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## DNA Extraction from 0.22µm Sterivex Filters - Qiagen Blood and Tissue Kit

 In 1 collection

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### Abstract

This protocol is used to extract genomic DNA from 0.22µm sterivex filters using Quiagens Blood and Tissue Kit. The protocol was developed as an equivalent replacement for the Phenol Chloroform extraction protocol. This protocol is developed to work across all domains of life, from viruses to prokaryotes to eukaryotes, allowing for both amplicon sequencing and shotgun sequencing.

Guidelines

MIOP: Minimum Information about an Omics Protocol

| MIOP Term                         | Value                                                                      |
|-----------------------------------|----------------------------------------------------------------------------|
| analyses                          | Nucleic Acid Extraction                                                    |
| audience                          | scientists                                                                 |
| broad-scale environmental context | marine biome ENVO_00000447                                                 |
| creator                           | Colleen Kellogg                                                            |
| environmental medium              | sea water [ENVO:00002149]                                                  |
| geographic location               | North Pacific Ocean [GAZ:00002410]                                         |
| hasVersion                        | 1                                                                          |
| issued                            | 2017                                                                       |
| language                          | en                                                                         |
| license                           | CC BY 4.0                                                                  |
| local environmental context       | coastal sea water [ENVO: 00002150]                                         |
| materials required                | Sterile workbench, Fume Hood, Centrifuge, Incubator                        |
| maturity level                    | Mature                                                                     |
| methodology category              | Sample collection                                                          |
| personnel required                | 1                                                                          |
| project                           | Biomolecular surveys of marine biodiversity in the Northern Salish Sea, BC |
| publisher                         | Hakai Institute, Ocean Observing Program                                   |
| purpose                           | DNA Extraction                                                             |
| skills required                   | sterile technique   pipetting skills                                       |
| target                            | DNA                                                                        |
| time required                     | 1 day                                                                      |

AUTHORS

|                                                                                                                                    |                 |                                                                         |
|------------------------------------------------------------------------------------------------------------------------------------|-----------------|-------------------------------------------------------------------------|
| PREPARED BY All authors known to have contributed to the preparation of this protocol, including those who filled in the template. | AFFILIATION     | ORCID (visit <a href="https://orcid.org">https://orcid.org</a> )        |
| Colleen Kellogg                                                                                                                    | Hakai Institute | <a href="https://orcid.org/0000-0003-">https://orcid.org/0000-0003-</a> |

RELATED PROTOCOLS

| PROTOCOL NAME AND LINK | ISSUER / AUTHOR | RELEASE / ACCESS DATE |
|------------------------|-----------------|-----------------------|
| Seawater filtration    | Hakai Institute |                       |

This is a list of other protocols which should be known to users of this protocol. Please include the link to each related protocol.

ACRONYMS AND ABBREVIATIONS

| ACRONYM / ABBREVIATION | DEFINITION |
|------------------------|------------|
|                        |            |

GLOSSARY

| SPECIALISED TERM | DEFINITION |
|------------------|------------|
|                  |            |



## BACKGROUND

This protocol is used to extract genomic DNA from 0.22µl sterivex filters using a modified version of the

☒ QIAgen DNeasy Blood and Tissue Kit, 50 rxn **Qiagen Catalog #69504** .

This protocol was developed as an equivalent to the Phenol Chloroform protocol for newly started projects that does not require comparable results to the weekly sampling series.

### ***Spatial coverage and environments of relevance***

As part of the Hakai Institute Ocean Observing Program, biomolecular samples have been collected weekly, from 0 to near bottom (260 m), to genetically characterize plankton communities in the Northern Salish Sea since 2015, developing a climatology from which we can begin uncover the physical, chemical and biological drivers of community and functional change in the dynamic coastal waters of coastal British Columbia. This protocol is developed to work across all domains of life, from viruses to prokaryotes to eukaryotes, allowing for both amplicon sequencing and shotgun sequencing.

### ***Personnel Required***

1 Technician

### ***Safety***

Identify hazards associated with the procedure and specify protective equipment and safety training required to safely execute the procedure!

