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Efficient DNA extraction and purification protocol of medicinal plants which producing large amount of secondary metabolites

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Abstract

Using medicinal plants is very valuable and beneficial. So, it is essential that the genetic and other molecular properties must be determined for the purposes of economy, sanitary and health, as well as maintaining natural diversity and avoiding the disappearance of endangered species in natural habitats. Although, Medicinal plants in various tissues and different stages of growth have varying amounts of organic compounds that make difficulties in the extraction process of genome in some cases or even impossible. Therefore, providing a convenient, fast, practical and lowcost method that works in all laboratories and situations with available materials seems very important. In this research, the genomic DNA has been extracted from various tissues and organs of different medicinal plant families. In addition, this protocol was achieved by studying, performing and using different methods of genomic extraction method on various medicinal plants. Whether the sample has been contaminated with different metabolites, rapid and efficient purification methods are available. The quantity and quality of the extracted DNA were determined by electrophoresis of 1% the Agarose gel and spectrophotometer tool respectively. The results show that the genomic DNA extracted is relatively pure and desirable. The results of this study have been used directly in various genetic molecular researches such as assessment of the genetic diversity with the AFLP molecular marker, transfer and gene over expression; it must be noted that the results of this study in similar resources were not observed and done for the first time.

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Introduction

Using medicinal plants are very valuable as the major and minor products (Majnoun Hosseini and Davazdah Emami, 2007). In addition, there are a lot of advantages through direct cultivation and sale of the extracts from these plants (Kadkhoda et al., 2011). This type of plant in different tissues and different stages of growth has variable and large amounts of organic compounds or secondary metabolites, which can be referred to as proteins, polysaccharides, colored pigments, alkaloids, tannins and phenolic compounds, terpenoves, etc. (Sahu et al., 2012). These compounds have medicinal and medical properties but recently due to the resistance of the pathogens to chemical agents and antibiotics, alternative sources are needed to meet the sanitary and health needs and also reduce the harmfulness of chemicals drugs (Pirttii, 2001; Hariri Akbari et al., 2010; Kazemi and Seyed Hajizadeh, 2012). therefore, clear that the determination of genetic, molecular, biochemical, morphological, physiological and ecological characteristics of this group of plants for the purpose of sustainable economic exploitation, sanitary and health goals, as well as maintaining their diversity in natural areas, preserving and saving of endangered species from their natural habitat seems necessary (Karimi and Farokhi, 1998).

In the meantime, molecular topics are important in various biotechnology studies. With using biotechnology tools such as genomics, genetic engineering and gene library development, it is possible to maintain and protect billions of genotypes in low volume and low cost. It can be said that the extraction of nucleic acids is the first and most important step in molecular genetic studies (Ghareyazi, 1996; Farsi and Zolali, 2003; Kazemi and SeyedHajizadeh,2012). In many cases, the extraction of the genome has also had limitations because of organic compounds, conditions as well as the reagents used for that purpose usually are expensive or cause a high environmental impact (Kazemi and Seyed Hajizadeh, 2012). Although, several successful DNA extraction protocols for plant species that contain polyphenolics and polysaccharides compound have been developed, none of these are universally applicable to all plants (Varma and Padh, 2007) and the published protocols are also limited (Kazemi and Seyed Hajizadeh, 2012; Sahu *et al.*, 2012). That it is necessary to provide a convenient, fast, practical and low-cost method that can be done in all laboratories with available materials (Shafiee *et al.*, 2009).

The search for efficient protocol for extracting genomic DNA that have both higher quality and yield has led to the development of several protocols for isolating and extracting DNA from plants containing high levels of secondary metabolites (Sahu *et al.*, 2012), in some cases, changing in the physical conditions and the materials of the experiment will be improved the quantity and quality of the extracted DNA (Vojdani, 1996; Naghavi *et al.*, 2005).

In this study, by studying and conducting various experiments on variety of medicinal plants such as *Anethum graveolense, Artemisia annua, Mentha arvensis, Ferula assa-foetida, Datura stramonium, Ducrosia anethifolia, Aloe vera* and Callus of *Taxus baccata* was achieved an easy, convenient, affordable and low cost way to extract the genome from medicinal plants. Most of these plants are native to Iran and parts of Afghanistan. In order to demonstrate the importance and applicability of this method in molecular studies, some genomic DNA that were extracted by fallowing method as well as *Anethum graveolense, Ducrosia anethifolia,*

Artemisia annua which were used directly to determine the genetic diversity with using the AFLP molecular marker, genome of opium poppy was used for the effect of exacerbating the expression of the TYDC gene for increasing the production of important alkaloids (Koohzadi, 2009) and for Callus of *Taxus baccata* the method Just used for proof testing that this method could extract DNA from different tissues (Fig. 3) (Behjat Sasan *et al.*, 2014) and all of the genome samples which were extracted by this method used in molecular studies successfully.

