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Mitochondria and Endoplasmic Reticulum Imaging by Correlative Light and Volume Electron Microscopy --Manuscript Draft--

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1 TITLE:

2 Mitochondria and Endoplasmic Reticulum Imaging by Correlative Light and Volume Electron

Microscopy

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SUMMARY:

We present a protocol to study the distribution of mitochondria and endoplasmic reticulum in whole cells after genetic modification using correlative light and volume electron microscopy including ascorbate peroxidase 2 and horseradish peroxidase staining, serial sectioning of cells with and without the target gene in the same section, and serial imaging via electron microscopy.

ABSTRACT:

Cellular organelles, such as mitochondria and endoplasmic reticulum (ER), create a network to perform a variety of functions. These highly curved structures are folded into various shapes to form a dynamic network depending on the cellular conditions. Visualization of this network between mitochondria and ER has been attempted using super-resolution fluorescence imaging and light microscopy; however, the limited resolution is insufficient to observe the membranes between the mitochondria and ER in detail. Transmission electron microscopy provides good membrane contrast and nanometer-scale resolution for the observation of cellular organelles; however, it is exceptionally time-consuming when assessing the three-dimensional (3D) structure of highly curved organelles. Therefore, we observed the morphology of mitochondria and ER via correlative light-electron microscopy (CLEM) and volume electron microscopy techniques using enhanced ascorbate peroxidase 2 and horseradish peroxidase staining. An en bloc staining method, ultrathin serial sectioning (array tomography), and volume electron microscopy were applied to observe the 3D structure. In this protocol, we suggest a combination of CLEM and 3D electron microscopy to perform detailed structural studies of mitochondria and ER.

INTRODUCTION:

Mitochondria and endoplasmic reticulum (ER) are membrane-bound cellular organelles. Their connection is necessary for their function, and proteins related to their network have been

described¹. The distance between the mitochondria and ER has been reported as approximately 100 nm using light microscopy²; however, recent super-resolution microscopy³ and electron microscopy (EM)⁴ studies have revealed it to be considerably smaller, at approximately 10-25 nm. The resolution achieved in super-resolution microscopy is lower than EM, and specific labeling is necessary. EM is a suitable technique to attain a sufficiently high-resolution contrast for structural studies of the connections between mitochondria and ER. However, a disadvantage is the limited z-axis information because the thin sections must be approximately 60 nm or thinner for conventional transmission electron microscopy (TEM). For sufficient EM z-axis imaging, three-dimensional electron microscopy (3DEM) can be used⁵. However, this involves the preparation of hundreds of thin serial sections of whole cells, which is very tricky work that only a few skilled technologists have mastered. These thin sections are collected on fragile formvar film-coated one-hole TEM grids. If the film breaks on one gird, serial imaging and volume reconstruction is not possible. Serial block-face scanning electron microscopy (SBEM) is a popular technique for 3DEM that uses destructive en bloc sectioning inside the scanning electron microscope (SEM) vacuum chamber with either a diamond knife (Dik-SBEM) or a focused ion beam (FIB-SEM)⁶. However, because those techniques are not available at all facilities, we suggest array tomography using serial sectioning and SEM. In array tomography, serial sections cut using an ultramicrotome are transferred to a glass coverslip instead of a TEM grid and visualized via light microscopy and SEM8. To enhance the signal for backscatter electron (BSE) imaging, we utilized an en bloc EM staining protocol employing osmium tetroxide (OsO₄)-fixed cells with osmiophilic thiocarbohydrazide (TCH)⁹, enabling us to obtain images without postembedding double staining.

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Additionally, the mitochondrial marker SCO1 (cytochrome c oxidase assembly protein 1)ascorbate peroxidase 2 (APEX2)10 molecular tag was used to visualize mitochondria at the EM level. APEX2 is approximately 28 kDa and is derived from soybean ascorbate peroxidase¹¹. It was developed to show the detailed location of specific proteins at the EM level in the same way that green fluorescent protein-tagged protein is used in light microscopy. APEX2 converts 3,3' diaminobenzidine (DAB) into an insoluble osmiophilic polymer at the site of the tag in the presence of the cofactor hydrogen peroxide (H₂O₂). APEX2 can be used as an alternative to traditional antibody labeling in EM, with a protein localization throughout the depth of the entire cell. In other words, the APEX2-tagged protein can be visualized by specific osmication¹¹ without immunogold labeling and permeabilization after ultra-cryosectioning. Horseradish peroxidase (HRP) is also a sensitive tag that catalyzes the H₂O₂-dependent polymerization of DAB into a localized precipitate, providing EM contrast after treatment with OsO4. The ER target peptide sequence HRP-KDEL (lys-asp-glu-leu)¹² was applied to visualize ER within a whole cell. To evaluate our protocol of utilizing genetic tags and en bloc staining with reduced osmium and TCH (rOTO method), using the osmication effect at the same time, we compared the membrane contrast with and without the use of each genetic tag in rOTO en bloc staining. Although 3DEM with array tomography and DAB staining with APEX and HRP have, respectively, been utilized for other purposes, our protocol is unique because we have combined array tomography for 3DEM and DAB staining for mitochondria and ER labeling. Specifically, we showed five cells with and without APEX-tagged genes in the same section, which aided in investigating the effect of the genetic modification on cells.

