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Visualization of endoplasmic reticulum subdomains in cultured cells

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Abstract:	<p>The lipids and proteins in eukaryotic cells are continuously exchanged between cell compartments, although these retain their distinctive composition and functions despite the intense inter-organelle molecular traffic. The techniques described in this paper are powerful means of studying protein and lipid mobility and trafficking in vivo and in their physiological environment. Fluorescence recovery after photobleaching (FRAP) and fluorescence loss in photobleaching (FLIP) are widely used live-cell imaging techniques for studying intracellular trafficking through the exo-endocytic pathway, the continuity between organelles or sub-compartments, the formation of protein complexes, and protein localisation in lipid microdomains, all of which can be observed under physiological and pathological conditions. The limitations of these approaches are mainly due to the use of fluorescent fusion proteins, and their potential drawbacks include artifactual over-expression in cells and the possibility of differences in the folding and localisation of tagged and native proteins. Finally, as the limit of resolution of optical microscopy (about 200 nm) does not allow investigation of the fine structure of the ER or the specific sub-compartments that can originate in cells under stress (i.e. hypoxia, drug administration, the over-expression of transmembrane ER resident proteins) or under pathological conditions, we combine live-cell imaging of cultured transfected cells with ultrastructural analyses based on transmission electron microscopy.</p>
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Question	Response

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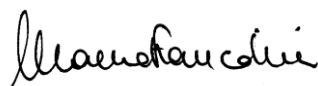
Dear Editor,

Enclosed you will find our revised manuscript entitled “**Visualization of endoplasmic reticulum subdomains in cultured cells**” by M. Fossati, N. Borgese S. Colombo, and myself (JoVE50985). As indicated in the submission site we would like the article to be filmed by the end of October 2013 as the first author and the main character of the movie will leave the laboratory. We hope that you will now consider the manuscript suitable for publication.

Thank you in advance for your consideration and please do not hesitate to contact us if you have any further question.

Looking forward to hearing from you,

Sincerely yours,



Maura Francolini

Visualisation of endoplasmic reticulum sub-domains in cultured cells

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Endoplasmic reticulum (ER); fluorescent proteins (FPs); confocal microscopy; fluorescence recovery after photobleaching (FRAP); fluorescence loss in photobleaching (FLIP); ultrastructure; transmission electron microscopy (TEM),

SHORT ABSTRACT (50 words maximum)

We describe the imaging approaches we use to investigate the distribution and mobility of the transfected fluorescent proteins resident in the endoplasmic reticulum (ER) by means of the confocal imaging of living cells. We also ultrastructurally analyse the effect of their expression on the architecture of this subcellular compartment.

LONG ABSTRACT (150 words minimum, 300 words maximum)

The lipids and proteins in eukaryotic cells are continuously exchanged between cell compartments, although these retain their distinctive composition and functions despite the intense inter-organelle molecular traffic. The techniques described in this paper are powerful means of studying protein and lipid mobility and trafficking *in vivo* and in their physiological environment. Fluorescence recovery after photobleaching (FRAP) and fluorescence loss in photobleaching (FLIP) are widely used live-cell imaging techniques for studying intracellular trafficking through the exo-endocytic pathway, the continuity between organelles or sub-compartments, the formation of protein complexes, and protein localisation in lipid microdomains, all of which can be observed under physiological and pathological conditions.

The limitations of these approaches are mainly due to the use of fluorescent fusion proteins, and their potential drawbacks include artifactual over-expression in cells and the possibility of differences in the folding and localisation of tagged and native proteins. Finally, as the limit of resolution of optical microscopy (about 200 nm) does not allow investigation of the fine structure of the ER or the specific sub-compartments that can originate in cells under stress (i.e. hypoxia, drug administration, the over-expression of transmembrane ER resident proteins) or under pathological conditions, we combine live-cell imaging of cultured transfected cells with ultrastructural analyses based on transmission electron microscopy.

INTRODUCTION

The discovery of green fluorescent protein (GFP) and its spectral variants, and the parallel development of fluorescence microscopy, have opened up completely new avenues for the investigation of protein behaviour in cells. Techniques such as fluorescence recovery after photobleaching (FRAP) and fluorescence loss in photobleaching (FLIP), which are possible because of the intrinsic capacity of fluorophores to extinguish their fluorescence under intense illumination, are based on confocal live-cell imaging and the use of transfected fluorescent fusion proteins¹⁻³. They are widely used to assess not only the localisation of proteins, but also their mobility and vesicular transport, which can reveal important clues concerning their function⁴.

The unique feature of eukaryotic cells is the presence of intracellular compartments that have specific lipid and protein compositions. Although organelles are physically isolated, they need to communicate with each other and share molecular components in order to maintain cellular homeostasis. The secretory pathway guarantees that the proteins and lipids synthesised in the ER reach the correct final destination in which they exert their function. Intracellular organelles can also be connected by dynamic contact sites that allow molecules (lipids) to be directly exchanged between compartments. Moreover, many proteins have to assemble in large heteromeric complexes or associated with specific lipid species (lipid rafts/microdomains) in order to become functionally active or to be transported to their final destination. All of these biological aspects greatly influence the kinetic properties of proteins, and can therefore be appropriately investigated by means of the techniques described below. Our group has widely used FRAP and FLIP combined with electron microscopy in order to study the architecture of the ER and its different sub-domains. The ER is the first station of the secretory pathway and plays a key role in protein and lipid sorting⁵. It is a highly dynamic organelle whose distinct sub-domains reflect its many different functions (i.e. protein and lipid biosynthesis and trafficking, protein folding, Ca^{2+} storage and release, and xenobiotic metabolism). However, although they are morphologically, spatially and functionally distinct, these domains are continuous with each other, and their relative abundance can be modified in cells under physiological and pathological conditions. The best known and usually spatially segregated domains of the ER are the nuclear envelope, and the smooth and rough ER; however, we and others have demonstrated that there are ER structures with a more elaborate architecture and three-dimensional organisation in various cell types and tissues under physiological conditions that can also be induced by means of stressful stimuli such as hypoxia, drug administration or the over-expression of ER-resident transmembrane proteins^{2,6} (and references therein).