Material and methods

Plant cultivation and callous production

Seeds of *Anethum graveolense* have been collected from natural habitats and placed in dish pads on wet paper and then transferred to plastic pots after germination. When the plant length reaches 10 to 15 centimeters and the leaves are well grown, it is ready to perform extraction (Fig. 1).

Seeds of *Ducrosia anethifolia* were grown in Murashige and Skoog medium (Mostafavi and Afzali, 2005; Shafiee *et al.*, 2012) with glucose in 2-2% and agar in 8 g/L, growth regulators including auxin and cytokinin at concentrations of 2 mg / L and 1 culture medium, in dark space and temperatures of 26 and 24 degrees Celsius were cultivated for the production of calluses (Fig. 2) (Ashtari, 2008; Kadkhoda *et al.*, 2011; Omidi *et al.*, 2012).

Taxus was occurred on ¹/₂ MS medium which had one-fourth nitrogen (KNO3, NH4NO3) supplemented with glutamine, 1mg/l 2,4-D and 1 mg/l Kin from stem(Fig. 3) (Behjat Sasan *et al.*, 2014) and the Callus was use for DNA ectraction.

Artemisia annua (Lari Yazdi *et al.*, 2002; Baraldi *et al.*, 2008) and other plants were planted in the field and greenhouse for the production of seedlings and fresh leaves (Fig. 4) (Bovard *et al.*,2016).

DNA extraction method

Plant organs and calluses were put in a mortar which autoclaved and placed in a freezer at -20 ° C and with helping of liquid nitrogen, the specimens are completely ground (Naghavi and Ghareyazi, 2007) and transferred to tubes of 1.5 ml. into each of the tube, add 900 μ l of the SDS solution 4% (0.4 g SDS in 10 cc of Tris solution, EDTA, NaCl) to the buffer solution and place it at 65 degrees Celsius for 45 minutes. It should be noted that the inverting procedure should be done alternately. Add 300 μ l of potassium acetate to each tube and place it in a container of ice for 25 minutes. The tubes are centrifuged at 3 ° C for 15 minutes and 12000 rpm. Remove 750 μ l of the upper liquid and transfer to a new tube, then add 750 μ L of isopropyl alcohol and place it at 25 ° C for 5 minutes. The tubes were again centrifuged at 3 ° C for 15 minutes and 12000 rpm. Discard the upper liquid and place the tubes at 37 ° C in the incubator for 20-30 minutes. Until the pellet (Fig. 5) is completely becoes dry.

Purification

Add 700 ml of autoclaved DDW to each of the tubes, It is kept at 4 ° C for 1 hour.Then we slowly tap into the Pellet formed at the end of the tube to be completely dissolved after that the chloroform solution 24/1 (24: 1) is added to the volume of 700 microliters next, Shake gently for 20 seconds to obtain a uniform emulsion.

Centrifuge with 13000 rpm for 10 minutes, which consists of two phases: The lower phase is chloroplast isoamyl alcohol and the supernatant phase contains DNA. The supernatant phase is transferred to a new 2 ml tube And 0.1 volume of upper liquid, Sodium acetate (3 mol, pH = 8) was added. 2.5 times the upper liquid volume, absolute alcohol (100%) added and then waiting 5 minutes to dewater.

Centrifuge 13000 rmp for 10 minutes, Discard the upper liquid and pellet, 100 μ l of alcohol was added to 70% . Removing the alcohol and place in the incubator for 20-30 minutes at 37 ° C to dry completely. Then add 100 μ l of TE or distilled water (DDW).

Electrophoresis of Agarose gel

Different methods such as ion exchange chromatography and electrophoresis can be used for separation of nucleic acids. The performance of all these methods is based on the difference in electric charge (Clark and Pazdernik, 2005). In this study, simple and fast electrophoresis method of 1% agarose gel was used.

Mix 5 μ l of prepared DNA samples with 5 μ l of dye, after that 9.5 μ l of DNA and dye mixture were placed

in 0.1% agarose gel wells. Agarose gel for 35 minutes at a constant voltage of 90 V, was electrophoresis. after staining with ethidium bromide (for 30 minutes), DNA is observed and photographed under UV light on the Geldoc device. It is also possible to measure the DNA quantity by spectrophotometer (Fig. 6).