PROTOCOL:

1. Cell culture with patterned grid culture dish and cell transfection with SCO1-APEX2 and HRP-KDEL plasmid vector

1.1. Seed 1 x 10^5 HEK293T cells by placing them into 35-mm glass grid-bottomed culture dishes in a humidified atmosphere containing 5% CO₂ at 37 °C in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum, 100 U/mL penicillin, and 100 U/mL streptomycin.

1.2. The day after seeding the cells, when they have grown to 50%–60% confluency, introduce the SCO1–APEX2¹⁰ and HRP–KDEL¹² plasmid to the cells using transfection reagent according to the manufacturer's instructions (SCO1–APEX2 cDNA 0.5 μ g + HRP–KDEL plasmid DNA 0.5 μ g per 3 μ L transfection reagent).

2. Light microscopy of cells growing on patterned culture dishes and DAB staining for APEX2 and HRP

2.1. At 16–24 h after transfection, remove all the culture media and immediately add 250 μ L of warm (30–37 °C) fixation solution (**Table 1**) by gentle pipetting. Immediately remove the fixation solution and replace it with 1.5 mL of fresh fixation solution. Incubate on ice for 60 min, and then wash three times for 10 min each in 1 mL of ice-cold 0.1 M sodium cacodylate buffer (**Table 1**).

CAUTION: Aldehyde fumes are extremely toxic. Perform all work under a ventilated fume hood.

2.2. Add 1 mL of cold (0–4 °C) 20 mM glycine solution and incubate for 10 min on ice followed by three washes of 5 min each in 1 mL of cold 0.1 M sodium cacodylate buffer.

2.3. Prepare a fresh 1x DAB solution (3.33 mL of 0.3 M cacodylate solution + 10 μ L of 30% H₂O₂ + 5.67 mL of cold water + 1 mL 10x DAB solution).

2.4. Add 500 μL of the freshly prepared 1x DAB solution (step 2.3) and incubate on ice for approximately 5–45 min until a light brown stain is visible under an inverted light microscope (Figure 1A).

2.5. Gently remove the DAB solution and rinse three times with 1 mL of cold 0.1 M sodium cacodylate buffer for 10 min each.

2.6. Use a phase-contrast inverted microscope (or a bright-field light microscope) to visualize the DAB staining at a magnification of 100x or higher. Use a marker pen to mark the bottom of the glass where the region of interest (ROI) is located (**Figure 1B,C**).

3. Sample preparation for the EM block

3.1. Perform cell culture and DAB staining as described in steps 2.1–2.6. 3.2. Post-fix the samples with 1 mL of 2% reduced OsO₄ for 1 h at 4 °C. CAUTION: OsO₄ fumes are highly toxic. Perform all work under a ventilated fume hood. 3.3. Prepare a new TCH solution (Table 1) during step 3.2 and pass through a 0.22-µm filter. CAUTION: TCH fumes are highly toxic. Perform all work under a ventilated fume hood. 3.4. Remove the fixative and rinse three times with 1 mL of distilled water for 5 min each at room temperature (RT). 3.5. Place the cells in 1 mL of previously prepared and filtered TCH solution for 20 min at RT. 3.6. Rinse the cells three times with 1 mL of distilled water for 5 min each at RT. 3.7. Expose the cells a second time to 1 mL of 2% osmium tetroxide in distilled water for 30 min at RT. 3.8. Remove the fixative and rinse three times with 1 mL of distilled water for 5 min each at RT. Add 1 mL of 1% uranyl acetate (aqueous), and leave overnight at 4 °C in the dark. 3.9. Wash the cells three times in 1 mL of distilled water for 5 min each at RT. 3.10. Pre-warm Walton's lead aspartate solution (Table 1) in an oven at 60 °C for 30 min. 3.11. Stain the cells with Walton's lead aspartate solution by adding 1 mL of the pre-warmed lead aspartate solution, and then place in an oven for 30 min at 60 °C. 3.12. Rinse the cells three times with 1 mL of distilled water for 5 min each at RT. 3.13. Incubate in a graded series of 2-mL ethanol aliquots (50%, 60%, 70%, 80%, 90%, 95%, 100%, 100%) for 20 min each at RT. 3.14. Decant the ethanol and incubate for 30 min in 1 mL of 3:1 ethanol:low-viscosity embedding mixture medium at RT. 3.15. Remove the medium and add 1 mL of 1:1 ethanol:low-viscosity embedding mixture medium. Incubate for 30 min at RT. 3.16. Remove the medium and add 1 mL of 1:3 ethanol:low-viscosity embedding mixture

medium. Incubate for 30 min at RT.

