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Cryo-focused Ion Beam Sample Preparation for Imaging Vitreous Cells by Cryo-electron Tomography

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Abstract

Cryo-electron tomography (CET) is a well-established technique for imaging cellular and molecular structures at sub-nanometer resolution. As the method is limited to samples that are thinner than 500 nm, suitable sample preparation is required to attain CET data from larger cell volumes. Recently, cryo-focused ion beam (cryo-FIB) milling of plunge-frozen biological material has been shown to reproducibly yield large, homogeneously thin, distortion-free vitreous crosssections for state-of-the-art CET. All eukaryotic and prokaryotic cells that can be plunge-frozen can be thinned with the cryo-FIB technique. Together with advances in low-dose microscopy, this has shifted the frontiers of in situ structural biology. In this protocol we describe the typical steps of the cryo-FIB technique, starting with fully grown cell cultures. Three recently investigated biological samples are given as examples.

Materials and Reagents

1. Biological material

Note: The FIB-milling procedure is compatible with a wide range of cell types, including single-celled eukaryotes, prokaryotes, and mammalian cells such as HeLa and neuronal cultures. The following examples are used in this protocol:

2. Tris-acetate-phosphate (TAP) medium (Harris et al., 2009; Culture media recipe is available at [http://www.chlamy.org/media.html\)](http://www.chlamy.org/media.html)

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Equipment

- **2.** Tweezers
- **3.** Screwdrivers
- **4.** Light microscope
- **5.** Teflon sheets (custom made, cut from larger sheets in the exact shape and size as the filter paper used for plunge-freezing)
- **6.** Glass petri dish (9-12 cm)
- **7.** Glass microscopy slides (Thermo Fisher Scientific, catalog number: 10144633B)
- **8.** Cryo grid boxes (custom made, or FEI, Eindhoven, The Netherlands)
- **9.** Cryo AutoGrid boxes (custom made, or FEI, Eindhoven, The Netherlands)
- **10.** AutoGrids (custom made and modified for FIB work, see Figure 1a)
- **11.** Clip rings (FEI, Eindhoven, The Netherlands, see Figure 1b)
- **12.** Liquid nitrogen Dewars
- **13.** Personal protection equipment for work with liquid nitrogen (safety glasses, face shield, and cold-resistant gloves)
- **14.** Hemocytometer (Neubauer)
- **15.** Pipets and tips
- **16.** Clipping tools (custom made, or FEI, Eindhoven, The Netherlands)
- **17.** Personal protective equipment for work with liquid nitrogen and liquid ethane/propane
- **18.** Plasma cleaner (Harrick, model: PDC-3XG)
- **19.** Vitrobot Mark 4 (FEI)

1. FIB software

Procedure

Note: Working with liquid nitrogen and liquid ethane/propane mixture is potentially dangerous. Personal protective equipment should be used.

A Vitrification by plunge-freezing

Note: Standard protocols can be used for plunge-freezing cells (e.g. Iancu et al., 2006). For proper vitrification (freezing in non-crystalline ice) and cell density, parameters must be optimized for each specific cell type.

- **1.** Cell concentration is determined by counting using a hemocytometer. (*C.* reinhardtii cells are fixed with Lugol's iodine solution for the counting process in order to stop cell motility. A Lugol's solution to cell culture of ratio 1:10 is sufficient.)
- **2.** The concentration of the cells is diluted to 200-750 cells/μl in fresh TAP for the C. reinhardtii wild-type strain, 500-4,000 cells/μl in fresh TAP for the C. reinhardtii mat3-4 strain, and 10,000-15,000 cells/μl for S. cerevisiae cells in YPD medium.
- **3.** The carbon-coated 200-mesh copper TEM grids placed carbon side up on a glass slide are glow discharged by 30 sec plasma cleaning. The slide is then stored in a glass petri dish until plunging, which should proceed immediately.
- **4.** The cells are plunge-frozen using the Vitrobot:
	- **a.** The Vitrobot is set to 90% humidity, blot force 10, 7 to 10 sec blot time, room temperature (C. reinhardtii cells) or 27 °C (S. cerevisiae cells).