Electrophoresis of polyacrylamide gel

Molecular markers, in particular DNA based markers provide reliable genetic information because of the independence of the confounding effects of environmental factors (Powell *et al.*, 1996; Etminan *et al.*, 2012). The AFLP procedure was performed with appropriate modifications of the method described by Vos *et al.*, (1995). In order to demondtrarte the appicibility, high quality and quantity of the genomic DNA which was extracted by this method, assessment of genetic diversity by AFLP molecular markers for *Anethum graveolense*, *Artemisia annua* and *Ducrosia anethifolia* (Fig. 8) has been done.

Results and discussion

Resuls of extraction and purifiction process

The DNA obtained was free of any contaminating proteins, polysaccharides and coloured pigments.

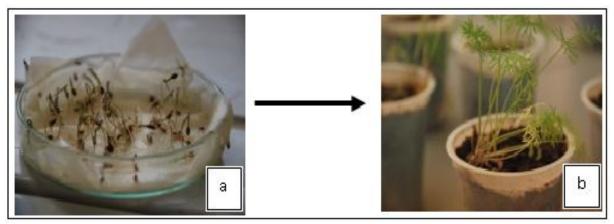


Fig. 1. A view of the cultivated plant samples of *Anethum graveolense*. The seeds were put on Wet paper. (a) and transferred to the plastic pot after germination(b) A view of the cultivated plant samples.

The study of gel electrophoresis shows high-weight and good resolution bands for all specimens, and also these bands prove that DNA does not have fracture and also are desirable quality for molecular experiments (Fig.6).

Genome quantitative determination was done by spectrophotometer and the purity Index with radiating two different wavelengths ranging from 260 to 280 nm shows 1.76 to 2.01 and prove that genomic DNA has a good quantity.

Considering that the extraction of DNA from medicinal plants due to the high level of phenolic, alkaloid, tannin, oily compounds, etc. is a problem and requires purification methods. However, using non-differentiated tissues in this method, such as fresh leaves, young ones, as well as callus, allowed the removal of the purification step. consequently, DNA extraction can be made at a faster rate and cost less.

As shown in Fig. 6 of the electrophoresis gel, without applying RNase, Protease and purifying process with phenol and chloroform isoamyl alcohol, the resulting DNA has a relatively good quality.

In the case of contamination with metallolites, the purification step can be used to extract pure DNA, Of course, this should be noted that the purification steps lead to the fracture and compression of the DNA, therefore, carefulness in the work process is important so that there is no need for repetition.

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Fig. 2. View of callus of *Ducrosia anethifolia* (Shafiee *et al.*, 2012).

The right side genomic DNA is much purer than the left one. It should be noted that this DNA is so pure and after purification step, it has been used directly in molecular tasks like AFLP marker for assessment of genetic diversity (Fig. 7 and Fig. 8).

Using the extracted genome in molecular studiese The isolated genomic DNA was found suitable for restricted enzym and digestion process. In addition,



Fig.3. Callus of *Taxus baccata* was used for extracting genome by the method (Behjat Sasan *et al.,* 2014).

This DNA extraction protocol can also be used in molecular studies such as genomics and genetic engineering, some of which are PCR-based protocols. Genome required for using in molecular markers, determination of polymorphism and genetic diversityshould have high quality and quantity and the results of the polyacrylamide gel and the study of the genetic diversity with the AFLP molecular marker showed that the extracted genome has been suitable for molecular studies (Fig. 8). As well as TheGenome of Opium poppy which was extracted by the method for the effect of exacerbating the expression of the TYDC gene for increasing the production of important alkaloids (Fig. 9). (Koohzadi, 2009; Koohzadi *et al.*, 2013).



Fig. 4. View of the greenhouse.

Discussion

The extraction of the genomic DNA from any plant sample needs the basic requirement that is first to break the cell to release all cellular constituents like DNA, RNA, polysaccharides, carbohydrates, enzymes, etc.



Fig. 5. Shows that a very clear pellet and does not indicate any contamination.

The cell membrane can be ruptured by detergents like SDS or CTAB. EDTA is used as a chelator of most metal ions requires for cellular nucleases activity. Most proteins are removed by chloroform extraction while the polysaccharides are removed by salt (NaCl, KCl or NaAc) together with detergent (Murray and Thompson, 1980). Some changes in the process of extraction and purification are required in terms of temperature, time, and amounts of materials needed, which can provide a suitable method for the extraction of genomic DNA in molecular research (Keb-Llanes, 2002).