We have also recently demonstrated the presence of such structures in cell models of human diseases^{1,7}. Originating from the stacked cisternae of smooth ER, they were given the collective name of organised smooth endoplasmic reticulum (OSER) in 2003⁶, although they are also known as *karmellae*, *lamellae* and crystalloid ER on the basis of their architecture

which, like their size, can vary. After the cells are transfected with GFP fused to the cytosolic region of tail-anchored (TA) ER-resident proteins (Δ EGFP-ER), the weakly dimerising tendency of GFP in *trans* dramatically alters the organisation and structure of the ER. FRAP and FLIP experiments showed that Δ EGFP-ER is free to diffuse within OSERs, and the fact that it moves from the reticular ER to the OSER and *vice versa* indicates that the aggregates are continuous with the surrounding reticular ER. Ultrastructural analysis has allowed us to correlate the fluorescence data with a detailed description of OSER architecture and organisation at nanoscale level: OSERs are always made up of stacks of paired cisternae of smooth ER but may have different forms of spatial organisation, such as regularly arranged sinusoidal arrays or whorls, or hexagonal “crystalloid” tubular arrays. These rearrangements lead to cubic morphologies⁸ which, as they have been found in cells under physiological conditions⁹ and following stresses such as hypoxia¹⁰, drug treatment¹¹ and cancer⁹, may have significant potential as ultrastructural markers.

After this first demonstration using GFP fusion proteins, we used imaging experiments to analyse the proliferation of ER domains in response to pharmacological treatments¹², assess the tendency of fluorescent proteins to oligomerise in cells¹³, and to investigate the role of a mutant, ALS-linked TA protein in the formation of intracellular aggregates of ER origin that may be relevant to its pathogenicity^{1,8}. It has been suggested that the formation of intracellular aggregates (which occurs in many neurodegenerative diseases¹⁴) may be a protective mechanism designed to prevent the interactions between toxic mutant proteins and the surrounding cell components¹⁵.

What follows is a description of a combination of optical and electron microscopy methods for investigating constructs whose C-terminal hydrophobic domains are inserted into the membrane of the ER, and an analysis of their dynamic behaviour and the effects of their over-expression on ER domain architecture in cultured cells (see Fig. 1 for a flowchart of the experimental protocol).

PROTOCOLS

1) Plasmid, cell culture and transfection with ER fluorescent proteins

1.1) The plasmid used in this study consists of an enhanced version of GFP fused at its C-terminus to the tail region of the ER isoform of rat cytochrome b(5) (abbreviated here as b(5)) via a linker sequence. The tail region contains the entire sequence (Pro94-Asp134) that remains membrane associated after the trypsin cleavage of native b(5), including the 17-residue TMD (Transmembrane domain), flanked by upstream and downstream polar sequences (UPS and DPS). The linker consists of the myc epitope followed by [(Gly)₄Ser]₃, and the entire cDNA is inserted into the Hind3-Xba1 sites of the mammalian expression vector pCDNA3. The details of the construction of this plasmid have been described in a previous publication in which it is referred to as GFP-ER¹⁶.

1.2) Grow COS-7 cells in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% fetal bovine serum, 2 mM L-glutamine, 1% penicillin/streptomycin in an incubator at 37°C and 10% CO₂.

1.3) Transfection. Plate 3x10⁵ cells on a round glass coverslip in a 6-well plate and, on the following day, transfect with the JetPEI system as described by the manufacturer. Note that the optimal JetPEI/DNA ratio has been tested in order to establish the maximum transfection efficiency depending on the plasmid and cell line used: in our case, a JetPEI:DNA ratio of 2:1 leads to 70-80% transfection efficiency.

2) Live fluorescence scanning confocal microscopy

2.1.) Live-cell imaging. Put the coverslip on which the transfected cells were seeded into a steel culture cell chamber for 24 mm coverslips filled with DMEM w/o phenol red, supplemented with 10% FBS, 2 mM L-glutamine, 1% pen/strep, 25 mM Hepes, 50 µg/ml cycloheximide and 1:100 OxyFluor to prevent the samples from photobleaching. An SP5 confocal microscope equipped with a temperature-controlled CO₂ incubator (37°C and 5% CO₂) is used for live cell imaging experiments, with dGFP-ER being visualised using a 488 nm laser and a 525/50 band pass emission filter.

2.2.) Fluorescence recovery after photobleaching (FRAP). Draw a region of interest (ROI), corresponding to an OSER structure, and bleach it using 20 iterations and a combination of 488 nm (100% of a 30 mW Argon laser, corresponding to 5.5-6 µW at the sample) and 405 nm (60% of a 30 mW Diode 405 laser, corresponding to 11.6 µW at the sample) lasers which, in our experience, leads to efficient and rapid photobleaching.

2.3) Record the recovery of fluorescence in the bleached ROIs by taking a single frame every 10 seconds for 10 minutes (pixel time = 1.61 µs/px).

2.4.) Fluorescence loss in photobleaching (FLIP). Draw a ROI corresponding to an OSER structure, and bleach as described above. The bleaching is repeated every 30 sec, and post-bleaching images are recorded every 10 seconds for 30 minutes (pixel time = 1.61 µs/px).

2.5) FRAP and FLIP analysis. All of the images are analysed using ImageJ software (<http://rsbweb.nih.gov/ij/download.html>). In the FRAP experiments, the fluorescence recovery of the bleached ROI is measured over time and normalised to the total fluorescence of bleached cell, which is always checked to be constant over time.

2.6) For the FLIP experiments, draw an ROI outside the bleached OSER and covering the whole cell. Measure its fluorescence intensity over time and normalise to the fluorescence levels of an ROI drawn on an unbleached cell in order to correct for any decrease in fluorescence caused by the imaging itself.

2.7) In all of the experiments, subtracted the background signal (determined in an area outside the cells) from the fluorescent intensities of the ROIs. Finally, plot the results using GraphPad Prism software.

3) Ultrastructural analysis by means of transmission electron microscopy

Given the toxicity of many of the reagents, all of the procedures should be carried out wearing an appropriate lab. coat and gloves under a fume hood.

3.1) After removing the coverslip from the Petri dish, fix the remaining cells grown on the bottom of the dish as a monolayer using filtered 2% glutaraldehyde in 0.1 M cacodylate buffer, pH 7.4, for 10 min at room temperature.

3.2) Scrape the cells using a Teflon scraper and transfer them into 1.5 ml eppendorf tubes. Pellet the cells by means of centrifugation at 9,000 g for 10 min. Remove the supernatant, add fresh fixative and leave overnight at 4°C.

3.3) Wash the pellets with the buffer, then post-fix with a solution of 1% osmium tetroxide in cacodylate buffer for 1 hour at room temperature.

3.4) Rinse with MilliQ water, and *en bloc* stain with 1% uranyl acetate in distilled water for between 20 min and 1 h.

3.5) Dehydrate the samples in increasing ethanol series (70%, 80%, 90%, 100% and 100% for 10 min each), and wash briefly twice in propylene oxide (15 mins each).

3.6) Infiltrate the samples in a mixture of propylene oxide + Epon (1:1) (from 2 h to overnight).

3.7) Embed in Epon epoxy resin cured at 60°C for at least 24 hours.

