



Published in final edited form as:

Arterioscler Thromb Vasc Biol. 2018 June ; 38(6): 1333–1345. doi:10.1161/ATVBAHA.118.310951.

CaMKII (Ca²⁺/calmodulin-dependent kinase II) in mitochondria of smooth muscle cells controls mitochondrial mobility, migration and neointima formation

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Abstract

Objective—To define the mechanisms by which mitochondria control VSMC migration and impact neointimal hyperplasia.

Approach and Results—The multifunctional Ca²⁺/calmodulin-dependent kinase II (CaMKII) in the mitochondrial matrix of VSMC drove a feed-forward circuit with the mitochondrial Ca²⁺ uniporter (MCU) to promote matrix Ca²⁺ influx. MCU was necessary for the activation of mitochondrial CaMKII (mtCaMKII), whereas mtCaMKII phosphorylated MCU at the regulatory site S92 that promotes Ca²⁺ entry. mtCaMKII was necessary and sufficient for PDGF-induced mitochondrial Ca²⁺ uptake. This effect was dependent on MCU. mtCaMKII and MCU inhibition abrogated VSMC migration and mitochondrial translocation to the leading edge. Overexpression of WT MCU, but not MCU S92A mutant in MCU^{-/-} VSMC rescued migration and mitochondrial mobility. Inhibition of microtubule, but not of actin assembly blocked mitochondrial mobility. The

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Disclosures: One author is a named inventor on awarded patents related to targeting CaMKII inhibitors to mitochondria (OMK). All other authors declare no conflict of interest exists

outer mitochondrial membrane GTPase Miro-1 promotes mitochondrial mobility via microtubule transport, but arrests it in subcellular domains of high Ca^{2+} concentrations. In Miro-1^{-/-} VSMC, mitochondrial mobility and VSMC migration were abolished, overexpression of mtCaMKII or a CaMKII inhibitory peptide in mitochondria (mtCaMKIIN) had no effect. Consistently, inhibition of mtCaMKII increased and prolonged cytosolic Ca^{2+} transients. mtCaMKII inhibition diminished phosphorylation of focal adhesion kinase and myosin light chain, leading to reduced focal adhesion turnover and cytoskeletal remodeling. In a transgenic model of selective mitochondrial CaMKII inhibition in VSMC, neointimal hyperplasia was significantly reduced after vascular injury.

Conclusions—These findings identify mitochondrial CaMKII as a key regulator of mitochondrial Ca^{2+} uptake via MCU, thereby controlling mitochondrial translocation and VSMC migration following vascular injury.

Keywords

Mitochondria; CaMKII; Ca^{2+} ; smooth muscle cell; migration; neointima

INTRODUCTION

Atherosclerotic vascular disease is the leading cause of mortality in the industrialized world, and commonly treated by percutaneous balloon angioplasty and stent placement. However, even with contemporary drug-eluting stents, restenosis via neointimal hyperplasia occurs after 10–30% of percutaneous arterial interventions¹. Neointimal hyperplasia develops from excessive vascular smooth muscle cell (VSMC) migration and proliferation from the medial layer to the arterial lumen, narrowing the luminal diameter leading to decreased blood flow and recurrence of anginal symptoms². Thus, neointimal hyperplasia remains a significant clinical problem in patients with vascular disease.

Previous studies have supported that mitochondrial physiology impacts on VSMC phenotypes and vascular disease such as neointimal hyperplasia^{3,4}, atherosclerosis,⁵ and hypertension⁶. These studies primarily interrogated well-established concepts in VSMC phenotypes in vascular disease, such as mitochondrial reactive oxygen species (ROS) production and mitochondrial fission and fusion. For example, neointimal hyperplasia was blocked by delivery of mitochondrial manganese superoxide dismutase to VSMC³. Since mitochondria undergo dynamic fission and fusion during the cell cycle, inhibition of mitochondrial fission as anticipated decreased neointimal hyperplasia and VSMC proliferation⁴. While these studies implicate that mitochondria affect vascular function and disease, a detailed mechanistic understanding of how intra mitochondrial events alter VSMC phenotypes remains elusive.

Very recent evidence in cancer and epithelial cells has suggested that mitochondrial translocation to the leading edge is necessary to support cell mobility and invasiveness^{7–10}. At the leading edge, mitochondria localize to the vicinity of focal adhesions¹¹ and support local energy production⁷, necessary for focal adhesion turnover and cytoskeletal remodeling. Along with providing energy for VSMC, mitochondria act as major Ca^{2+} buffering organelles^{12,13}. Mitochondrial Ca^{2+} influx is primarily controlled by mitochondrial Ca^{2+}

uniporter (MCU), which resides in the inner mitochondrial membrane. MCU activity is modulated by multiple regulators, including MICU and potentially multifunctional Ca^{2+} /calmodulin-dependent kinase II (CaMKII)^{14,15}. In cancer cells, MCU inhibition perturbs cell migration¹⁶. For example, studies in breast cancer¹⁷ and cervical cancer¹⁸ cells demonstrated that migratory capacity directly correlates with the expression of MCU or its regulator MICU. The mechanisms by which MCU inhibition impairs migration remain unknown. While incompletely studied in VSMC, data in neurons and cardiac myoblasts suggest that mitochondrial mobility is reduced when local Ca^{2+} concentrations are high¹⁹. Therefore, abrogation of MCU activity may lead to local increase in Ca^{2+} concentrations in the vicinity of MCU-deficient mitochondria and thereby, decrease cell migration via arresting mitochondrial mobility.

Emerging studies have suggested that CaMKII, a coordinator of Ca^{2+} handling in multiple cell types, resides within the mitochondrial matrix of cardiac myocytes²⁰ and lung epithelial cells²¹. Mitochondrial CaMKII has been suggested to regulate MCU in cardiomyocytes, though the data are controversial^{20,22,23}. Herein we test the hypothesis that CaMKII in mitochondria of VSMC controls mitochondrial Ca^{2+} uptake and thereby mitochondrial mobility and MCU-dependent VSMC migration, ultimately contributing to neointimal hyperplasia.

MATERIALS AND METHODS

Materials

The detailed usage of materials and antibodies are included in the Supplemental Material and Major Resource Tables.

Mice

All protocols were approved by the University of Iowa Institutional Animal Care and Use Committee and in compliance with the standards for the care and use of laboratory animals of the Institute of Laboratory Animal Resource, National Academy of Science. Mice were maintained in the University of Iowa Animal Facility and treated in accordance with Institutional Animal Care and Use Committee guidelines (PHS Animal Welfare Assurance, A3021-01).

Mice with tamoxifen-inducible Cre recombinase (driven by the SMMHC-promoter) on a C57BL/6 background were used (SM-Cre)²⁴. These mice carry the Cre gene on the Y chromosome; hence only male mice were used. HA-tagged mtCaMKIIN mice were generated as previously described²¹. Double-transgenic mice with VSMC-specific expression of mtCaMKIIN (SM-mtCaMKIIN mice) were generated by crossing SM-Cre mice with HA-tagged mtCaMKIIN mice, as diagrammed in Supplemental Figure X A. All mice were genotyped as we previously described²¹. All studies used tamoxifen-treated SM-Cre mice as littermate controls (WT).

Smooth muscle-specific expression of mtCaMKIIN was induced in 6- to 8-week-old male mice via injection of tamoxifen (20 mg/mL, i.p., for 5 days). Recombination was verified by detection of the HA tag in aortic lysates by immunoblot, and by immunofluorescence in 10-

µm frozen carotid sections. Sections were imaged using a Zeiss LSM 510 confocal microscope.

MCU^{-/-} mice in CD1 background were a kind gift of Dr. Toren Finkel (NIH), Miro-1^{fl/fl} mice were graciously provided by Dr. Janet Shaw (Univ. of Utah). Information on strains and sources are provided in the Major Resources Table.

Vascular smooth muscle cell culture

Primary vascular smooth muscle cells were isolated from aortas and cultured in DMEM (Gibco, #11885-092) supplemented with 10% fetal bovine serum (FBS), 100 U/ml penicillin, 100 µg/ml streptomycin, 8 mM HEPES, MEM vitamins, and non-essential amino acids at 37°C in a humidified 95% air and 5% CO₂ incubator²⁵. VSMC at passages 4–10 were used for all experiments.

Adenoviral transduction

VSMC were incubated with adenoviruses expressing mtCaMKIIN, mtGFP, or control at a multiplicity of infection (MOI) of 50 in serum-free media overnight. Subsequent experiments were conducted 48–72 h after adenoviral transduction as described previously²¹. Miro-1^{-/-} were generated by infecting VSMC from Miro^{fl/fl} mice with adenovirus expressing cre recombinase at MOI of 10²⁶. Deletion of Miro-1 was confirmed 72 hours after infection by immunoblot.