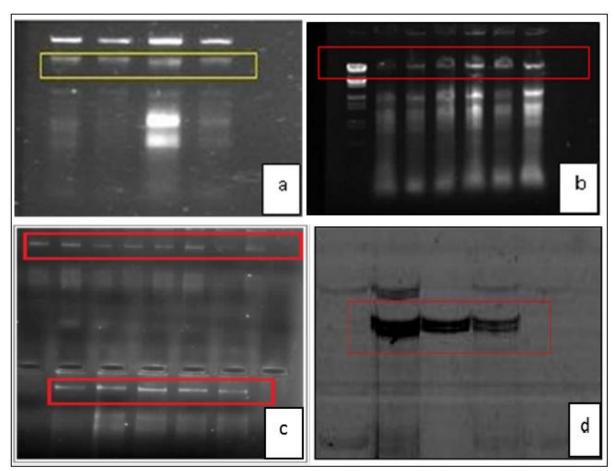


Fig. 6. 1% agarose gel was used for extracting the genome of medicinal plant sampels: *Anethum graveolense*(a), *Ducrosia anethifolia*(b),*Artemisia annua*(c) and*Taxus baccata* (d).

(a)Agarose gel electrophoresis containing DNA samples along with a DNA ladder Which represents the concentration of extracted DNA.

(b) Agarose gel electrophoresis of samples containing DNA from callus of Ducrosia anethifolia, which has transparent bands in all four replicates.

- (c)DNA extracted from leaves of Artemisia annua.
- (d) DNA extracted from callus of Taxus baccata.

The isolation of pure, intact, and high-quality DNA is very crucial for any molecular studies. However, DNA isolation from plants is usually compromised by excessive contamination by secondary metabolites. The DNA isolation methods need to be adjusted to each plant species and even to each plant tissue because of the presence of these unlike metabolites (Lutz *et al.*, 2011). Some changes in the process of extraction and purification are required in terms of temperature, time, and amounts of materials needed,

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which can provide a suitable method for the extraction of genomic DNA in molecular research (Keb-Llanes, 2002). The search for a more efficient method of extracting DNA of both higher quality and

yield has led to the development of several protocols for isolating DNA from plants containing high levels of secondary metabolites (Sahu *et al.*, 2012).

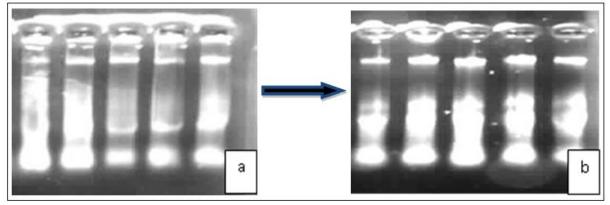


Fig. 7. Extracting Genomic DNA from the *Anethum graveolense*(a) Shape left before purification.(b) Shape right after purification.

In this research, applying various methods such as CTAB, Dellaporta, Qiagen DNeasy Mini Plant Kit to extract DNA on medicinal plants, it was concluded that the DNA produced by this method has a much and quantity better quality for molecular experiments. The method is very simple, easy, functional and low costcompared with the use of genomic extraction kits that are common in genetic laboratories today, it significantly reduces the cost of the test.On the other hand, this method has fewer steps than CTAB methods, so in a short time it is possible to extract more samples with better quality and quantity (Kazemi and Seyed Hajizadeh, 2012).

By comparing the various methods of extracting DNA, if the extracted specimen from the genomic plant is not rich in metabolites, Using routine laboratory methods are efficient. But if the herb has a high level of metabolism, especially when exposed to environmental stress in this case, the use of common protocols is not efficient or it should take a lot of time to optimize it. But this method is applied in various medicinal plants which are very diverse in terms of treatment conditions or culture media and showed that good and acceptable genomic DNA can be obtained at little cost and time. In this way, there's no need to use the Triton X-100, the polyvinylpyrrolidone (PVP), which is used in a CTAB buffer-based method.

According to Ribeiro and Lovato (2007), the extraction of the genome by using the Mini Plant Kit from young leaves yields very good DNA but if the plants is somewhat were affected by environmental stress or become elderly, the extracted genome greatly reduced in terms of quality and quantity or will be not efficient. Polymerase chain products (PCR products) prove this, because the polymerase enzyme (Taq DNA Polymerase) does not perform well in the presence of metabolites, metabolites inhibit the activity of the substances which were used in various stages of extraction, also, if the number of samples or the repetition of the test increases, good results are not achieved with plant DNA extraction kit. But after the extraction of the genome, if contamination with the metabolites will be observed, the purification steps that provided in this protocol could be performed. It is better to perform the purification step once; otherwise, the DNA may be squeezed or broken.