### ***Training requirements***

Sterile technique, pipetting skills. Work-safe laboratory practices.

### ***Time needed to execute the procedure***

1 Day (for 24 samples).

## Protocol materials

☒ QIAgen DNeasy Blood and Tissue Kit, 50 rxn **Qiagen Catalog #69504**

☒ Proteinase K, 2mL **Qiagen Catalog #19131**

## Before start

Read background information, MIOP and BePOP-OBON information under the "Guidelines" tab.

**PREPARATION - must be done in Clean Room 1 or Clean Room 2**

1

***This protocol assumes that samples have been collected and preserved according to this procedure:***

Protocol

 NAME  
**Seawater Filtration for Microbial or Environmental DNA**

CREATED BY  
Andreas Novotny

Preview

2

## Note

We are aiming to do about 24 samples per day, but you can aim for less than that until you get comfortable with the protocol.

**Materials needed:**

- ☒ Proteinase K, 2mL Qiagen Catalog #19131
- 0.5 mm glass beads, silica. Molecular grade
- Molecular grade ethanol (100%)
- ☒ QIAgen DNeasy Blood and Tissue Kit, 50 rxn Qiagen Catalog #69504

**The kit Includes:**

- ATL (lysis buffer)
- AL (lysis buffer)
- RNase
- AW1 (Wash buffer)
- AW2 (Wash buffer)
- AE (Elution buffer)
- Spin Columns

3 **UV for 30 minutes the following:**

- Silica beads - you will need a 5mL tube full of beads to extract DNA from 12 samples  
(See bench top guide in the end of this protocol to check the amount of tubes you will need)
- 2mL tubes
- 50mL falcon tubes
- Racks
- Pipettes
- pipette tips

30m

*Do not forget to UV tubes for that will be used to aliquot the buffers, and silica beads.*

4 Wipe down the benches, centrifuge, and working areas using the PREempt solution/wipes.



Turn on the incubator and set the temperature to 56°C.

5 Set aside ATL buffer, AL buffer, proteinase K, RNase A and anhydrous ethanol.

*Put the ATL and AL buffers in the incubator to eliminate any precipitate that may be in the solution.*

There is a cardboard box in the mini freezer with pro K aliquots. Each aliquot has enough volume for 12 samples. The anhydrous ethanol is stored in the CR1 mini fridge, and in the CR2 in the mini freezer.

6 Calculate the volume of each reagent you will need for each step and have a one-time-use tube to make an aliquot for that specific reagent. Try to add a little bit more than you



need and dispose of the leftover. *Prepare the aliquots inside the workstation (with HEPA filter).*

- 7 Cut the parafilm to a size of 1 cm x 5 cm, two or three per Sterivex – sometimes you will need to replace the parafilm in the Sterivex.

## BEADS BEATING AND INITIAL INCUBATION

- 8 Thaw the Sterivex filters.
- 9 Remove the parafilm and remove Longmire's buffer/SLB using a syringe. You can use a plastic "tripour" to dispose the buffer and then pour all of the volume in the sink. *Rinse the tripour with water after use, dry and wipe it down using a paper towel and PREempt solution.*
- 10 If needed, dry the Sterivex inlet using a Kimwipes (one wipe per Sterivex). Place the Sterivex on a clean Kimwipe while preparing the other one Sterivexes.
- 11 Add 0.1 mm silica beads (*about 0.3 g or three spoons\**) into the Sterivex using a weighting paper (make a funnel with the paper to slide in the beads, use one per Sterivex). *\*It is a white spoon that is stored in the drawer with the silica beads.*
- 12 Seal the outlet port of the Sterivex filter unit with the parafilm.
- 13 Inject 720 µL ATL buffer into the Sterivex.
- 14 One more Sterivex +ATL buffer should be prepared for the extraction blank for detecting contamination during DNA extraction.
- 15 Place the Sterivex in the vortex adapter and do the "bead-beating" for 10 min to promote cell lysis.
- 16 Get one 50mL tube per sample, and put the Sterivexes inside the 50mL tube. Incubate the Sterivex at 56°C for 30 min while tilting or rotating.
- 17 Repeat steps 15 and 16 one more time.