3.8) Section the manually trimmed resin blocs using an ultramicrotome LEICA UC6 equipped with a 45° diamond knife to obtain sections with a thickness of 60-70 nm. Collect the sections on 300 mesh copper grids.

3.8) Stain the sections on the grid with a saturated solution of uranyl acetate (20 min) and lead citrate (7 min), thoroughly wash the grids by immersing them in bi-distilled filtered water, and allow them to dry at room temperature.

3.9) The stained grids are observed using a TECNAI G2 transmission electron microscope, and the images are captured using a bottom-mounted CCD camera at different final magnifications (generally ranging from 6,000 to 39,000x).

REPRESENTATIVE RESULTS

Figure 2 shows an example FRAP study of protein mobility. The mobility of *dEGFP-ER* protein is demonstrated by the rapid fluorescence recovery after photobleaching in bleached OSERs. For the quantitative analysis, the half time and mobile fraction were derived from experimentally measured data by fitting the following monoexponential equation:

$$F(t) = F_{post} + (F_{rec} - F_{post}) \left(1 - e^{-\frac{t}{\tau}}\right)$$

where F_{post} is the fluorescence signal after photobleaching, F_{rec} is the maximum fluorescence recovery value that is reached after bleaching, t the final time of registration and τ the mid time of registration.

Please note the importance of acquiring images without saturated pixels that could alter the fluorescence recovery and, consequently, the protein mobility analysis. It is also essential to always normalize the fluorescence signal in the bleached ROI to the total fluorescence of the same cell in order to consider fluorescence intensity variations due to bleaching during image acquisition or small changes in the focus plane.

An example of a FLIP experiment to study the continuity between intracellular compartments is shown in Fig. 3. OSERs are physically connected with the rest of the ER as demonstrated by the progressive emptying of the ER when the OSER domain is continuously bleached.

For a proper analysis, the acquisition of saturated pixels must be avoided (see above); furthermore, the acquisition parameters must be set up with laser powers as low as possible in order to avoid photobleaching due to image acquisition. For this reason it is strongly recommended to image an unbleached cell in the same field that will be used to normalize the fluorescence signal of the bleached cell.

All experiments have to be performed in the presence of cycloheximide, a translation inhibitor, in order to avoid any increase in the ER fluorescence signal (and consequently total fluorescence) due to protein biosynthesis.

Transmission electron microscopy demonstrated that the fluorescent aggregates observed in cultured cells transfected with *dEGFP-ER* represent patches of smooth and flattened ER cisternae that spatially organised themselves into well-defined 3D geometries classified on the basis of their patterns: linear or curved stacks (often associated with the nuclear envelope, not shown) (Figs. 4A and B) that may be continuous with regions of sinusoidal ER (Fig.4A); the membranes in some regions are organised into lattices with a square or hexagonal symmetry (crystalloid ER, not shown). Adjacent cisternae are separated by a thin layer of slightly electron-dense cytoplasm about 11 nm thick that is continuous with the cytoplasm surrounding the aggregates.

TABLES AND FIGURES

Figure 1: Flow chart of the experimental procedure. The cultured cells are first transfected with jetPEI (see Protocol) in order to over-express the fluorescent fusion protein of interest. After 24 h, the live transfected cells are visualised and FRAP and FLIP experiments are performed using a confocal microscope equipped with a controlled temperature CO₂ incubator, and the recorded images are exported and analysed using appropriate software (e.g. ImageJ). For the ultrastructural analysis, the transfected cells are fixed, pelleted and embedded in epon epoxy resin blocs. Ultrathin sections are obtained using a diamond knife, collected on copper grids, and observed under a transmission electron microscope.

Figure 2: FRAP experiment using COS-7 cells transiently transfected with *dEGFP-ER*. A) Two OSER structures (red ROIs) were bleached, and fluorescence recovery was recorded over time. Clear fluorescence recovery can be detected 1 min post-bleaching, and the signal further increases 4 min later (scale bar 10 μ m). B): Quantitative analysis of the FRAP experiment showing the recovery half-time and the mobile fraction of the *dEGFP-ER* protein.

Figure 3: FLIP experiment using COS-7 cells transiently transfected with *dEGFP-ER*. A) The continuous bleaching of an OSER (indicated by the red ROI) causes a progressive decrease in fluorescence in the rest of the ER and in other OSER structures within the same cell (indicated by the yellow ROI). The yellow arrow indicates a portion of an unbleached cell in which the fluorescence signal is constant over time. (Scale bar 10 μ m). B) Quantitative analysis of the FLIP experiment.

Figure 4: After fixation and embedding, cells expressing high levels of *dEGFP-ER* in which OSER structures could be detected by means of fluorescence optical microscopy were observed through a transmission electron microscope. A) Low magnification view of a portion of cytoplasm of a cell containing an OSER consisting of stacked cisternae and undulating sinusoidal membranes. Mitochondria (M) can be seen clustered around the OSER structures,

whereas ribosomes decorate only the membranes of the outermost cisternae (arrowheads and inset). The 11 nm thick electron-dense space between the membranes is continuous with the cytoplasm (arrow and inset) (L = lysosomes/(auto-)phagosomes) (scale bar 1.5 μm ; inset 0.25 μm). B) An OSER can be formed by lamellar ER: i.e. stacks of flattened ER cisternae that can be continuous or fragmented in their appearance in thin sections. Vesicles budding from the outermost cisternae of the stack can occasionally be observed (asterisk) (PM, plasma membrane) (Scale bar 150 nm).

DISCUSSION

The protocols and imaging approaches described in this paper have been used to investigate the distribution and mobility of transfected TA fluorescent proteins resident in the ER of living cells. We have also analysed the effect of the over-expression of these proteins on the architecture of this sub-cellular compartment by means of ultrastructural analyses.

The combination of live-cell confocal imaging and electron microscopy represents a very powerful means of investigating the dynamic properties of proteins, and may provide important information concerning protein function. The described methods are not time consuming (typically three days of work), and the development of many user-friendly software applications for image acquisition and analysis makes photobleaching-based, live-cell imaging relatively simple.

The main limitation of these techniques is the use of fluorescent fusion proteins because the fluorescent tag can affect the proper folding and/or assembly of the protein of interest. In addition, over-expression can alter the behaviour of transfected, fluorescently tagged proteins, and may therefore not reflect the real properties of endogenous proteins; however, this can be overcome by using of inducible and stably transfected cells in which the expression level can be precisely modulated to obtain levels comparable with those of the endogenous protein^{1,7}. The tendency of FPs to oligomerise has been widely documented and could significantly alter the behaviour (i.e. kinetics, unwanted protein-protein interactions and formation of aggregates) of chimeric proteins. The use of optimised monomeric fluorescent proteins should therefore be considered¹⁷.