Isolation of mitochondrial fractions and mitoplasts

Cleaned, segmented mouse aortas or cultured VSMC were suspended in MSE (5 mM 3-(N-morpholino)propanesulfonic acid, 70 mM sucrose, 2 mM ethyleneglycol-*bis*-(β-aminoethyl ether)-*N,N'*-tetraacetic acid, 220 mM mannitol, pH 7.2, with KOH) on ice followed by homogenization by mortar and pestle. Nuclei and unbroken cells were pelleted by centrifugation at 600 × *g* for 10 min. Then, centrifugation of the supernatant at 8,500 × *g* for 20 mins separated crude mitochondrial from cytosolic fractions. The mitochondrial pellet was resuspended in MSE with protease inhibitors. For mitoplast preparations, crude mitochondria were digested in 20 nM Proteinase K in MSE for 5 minutes on ice. The reaction was stopped by adding PMSF (1 mM), and mitoplasts were pelleted at 10,000×*g* for 10 min and resuspended in MSE with protease inhibitors.

Immunoblotting

Immunoblotting experiments were performed following the general protocol for western blotting by BioRad and detailed protocol in the Supplemental Materials. Equivalent amounts of protein of were separated by SDS/PAGE on 4–20% Tris/glycine gels (BioRad) and transferred to PVDF membranes. Blots were scanned and analyzed using ImageJ.

Determination of mitochondrial Ca²⁺

Ratiometric Ca²⁺ measurements in mitochondria were performed in VSMC after transduction with adenovirus expressing mtPericam (Ad-mtPericam)²⁷. Pericam ratiometric fluorescent imaging with the Leica SP8 STED imaging system was used to determine fluorescence signal intensity, with an excitation at 405nm/480nm and acquisition at 510nm.

Real-time Pericam fluorescence ratios were recorded after addition of PDGF. Peak amplitude (R) was calculated by subtracting the baseline fluorescence ratio from the highest fluorescence ratio. The area under the curve (AUC) from baseline was determined using GraphPad Prism. Summary data represent the average difference in basal and peak mitochondrial $[Ca^{2+}]$.

The o-Cresolphthalein conjugation colorimetric plate assay was used to measure Ca^{2+} concentration of isolated mitochondria from thoracic aortas or cultured VSMC. Mitochondrial Ca^{2+} was assessed per the manufacturer's protocol (Cayman Scientific) and normalized to total mitochondrial protein concentration.

Determination of cytosolic Ca^{2+} transients

Cells were loaded with 2 μ M Fura-2 acetoxyethyl ester (Fura-2AM) Ca^{2+} -free HBSS for 20 min at 25°C, then washed with Ca^{2+} -containing HBSS at 37° for 20 min. Cells were excited alternatively at 340 and 380 nm. Fluorescence signal intensity was acquired at 510 nm. Real-time shifts in Fura-2AM fluorescence ratio were recorded as PDGF was acutely added using Olympus IX81 Inverted Light Microscope. Peak amplitude (R) was calculated by subtracting the baseline fluorescence ratio from the highest fluorescence ratio. Summary data was calculated using GraphPad Prism.

Migration assays

Boyden chamber and traditional scratch wound assays were performed as previously described and detailed in the Supplemental Material²⁸. To perform high throughput migration assays, VSMC were grown to confluence in a 96-well Black, Clear Bottom, Tissue Culture 96-Well with Lid (Perkin Elmer #6005550). Wounding was performed by inserting a conical 96-well PCR plate and scraping to create a cell-free zone. Cells were washed with DMEM and treated in DMEM containing PDGF or vehicle control. Images were taken at 10 \times at 0 – 48 hr after injury using the Perkin Elmer Operetta High-Content Imaging System by Digital Phase Contrast (DPC). Semi-automated analysis was performed using Image J as detailed in Supplemental Figure III. Each condition was performed and analyzed in quadruplicate for each independent experiment.

Quantification of mitochondrial distribution

To visualize mitochondrial distribution in migrating cells, VSMC were simultaneously infected with Ad-mtGFP and Ad-control or Ad-mtCaMKIIN. Cells were subject to a scratch wound assay and allowed to migrate in DMEM/10% FBS and PDGF for indicated time points. Inhibitors for mitochondria Ca^{2+} (Ru360, 1 μ M), mtROS (mitoTEMPO, 10 μ M), actin polymerization (Cytochalasin D, 0.1nM) and microtubules (Nocodazole, 1 μ M) were given for the duration of migration. For some experiments, VSMC with Nocodazole were washed and left in DMEM/10% FBS 2 hr prior to fixation to allow microtubule re-polymerization. VSMC were then fixed and stained with phalloidin 568. Images were acquired using a Zeiss 510 confocal microscope with a 40 \times objective. Mitochondrial distribution was quantified using NIH ImageJ by line scan of mitochondria from the nucleus to the leading edge and by region of interest at the leading edge as outlined in detail in Supplemental Figure V. For both methods, data are expressed as percent of mitochondria in the leading edge area or segment.

The image analysis was performed independently by two scientists who were blinded to the treatment group.

Focal adhesion immunostaining and analysis

VSMC infected with Ad-control or Ad-mtCaMKIIN, were grown to confluence on glass coverslips. A scratch wound assay was performed with PDGF. After 6 hr, cells were washed and fixed in 4% PFA, then subject to the staining protocol described in the supplemental detailed methods. Cells were stained with anti-vinculin primary antibody and phalloidin-568. Images were acquired using the Zeiss LSM 510 confocal microscope. Confocal images were thresholded equally across experiments by ImageJ. Region of interest (ROI) was selected at the leading edge of every cell and “Analyze Particles” function was used to identify and measure all FA.

Focal Adhesion Turnover

VSMC were nucleofected with GFP-Vinculin plasmid. Images of labeled FA in VSMC were taken after addition of DMEM/10% FBS containing PDGF every 15 minutes for a total of 90 minutes. Imaging was performed using the custom-built Nikon BX-81 microscope at 40× objective. Images were automatically thresholded by CellProfiler and FA were identified by “Primary Objects” function. The first image (green) and last image (red) were pseudocolored and overlaid in CellProfiler. Colocalization of green and red signal of FA at times 0 min and 90 min was expressed by Mander’s coefficient.

Carotid injury model

Male mice (10–12 weeks-old) were subject to carotid injury by endothelial denudation using a resin-bead coated suture as described in the Supplemental Materials²⁹. At 28 days after injury, all animals were anesthetized and perfused with PBS followed by 4% PFA for 3 min. The carotid arteries were excised and paraffin-embedded. Carotid artery cross sections (5 µm) were obtained at 50 µm intervals from the carotid bifurcation site for up to 500 µm and stained by Verhoeff’s Van Gieson. Luminal and intimal areas were determined by tracing the circumference of the internal elastic lamina (IEL), and the luminal area using NIH Image J. The neointimal area was calculated by subtracting the luminal area from the IEL area.

Nucleofection

Cells were nucleofected, following manufacturer’s protocol (Lonza #VPI-1004). Briefly, 600,000 cells were nucleofected in the presence of 5 µg plasmid DNA and plated onto 3 cm glass coverslip dishes. For focal adhesion turnover assays, VSMC were infected with either Ad-mtCaMKIIN or Ad-Control the next day and allowed to express for 48 hour.

Statistical Analyses

Data are expressed as mean±SEM and analyzed with GraphPad Prism 7.0 software. All data sets were analyzed for normality and equal variance. Kruskal-Wallis test with Dunn’s post hoc test was used for data sets where normal distribution could not be assumed. Two-tailed unpaired Student’s T-test and 1-way ANOVA followed by Tukey’s multiple comparison test were used for data sets with normal distribution. Two-way ANOVA followed by Tukey’s

multiple comparison test was used for grouped data sets. A p-value < 0.05 was considered significant.

RESULTS

CaMKII is present and active in mitochondria of VSMC

We first established that CaMKII is present in mitochondria of VSMC. We detected CaMKII in whole mitochondria and in mitoplasts, mitochondrial preparations that contain only the matrix and inner mitochondrial membrane (Figure 1A). Next, we tested whether CaMKII in mitochondria is activated by PDGF, a well-established agonist in VSMC migration and neointimal hyperplasia³⁰. PDGF increased the Ca²⁺/calmodulin-dependent autophosphorylation of CaMKII at Thr-287 in particular in mitoplasts (Figure 1B).