⇒ [go to step #15](#)



## DIGESTION WITH PRO-K AND INCUBATION

- 18 Add 80 µL proteinase-K to each Sterivex.
- 19 Seal the outlet port of the Sterivex filter unit with a parafilm if you notice that some lysate is leaking.
- 20 Vortex tubes for ~10 s (or simply move it to mix the solution). Place the Sterivexes back to the 50mL. Incubate tubes at 56°C for 2h while rotating.



## COLLECTING THE LYSATE

- 21 While warming the Sterivex filter unit to 56°C, prepare a 2.0 mL tube for DNA recovery (ioBind DNA tubes). **Note:** write the necessary information on the cap of the 2.0 mL tube.
- 22 After completion of warming, carefully remove the parafilm and the luer fitting on the inlet port of the Sterivex filter unit, while preventing liquid inside from leaking.



- 23 Insert the inlet port of the Sterivex filter unit into the 2.0 mL tube and lightly push it down to the bottom of the 50mL conical tube. Then, close the cap of the conical tube firmly.
- 24 Put the conical tubes in the Megafuge adapters. Centrifuge the conical tube containing the Sterivex filter unit at 6,000 x g for 1min and collect the extracted DNA in a 2 mL tube.
- 25 Remove the 50 mL conical tube from the centrifuge and remove the Sterivex filter unit and 2.0 mL tube using tweezers.  
**Note:** The 2.0 mL tube is uncapped; handle it carefully. Wipe down the tweezers with PREempt wipes between samples.
- 26 Discard the used conical tubes (*keep one conical tube and use it as a provisory waste container*) and Sterivex filter unit.  
Firmly cap the 2.0 mL tube and proceed with these vials and lysate



## FINAL INCUBATION AND PRECIPITATION

12m

- 27 Add 4  $\mu$ L of RNaseA (100 mg/mL).  
Mix pipetting up and down (or vortexing).  
Incubate at room temperature for 2 min.
- 28 Add 200  $\mu$ L buffer AL.  
Mix thoroughly pipetting up and down (or by vortexing). It may form some precipitate.  
Incubate at 56°C for 10 min (it doesn't need to be in the rotisserie).
- 29 Add 200  $\mu$ L ethanol (96-100%).  
Mix thoroughly pipetting up and down (or by vortexing).  
Total volume now is ~1.2 mL.



## DNA BINIDNG AND WASHING

- 30 Pipette 600  $\mu$ L the mixture into a DNeasy mini spin column placed in a 2 mL collection tube.  
Place the tubes in the centrifuge and spin the tubes at 8,000 rpm (~6,000 x g) for 1 min.  
Discard the flow through.
- 31 Repeat the previous step once more, using the remaining volume of the lysate.  
[⇒ go to step #30](#)
- 32 Place the spin column in a new 2 mL collection tube. *If after spinning down you still can see some buffer in the spin column, centrifuge the tube again with a higher speed (about 10,000 x g). If this still not work, spin down with a higher speed.*  
Add 500  $\mu$ L buffer AW1.  
Centrifuge for 1 min at 8,000 rpm (~6,000 x g).  
Discard the flow through and collection tube.
- 33 Place the spin column in a new 2 mL collection tube. Add 500  $\mu$ L buffer AW2.  
Centrifuge for 30 s. at 14,000 rpm (~20,000 x g).  
Discard the flow through and collection tube.
- 34 Transfer the spin column to a new 1.5 mL or 2 mL microcentrifuge tube.



## DNA ELUTION

2m

- 35 Elute the DNA by adding 200  $\mu$ L buffer AE to the centre of the spin column membrane.  
Incubate for 1 min. at room temperature.  
Centrifuge for 1 min at 8,000 rpm (~6,000 x g).
- 36 OPTIONAL: repeat the step 27 for increased DNA yield.





## Protocol references

This protocol is modified based on the manual of:

 QIAgen DNeasy Blood and Tissue Kit, 50 rxn **Qiagen Catalog #69504**