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| 178 | 3.17. Remove the medium and add 1 mL of 100% low-viscosity embedding medium and incubate |
| 179 | overnight. |
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| 181 182 | 3.18. Embed the sample in 100% low-viscosity embedding mixture and incubate for 24 h at 60 °C. |
| 183 184 | 3.19. Prepare 90-nm thick sections using an ultramicrotome. |
| 185 186 | 3.20. Observe the grid under TEM at 200 kV. |
| 187 | 4. Serial sectioning and mounting on indium-tin-oxide coated coverslips for SEM imaging |
| 188 189 | 4.1. Substrate preparation |
| 190 | |
| 191 | 4.1.1. Clean indium-tin-oxide (ITO)-coated glass coverslips (22 mm x 22 mm) by gentle agitation |
| 192 193 | in isopropanol for 30–60 s. |
| 194 | 4.1.2. Remove the coverslips, drain off the excess isopropanol, and leave in a dust-free |
| 195 | environment until dry. |
| 196 | • |
| 197 | 4.1.3. Treat the ITO-coated glass coverslips by glow discharge using a plasma coater for 1 min. |
| 198 | 7,0 0 0 1 |
| 199 | NOTE: Plasma activating confers a hydrophilic property on the substrate surface. It creates a very |
| 200 | thin film of water on the substrate to prevent wrinkle formation in the sections when the section |
| 201 | is attached to the substrate. |
| 202 | |
| 203 | 4.1.4. Insert the ITO-coated glass coverslips into the substrate holder, and place into the knife |
| 204 | boat. |
| 205 | |
| 206 | 4.2. Trimming of the sample block and serial sectioning |
| 207 | |
| 208 | 4.2.1. Insert the sample block into the sample holder of the ultramicrotome and set into the |
| 209 | trimming block. |
| 210 | |
| 211 | 4.2.2. Use a razor blade to trim away all excess resin around the target position (identified in step |
| 212 | 2.6, Figure 1D-G). The shape of the block face should be trapezoid or rectangular. The leading |
| 213 | edge and trailing edge must be absolutely parallel (Figure 1H,I). |
| 214 | |
| 215 | 4.2.3. Insert the sample holder on the arm of the ultramicrotome and place the diamond knife in |
| 216 | the knife holder. Insert the ITO glass coverslips into the ribbon carrier and clamp the carrier with |
| 217 | the handle (Figure 1J). Set the ribbon carrier into the knife boat and fill the knife boat with filtered |
| 218 | distilled water (Figure 1K). |
| 219 | |
| 220 | 4.2.4. Adjust the carrier position with the slide of the knife by carefully pushing the handle of the |

- 221 holder to set the edge of the ITO glass close to the knife (**Figure 1L**).
- 222
- 4.2.5. After cutting the section, stop the sectioning process, and slowly open the clamping screw
 of the tube and drain the water boat (flow rate of one drop of water per second).

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4.2.6. After completing the ribbon-collection process, remove the substrate with the handle of the clamping device and dry the ribbon (**Figure 1M**).

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5. Imaging in the SEM and alignment of the SEM image stack

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5.1.1. Mount the ITO-coated coverslip on aluminum stubs with sticky carbon tape. Seal the glass surface and the surface in the stub with sticky carbon tape, and then coat with a 10-nm thick carbon layer (Figure 1N).

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5.1.2. Observe the ITO-coated coverslip in a field emission SEM at a low acceleration voltage of
 5 kV and a suitable working distance for the efficient collection of BSEs.

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5.1.3. Import the serial images into the Image J software (Fiji)¹³ using the virtual stack option.
Open a new TrakEM¹⁴, and import the image stack into TrakEM. Click the right-mouse button and choose the **align** menu.

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5.1.4. Then select the image range (from the first image to the last image). Finish the autoalignment, save the aligned dataset, and choose **export** to compile a flat image from the selected image range (from the first image to the last image). Finally, save the flat image data in AVI format in the Image J main menu.

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NOTE: **Supplemental Movie 1** and **Supplemental Movie 2** show the SEM image stack and cropped image stack, respectively.

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6. Segmentation of mitochondria and ER from serial images

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252 6.1.1. Start the 3dmod in IMOD¹⁵ software and open image files.

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254 6.1.2. In the ZaP window, draw the contour of the mitochondria and ER using middle-mouse button.

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6.1.3. To visualize the segmented volume, open the Model View window (Supplemental Movie3).

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REPRESENTATIVE RESULTS:

- 261 Figure 1 describes the schedule and workflow for this protocol. The protocol requires 7 days;
- 262 however, depending on the time spent on SEM imaging, this may increase. For cell transfection,
- the confluency of the cells should be controlled so as not to cover the bottom of the entire grid
- plate (Figure 1A). A high cell density could prevent the identification of the cell of interest during

light microscope and EM observation. We used genetically tagged plasmids that expressed APEX2 and HRP to select efficiently transfected cells among the numerous cultured cells in the culture dish. We cultured HEK293T cells and confirmed the expression of SCO1-linked APEX2 (mitochondrial intermembrane space [IMS]) and HRP-conjugated KDEL (ER) in co-transfected cells. Under light microscopy, APEX2-transfected cells were stained a brown color, whereas cells without transfection remained unstained (Figure 1A and Figure 2). This allowed the identification of the transfected target cells, which were then used for correlative light-electron microscopy (CLEM), using DAB staining in a cultured cell population (Figure 3D-F and Figure 4B). It was helpful to mark the glass bottom (Figure 1B,C) to make it easy to identify the location of the target cell during the flat embedding step (Figure 1E,F). When the HEK293T cells were treated with an enhanced "double osmium" staining protocol (rOTO), whole cells were stained a dark color (Figure 1D). After removing the gridded coverslip from the culture dish, we identified the target location on the block surface under a stereo microscope (Figure 1G). We trimmed the cells in the ROI in a trapezoid shape, and the leading and trailing edges were made parallel (Figure 1H,I). To implement mitochondria and ER network reconstruction, we used a large diamond knife with a large water boat to serially section SCO1-APEX2 and HRP-KDEL-expressing HEK293T cells (Figure 1J-L). Serial 90-nm thick ribbon sections were successfully attached to the ITO-coated glass coverslip (Figure 1M), and the surface was coated with 10-nm thick carbon for observation via SEM (Figure 1N).

