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# Annonaceae DNA extraction protocol from silicage dried and herbarium preserved leaves

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#### DISCLAIMER

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# OPEN ACCESS



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Protocol status: Working We use this protocol and it's working

#### **ABSTRACT**

This protocol is used for DNA extraction of samples from the tropical plant family Annonaceae for leaves dried using silicagel or sampled from herbarium sheets.

This protocol is made for generation of small to long fragments (depending quality of sample) to prepare NGS libraries.

This protocol is designed to extract DNA in batches of 48 samples, but this can also be undertaken in 2 times 48 (96) samples.

#### **IMAGE ATTRIBUTION**

Art work by Vincent Soulé

#### **GUIDELINES**

Work in a clean environment to avoid contamination, use as much as possible filter tips, wear gloves and lab coat. Wash work space and pipettes before and after use, with DNAaway and DNAse away.

Manipulate with extreme caution rare or old samples.

#### **MATERIALS**

2mL Screw tube 2mL secure lock ependorf tube

**REF MATAB** 

Created: Jan 18, 2023

Oct 5 2023

Last Modified: Dec 05, 2023

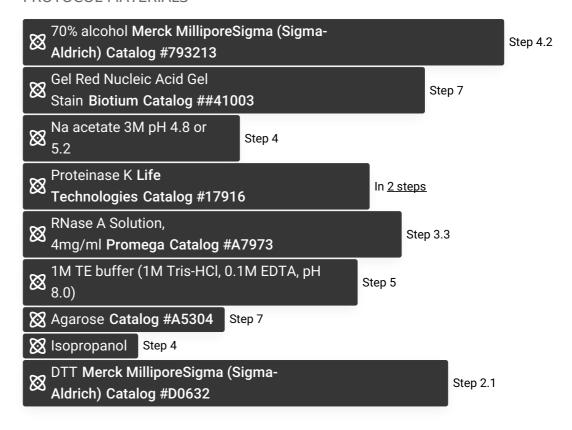
# **PROTOCOL integer ID:** 75464

**Keywords:** DNA extraction, NGS extraction, MATAB, CTAB, aDNA, Illumina sequencing, Angiosperm, magnoliales, herbarium

#### Funders Acknowledgement:

ERC Consolidator Grant ID: 865787

#### PROTOCOL MATERIALS



#### SAFETY WARNINGS

Always work under an extractor hood when manipulating of Chloroform, DTT or Isopropanol

## Leaf grinding

- 1 Prepare 48 2 mL Screw-Top tubes in rows of 8 in a 96 well rack. Add one 1/4" ceramic beads (MP Biomedical REF 116540422).
- **1.1** Add leaf sample inside the tube using clean tweezers. The leaf samples can be between 1x1 cm and 3x3 cm in size. Closes the tubes.
- 1.2 Grind samples using a MP FastPrep grinder, twice for 00:00:40 at 4m/second speed with a 2 4m minute pause in between each grind as not to over heat the samples.



# Lysis buffer preparation and lysis

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Lysis buffer LB needs to be freshly made the day of the extraction using a previously made LBmix +

MATAB, Proteinase K Life
Technologies Catalog #17916

and DTT (DL-Dithiothreitol) (final

concentration 1mM).

Preparation of LBmix ( 🔼 1000 mL ) for 1000 samples:

△ 1000 mL miliQ water

Д 9.31 g EDTA

△ 15.76 g Tris-HCL

∆ 81.82 g NACI

Final concentration

[м] 25 millimolar (mM)

[M] 100 millimolar (mM)

[M] 1.4 Molarity (M)