Since CaMKII is activated by Ca²⁺/CaM binding and subsequent autophosphorylation, we examined whether deletion or inhibition of the mitochondrial Ca²⁺ influx channel MCU alters PDGF-induced activation of CaMKII in mitochondria (mtCaMKII). Deficiency of MCU or inhibition of MCU with the pharmacologic inhibitor Ru360 abrogated mtCaMKII activation in mitoplasts (Figure 1B, Supplementary Figure IA). Phosphorylation of MCU at S92, a highly conserved site on the N-terminal domain of MCU, is essential for mitochondrial Ca²⁺ uptake¹⁵. Thus, we overexpressed WT MCU and a mutant of MCU that cannot be phosphorylated at S92 (S92A) in MCU^{-/-} VSMC (Figure 1C). Whereas WT MCU expression restored the phosphorylation of CaMKII, this effect was absent with mutant MCU. Of note, we confirmed that expression of MCU WT, but not of the MCU S92A mutant in MCU^{-/-} markedly augmented mitochondrial Ca²⁺ uptake (data not shown). These data suggest that Ca²⁺ influx via MCU is necessary and sufficient for CaMKII activation in mitoplast of VSMC.

Studies in other cell types have suggested that mtCaMKII phosphorylates MCU at S92 although direct evidence is currently missing¹⁵. To test the effects of mtCaMKII, we developed a model of mitochondrial CaMKII inhibition by adenoviral delivery of CaMKIIN, a specific peptide that blocks substrate binding to all CaMKII isoforms³¹. A COX8 mitochondrial targeting sequence was used to target CaMKIIN to the mitochondrial matrix (mtCaMKIIN). In immunoblots, we confirmed mtCaMKIIN expression in mitoplasts, with minimal detection in the cytosol (Supplemental Figure IB, C). Using immunoblots for activated ERK1/2, a bona fide cytosolic CaMKII signaling target^{30,32} we excluded additional cytosolic effects of mtCaMKIIN (Supplemental Figure ID). To provide direct evidence that mtCaMKII regulates MCU phosphorylation, we utilized an antibody that specifically detects phosphorylation of S92 on MCU (Supplemental Figure IE). In isolated mitochondria of WT cells, PDGF induced phosphorylation of MCU, which was abrogated with mtCaMKIIN expression at baseline and after PDGF (Figure 1D). Taken together with the data demonstrating that MCU is necessary for mtCaMKII activation, our findings support a feed-forward circuit by which mitochondrial Ca²⁺ uptake via MCU activates mtCaMKII that phosphorylates MCU at S92 and further augments mitochondrial Ca²⁺ influx.

Therefore, we sought to confirm that mtCaMKII inhibition decreases mitochondrial Ca^{2+} uptake using the ratiometric mitochondria-targeted Ca^{2+} indicator protein Pericam (mtPericam)³³. PDGF induced mitochondrial Ca^{2+} uptake, and mtCaMKIIN significantly blunted the increase in Ca^{2+} after PDGF treatment (Figure 1E). Moreover, the peak amplitude of the Ca^{2+} signal and the area under the curve were reduced (AUC, Figure 1E). Accordingly, we observed significantly lower mitochondrial Ca^{2+} levels in VSMC with mtCaMKIIN expression compared to control-infected cells based on Ca^{2+} complex formation with O-Cresolphthalein (Figure 1F). To further interrogate the regulatory circuit between mtCaMKII and MCU, we measured mitochondrial Ca^{2+} uptake in MCU^{-/-} VSMC. Overexpression of mitochondria-targeted CaMKII in WT VSMC was sufficient to augment PDGF-induced mitochondrial matrix Ca^{2+} uptake (Figure 1G, Supplemental Figure IF). MCU was necessary for the effect since the Ca^{2+} influx was completely abrogated in MCU^{-/-} VSMC with mtCaMKII overexpression (Figure 1G). These data further support the presence of a feed-forward mtCaMKII and MCU.

To determine whether other agonists that also increase cytoplasmic Ca^{2+} levels have an effect on CaMKII activation in mitochondria, we confirmed our findings using histamine stimulation. Specifically, histamine promoted CaMKII phosphorylation in mitoplasts (Supplemental Figure IG), and treatment with mtCaMKIIN blunted mitochondrial Ca^{2+} uptake (Supplemental Figure IH). These data support that mitochondrial CaMKII activation is a general mechanism in mitochondrial Ca^{2+} uptake.

Inhibition of mitochondrial Ca^{2+} uptake prevents VSMC migration

We next tested whether inhibition of mitochondrial CaMKII is sufficient to alter VSMC phenotypes. mtCaMKIIN had no significant effect on cell counts following agonist stimulation (Supplemental Figure IIA), where as VSMC migration was profoundly inhibited by mtCaMKIIN in Boyden chamber migration (Figure 2A) or wounding assays (Figure 2B). These findings were confirmed using siRNA-mediated MCU silencing (Supplemental Figure IIB, C).

To overcome the limitations of conventional migration assays, we developed a novel high-throughput scratch wound migration assay with semi-automated data analysis (Supplemental Figure IIIA). mtCaMKIIN blocked PDGF-induced VSMC migration in a dose-dependent manner at 24 hours after scratch wound in the presence of a proliferation inhibitor (Figure 2C, D). Of note, mtCaMKII overexpression in WT VSMC moderately increased VSMC migration (Figure 2E).

As anticipated, PDGF-induced migration of VSMC from MCU^{-/-} mice was significantly impaired using the high throughput scratch wound migration assay (Figure 2F). Expression of mtCaMKIIN or mtCaMKII in MCU^{-/-} VSMC had no significant additional effect on VSMC migration (Figure 2F). As a separate strategy for MCU inhibition, we examined increasing concentrations of the MCU inhibitor Ru360. As expected, we observed a dose-response to Ru360 (Supplemental Figure IIIB). Under mtCaMKII overexpression, higher doses of Ru360 were required to delay wound closure. These data support that mitochondrial Ca^{2+} uptake via MCU is necessary for the action of mitochondrial CaMKII on VSMC migration.

In addition to mitochondrial Ca^{2+} uptake, both mitochondrial metabolism and mitochondrial ROS production have been implicated in cell migration. We measured oxygen consumption (OCR), an indicator of mitochondrial respiration, following PDGF treatment and did not observe appreciable differences with expression of mtCaMKIIN (Supplemental Figure IVA). Next, we tested the effect of mtCaMKII inhibition or overexpression on mitochondrial ROS generation. As anticipated, mtCaMKII promoted while mtCaMKIIN abolished PDGF-induced mitochondrial ROS production (Supplemental Figure IVB, C). Treatment with the mitochondrial ROS scavenger mitoTEMPO attenuated migration in mtCaMKII-expressing VSMC, but did not alter migration in cells expressing mtCaMKIIN (Supplemental Figure IVD). These data are consistent with the concept of mitochondrial Ca^{2+} uptake via mtCaMKII as an upstream regulator of mitochondrial ROS production.

Mitochondrial CaMKII inhibition blocks mitochondrial translocation towards the leading edge

Studies in non-vascular cells demonstrate that mitochondrial translocation to the leading edge is required for cell migration^{7,9,10}. In growth-arrested VSMC, mitochondria were predominantly localized in the perinuclear area (Figure 3A). PDGF treatment of WT VSMC for 6–12 hr after scratch wound induced mitochondrial translocation to the anterior edge (Figure 3A, B, Supplemental Figure V), providing evidence that mitochondrial mobility occurs in migrating VSMC. In contrast, mtCaMKIIN significantly inhibited the PDGF-induced mitochondrial redistribution at 6–24 hr (Figure 3C). This effect was phenocopied in $\text{MCU}^{-/-}$ VSMC or by Ru360 (Figure 3C). While we found that mtCaMKIIN reduced mitochondrial ROS production, treatment of WT VSMC with mitoTEMPO had no effect on redistribution of mitochondria to the leading edge (Figure 3C). We also tested whether acute MCU inhibition with Ru360 could arrest translocating mitochondria in migrating WT VSMC. Indeed, when Ru360 was added at 6 hr after initiation of migration with PDGF, further mitochondrial redistribution was prevented (Supplemental Figure VI). Together, these data suggest that inhibition of mitochondrial Ca^{2+} uptake arrests mitochondrial translocation.

To provide direct experimental evidence that mitochondrial translocation is Ca^{2+} -dependent, we expressed WT MCU and the MCU S92A mutant with decreased mitochondrial Ca^{2+} influx in $\text{MCU}^{-/-}$ VSMC. Whereas WT MCU recovered VSMC migration and mitochondrial translocation to the leading edge, MCU mutant S92A did not, confirming that mitochondrial mobility depends on mitochondrial matrix Ca^{2+} uptake (Figure 3D, E).