Another critical aspect of dynamic imaging studies using fluorescence and photobleaching is the time needed to bleach the fluorescence efficiently and measure fluorescence recovery (and thus protein mobility) precisely, which also depends on the area of the ROI and local cell thickness. If a given GFP-tagged protein has a high diffusion coefficient, diffusion could occur during the bleaching and thus interfere with recovery time measurements. In order to obtain rapid and efficient bleaching, it is strongly recommended that a “zoom in” function (if available) and more than one laser line be used. Although the use of a fast scan module (i.e. a resonant scanner) can greatly improve the speed of imaging during the recovery phase of an experiment, in our hands it also considerably reduces bleaching efficiency. However, alternative scanning systems (such as a spinning disc equipped with a dedicated photobleaching device), and more powerful lasers can improve both bleaching efficiency and acquisition speed.

Most fluorescent proteins used in FRAP and FLIP experiments show some degree of reversible photobleaching and blinking that must be considered when performing quantitative analyses. The fluctuations between fluorescent and dark states occur in the second to minute time-scale. For EGFP, it has been shown that during bleaching experiments, fluorescence variations might involve less than 10% of the molecules, thus in the present protocol this phenomenon is negligible. If all conditions are kept constant, this will introduce a constant bias in the results. If other fluorescent proteins are used, in which the reversible fraction is

significantly higher (i.e. YFP), or to detect and evaluate photobleaching reversibility, this can be done by measuring fluorescence recovery after photobleaching in the entire living cell; if recovery is observed this can only be the result of photobleaching reversibility¹⁸.

The potential toxicity of light during the experiments is another critical factor, particularly because photobleaching requires strong lighting. It is well known that excited fluorophores tend to react with oxygen to produce free radicals that can affect various intracellular processes and even cell viability¹⁹, and so it is necessary to establish a balance between efficient bleaching and minimal phototoxicity; furthermore, cell viability should always be checked after live-cell imaging experiments. Given the short recording time, we did not consider the genotoxic effect of short wavelength light (405 nm) in the example described in this paper but, if a longer experiment is needed, a 405 nm laser line should not be used.

We chose not to use a correlative approach to transmission electron microscopy because of the heterogeneous nature of OSER architecture and the fact that we wanted to observe as many cells (and structures) as possible. The diversity of the fine structure of protein aggregates in cells may be a key feature of different diseases and we were interested in obtaining a broad range of samples, whereas a correlative approach allows the observation of fewer events during the same period time. However, correlative light-electron microscopy (CLEM) should be the first choice when investigating events in structures that cannot be easily identified (such as less prominent ER sub-domains) or in a limited number of cells (such as micro-injected cells). It is worth noting that our experiments were characterised by a high degree of transfection efficiency (at least 30% of the cells were transfected), otherwise the possibility of observing OSER structures non-correlatively is quite limited.

Disclosure

The authors have nothing to disclose.

