

# High quality DNA from Fungi for long read sequencing e.g. PacBio Version 3

Benjamin Schwessinger

## Abstract

Extraction of high quality DNA for long read sequencing e.g. PacBio

Optimized for DNA extraction from wheat stripe rust spores and also tested on barley leaf rust.

Buffers are best when fresh and not older than 3-6 months. Buffered Phenol:Chloroform:Isoamylalcohol (25:24:1) should not be older than 3 months.

Critical steps to obtain high quality DNA:

- Do NOT heat samples during DNA extractions! Perform all steps at RT or 40C as indicated.
- Do NOT incubate samples with KAc for prolonged time periods
- Perform two steps of buffered Phenol:Chloroform:Isoamylalcohol purification to reduce co-purifying metabolites.

DNA fragments were well above the 40kb mark based on Pippin Pulse Gels. The sequencing center performed a second AMPure purification step before library construction. Summary statistics of sequencing runs to follow.

**Citation:** Benjamin Schwessinger High quality DNA from Fungi for long read sequencing e.g. PacBio. **protocols.io** dx.doi.org/10.17504/protocols.io.evqbe5w

**Published:** 19 Apr 2016

## Guidelines

Modified from protocols of Prof. Pietro Spanu (Imperial College, London) and T. M.

Fulton, J. Chunwongse, S. D. Tanksley, *Pl Mol Biol Rep* 13, 207 (1995)

Optimized for DNA extraction from wheat stripe rust spores and also tested on barley leaf rust

**Buffers are best when fresh and not older than 3-6 months. Buffered Phenol:Chloroform:Isoamylalcohol (25:24:1) should not be older than 3 months.**

Critical steps to obtain high quality DNA:

- Do NOT heat samples during DNA extractions! Perform all steps at RT or 4°C as indicated.
- Do NOT incubate samples with KAc for prolonged time periods
- Perform two steps of buffered Phenol:Chloroform:Isoamylalcohol purification to reduce co-purifying metabolites.

## Reagents required

**BUFFER A:** 0.35 M sorbitol

0.1 M Tris-HCl, pH 9

5 mM EDTA, pH 8

autoclave to sterilize

**BUFFER B:** 0.2 M Tris-HCl, pH 9

50 mM EDTA, pH 8

2 M NaCl

2% CTAB

autoclave to sterilize

**BUFFER C:** 5% Sarkosyl (N-lauroylsarcosine sodium salt SIGMA L5125)

Filter-sterilize

## Other solutions:

Potassium Acetate 5M (KAc precipitate polysaccharides) pH 7.5

PVP 1 %

Sodium Acetate (NaAc) 3M pH 5.2

Filter-sterilize

Isopropanol 100%

Ethanol 70%

Buffered Phenol:Chloroforme:Isoamylalcohol P:C:I (25:24:1, Sigma P2069)

Autoclave acid washed Sand

## Enzymes

RNAse T1 (1000 U/ml, Thermo Fisher EN0541)

Proteinase K (800U/ml, NEB P81072)

AMPure beads from Beckman

Lysis Buffer For 17.5 ml for 500 mg starting material

2.5 volume of Buffer A 6.5 ml

2.5 volume of Buffer B 6.5 ml

1.0 volume of Buffer C 2.6 ml

PVP 0.1 % 1.75 ml

## Protocol

### Extraction II

#### Step 1.

use AMPure beads for secondary clean up at beads 0.45 (Vol/Vol) following the PacBio protocol

### Extraction I

#### Step 2.

Mix buffers lysis buffer by vortexing and briefly heat to 64 °C. Let cool to room temperature for use in 50mL Falcon tubes.

### Extraction I

#### Step 3.

add 10uL (10kU) RNAse T1 to lysis buffer

### Extraction I

#### Step 4.

Grind tissue/spores with liquid nitrogen in a mortar with sand, use 1g of sand per 100mg of starting material, grind for 2 mins in 4x 15 sec burst adding liquid nitrogen after each 15 sec grinding burst

### Extraction I

#### Step 5.

transfer powder to 50mL Falcon containing lysis buffer and RNAse, mix well by vortexing

### Extraction I

**Step 6.**

incubate at RT for 30 mins mixing by inversion every 5 mins

 DURATION

00:30:00

Extraction I

**Step 7.**

add 200uL Proteinase K, incubate at RT for 30 mins mixing by inversion every 5 mins