- **b.** 3.5 μl of the diluted cell culture is pipetted onto TEM grids inside the Vitrobot.
- **c.** The grids are blotted from the reverse side using Teflon sheets on both sides and filter paper on the backside. Then they are immediately plunged into the liquid ethane/ propane mixture at liquid nitrogen temperature.
- **d.** The plunge-frozen grids are then stored in sealed boxes under liquid nitrogen until used.

B Sample thinning using cryo-FIB milling

- **1.** Cooling the FIB system from room temperature to cryo conditions.
	- **a.** Before starting the cooling, the vacuum in the FIB chamber and in the prep-chamber must be lower than $4 \times$ 10⁻⁶ mbar to avoid contamination from water vapor. **b.** The N_2 gas pipeline between the liquid nitrogen Dewar and the FIB chamber (vacuum isolated line) is pumped to
	- **c.** The nitrogen gas flow for the stage and anti-contaminator are adjusted to 3.8 L/min and 4.2 L/min, respectively. These values ensure that temperatures of -182 °C and -192 °C are reached after cooling, respectively.
	- **d.** The cooling is started by slowly inserting the cooling rod into the liquid nitrogen Dewar.
- **2.** Sample clipping and loading the AutoGrids into the FIB shuttle.

 2×10^{-2} mbar.

Note: Clipping and loading is started when the cryo-stage and anticontaminator reach temperatures below -160 °C. Using a surgical mask can minimize water vapor contamination of the work area.

- **a.** The shuttle and the clipping support base are placed into the loading box (Figure 2).
- **b.** The loading box is filled with liquid nitrogen.
- **c.** After boiling has finished, the double wall tank is filled with liquid nitrogen by slightly tilting the loading box (Figure 2).
- **d.** The sample boxes from the storage Dewar are transferred into the loading box and opened there. Transfer time should be minimized to avoid contamination of the sample.
- **e.** All tools that will contact the TEM grids are pre-cooled by liquid nitrogen in the loading box immediately before use.

4. Lamella milling.

(GIS). For this, a relative stage rotation of 180° is performed using the compucentric rotation. The AutoGrid is then centered at the GIS position in the electron image (Figure 4b). **iii.** The GIS temperature is set to 26 °C. **iv.** The GIS needle is inserted and opened for 4 to 8 sec. **v.** The GIS needle is retracted. **vi.** The stage is moved back to the initial position where it was before the procedure. **m.** The stage is tilted to the milling position with the ion beam almost parallel (typically 6 to 12°) to the grid surface. For a shuttle that is 7° pre-tilted, and a desired milling angle of 10° with respect to TEM grid surface, the stage is tilted to 17°. **n.** The ion beam parameters are set to: 30.0 kV beam energy, 10 pA beam current, $1,024 \times 884$ or $1,536 \times 1,024$ scan resolution, 1 μs dwell time. **o.** The focus and astigmatism of the ion beam are adjusted while scanning the grid bar at increased zoom. **p.** A target cell is localized in both electron and ion beam images (Figure 4c-e). Note: The three meshes closest to the edge of the TEM grid are often not accessible in the TEM microscope. Generally, central meshes are preferred. **q.** The eucentric height is adjusted using stage movement in the z-direction so that the ion beam and the electron beam show the same sample surface. Note: The eucentric height must be separately adjusted for each milling position. **r.** Two parallel rectangular standard milling patterns are drawn (Figure 4e). With pre-tilt correction disabled, the size of the pattern is approximately 10×6 µm and the distance between the patterns is more than 5 μm. The milling direction is set to top-to-bottom for one pattern and to bottom-to-top for the other, so that the milling direction of the pattern is always towards the lamella edge. The milling parameters are set to: Ice material (or Si), 1 μs

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dwell time, 60% overlap.

- **t.** The milling process is started. The milling is stopped as soon as the material is completely removed, as observed by live imaging of the scanned area.
- **u.** Iteratively, the beam current is reduced, pattern heights on both sides are made slimmer (while keeping pattern widths constant) and patterns are shifted closer to the lamella edge (Figure 4f and Video 1). Typical steps for the beam current are 0.1 nA, 50 pA and then 30 pA.
- **v.** At a sample thickness of about 500 nm, the final milling is performed using 30 pA and optionally the cleaning-crosssection pattern. The target lamella thickness is between 300 and 100 nm (Figure 4g). During this step, thickness is estimated using electron images (Figure 4h-i).
- **w.** It is possible to prepare multiple lamellas (~10) during one FIB session. For each new lamella, first set the ion beam current back to 10 pA and then repeat steps B4p-v).