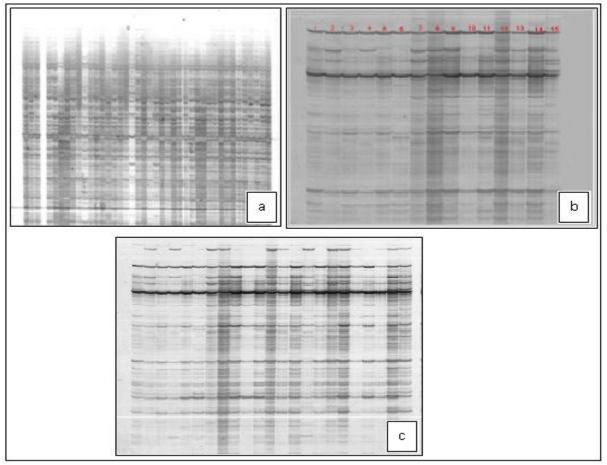
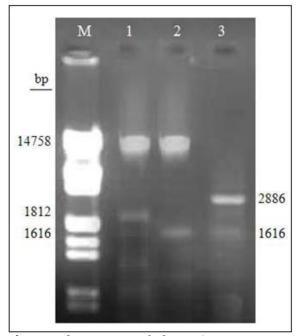


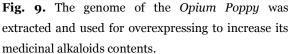
Fig. 8. Polymorphism investigation of *Anethum graveolense*, (a) (Hariri Akbari *et al.*, 2014), *Artemisia annua* (Bovard *et al.*, 2016) (b), and *Ducrosia anethifolia* (c) by using the amplified fragment length polymorphism (AFLP) technique with using the genome which was extracted by mentioned method.

Detergent sodium dodecyl sulfate (SDS), which is used in the first steps, has the potential for uniform zing the electrical charge of the proteins and destroying of the membrane of the cell, in contrast of other methods that has used simpler way but SDS could be tangible in laboratories.

According to Al-Saghir (2009), it should be noted that none of these methods are suitable for woody and rough texture such as rough stems and their seeds and to extract the genome from these tissues, there is a need for alternative methods. Because of crushing plant tissues at the sub- cellular levels and the collapse of cellular organelles are not possible with the simple methods available, in other hand not only the genome of fresh organs could be extracted by this method but also Somewhat old and rough organs too. In this genome extraction method, liquid nitrogen due to reduced cost and the unavailability of advanced tools crushing plant tissue is used, in addition plays the role of brittle plant tissue and it is prevented from the rapid corruption of crushed texture. In this study, different tissues of the plant are used to extract the genome successfully like fresh leaves, green and Grass Shoot or even callus of *Ducrosia anethifolia* and *Taxus baccata*.

Maria *et al.*, (2001), by extracting DNA from medicinal plants with aromatic compounds using CTAB, managed to extract the desired quality genome, but the time and number of steps have diminished DNA quality and their research required the use of PVP and Mercaptoethanol. These materials should be used with special tools and Laminar flow, as well as adding lithium chloride (LiCl) in the CTAB buffer, it prevents DNA from being isolated from the RNA However, in this method, we have removed the RNA at the last step by adding 2 Macro liters of RNase. In spite of, This method does not require RNAase, making it advantageous over common protocol.





Various genomic DNA isolation methods like Dellaporta *et al.*, (1983), CTAB (Murray and Thompson, 1980), and methods were tried and Khanuja *et al.*, (1999) method is the well suited to most of the medicinal plants. Further improvement of Khanuja *et al.*, (1999) method was developed by modification of few steps in the genomic DNA isolation protocol to get the good quantity and quality of the genomic DNA which is used for further downstream processes like Polymerase Chain Reaction etc.

The age of the leaf also affects the quality of extracted DNA (Moreira and Oliveira, 2011).

The young leaves yield a good quality and quantity of DNA with fewer impurities (secondary metabolites etc.). It was found that the young, frozen leaves yield good quality of DNA. (Shafiee *et al.*, 2009).

Conclusion

Using the methodthat presented in this study, with such a wide variety of medicinal plants and their various tissues including herbs, fresh leaves, old tissues and even calluses can extract the genome and use it in various molecular experiments, has not been observed. The results of this study, has been used in molecular research, including determining genetic diversity with molecular markers AFLP, transfer and gene overexpression. This research, due to the easy method and the use of available materials, can be a good alternative to kits-based methods.

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