SCO1–APEX2 and HRP–KDEL proteins generate highly dense electronic signals derived from DAB conversion that are detectable in TEM (Figure 3) and SEM (Figure 4). The dark stain generated by SCO1–APEX2 was observed exclusively in the IMS and not in the matrix space of mitochondria (Figure 3D). Co-transfected cells (the left cell in Figure 3D,E) with both SCO1–APEX2 and HRP–KDEL plasmids expressed a highly dense electron signal in mitochondrial IMS and ER; however, we observed no ER staining in cells that were transfected only with SCO1–APEX2 (the right cell in Figure 3D,F). For serial images using SEM, first, we created an overview of the whole array image using the BSE detector over a large area (Figure 4A). Second, the ROI was placed in the first section and propagated to all other sections (Figure 4B). Finally, we visualized the ROI containing five target cells with 5-nm image pixels (Figure 4C). Zoomed-in images revealed detailed subcellular structures (Figure 4D) such as Golgi apparatus, mitochondria, nuclei, and ER. The serial images clearly showed that ER–mitochondria contacts were occurring on different z-planes (Supplemental Movie 2 and Supplemental Movie 3).

FIGURE AND TABLE LEGENDS:

Figure 1: Sample preparation workflow for SEM and TEM. (A) A culture dish containing gridded coverslips was seeded with cells and stained with DAB. (B,C) After DAB staining, a marker pen was used to mark the bottom of the glass where the target cells were located. (D) After O₅O₄ staining, the cells become a dark color. (E,F) Polymerase chain reaction (PCR) tubes (or any type of embedding capsules) were used to easily make an EM block that contained the marked positions. (E) Top view. (F) Bottom view. (G) A low-magnification stereo microscopy image of the surface of an EM block. (H) The ROI is in the middle of the flat surface. (I) A higher-magnification stereo microscopy image of the rectangular ROI. (J) ITO-coated glass coverslips (white asterisk)

are inserted into the ribbon carrier (blue arrow), and the carrier is clamped by turning the handle clockwise. (**K,L**) The handle of the holder is carefully pushed, and the carrier is adjusted to position the edge of the ITO-coated glass coverslip close to the knife by sliding. (**M**) The ribbons are attached to the ITO-coated glass coverslips. (**N**) The ITO-coated glass coverslips are attached to the SEM stubs, and the residual glass is sealed with sticky carbon tape and coated with a 10-nm carbon thread layer. White asterisks indicate the ITO-coated glass coverslip, and black asterisks indicate the carbon tape.

Figure 2: Inverted phase-contrast microscopy image of cultured HEK293T cells stained with DAB. (A) Staining of cells with DAB only (without O_sO_4 staining). White arrows indicate the unstained cells, and black arrows indicate DAB-stained cells. (B) Higher-magnification image of the ROI.

Figure 3: TEM imaging of HEK293T cells exhibiting the targeted mitochondrial IMS (SCO1–APEX2) and ER (HRP–KDEL). (A–C) Untransfected HEK293T cells showing the double-membrane of mitochondria (M) and endoplasmic reticulum (ER). (D–F) APEX2 and HRP catalyze the polymerization of DAB into a local precipitate, which is subsequently stained with electron-dense OsO₄. A dark contrast is apparent in the mitochondrial IMS (black arrowhead) and ER (black arrow); however, cells that were not transfected with HRP–KDEL exhibit unstained ER (white arrow). Scale bars: 1 μm.

Figure 4: Serial SEM imaging of HEK293T cells exhibiting the targeted mitochondrial IMS (SCO1–APEX2) and ER (HRP–KDEL). (A) Overview of the serial section ribbons observed using the BSE detector. (B) Correlation of low-magnification image (inset) with high-magnification BSE image (white dotted-line box indicates the ROI of DAB-stained cells). (C) High magnification of the ROI target cells with 5-nm image pixels. (D,E) A dark contrast is apparent in the mitochondrial IMS and ER but not the Golgi apparatus. (F–I) ER–mitochondria contacts (white arrow) occur on different z-planes. N, nucleus; M, mitochondria; ER, endoplasmic reticulum; G, Golgi apparatus.

Table 1: Solution recipes.

Supplemental Movie 1: SEM image stack. Fiji¹³ with TrakEM¹⁴ software was used to align 91 images. The original aligned data set is 11 GB. To downsize the stack, resized and cropped image set was used.

Supplemental Movie 2: Cropped image stack. To visualize mitochondria, ER, and their contact sites in detail, images were cropped from original data set (5 nm/pixel). Scale bars: 1 µm.

Supplemental Movie 3: 3D Reconstruction of mitochondria and ER. For 3D visualization, the contour of mitochondria and ER was segmented and visualized using IMOD¹⁵ software. Mitochondria were visualized as long tubular structures (red), and the ER networks (green) showed their complicated morphology. Yellow represented a large surface area of contact site between mitochondria and ER in different z-planes.

DISCUSSION:

Determining the cellular localization of specific proteins at a nanometer resolution using EM is crucial to understand the cellular functions of proteins. Generally, there are two techniques to study the localization of a target protein via EM. One is the immunogold technique, which has been used in EM since 1960, and the other is a technique using recently developed genetically encoded tags¹⁶. Traditional immunogold techniques have employed antibody-conjugated gold particles or quantum dots to show the location of the labeled protein. However, due to the requirement for high-quality antibodies and the penetration efficiency of antibodies affected by resin and fixative, this technique is significantly limited¹⁷. Specifically, because immunogold labeling is predominantly restricted to the surface of an ultrathin section without en bloc metal staining and strong osmium fixation, this technique is not directly applicable to modern 3DEM¹⁸. To use recent 3DEM methods, including SBEM and array tomography, with protein labeling, we utilized genetically encoded EM tags in this protocol. Genetically encoded tags do not require permeabilization, technically demanding ultra-cryosectioning, and immunostaining of individual sections because they localize to the site of interest prior to fixation.