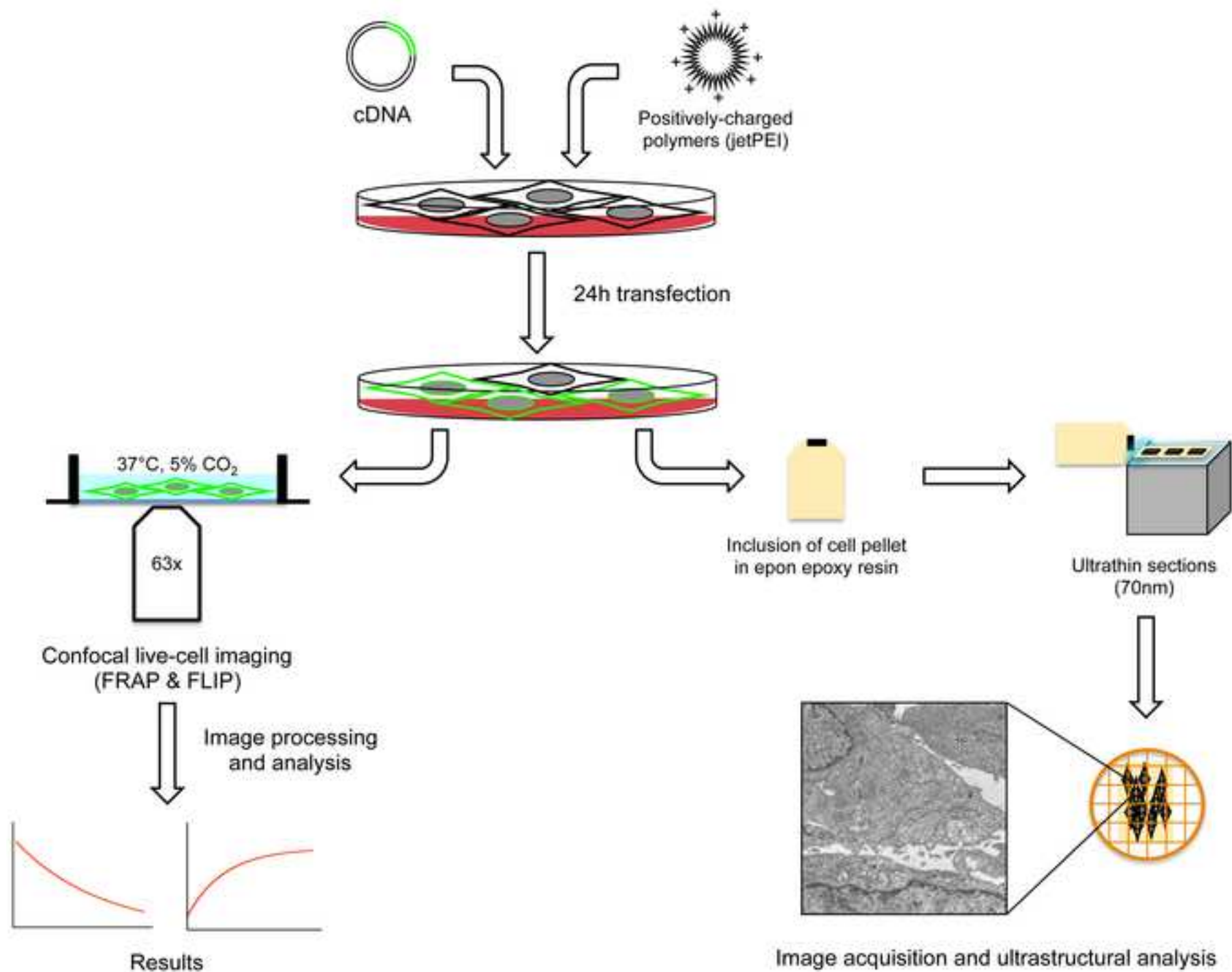
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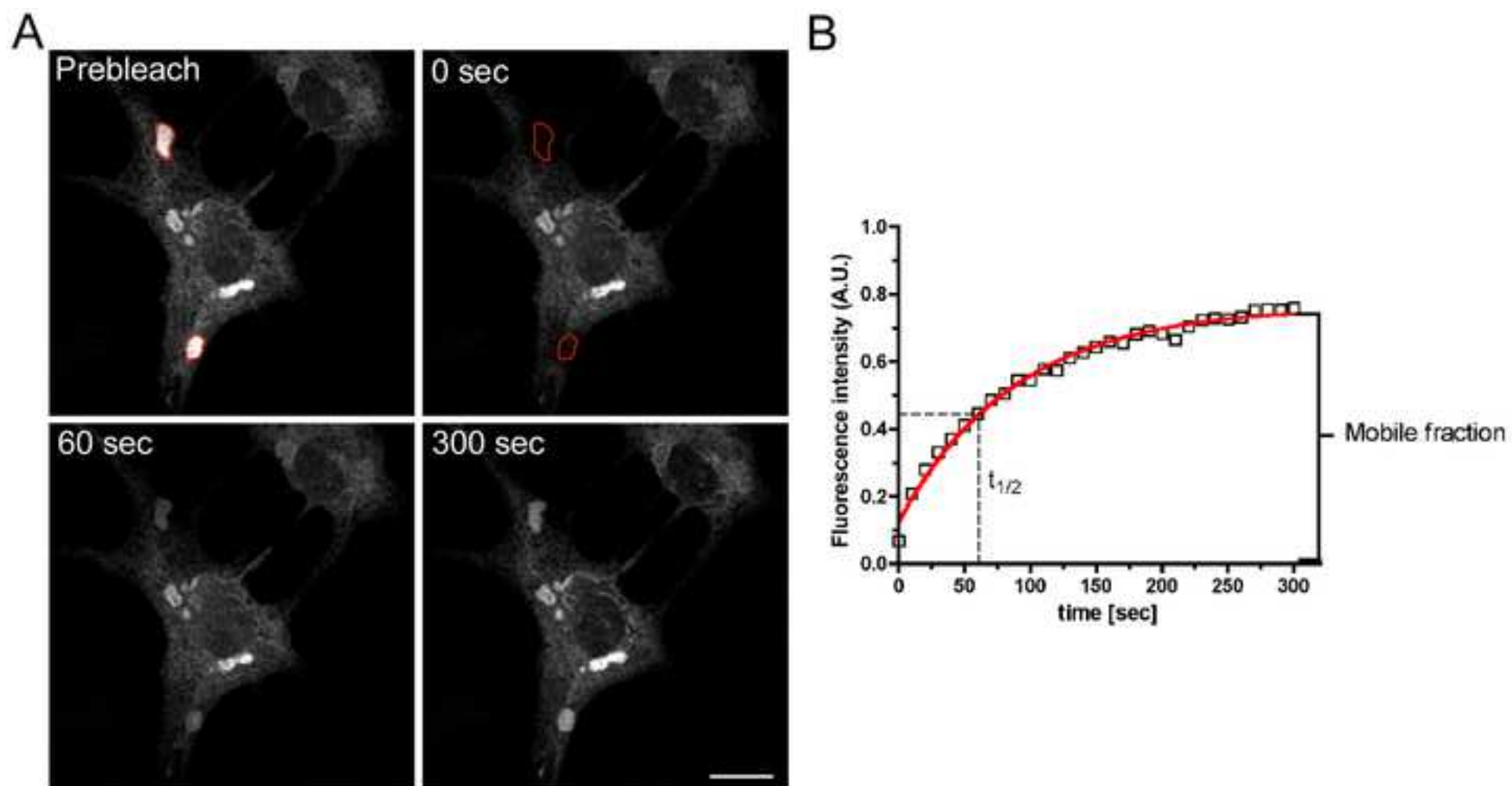
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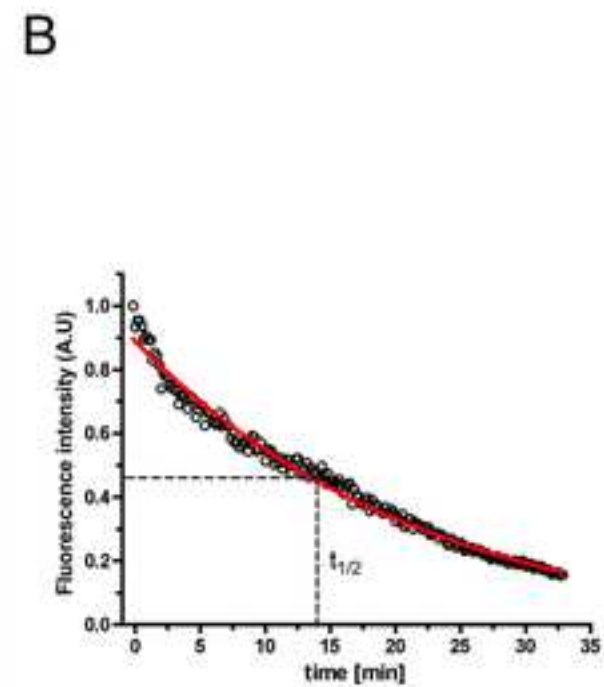
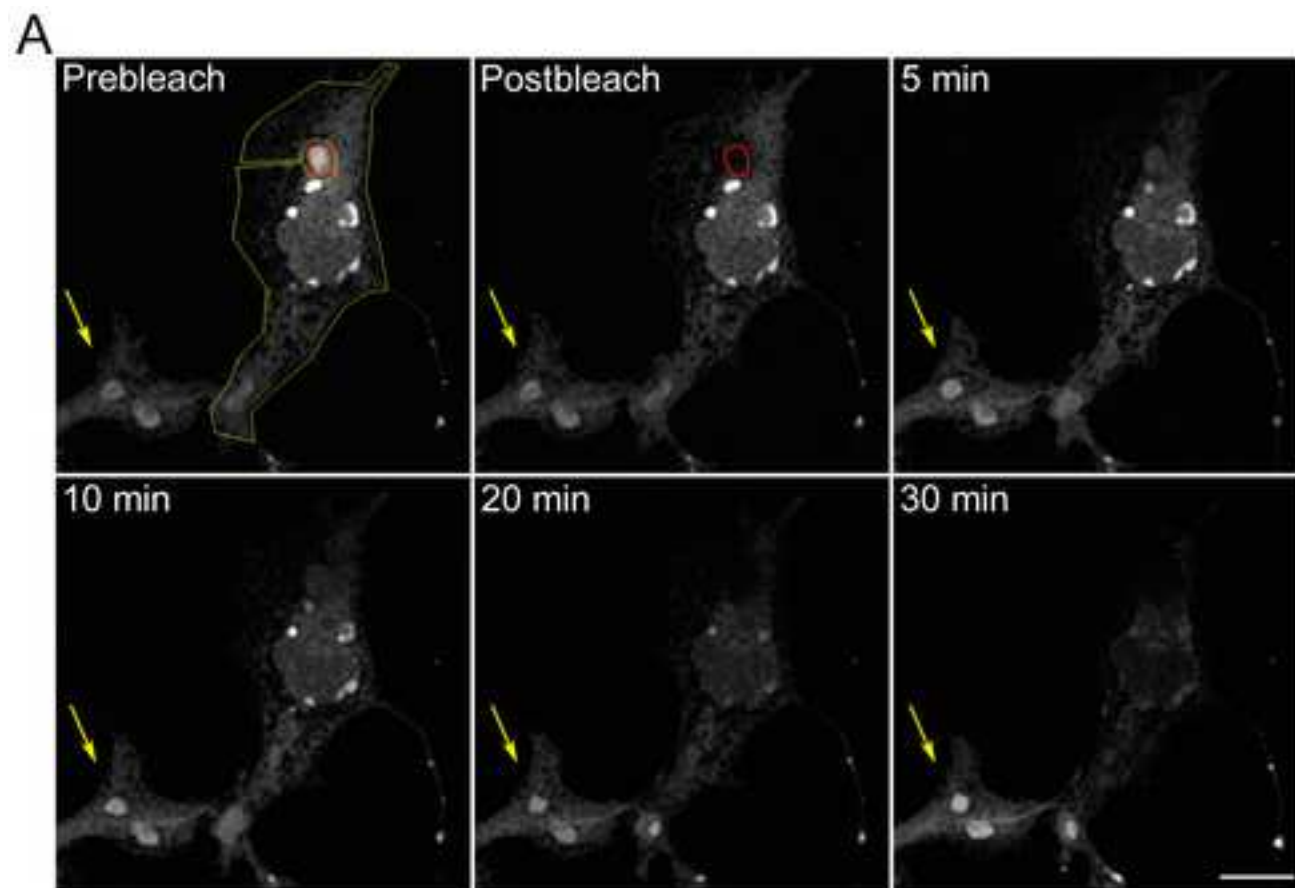
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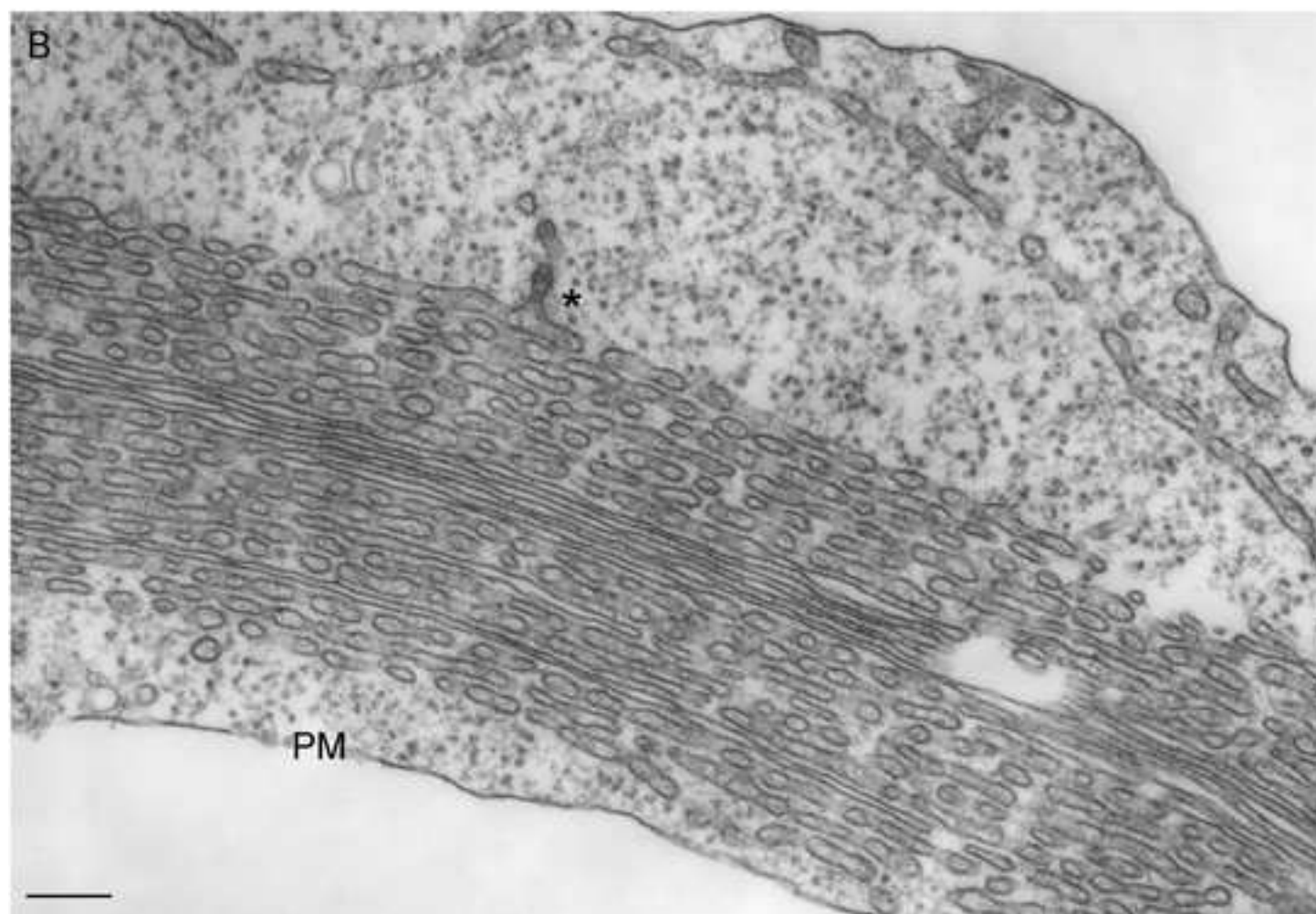
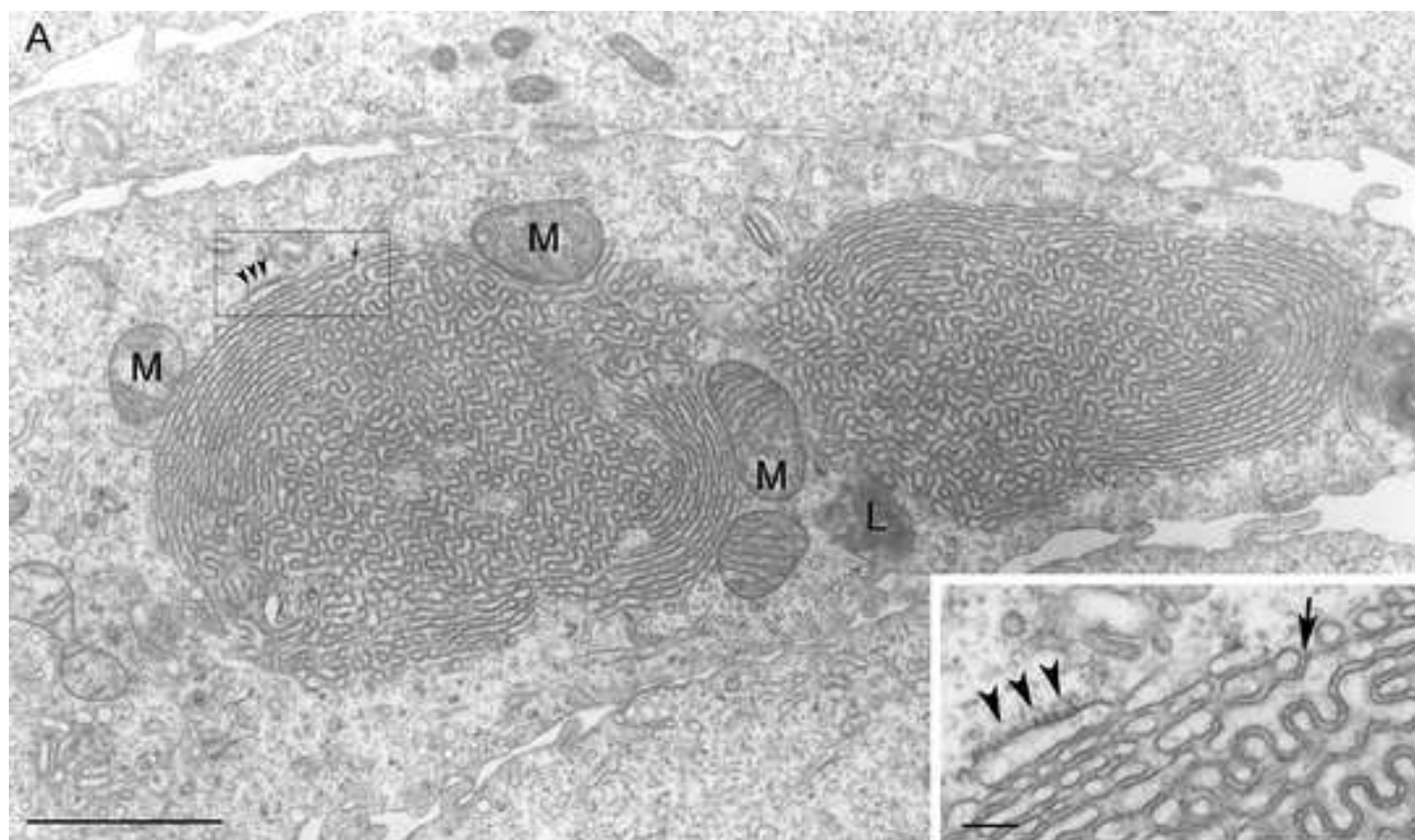
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Name of Material/ Equipment	Company	Catalog Number	Comments/Description
Dulbecco's Modified Eagle medium (DMEM)	Invitrogen	41966029	
Dulbecco's Modified Eagle medium (DMEM) w/o phenol red	Invitrogen	31053028	
Fetal Bovine Serum (FBS)	Invitrogen	10270106	
Pen/Strep	Invitrogen	15140-122	
L-Glutamine 200 mM solution	Invitrogen	25030-024	
jetPEI	Polyplus Transfection	PP10110	
OxyFluor	Oxyrase Inc.	OF-0005	
Glutaraldehyde Grade I	Sigma Aldrich	G5882	
Sodium Cacodylate Trihydrate	Sigma Aldrich	C0250	
Osmium Tetroxide 4% solution	Electron Microscopy Science	19150	
Uranyl Acetate dihydrate	Sigma Aldrich	73943	slightly radioactive
Propylene Oxide	Sigma-Aldrich	82320	
EPON embedding medium kit	Sigma-Aldrich	45359-1EA-F	
Lead Citrate	Electron Microscopy Science	17800	
Bench top centrifuge	Eppendorf	5415 D	
Spectral Confocal Microscope	Leica Microsystems	TCS SP5	
CO ₂ Microscope Cage Incubation System	OkoLab		
Ultramicrotome	Leica Microsystems	UC6	
Diamond knife	Diatome	Ultra 45°	
Transmission Electron Microscope	FEI	Tecnai G2	
GraphPad Prism Software	GraphPad Software, Inc		
steel culture cell chamber for 24mm coverslip	Bioscience Tools	CSC-25	
Electron Microscopy grids	Electron Microscopy Science	G300Cu	