2.1 Preparation of LB for 48 samples:



[м] 4 Mass / % volume

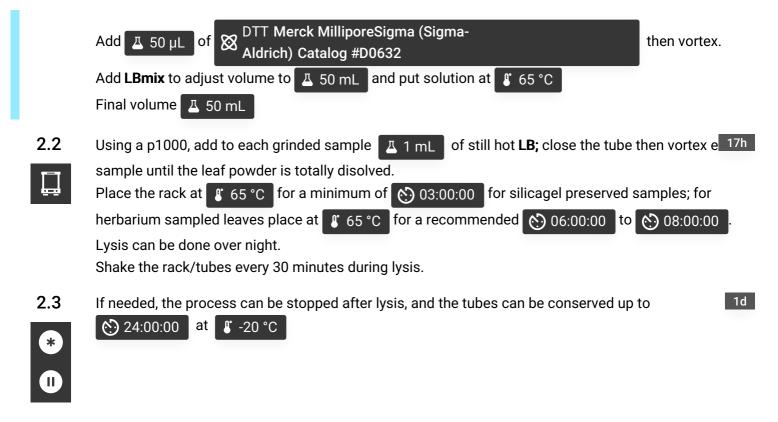
Disolve MATAB in \$\ 65 \cdot C \ water bath and vortex (aprox 10 min).

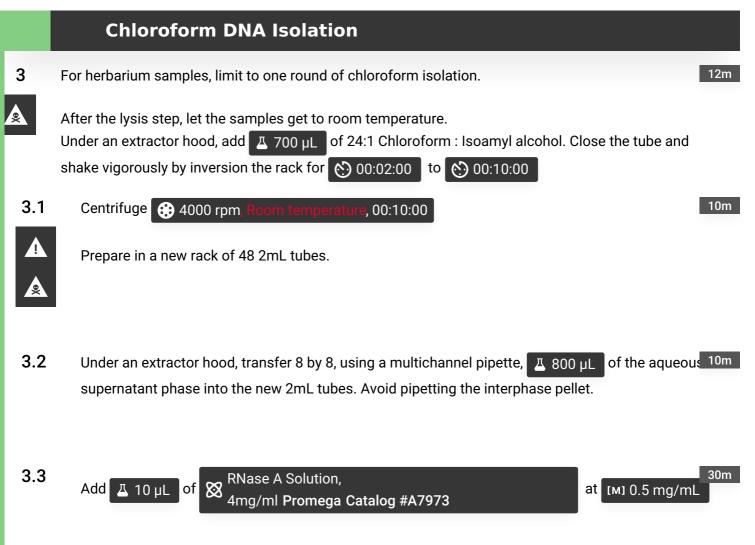
Add Δ 250 μL of

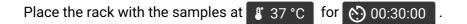


at [м] 1 mg/mL then

vortex.







3.4 Under an extractor hood, proceed with the second chloroform cleaning step. Add Δ 700 μL of 10m Chloroform Isoamyl alcohol; close tubes and shake the rack of tubes.