The procedures for sample preparation in 3DEM generally include a combination of common chemical fixation and heavy metal staining methods because cells are composed mainly of C, H, O, and N, requiring staining with heavy metals to acquire contrast under EM⁹. Therefore, we employed reduced osmium fixation and metal staining to enhance contrast and conductivity for serial imaging. The procedure to stain samples before sectioning, known as en bloc staining, has been reported as an essential step for 3DEM methods such as SBEM and FIB-SEM¹⁹. We confirmed that the en bloc-stained cells in our protocol demonstrated clear SCO1–APEX2 and HRP–KDEL EM contrast exclusively in the mitochondrial IMS and ER, respectively, in TEM (**Figure 3**). Furthermore, the SEM images from 90-nm serial sections revealed a clear contrast in both organelles (**Figure 4**). Notably, the enhanced contrast by en bloc staining was distinctly distinguishable from the DAB signal, and the contrast and conductivity resulted in good-quality serial images (**Figure 4**). Additionally, this high contrast aids the facilitation of subsequent tasks such as alignment and segmentation with three-dimensional (3D) image software.

In recent years, volume electron microscopy techniques (dik-SBEM, FIB-SEM, and array tomography) have answered biological questions that required the observation of a large field of view and a 3D view. Dik-SBEM and FIB-SEM do not involve the physical handling of sections, so time consuming for alignment of images can be reduced. However, the sample has to be destroyed to obtain serial images, and the field of view is smaller than that of array tomography. Serial SEM imaging using array tomography is employed increasingly as an alternative to TEM serial sectioning, and the major advantage of this technique is its non-destructive manner and large field of view. Unlike other 3DEM techniques such as dik-SBEM and FIB-SEM, sections can be stored on a coverslip, an ITO-coated coverslip, a silicon wafer, or a tape and can be repeatedly imaged⁷.

APEX2 is easy to use and can give a wide range of staining densities without special equipment, unlike mini singlet oxygen generator²⁰ or fluorescent protein²¹ techniques, generating DAB precipitation via a photooxidation. Its variable application has been tested in several cellular

organelles including nucleus, plasma membrane, mitochondria matrix, mitochondrial cristae, ER, tubulin, and actin in COS 7 and HEK293T cell²². However, there are some limitations and several checkpoints for the use of genetically encoded tagging in electron micrographs. The expression levels of the exogenous genes should be controlled to achieve reasonable staining at EM level because if the expression of the genetic tag is too high, it may induce false-positive signals and perturb the ultrastructure of cells via membrane rupture and subcellular organelle aggregation²³. Another possible problem is DAB overstaining, which has been reported to cause blurriness and membrane destruction²². To ensure the appropriate expression of genes, DAB-stained cells were compared with unstained cells using both light microscopy and EM (Figure 2 and Figure 3). Additionally, the fixation level should be well regulated to ensure that the endogenous oxidases are fully inactive. To prevent any artifacts from endogenous oxidases during processing, we fixed a monolayer of cells instead of using detached and pelleted cells²⁴. This also helped to identify the cells of interest when we checked the DAB signal under light microscopy. Thus, our results indicate that the staining and fixation of cell monolayers are useful for CLEM using DAB staining (Figure 2). The serial images with array tomography and 3D model revealed that the ERmitochondria contact sites occur on different z-planes (Supplemental Movie 2 and Supplemental Movie 3). The image produces a complete 3D visualization of the mitochondrial and ER networks in whole cells (Supplemental Movie 1). It suggests 3D volume analysis is essential for quantitative comparison of ER-mitochondria contacts. When studying the complex networks of intracellular organelles, this is an exceptionally useful technique.

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In conclusion, this protocol was an efficient combination of CLEM and 3DEM techniques that allowed whole-cell investigation at EM level. Notably, two different tags at the same time and DAB signals in two different organelles were visible in a whole cell. In addition, labeled cells and unlabeled cells in same section can be compared, because of large scale EM. In this protocol, en bloc staining and DAB signals from genetically encoded tags were useful to investigate the interaction between membranous organelles in whole cells. This could be a suitable application for large-scale EM to investigate other cellular interactions.

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DISCLOSURES:

The authors have nothing to disclose.