Miro-1 is required for mtCaMKII-mediated active mitochondrial translocation in VSMC

Mitochondria rely on intact cytoskeletal proteins to efficiently traffic throughout the cell. We tested whether mitochondrial mobility in migrating cells is an active process or whether it passively follows cell movement. We treated cells with either a microtubule or an actin inhibitor, both of which arrest cell migration^{34,35}. Only the microtubule inhibitor, nocodazole, prevented mitochondrial mobility to the leading edge (Figure 4A), suggesting that mitochondrial translocation in migrating cells is an active process that is selectively regulated by microtubule dynamics. In addition, PDGF treatment of contact-inhibited, confluent VSMC promoted redistribution of mitochondria away from the nucleus to the cell

periphery (Supplemental Figure VII A), further substantiating that mitochondrial mobility is not a passive event.

Precedence for active mitochondrial motility comes from studies in neurons that identified the outer mitochondrial membrane GTPase Miro-1 as a coordinator of mitochondrial translocation along microtubules³⁶. Upon Ca^{2+} binding to the two EF hands of Miro-1, mitochondria and microtubules dissociate, which induces mitochondrial arrest. Thus, we isolated aortic VSMC from Miro-1^{fl/fl} mice and induced Miro-1 deletion by cre recombination (Miro-1^{-/-}, Figure 4B). In Miro-1^{-/-} VSMC, we detected mitochondrial arrest and strongly impaired VSMC migration in the presence of PDGF (Figure 4C–E). Overexpression of mtCaMKII or mtCaMKIIN had no effect on mitochondrial translocation or VSMC migration in Miro-1^{-/-} VSMC. Similar results were obtained by overexpressing wild-type MCU or a dominant negative mutant that decreases the Ca^{2+} influx³⁷ in Miro-1^{-/-} VSMC (Supplemental Figure VII B, D). These data demonstrate that in VSMC, Miro-1 is necessary for migration and mitochondrial translocation to the leading edge.

Mitochondrial mobility is abrogated by increases in local ‘peri-mitochondrial’ Ca^{2+} levels³⁶. Since we observed a significant reduction in mitochondrial Ca^{2+} uptake with MCU or mtCaMKII inhibition, we examined their impact on cytosolic Ca^{2+} transients using the ratiometric indicator Fura-2AM. Expression of mtCaMKIIN did not alter baseline cytosolic Ca^{2+} levels (data not shown). Whereas total cytosolic Ca^{2+} levels were transiently increased in control-infected cells following PDGF treatment, the decay of the cytosolic Ca^{2+} signal was significantly prolonged under mtCaMKII inhibition, as evidenced by greater tau (τ), residual amplitude, and AUC (Figure 4F). Together with the data in Figure 1, these findings suggest that mtCaMKII inhibition prevents mitochondrial matrix Ca^{2+} uptake and thereby prolongs the PDGF-induced transient increases in total cytosolic Ca^{2+} . We posit that the perturbed cytosolic Ca^{2+} transients by mtCaMKII inhibition disrupt Miro-1-dependent mitochondrial translocation towards the leading edge and arrest migration of VSMC.

Since VSMC with small, fragmented mitochondria are reported to have a higher propensity to migrate⁴, we assessed mitochondrial morphology³⁸. In accordance with published evidence³⁹, PDGF induced mitochondrial fission in control-infected VSMC (Supplemental Figure VIII). With mtCaMKII inhibition, mitochondria were fragmented at baseline without further change in morphology with PDGF.

Mitochondrial CaMKII-dependent mitochondrial translocation is necessary for focal adhesion dynamics

Mitochondria provide the energy source for dynamic focal adhesion (FA) turnover at the leading edge, which is necessary for cell migration^{10,40}. Since mtCaMKIIN prevented mitochondrial translocation to the leading edge, we next interrogated the effect of mtCaMKII inhibition on FA dynamics. We first assessed FA turnover by time-lapse imaging after scratch wounding and PDGF treatment. Here, mtCaMKIIN prevented the dynamic changes in FA redistribution observed in control-infected VSMC after 90 min (Figure 5A). We also assessed FA size as a surrogate for FA turnover since FA size predicts cell migration⁴¹. In migrating VSMC, FA size was decreased after PDGF treatment (Figure 5B).

Conversely, mtCaMKIIN-expressing VSMC exhibited large, stable FA, suggesting that mtCaMKII inhibition promotes static FA associated with reduced cell migration.

In addition, we analyzed phosphorylation of focal adhesion kinase (FAK) at Y577 as a marker for FA activity⁴². As compared to control-infected cells, the phosphorylation was reduced in VSMC expressing mtCaMKIIN (Figure 5C). MLC inserts at the vicinity of FA and is phosphorylated to coordinate forward migration forces⁴³. Accordingly, colocalization of pMLC to FA was reduced in VSMC expressing mtCaMKIIN compared to controls (Supplemental Figure IX). These data suggest that, under mtCaMKII inhibition, reduced localization of mitochondria to the leading edge depletes the energy source necessary for dynamic FA turnover.

Mitochondrial CaMKII inhibition ameliorates neointimal hyperplasia in an in vivo model of endothelial injury

To test whether mtCaMKII inhibition reduces neointimal hyperplasia in vivo, we engineered a novel transgenic mouse model with inducible, smooth muscle-specific mtCaMKIIN expression (termed “SM-mtCaMKIIN” mice, Supplemental Figure XA). We confirmed robust transgene expression by qrtPCR and immunofluorescent staining of mtCaMKIIN in the carotid media after tamoxifen-induced cre activation (Supplemental Figure XB, Figure 6A). Immunoblots of cytosolic and mitochondrial fractions confirmed the presence of the transgene predominantly in mitochondria (Figure 6B). Functional mtCaMKII inhibition was confirmed by a decrease in mitochondrial Ca²⁺ concentration (Figure 6C).

Next, we performed vascular injury by endothelial denudation of the left common carotid artery. On day 28 after endothelial injury, the neointimal area in SM-mtCaMKIIN mice was significantly reduced compared to littermate controls (Figure 6D, Supplemental Figure XE). In uninjured right carotid arteries, there was no apparent difference in arterial morphology with mtCaMKIIN expression (Figure 6D).

To examine the translational potential of our findings, we performed co-immunostaining for CaMKII and a mitochondrial marker in human coronary arteries from autopsy samples (Supplemental Figure XF). 3D projections of z-stack images demonstrated colocalization of mitochondria and CaMKII in the intima. Most CaMKII-positive cells in areas of subintimal thickening also expressed smooth muscle actin.

Discussion

The goal of this study was to identify key regulators of mitochondrial function that contribute to VSMC migration and neointimal hyperplasia. First, we demonstrate that CaMKII resides in mitoplasts of VSMC and was activated by PDGF. Activation of CaMKII in mitochondria was abrogated when MCU was deleted. Inhibition of mtCaMKII lowered the phosphorylation of MCU at S92, a site that is crucial for mitochondrial Ca²⁺ uptake by MCU activity. MtCaMKII inhibition blocked mitochondrial translocation to the leading edge and VSMC migration. These effects were recapitulated by deletion of MCU. Overexpression of WT MCU but not of the MCU mutant S92A in MCU^{-/-} VSMC recovered mitochondrial translocation and migration, suggesting that the effects of MCU or mtCaMKII on these

phenotypes are caused by altered mitochondrial Ca^{2+} uptake. Ca^{2+} -dependent mitochondrial mobility is coordinated by Miro-1, an outer mitochondrial membrane GTPase. In agreement, in Miro-1^{-/-} VSMC, mitochondrial mobility and migration were abolished, establishing Miro-1 as a key regulator of mitochondrial function in VSMC. mtCaMKII overexpression or inhibition did not have any effect in Miro-1^{-/-} VSMC, suggesting that Miro-1 mediates the effect of mtCaMKII on mitochondrial mobility and migration. Consistent with the notion that increased Ca^{2+} levels arrest mitochondria, Ca^{2+} clearance from the cytosol was delayed with mtCaMKII inhibition. Moreover, mtCaMKII inhibition led to impaired FA turnover and phosphorylation of cytoskeletal proteins necessary for coordinated anterior cell movement. In agreement with in vitro findings, transgenic CaMKII inhibition selectively in mitochondria of VSMC significantly reduced neointimal hyperplasia after endothelial vascular injury. Together these data provide key mechanistic insight into how mitochondrial function regulates VSMC migration and neointimal hyperplasia: mtCaMKII controls mitochondrial Ca^{2+} uptake through activation of MCU and is necessary for mitochondrial translocation to the leading edge of migrating VSMC where mitochondria support FA and cytoskeletal remodeling (Figure 6E).