Note: To minimize time-dependent ice contamination, it is recommended to perform steps B4p-U at all sample locations first, then afterwards perform step B4v for each lamella.

5. Shuttle transfer out of the FIB

- **a.** The column valves are closed ("Beam on\off" buttons, or "Sleep" button to end the FIB session). **b.** The stage is moved to the transfer position. **c.** The loading box is filled with liquid nitrogen and then placed onto the pumping station. **d.** The transfer unit is docked to the airlock of the FIB. **e.** The airlock is pumped to the vacuum level required to safely open the airlock valves. The airlock valves and the transfer unit valve are then opened. **f.** The shuttle is retrieved from the cryo-stage with the insertion rod and retracted out of the FIB chamber into the transfer unit. **g.** The airlock valves and the transfer unit valve are closed.
- **h.** The airlock is vented.
- **i.** The transfer unit is attached to the loading box.

- **2.** The lamella positions are localized using low magnification imaging.
- **3.** Tilt-series acquisition is performed using SerialEM software under lowdose conditions (<100 e/ \AA ² cumulative dose). K2 images are recorded at 2° tilt increments, with −4 μm to −8 μm defocus, typically with pixel sizes of 3 to 5 Å.

Representative data

Figure 5 shows examples of final cryo-FIB-prepared lamellas of Chlamydomonas and yeast cells. Samples of this quality are reproducibly produced by the described technique (Rigort et al., 2012) and have been used for data collection published elsewhere (Engel et al., 2014; Villa et al., 2013).

Recipes

C Cryo-ET

- **1.** YPD liquid medium
	- 1% yeast extract
	- 2% peptone
	- 2% D-glucose

Sterilize by autoclaving

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Figure 1. AutoGrids modified for cryo-FIB.

a) Top and b) bottom side of an AutoGrid holding a clipped TEM grid. The flat top side shows the cutout required for cryo-FIB milling. c) The FIB shuttle loaded with two AutoGrids. Detailed view showing a properly oriented AutoGrid loaded into the shuttle. Note that the AutoGrid cutout faces up.

Figure 2. Sample clipping and loading.

a-c) The sample loading box with double-walled reservoir (9). The second reservoir is filled with liquid nitrogen through the filling gaps (2, 8). The AutoGrid notch (6) aids the fast and easy handling of Autogrids under liquid nitrogen. The clipping tool (1) and tweezers can be cooled in the round bore (7). The shuttle (3) (in loading position), sample storage box (4) and clipping metal support (5) are immersed under liquid nitrogen.

Figure 3. Sample transfer system.

a) The Quorum cryo-system with the transfer unit (1). The pumping station (2) with the loading box inside. b) The sample transfer unit with the small transfer chamber (3) and the shuttle (4) attached to the transfer rod. c) The loading box (5) inside the pumping station (7). Here, the shuttle is in the transfer position (6). d) The transfer unit attached to the loading box for shuttle pick-up/drop-off. The small transfer chamber (3) is closed/opened using the transfer unit valve (8).

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Figure 4. Lamella milling.

a). Scanning electron microscope (SEM) image of an AutoGrid aligned with the incident direction of the ion beam. b). The AutoGrid is centered at the GIS position in the SEM image and the GIS needle is inserted. c). SEM image of a TEM grid with Chlamydomonas cells. d). SEM image of two target Chlamydomonas cells before FIB milling. e). FIBinduced secondary electron (FIB SE) image of the two target cells with two rectangle standard milling patterns as a starting point for the milling procedure. f). FIB SE image showing the milling step at 50pA where patterns on both sides are made slimmer (but pattern width remains constant) and shifted closer to the lamella edge. g, i). FIB SE and h) SEM images of the finished lamella after cryo-FIB milling. See Video 1 for an overview of cryo-FIB milling.

Figure 5. TEM images of final lamellas.

a) Cross-section of a Chlamydomonas cell, with a lamella thickness of 100 nm. b) Crosssection through several yeast cells, with a lamella thickness of 250 nm.