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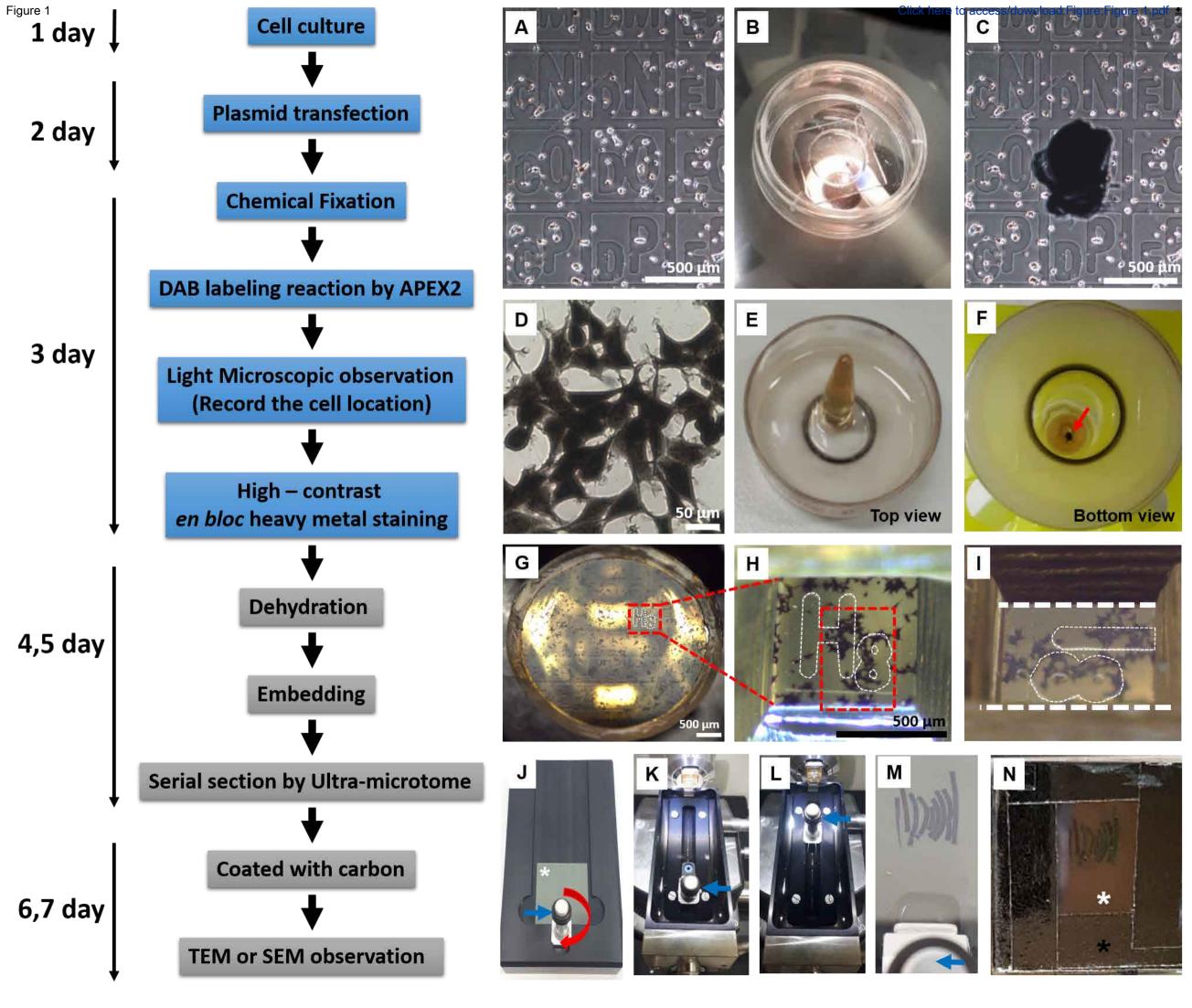
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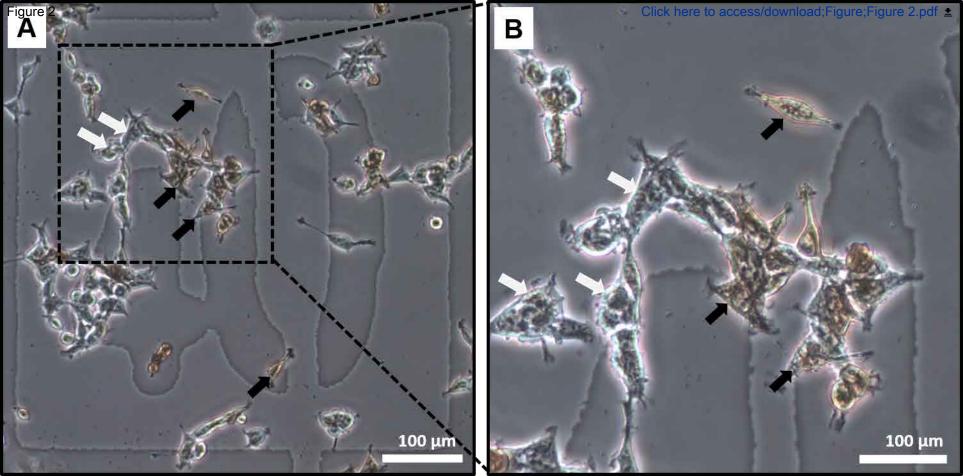
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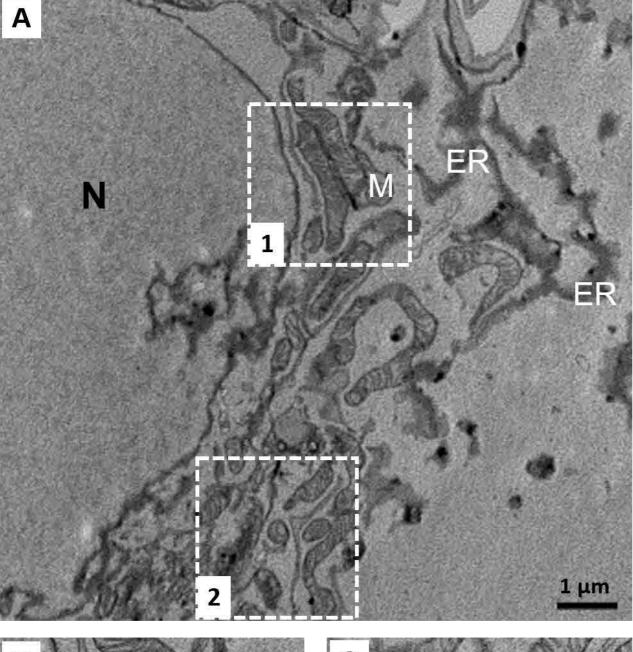