Several other studies support that mitochondrial Ca^{2+} uptake regulates cell migration¹⁷. For example, MCU inhibition or knockdown halts cell migration of cancer cells, whereas increased expression of MCU correlates with an invasive phenotype¹⁶. Our data in VSMC are in line with these observations and provide further insight into how regulation of mitochondrial Ca^{2+} uptake is regulated and affects VSMC migration. CaMKII has been detected in the mitochondrial matrix of cardiac myocytes and reported to blunt mitochondrial matrix Ca^{2+} uptake²⁰. Here, we provide further mechanistic evidence for the actions of mtCaMKII in mitochondria; phosphorylation of MCU at S92, a validated strong regulatory site for MCU activity¹⁵, was reduced when mtCaMKII activity is inhibited. CaMKII activation requires an initial binding of calcified calmodulin that is abundant in the mitochondrial matrix⁴⁴. Accordingly, mtCaMKII activation was abrogated when MCU was deleted or inhibited. Moreover, mtCaMKII inhibition prevented further mitochondrial Ca^{2+} uptake, suggesting a feed forward circuit in which initial mitochondrial Ca^{2+} influx via MCU is required for mtCaMKII activation, which in turn controls MCU activity via phosphorylation at S92. mtCaMKII thereby drives further mitochondrial Ca^{2+} uptake. Alternatively, mtCaMKII may regulate Ca^{2+} uptake via phosphorylation of other sites on MCU, such as S57 as proposed by a recent study, phosphorylation of MCU regulators MICU or EMRE^{14,45}, or potentially by activating Ca^{2+} influx via another Ca^{2+} channel, such as the mitochondrial RyR receptor⁴⁶.

Previous studies reported that dynamic mitochondrial fission and fusion are required for VSMC migration. In particular, migration was abolished when a dominant negative mutant of Drp-1, a master regulator of mitochondrial fission, was expressed in VSMC. Based on this study and other reports, it has been proposed that VSMC with small, fragmented mitochondria have a higher propensity to migrate⁴. However, with mtCaMKII inhibition, mitochondria were fragmented at baseline without further change in morphology with PDGF, implying that mitochondrial size is not a major determinant of mobility when mitochondrial Ca^{2+} uptake is altered. Our study provides novel mechanistic insight by defining mitochondrial mobility as a function of Ca^{2+} levels and a prerequisite for VSMC

migration and likely neointimal hyperplasia. Mitochondrial mobility is arrested in microdomains of high Ca²⁺ concentrations, as may occur in the vicinity of mitochondrial/ER convergence zones when the mitochondrial Ca²⁺ uptake is impaired with MCU or mtCaMKII inhibition. In subcellular domains of high Ca²⁺ concentrations in neurons^{19,36}, Ca²⁺ binding to the EF hands of the Rho-GTPase Miro-1 induces the dissociation of mitochondria from microtubules, followed by mitochondrial arrest. Our findings are in agreement with these data and demonstrate that mitochondrial translocation in VSMC is an active process and controlled by Miro-1. Alternatively, tethering of mitochondria to actin filaments via myosin V, which is induced by locally increased Ca²⁺ levels, has been implicated to halt mobile mitochondria⁴⁷. However, our data do not support this mechanism since we detected mitochondrial redistribution to the leading edge despite disruption of the actin cytoskeleton. Once at the leading edge, mitochondria cluster in the vicinity of FA, in order to meet the significant energy demands for FA turnover and cytoskeletal remodeling in migrating cells^{7,10,11,40}. Consistent with this mechanism, we detected reduced FA activity under mtCaMKII inhibition.

CaMKII is well accepted to be present and active in the cytosol and nucleus where it fulfills distinct roles in the regulation of transcriptional events^{48,49} substrate phosphorylation of a wide array of signaling mediators⁵⁰. Different approaches to “globally” block intracellular CaMKII activity have revealed its regulatory function in cell migration. Using a mitochondria-targeted CaMKII inhibitory peptide, we discovered that the effects of CaMKII on migration are due, at least in part, to its actions in mitochondria. Previous data suggest that the spatial and functional specificity in CaMKII activation is elicited by mobilization of different Ca²⁺ stores⁵⁰. Thus, inhibiting mtCaMKII activity may be sufficient to block cell migration regardless of its actions in other cellular compartments. The CaMKII isoform(s) that are present or predominant in mitochondria are currently unknown. However, our approach of overexpressing an inhibitor that blocks all isoforms overcomes this obstacle.

Mitochondria-derived ROS promotes VSMC migration⁴. Here, we found that mtCaMKII inhibition diminished mitochondrial ROS production, in line with previous data for MCU⁵¹. Mitochondrial Ca²⁺ uptake is a prerequisite for ROS production in mitochondria, for example by increasing Krebs cycle activity and substrate delivery to the electron transport chain¹². Therefore, we consider mtCaMKII as a regulator of these upstream metabolic events leading to mitochondrial ROS production. Mitochondrial translocation to the leading edge was not altered in VSMC pretreated with a mitochondrial ROS scavenger, suggesting that mitochondrial ROS production in itself promotes migration through additional pathways, likely related to redox signaling⁵².

Together, this study identifies mtCaMKII as an important regulator of MCU and mitochondrial Ca²⁺ uptake and provides evidence that mitochondrial Ca²⁺ uptake promotes VSMC migration via control of mitochondrial mobility. The data presented here also synthesize several disparate concepts introduced in the literature. First, mitochondrial Ca²⁺ uptake determines cytosolic Ca²⁺ transients^{53,54}, high cytosolic Ca²⁺ arrests mitochondrial mobility³⁶, which in turn determines cell migration¹⁰. Moreover, our results link mtCaMKII and mitochondrial Ca²⁺ uptake with a recent report demonstrating that mitochondria colocalize to focal adhesions to maintain the subcellular energy demands of structural

remodeling in cell migration⁴⁰. Future work focusing on regulators of mitochondrial mobility may reveal novel therapeutic options to mitigate neointimal hyperplasia after vascular injury.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

The authors thank Dr. Kris DeMali (University of Iowa) for the kind gift of the GFP-Vinculin plasmid and Dr. Janet Shaw (University Utah and HHMI) for Miro-1^{fl/fl} mice.

Sources of Funding: The project was supported by grants from the NIH (R01 HL 108932 to IMG); the Veterans Affairs Iowa City (I01 BX000163 to IMG), the American Heart Association (14SDG18850071 to WHT, 17GRNT33660032 to IMG) and from the NIH NHLBI (F30 HL131078-01, T32 GM007337 to EKN).

ABBREVIATIONS

DN-MCU	Dominant Negative Mitochondrial Calcium Uniporter
FA	Focal Adhesion
PDGF	Platelet Derived Growth Factor
FAK	Focal Adhesion Kinase
MCU	Mitochondrial Calcium Uniporter
Miro-1	Rho-GTPase responsible for mitochondrial mobility
mitoTEMPO	mitochondrial reactive oxygen species scavenger
MLC	Myosin Light Chain
mtCaMKII	Ca ²⁺ /Calmodulin-dependent Kinase II in mitoplast
mtCaMKIIN	mitochondrially targeted peptide inhibitor of CaMKII
mtROS	mitochondrial reactive oxygen species
Ru360	pharmacologic inhibitor of MCU
VSMC	vascular smooth muscle cell

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HIGHLIGHTS

- Mitochondrial CaMKII is present in mitoplasts of VSMC and activated by PDGF in a mechanism that is dependent upon the mitochondrial Ca²⁺ uniporter.
- Inhibition of mitochondrial CaMKII or of the mitochondrial Ca²⁺ uniporter decreases VSMC migration by blocking mitochondrial matrix Ca²⁺ uptake.
- Inhibition of mitochondrial CaMKII prevents mitochondrial translocation to the leading edge of migrating cells, leading to decreased focal adhesion signaling and turnover.
- Selective inhibition of mitochondrial CaMKII in smooth muscle in mice reduces neointimal hyperplasia after vascular injury.