 DURATION

00:30:00

Extraction I

**Step 8.**

cool on ice for 5 mins

 DURATION

00:30:00

Extraction I

**Step 9.**

add 3.5 mL of KAc 5M, mix by inversion, incubate on ice for max 5 mins

Extraction I

**Step 10.**

spin at 4°C and 5000g for 12 mins

 DURATION

00:12:00

Extraction I

**Step 11.**

transfer supernatant to fresh Falcon tube containing 18ml P/C/I and mix by inversion for 2 mins

 DURATION

00:02:00

Extraction I

**Step 12.**

spin at 4 °C and 4000g for 10 mins

 DURATION

00:10:00

Extraction I

**Step 13.**

transfer supernatant (might be milky but do not worry) to fresh Falcon tube containing 18ml P/C/I and mix by inversion for 2 mins

 DURATION

00:02:00

Extraction I

**Step 14.**

spin at 4 °C and 4000g for 10 mins

 DURATION

00:10:00

Extraction I

**Step 15.**

transfer supernatant (17mL) to fresh Falcon tube and add 5uL RNase T1

## Extraction I

### Step 16.

incubate for 20-30mins at RT

 DURATION

00:20:00

## Extraction I

### Step 17.

add 1.8mL NaAc and mix by inversion

## Extraction I

### Step 18.

add 18mL RT isopropanol nad mix by inversion

## Extraction I

### Step 19.

incubate at RT for 5-10mins

 DURATION

00:05:00

## Extraction I

### Step 20.

spin at 4 °C and 10000g for 30 mins

 DURATION

00:30:00

## Extraction I

### Step 21.

carefully pipette off supernatant till about 1-2 mL left, DNA will form a mostly translucent to white film/pellet at the bottom of the tube

## Extraction I

### Step 22.

use 1mL pipette tip to transfer pellet and remaining liquid into fresh 1.7mL eppendorf tube

## Extraction I

### Step 23.

spin in table top centrifuge for 5 mins at 13000g

 DURATION

00:05:00

## Extraction I

### Step 24.

remove supernatant with pipette and wash with 1.5mL fresh 70% Ethanol, invert several times to dislodge pellet

## Extraction I

### Step 25.

spin in table top centrifuge for 5 mins at 13000g

 DURATION

00:05:00

## Extraction I

### Step 26.

remove supernatant with pipette and wash with 1.5mL fresh 70% Ethanol, invert several times to dislodge pellet

## Extraction I

### Step 27.

spin in table top centrifuge for 5 mins at 13000g

 DURATION

00:05:00

## Extraction I

### Step 28.

remove supernatant with pipette

## Extraction I

### Step 29.

spin in table top centrifuge for 1 min at 13000g

 DURATION

00:01:00

## Extraction I

### Step 30.

remove remaining ethanol with pipette

## Extraction I

### Step 31.

air-dry pellet for 7 mins

 DURATION

00:07:00

## Extraction I

### Step 32.

add 200uL of 10mM Tris pH9 leave at RT for 3 hours

 DURATION

03:00:00

## Extraction I

### Step 33.

flick tube slightly for mixing and add 200uL of TE buffer

## Extraction I

### Step 34.

leave at RT over night

 DURATION

16:00:00

## Extraction I

### Step 35.

next day add another 100uL TE buffer and incubate for 1h at 28 °C with 1400rpm shaking

 DURATION

01:00:00

## Extraction I

### Step 36.

Measure dsDNA concentration using BR Qubit and measure absorbance with Nanodrop. At this point Qubit to Nanodrop ratios were 1/1000

## Extraction II

### Step 37.

elute in 10mM Tris pH8

## Extraction II

### Step 38.

measure dsDNA concentration using BR Qubit and measure absorbance with Nanodrop

## Extraction II

### Step 39.

at this stage Qubit to Nanodrop ratios were 0.64, 260/280 1.87 and 260/230 1.37

## Extraction II

### Step 40.

Samples were submitted to Ramaciotti (<http://www.ramaciotti.unsw.edu.au/>) sequencing centre in Sydney. Excellent personel performed quality control, prepared 15-20kb libraries and we ran 13 SMRT cells with P6 chemistry. Some summary statistics are shown below.

#### 📄 EXPECTED RESULTS

Summary statistics for all 12 SMRT cells combined

\*\*\*\*\*  
\*\*\*\*\*

Total sequence amount:	1.263691e+10
Number of reads:	1.181543e+06
Median read length:	9632
Mean read length:	10695

## Pippin Pulse Gel: 9hr 10-48kb 0.75% KBB gel