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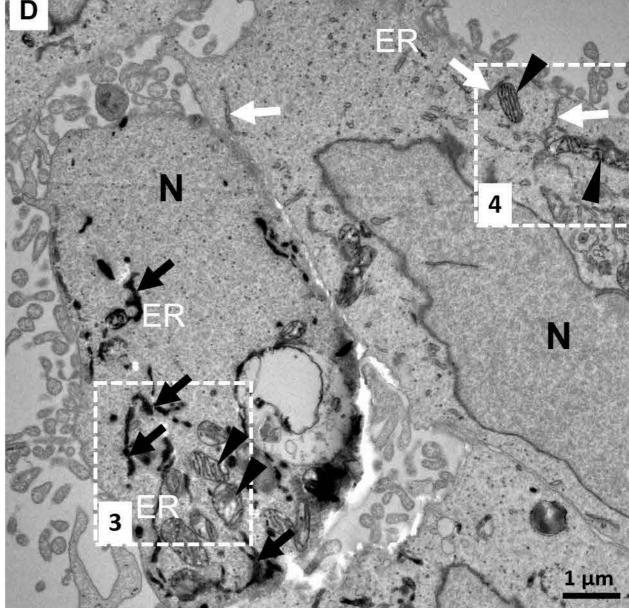
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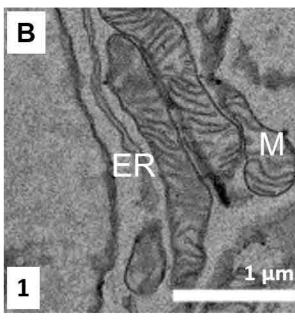
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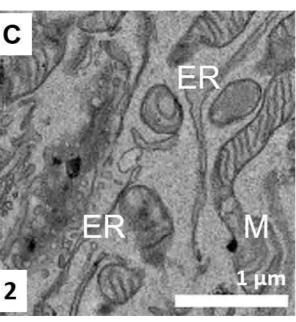