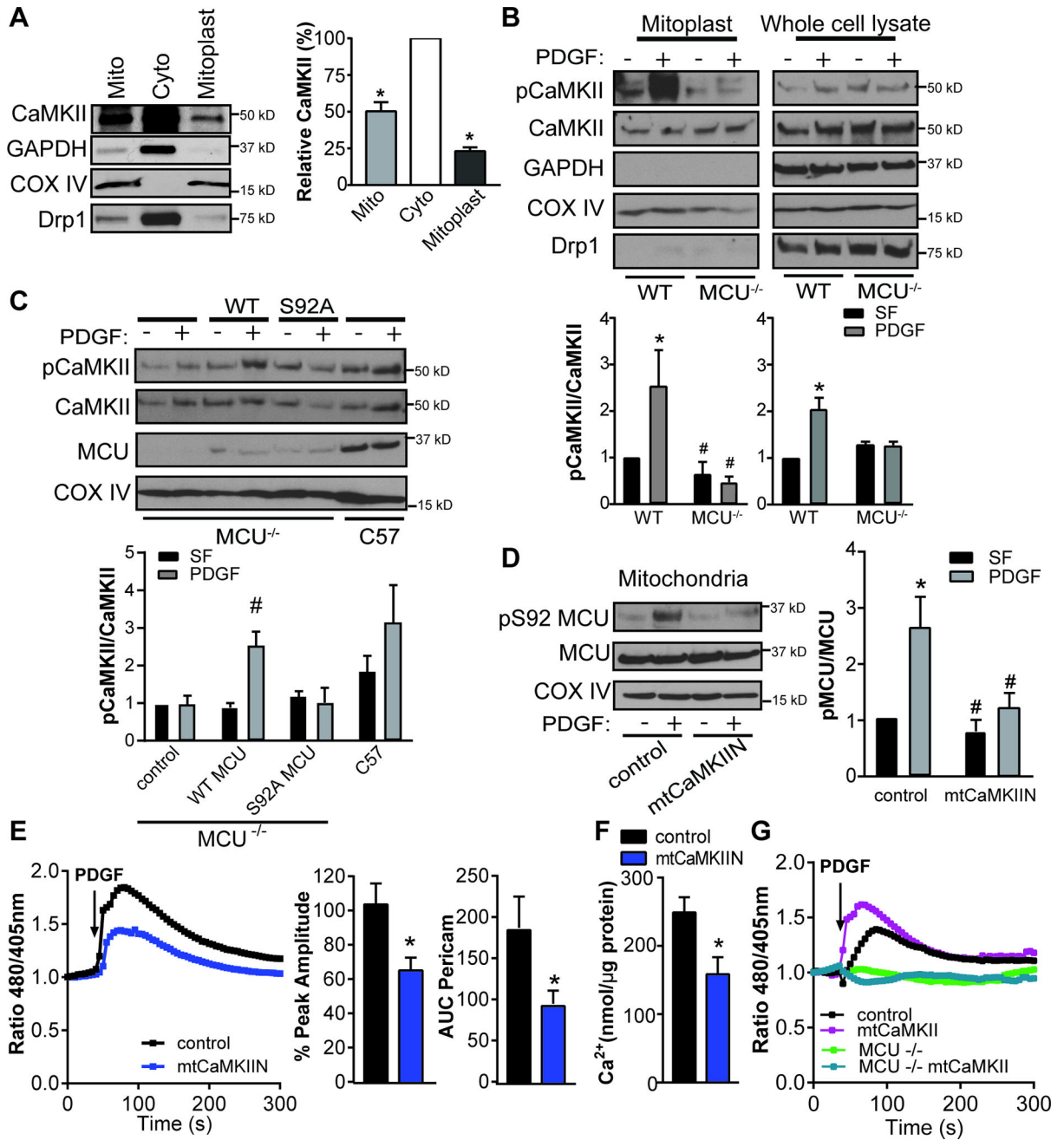


Figure 1. Mitochondrial CaMKII regulates a feed forward circuit promoting mitochondrial Ca²⁺ uptake

A) Representative immunoblot and summary data for CaMKII in mitochondrial (mito) and cytosolic (cyto) fractions and mitoplasts from VSMC. Mitoplasts (inner mitochondrial membrane and matrix) were generated by digestion of mitochondrial fractions with Proteinase K. GAPDH: cytosolic marker; Cox IV: marker of inner mitochondrial membrane; Drp1: marker of outer mitochondrial membrane. Data quantified as intensity of CaMKII to total amount of protein by BCA protein assay (n=4 independent experiments), *p<0.05 versus cytosolic fraction by Kruskal-Wallis. B) Immunoblot for active (phosphorylated, pCaMKII) and total CaMKII in whole cell lysate and mitoplast fractions of VSMC from

MCU^{-/-} or WT mice before or after treatment with PDGF (20 ng/mL) for 15 min after serum starvation (SF). (n=5 independent experiments). C) Immunoblot for pCaMKII in mitoplast fractions of MCU^{-/-} VSMC after transfection of WT MCU or MCU mutant Ser92 to Ala (S92A) or control and in mitoplasts of WT VSMC; treated as in (B). (n=5 independent experiments). D) Active (phosphorylated, pMCU, at S92) and total MCU in mitochondrial fractions from VSMC expressing mtCaMKIIN or control. COX IV: loading control. (n=5 independent experiments). For B-D, *p<0.05 versus control SF, #p<0.05 versus control PDGF by 2-way ANOVA. E) Representative mtPericam tracing in VSMC expressing mtCaMKIIN or control for 48 hr; arrow indicates addition of PDGF (20 ng/mL). Peak amplitude of mtPericam response normalized to peak amplitude in control cells and area under the curve (AUC) of mtPericam signal in 15 cells per condition (n=3 independent experiments). F) Ca²⁺ concentration by o-cresolphthalein assay in mitochondria isolated from VSMC expressing mtCaMKIIN or control for 48 hr; data were normalized to total mitochondrial protein content (n=5). G) Representative mtPericam tracing in WT or MCU^{-/-} VSMC expressing mtCaMKII or control for 48 hr with addition of PDGF, *p<0.05 versus control by Student's t-test.

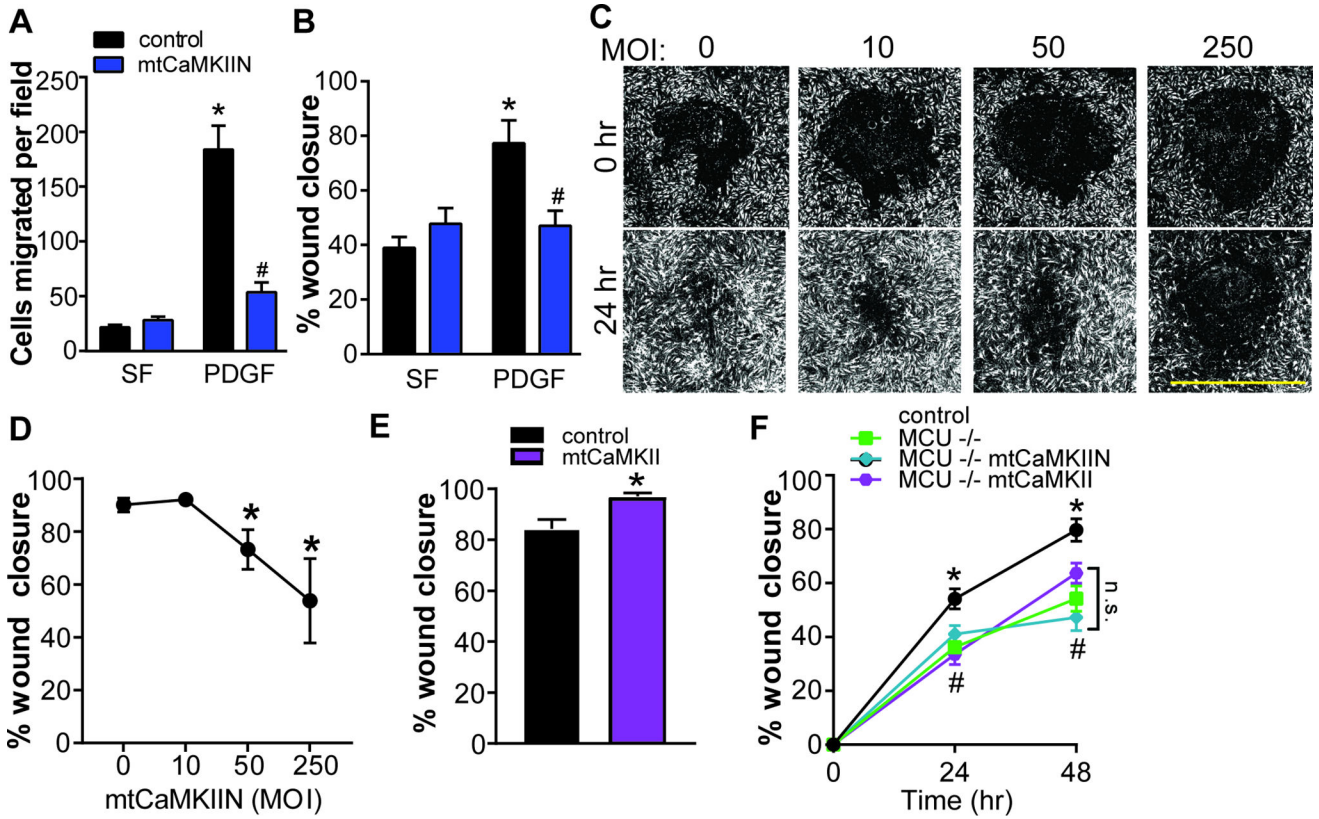


Figure 2. Mitochondrial CaMKII inhibition blocks VSMC migration

A) Boyden chamber migration assay in VSMC expressing mtCaMKIIN (MOI 50) or control in SF media or after treatment with PDGF (20 ng/mL) for 6 hr (n=5 independent experiments). B) Scratch wound assay in VSMC expressing mtCaMKIIN or control in SF media or after treatment with PDGF (20 ng/mL); data quantified as percent wound closure at 24 hr compared to 0 hr (n=5 independent experiments). C) Representative DPC images from high throughput scratch wound assay. WT VSMC were exposed to increasing MOIs of Ad-mtCaMKIIN; D) Migration in C quantified as percent wound closure at 24 hr compared to 0 hr; *p<0.05 versus MOI of 0 by 1-way ANOVA. E) Scratch wound assay in VSMC expressing mtCaMKII or control after treatment with PDGF; data quantified as percent wound closure at 24 hr as compared to 0 hr. *p<0.05 by Student's T-test. F) High throughput scratch wound assay in MCU^{-/-} or WT VSMC with expression of mtCaMKIIN or mtCaMKII after treatment with PDGF. High throughput experiments were conducted in quadruplicate, with biological replicates of three independent experiments. For A, B, and F, *p<0.05 versus control in SF, #p<0.05 versus PDGF-treated control by 2-way ANOVA.