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VISUALIZATION OF ENDOPLASMIC RETICULUM SUBDOMAINS IN CULTURED CELLS

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VISUALIZATION OF ENDOPLASMIC RETICULUM SUBDOMAINS IN CULTURED CELLS

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MS # (internal use):

The Authors are very grateful to the Reviewers for their thoughtful and stimulating reviews. A point-to-point response (in bold) to the criticisms is herewith provided.

Reviewer #1:

Major Concerns:

1) The manuscript reads as a hybrid between a purely methodological guide for studying ER subdomains and a "minireview" of OSERs. Related to this issue is that from the manuscript it is unclear whether the presented techniques are specific for the study of OSERs or that they would serve more generally for studying ER subdomains. If the latter is the objective of the authors, they may want to compare their practices on OSERs with approaches that have been employed elsewhere on ER (subdomains) with similar questions in mind, such as membrane fluidity and exchange of resident proteins between ER subdomains. In any case the "OSER angle" is an interesting example, but perhaps it is worthwhile to discuss in more detail how the authors think OSERs may reflect the physiology of the cell other than being a "freaky" phenomenon induced by over-expression by either ER-GFP or mutant VAPB.

In the "Introduction " we have added a paragraph in which we introduce studies by other groups describing the role and significance of ER membrane proliferation and more generally of intracellular membranes proliferation in physiological conditions and upon stressful stimuli (i.e. hypoxia, drug administration), disease (cancer) and in neurodegenerative disease where aggregates of mutant proteins (the causative agents of the disease itself) might represent a protection against unwanted and potentially harmful interaction of the mutants with the intracellular environment.

2) The EM part, while technically valid, doesn't really appear integrated with the live-cell imaging and doesn't add much beside the spectacular visualization of OSER structures. In the absence of a correlative analysis it is difficult to envision how these findings can serve in the analysis of other, less prominent ER subdomains etc. Perhaps, the authors can elaborate more comprehensively how EM should be employed to complement the FLIP and FRAP.