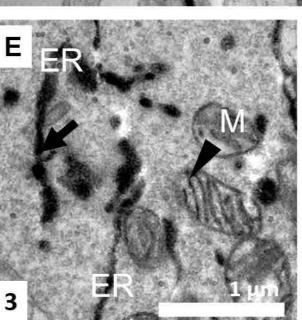


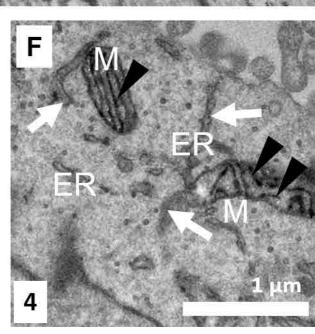


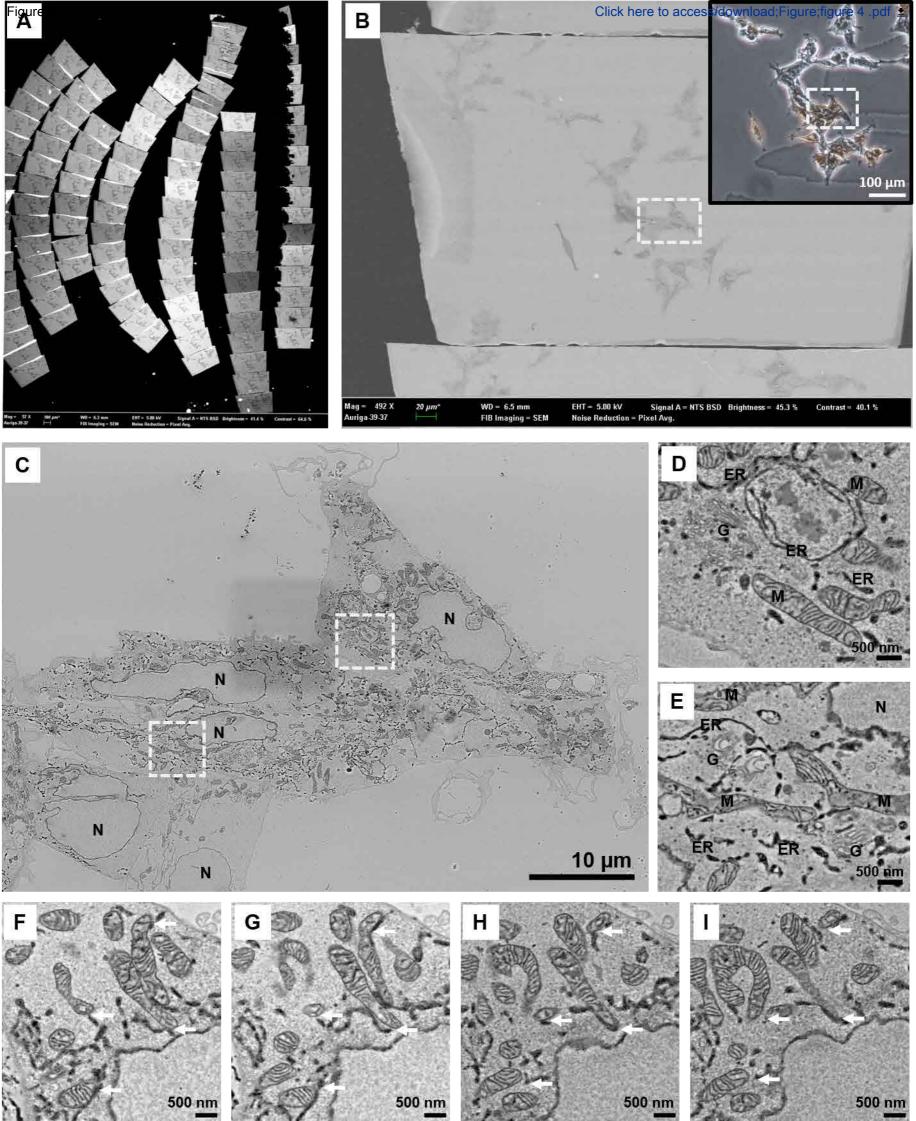












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| Solutions / mixtures | Concentration | | | | |
|-----------------------------------|---------------|--|--|--|--|
| Sodium cacodylate solution | 0.3 M | | | | |
| | 0.1 M | | | | |
| Cell fixation solution | - | | | | |
| Glycine solution | 0.02 M | | | | |
| DAB solution | 10x | | | | |
| | 1x | | | | |
| Potassium ferrocyanide | 3% (wt/vol) | | | | |
| Reduced osmium tetroxide solution | 2% (vol/vol) | | | | |
| Aqueous uranyl acetate | 1% (wt/vol) | | | | |
| Thiocarbohydrazide (TCH) solution | - | | | | |
| Aspartic acid solution | 0.03 M | | | | |
| Walton's lead aspartate solution | - | | | | |

Solution recipe

Dissolve 12.84 g of cacodylic acid in 160 mL of distilled water. Adjust pH to 7.4 with 0.1 M HCl then make up to 200 mL with distilled water.

Dilute the 3x sodium cacodylate solution threefold using distilled water.

1% glutaraldehyde and 1% paraformaldehyde in 0.1 M sodium cacodylate solution (pH 7.0).

Dissolve 75 mg of glycine in 50 mL of 1x sodium cacodylate buffer.

Total 50 mg of DAB powder dissolve in 10 mL of 0.1 M HCl solution at the room temperature with extensive vortexing for 10-20 min. Undissolved material is removed by centrifuge at $13,523 \times g$ at room temperature for 10 min. Small volume aliquots (e.g., 1 mL) of 10x DAB solution and store them at - 80 °C for several months.

Thaw a 1 mL aliquot of 10x DAB, and then mix it with 3.33 mL of cold 0.3 M sodium cacodylate solution and 5.67 mL of cold water, finally add 10 μ L of 30% H₂O₂.

Dissolve 1.5 g of tetrapotassium ferrocyanide in 50 mL of 0.2 M sodium cacodylate solution.

3% potassium ferrocyanide in 0.2 M sodium cacodylate solution is combined with equal volume of 4% aqueous osmium tetrovide

Dissolve 1 g of uranyl acetate in 90 mL of distilled water in RT. Almost all the uranyl acetate has dissolved, then make up to 100 mL with distilled water.

Add 0.1 g of thiocarbohydrazide to 10 mL of distilled water and dissolve in a 60 °C oven for 1 h.

Add 0.2 g of L-aspartic acid to 50 mL of distilled water.

Dissolve 0.066 g of lead nitrate in 10 mL of 0.03 M aspartic acid solution and adjust pH 5.5 with 1 N KOH.

| Name of Material/Equipment | Company | Catalog Number |
|---|--------------------|------------------|
| Glutaraldehyde | EMS | 16200 |
| Paraformaldehyde | EMS | 19210 |
| Sodium cacodylate | EMS | 12300 |
| Osmium tetroxide 4 % aqueous solution | EMS | 16320 |
| Epon 812 | EMS | 14120 |
| Ultra-microtome Leica ARTOS 3D | Leica | ARTOS 3D |
| Uranyl acetate | EMS | 22400 |
| Lead citrate | EMS | 17900 |
| 35mm Gridded coverslip dish | Mattek | P35G-1.5-14-CGRD |
| Glow discharger | Pelco | easiGlow |
| Formvar carbon coated Copper Grid | Ted Pella | 01805-F |
| Hydrochloric acid | SIGMA | 258148 |
| Fugene HD | Promega | E2311 |
| Glycine | SIGMA | G8898 |
| 3,3' -diaminobenzamidine (DAB) | SIGMA | D8001 |
| 30% Hydrogen peroxide solution | Merck | 107210 |
| Potassium hexacyanoferrate(II) trihydrate | SIGMA | P3289 |
| 0.22 um syringe filter | Sartorius | 16534 |
| Thiocarbonyldihydrazide | SIGMA | 223220 |
| Potassium hydroxide | Fluka | 10193426 |
| L-aspartic acid | SIGMA | A9256 |
| Ethanol | Merck | 100983 |
| Transmission electron microscopy | FEI | Tecnai G2 |
| Indium tin oxide (ITO) coated glass | | |
| coverslips | SPI | 06489-AB |
| Isopropanol | Fisher Bioreagents | BP2618-1 |
| Diamond knife | Leica | AT-4 |
| Inveted light microscopy | Nikon | ECLipse TS100 |
| Scanning electron microscopy | Zeiss | Auriga |

| Comments/Description | |
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