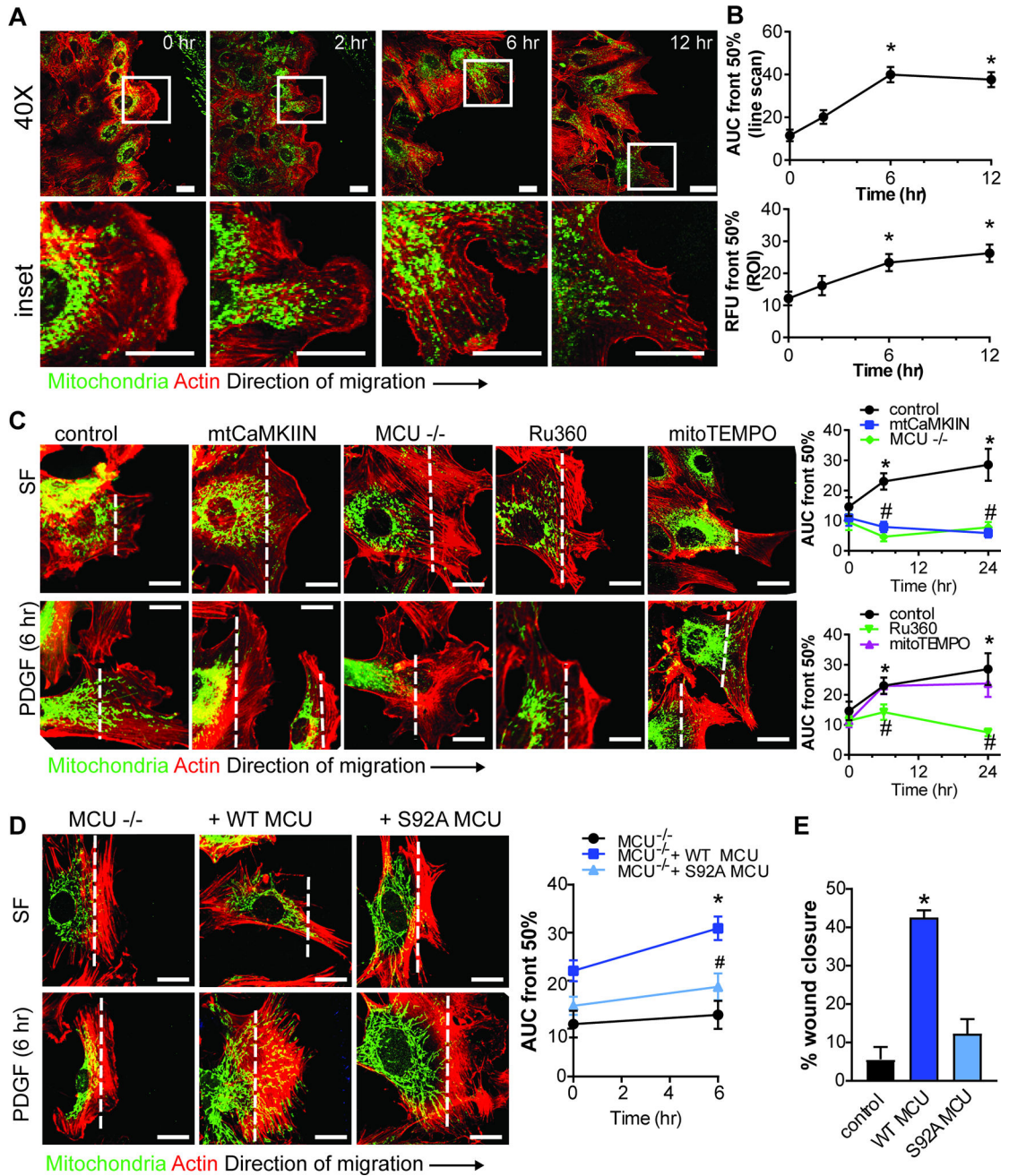


Figure 3. Mitochondrial CaMKII inhibition blocks translocation of mitochondria to the leading edge of migrating VSMC

A) Representative images of mitochondrial localization after scratch wound and PDGF treatment (20 ng/mL) at indicated time points; green: Ad-mtGFP; red: phalloidin-568. B) Quantification of mitochondrial distribution by line scan analysis in the leading to anterior cell areas and quantification of mitochondrial distribution expressed as percent mtGFP signal in the leading cell area (region of interest/ROI) relative to total mtGFP signal per cell (see details in methods and Supplemental Figure 5D); * $p < 0.05$ versus control at 0 hr by 1-way ANOVA. C) Representative images of mitochondrial localization in migrating VSMC before and after PDGF treatment. Studies were performed in WT VSMC expressing

mtCaMKIIN or control, MCU^{-/-} VSMC, or WT VSMC treated with Ru360 (1 μ M) or mitoTEMPO (10 μ M). Mitochondrial distribution was quantified by line scan analysis. D) Representative images of mitochondrial localization in migrating MCU^{-/-} VSMC transfected with control plasmid, WT MCU, or S92A MCU, before and after PDGF. Mitochondrial distribution was quantified by line scan analysis in the leading to anterior cell areas and expressed as percent mtGFP signal in the leading cell. Analyses were performed on 50 cells per condition (n=3 independent experiments). For C and D, *p<0.05 versus control at 0 hr, #p<0.05 versus control at the same time point by 2-way ANOVA. Scale bar= 10 μ m. E) Scratch wound assay in cells from D; data quantified as percent wound closure at 6 hr after scratch as compared to 0 hr (n=3 independent experiments). *p<0.05 versus control by 1-way ANOVA.

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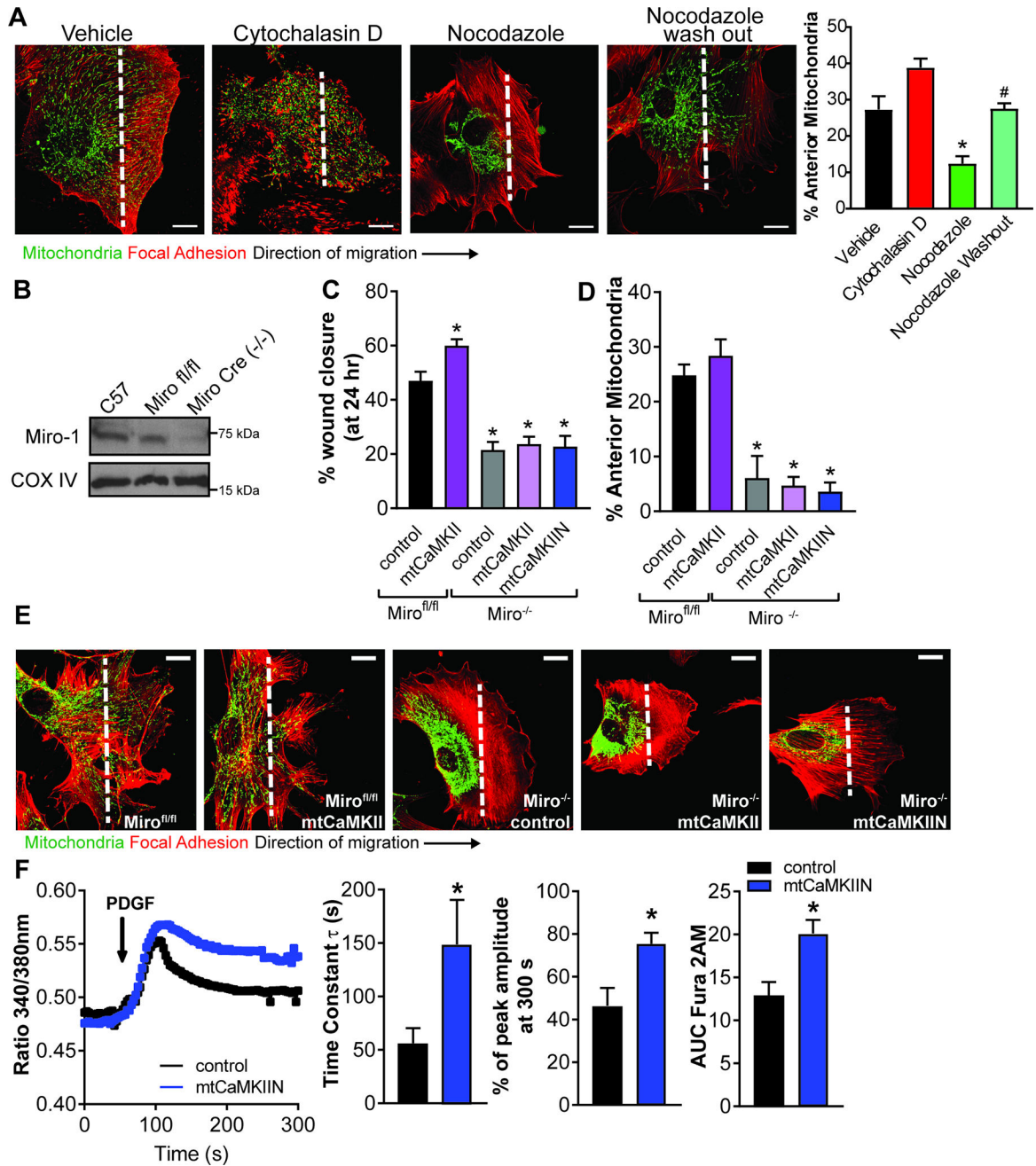