The importance of the investigation of the fine structure of subcellular aggregates and, more specifically in the present manuscript of these ER subcompartments, has been better explained in the "Introduction" and in the "Discussion" sections where we report the relevance of this approach in the identification of markers for ultrastructural pathology. Regarding the advantage of using a correlative microscopical approach in the study of less prominent ER subdomains, this has been fully acknowledge in the end of the "Discussion" section.

Minor Concerns:

1) I have interpreted that the authors refer to their constructs as ER resident, while this term is generally used for luminal proteins. To avoid confusion I suggest to explicitly state in each case that it concerns tail anchored proteins in the ER membrane facing the cytosol or find a term that fits such a profile.

To avoid confusion, throughout the text, we have specified that all our experiments were performed using tail anchored (TA) resident ER proteins, although we do not completely agree about "resident" being specific for luminal proteins.

2) The English can improve in some parts.

The new version of the manuscript was revised by a professional english translator

3) Ref 4: I believe Snappe should be Snapp.

The reference was corrected

Reviewer #2:

Minor Concerns:

1) The manuscript describes well how to prepare the sample, perform confocal imaging, and analyze the FRAP and FLIP measurements. However, to make the protocol less instrument-specific it would be convenient to report parameters as the laser power at the sample plane and the pixel dwell time, both during imaging and bleaching (see Additional Comments).

Additional Comments to Authors:

FRAP and FLIP: laser intensities for bleaching should be reported in mW, preferably at the sample, and not as "% of laser power", since this indication does not provide sufficient information about the actual energy delivered to the sample. Alternatively, if such a measure is not possible, measuring the laser power before the objective along with the transmission of the microscope objective at the wavelengths used for FRAP and FLIP would give a better idea about the laser intensity during the photobleaching experiments. It is not clear how the fluorescence intensity for a FLIP experiment is measured: please specify in section 2.3 whether the fluorescence was integrated over the whole image or if a specific ROI of the cell was selected. In the latter case, please report in Figure 3 panel A the ROI over which the loss of fluorescence shown in panel B was measured.

Scanning speed (pixel time) has been indicated and laser intensities during bleaching have been reported as mW at the sample. In fact we measured the laser intensities both before and after the objective using a Plan Neofluar 20x/0.5 objective. Very little differences were recorded in the two measures (less than 1 μ W). The value at the sample were included in the manuscript. We have specified the nature of the ROI in the FLIP experiment and it has been reported in Fig. 3 Panel A,

Reviewer #3:

Major Concerns:

1) In order to compare the light microscopy level and the ultrastructure, CLEM (correlative light-electron microscopy) is considered the method of choice. The possibility of correlation between FRAP and FLIP behavior and the ultrastructure of the same OSERs would be a great advantage for the study. This point should be better discussed and the reason why they do not use CLEM should be better explained.

As reported earlier, we stated at the end of the “discussion” section that we performed a non-correlative EM approach because we wanted to investigate the fine structure of as many aggregates as possible in many different cells in a limited amount of time. These fluorescent aggregates were very broad and abundant in cells and as the transfection efficiency was quite high we had no problem in tracking the structure of interest in many different samples. We clearly stated that, in case of less prominent features to be investigated or in case of a low number of cell presenting the wanted phenotype (i.e. microinjected cells), a correlative approach must be the method of choice.

2) the paper is missing an organic discussion of the limitations of the methods, and in particular of FRAP and FLIP experiments. Only some potential pitfalls are mentioned, but spread throughout the manuscript. Furthermore, other issues that affect photobleaching experiments should be discussed in addition to the ones already considered:

a) FRAP kinetics could be substantially affected by the area of the ROI and the local cell thickness.

b) fluorochrome intermittency (blinking or dark state) could affect the recovery curves

c) photo-toxicity induced by the strong laser exposure could affect several cellular processes, such as vesicular transport.

Due to these limitations, the FRAP and FLIP experiments presented in the paper demonstrate the continuity between the OSERs and the rest of the ER, but are not suitable for the determination of kinetics and diffusion parameters. This point should be discussed.

As indicated by the reviewer we have expanded the description of the limitations of the methods we propose in the “discussion”. In particular, as suggested, we mentioned the importance of the size of the ROI and the local cell thickness, while we had already indicated and discussed the fact that phototoxicity induced by high intensity irradiation can affect different intracellular processes and even viability.

A paragraph has been added in the “Discussion” to introduce the blinking behaviour of GFP and its potential influence on FRAP measurements, influence that is quite low due to the fact that 1) only a small fraction (less than 10%) of GFP molecules undergoes reversible photobleaching upon illumination and 2) if imaging conditions are kept constant, a constant bias will be introduced in the results.

3) the use of the 405 laser for bleaching in the FRAP and FLIP experiments is not justified. GFP is not significantly excited at this wavelength and photo-toxicity increases with shorter wavelengths. If there is a specific reason why they used this laser, it should be discussed.

We have described in the “Protocol” section of the manuscript the reason why we used 488 e 405 laser lines for bleaching, it is a common useful practice to use more than one laser line to increase the efficiency and the speed of bleaching. In the “Discussion” we discussed about the limitation of the use of the 405 laser line because of its genotoxic added to the more widespread phototoxicity of high intensity laser excitation.

Minor Concerns:

1) it is not clear what the authors mean by "round-shaped chamber" in paragraph 2.1. Manufacturer and cat number should be indicated as for the other equipment

The nature of the object has been clarified in the text and the manufacturer and cat. number indicated in the text and in the excel file.

2) EM grids are not listed in the table of reagents as well
The item has been included in the excel file.

3) references are poor (especially in the introduction) and mostly limited to the authors' publications

More references have been cited in the “Introduction” and in the “Discussion” sections.

4) english should be revised

As mentioned above this new version manuscript has been revised by a professional english translator.

Reviewer #4:

1. The authors may spend a couple of sentences in the discussion about the use of optimized monomeric fluorescent proteins (cf. Chudakov et al., Physiol Rev, 2010) to avoid unwanted protein-protein interactions or the formation of artefactual ER structures due to the mentioned oligomerization tendency of FPs.

A paragraph discussing this interesting and crucial aspect of the use of fluorescent proteins as tag has been added in the “Discussion”. We are grateful to the reviewer for the suggestion.

2. There is an inconsistency between the text and figure 1. It is reported that cells were grown and imaged in 10% CO₂ but the figure indicates a 5% concentration.

This inconsistency has been fixed in the revised version of the manuscript.

3. Please indicate the source of the softwares used for data analysis.

The source of the used softwares has been indicated in the text.