline habitat.

Universal A method: single protocol universally used for plant, algae, blood, bacteria, fungus will be more demanding (Kumar et al., 2012) than those suited specific to a particular biological material. The extraction buffer used in this case included 100mM Tris-HCl, pH 8.0, 25mM EDTA, 1.5M NaCl, 2% CTAB, β-mercaptoethanol, PVP(in case of plant sample). The method utilizes the classical protocol homogenization by liquid nitrogen, incubation in water bath at 65°C, deproteinization by chloroform-isoamyl alcohol followed by ethanol precipitation and washing. Alternative to the above, other universal methods termed as 'nuclei method' and 'protoplast method' may be successfully used to prepare highquality megabase-sized DNA (Zhang et al., 2012). In this method, nuclei are first isolated by physically grinding the source tissues. The protoplast method uses the cell wall hydrolases such as cellulose and pectinase to remove the cell walls of plants, algae, fungi, bacteria and yeast before isolating DNA. In case of 'nuclei method', nontarget cytoplast organellar genomes and other cytoplsmic organelles and cytosolic metabolites are removed by centrifugation and washing, thus maximizing the utility of the method and substantially improving the digestibility and clonability of the resultant DNA.

Rapid and a direct method: Jia *et al.*, (2014) designed a rapid and direct method that avoid precipitation step. They extracted DNA from stored desiccated (at -20°C) fungus grown on a piece of filter paper (0.5-1.0cm diameter). The fungal sample was placed in a 0.2 ml Eppendorf tube containing 100µl 10x TE. The suspension was heated for 10 min at 95 °C in a PCR machine. The tube was then

centrifuged for 1 min at 3000 rpm. One µl of 10x TE solution containing DNA can be suitably used for PCR amplification. The DNA prepared directly from the fungus on filter paper appeared suitable for a rapid survey of genetic identity of the rice blast fungus. The protocol proved to be the most safe, quickest and cost-effective method that took just 11min. to complete the process without use of any costly and hazardous chemicals.

# Checking for quantity and quality of fungal DNA

The PCR technique requires sufficient quantity and high quality DNA of pathogens. Success in development of a DNA isolation protocol needs to be verified by status of DNA in terms of quality and quantity of DNA. Concentration of DNA (ng/µl) samples was determined by spectrophotometry at 260 nm wave length, and the purity is assessed as  $OD_{260}/OD_{280}$ using **UV-VIS** spectrophotometer or NanoDrop (Thermo Electron Scientific Instruments LLC, USA). Further, the DNA quality may be assessed by electrophoresis following PCR amplification of genomic DNA using gene specific primers.

#### **Precautions**

Every precaution must be taken to avoid the laboratory borne contamination during DNA extraction. To make contamination free, the needle/loop needs to be flame sterilized. The bottles and culture tubes may be treated with 0.1% diethyl pyrocarbonate (DEPC) solution at 37°C overnight, autoclaved twice at 121°C for 20 min, and then dried at 100°C before use. Tips used for DNA extraction are required to be DNase-and RNase-free, while pipettes/Petri plates need steam sterilized before working. Besides, use of gloves and safety glasses are must as most of the protocols involve hazardous chemicals.

It can be concluded that the plants at different stages are suffered from a number of pathogenic fungi. Certain food and food products serve as high-risk substrate for growth of fungi. Besides, human health is threatened by notorious fungal infections. Now-a-days, PCR has become a common tool for detection. identification characterization of microbial clinical samples. Besides, PCR and advanced molecular analysis made it possible to study gene expression, cloning of genes, elucidation of factors underlying fungal evolution. population genetics, plant-fungus interactions. These demand a rapid and efficient protocol for isolation of pure fungal DNA. Several protocols are now available for this purpose but no single extraction method seems to be optimal for all fungal entities.

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