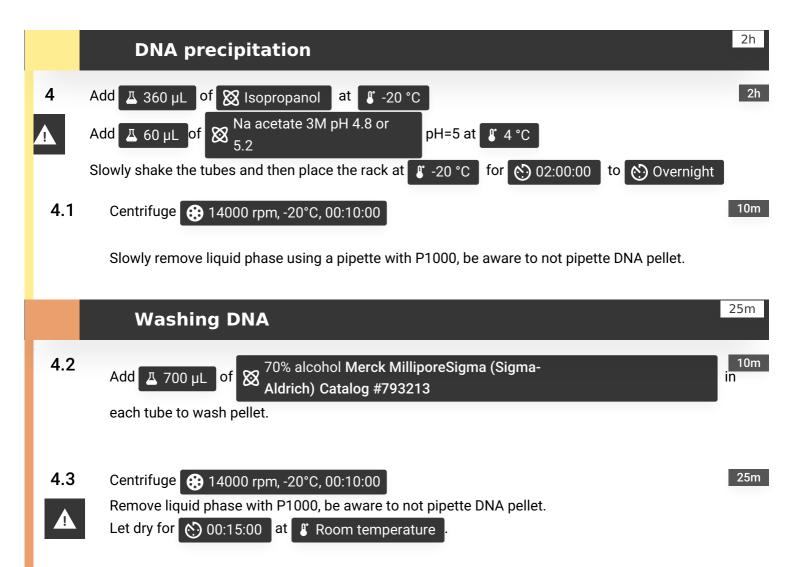


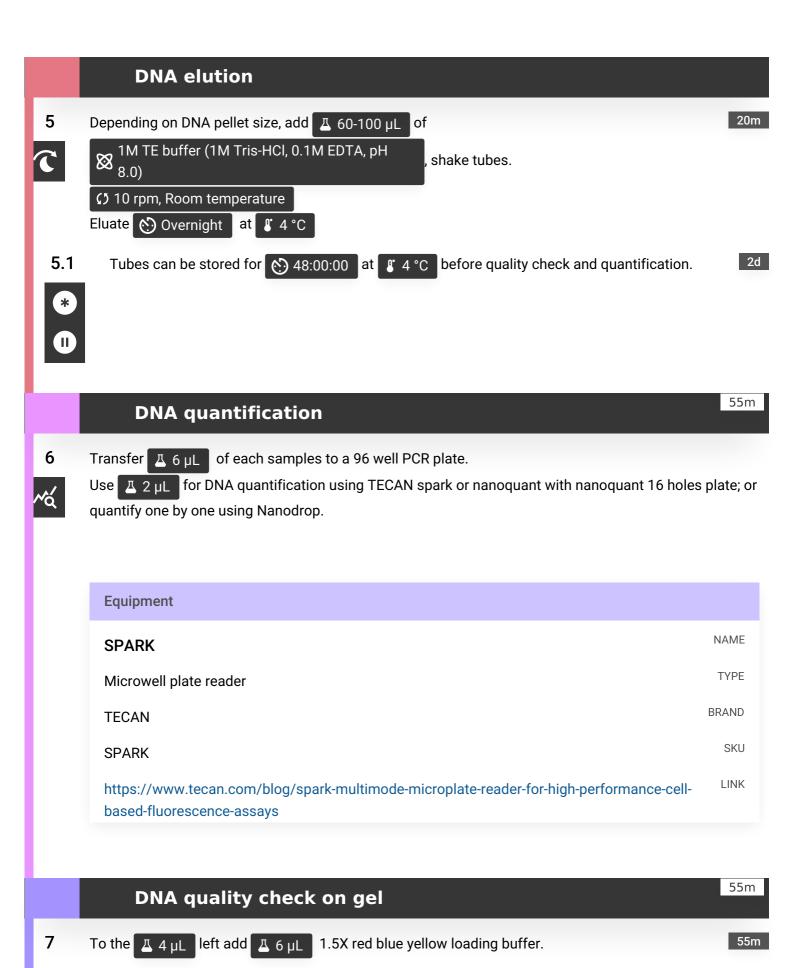
3.5 Centrifuge 4000 rpm, Room temperature, 00:10:00

10m

During centrifugation, prepare and name new 2ml eppendorf safe lock tubes.

3.6 Under an extractor hood, transfer 8 by 8 using a multichannel pipette, A 600-800 µL of the aque supernatant phase into the new 2mL tubes. Avoid pipetting the interphase pellet.





Prepare 1% of Agarose Catalog #A5304 gel with TAE 1X.

Add your samples and:

- + promega 100pb dna ladder
- + promega 2.5kb lambda eco R1 hind3 dna ladder on gel well

Then proceed with gel electrophoresis at 135V 00:40:00 on TAE 0.5X.

Put gel 00:15:00 in 1X Sel Gel Red Nucleic Acid Gel Stain Biotium Catalog ##41003

Place gel in imaging machine. Turn on UV light, take a picture.

### **DNA** conservation

55m

8 Extracted DNA needs to be stored at **§** -20 °C .

For long term conservation, transfert to barcoded screw-top tube on 96 rack. For the GLOBAL projet we used **Thermo Scientific™ Matrix™ 0.5mL 2d barcoded**.

# **Expected result**

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#### **Expected result**

Within the GLOBAL project, around 3600 DNA extractions were undertaken, some on silicagel leaves others on herbarium preserved leaves.

For silicagel dried samples we extracted 1050 specimens, with a max concentration of 979 ng/ul and a minimum of 0.9 ng/ul for a total elution volume of 100 ul. On average we had 213 ng/ul (Standard error: 205.8).

For herbarium preserved leaves 2600 samples were extracted: the highest concentration was 1088ng/ul and the lowest was 0,1 ng/ul for a total elution volume of 60 ul. On average we had 230 ng/ul per extraction (Standard error: 221.8).

Concentrations below 10 ng/ul were rarely used to sequenced or frequently failed.

DNA size ranged between 100pb-2.5kb, but longer fragments were also possible.