Figure 4. mtCaMKII regulation of VSMC migration and mitochondrial mobility is dependent on the Ca²⁺-sensitive Miro-1

A) Representative images of mitochondrial localization in migrating VSMC treated for 6 hr with PDGF and either actin inhibitor Cytochalasin D (0.1nM) or microtubule inhibitor Nocodazole (1 μ M) or Nocodazole washed out 1 hr before fixation. Quantification of mitochondrial distribution expressed as percent mtGFP signal in the leading cell area by line scan. * p<0.05 vs vehicle, # p<0.05 vs Nocodazole by 1-way ANOVA. (20 cells over 3 independent experiments) B) Representative immunoblot of Miro-1 expression in Miro^{fl/fl} VSMC with and without Ad5-Cre infection (MOI 10). C) VSMC migration by traditional scratch wound assay in Miro^{fl/fl} or Cre-infected Miro^{fl/fl} (Miro^{-/-}) VSMC co-expressing

mtCaMKII or mtCaMKIIN. Data quantified as percent wound closure at 24 hr as compared to 0 hr, (n = 3 independent experiments). D) Quantification of mitochondrial distribution by line scan analysis in the leading to anterior cell areas expressed as percent mtGFP signal in the leading cell (30 cells over 3 independent experiments). E) Representative images of mitochondrial localization after scratch wound and PDGF treatment (20 ng/mL) at 24 hr after scratch. Green: mitochondria, AdmtGFP; red: F-actin, phalloidin-568. For A-D, *p<0.05 versus control Mirofl/fl by 1-way ANOVA. Scale bar = 10 μ m. F) Representative cytosolic Ca²⁺ tracing by Fura-2AM after 20 ng/ml PDGF (arrow) in VSMC expressing control or mtCaMKIIN. Quantification of Fura-2AM signal as time constant of decay (τ , left), residual signal at 300 s after PDGF relative to peak response (middle) and AUC of Fura-2AM signal (right) in 25 cells per condition in 5 independent experiments. *p<0.05 versus control by Student's T-test.

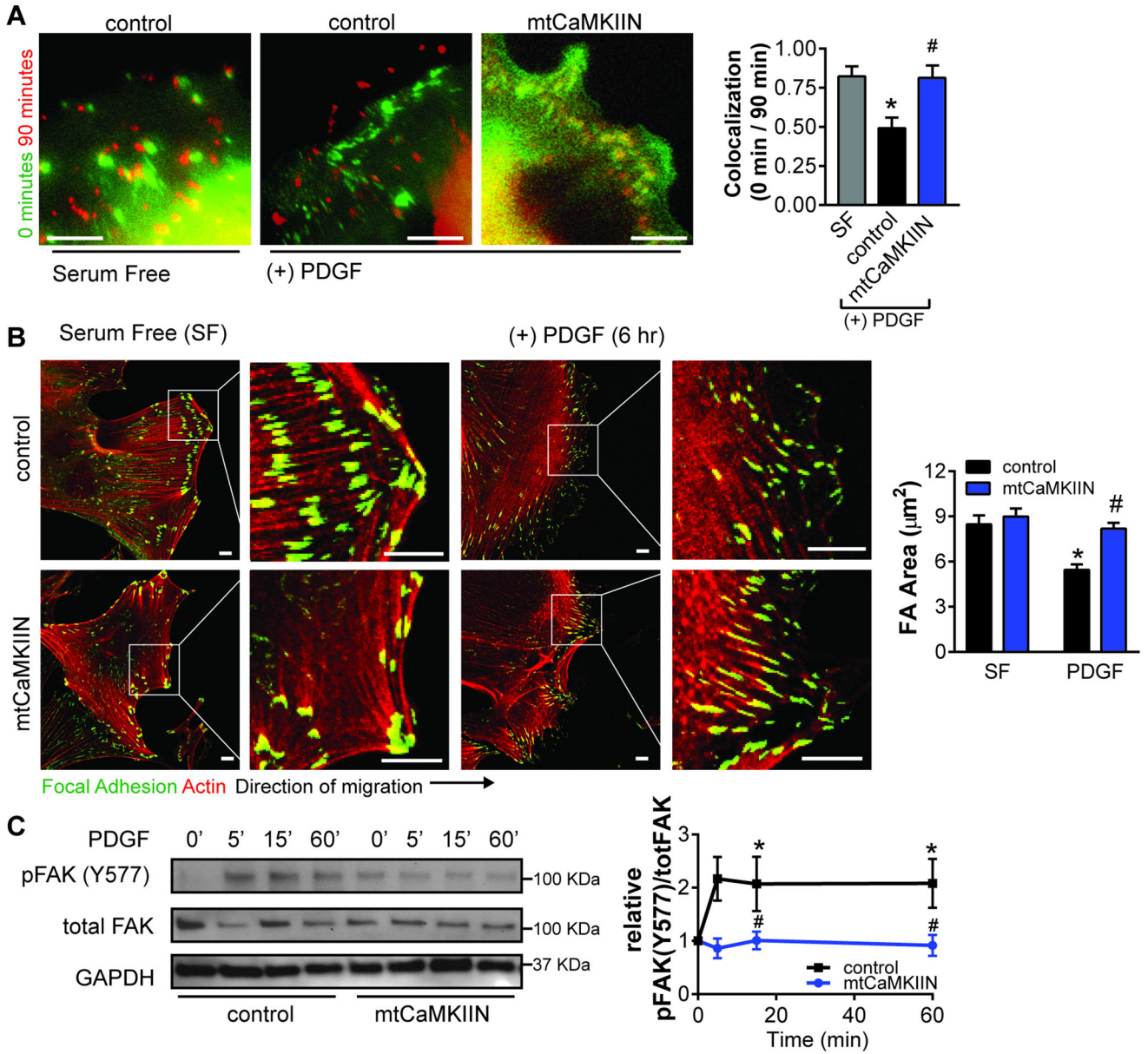


Figure 5. Mitochondrial CaMKII inhibition alters focal adhesions dynamics

A) Immunofluorescent overlaid time-lapse images of FA (GFP-Vinculin) at 0 (green) and 90 (red) min in VSMC expressing mtCaMKIIN or control, and in the presence of 20 ng/mL PDGF. FA colocalization at 0 and 90 min was quantified in 15 cells using CellProfiler software, * $p < 0.05$ vs SF, # $p < 0.05$ vs control PDGF by 1-way ANOVA. B) Representative images of focal adhesion (FA) at wound edge in VSMC expressing mtCaMKIIN or control at 0 or 6 hr after PDGF treatment in SF media with quantification of average focal adhesion size (red: phalloidin, actin; green: vinculin, FA marker). C) Immunoblots for phosphorylated (pFAK Y577) and total FAK in whole cell lysates from VSMC expressing mtCaMKIIN and treated with PDGF (20 ng/ml) for 0–60 min. Data were quantified as phosphorylated FAK (pFAK Y577) relative to total FAK, normalized to respective baseline at 0 min. GAPDH:

loading control (n=4 independent experiments). For B and C, *p<0.05 versus control SF, #p<0.05 versus control PDGF by 2-way ANOVA. Scale bar= 10 μ m.

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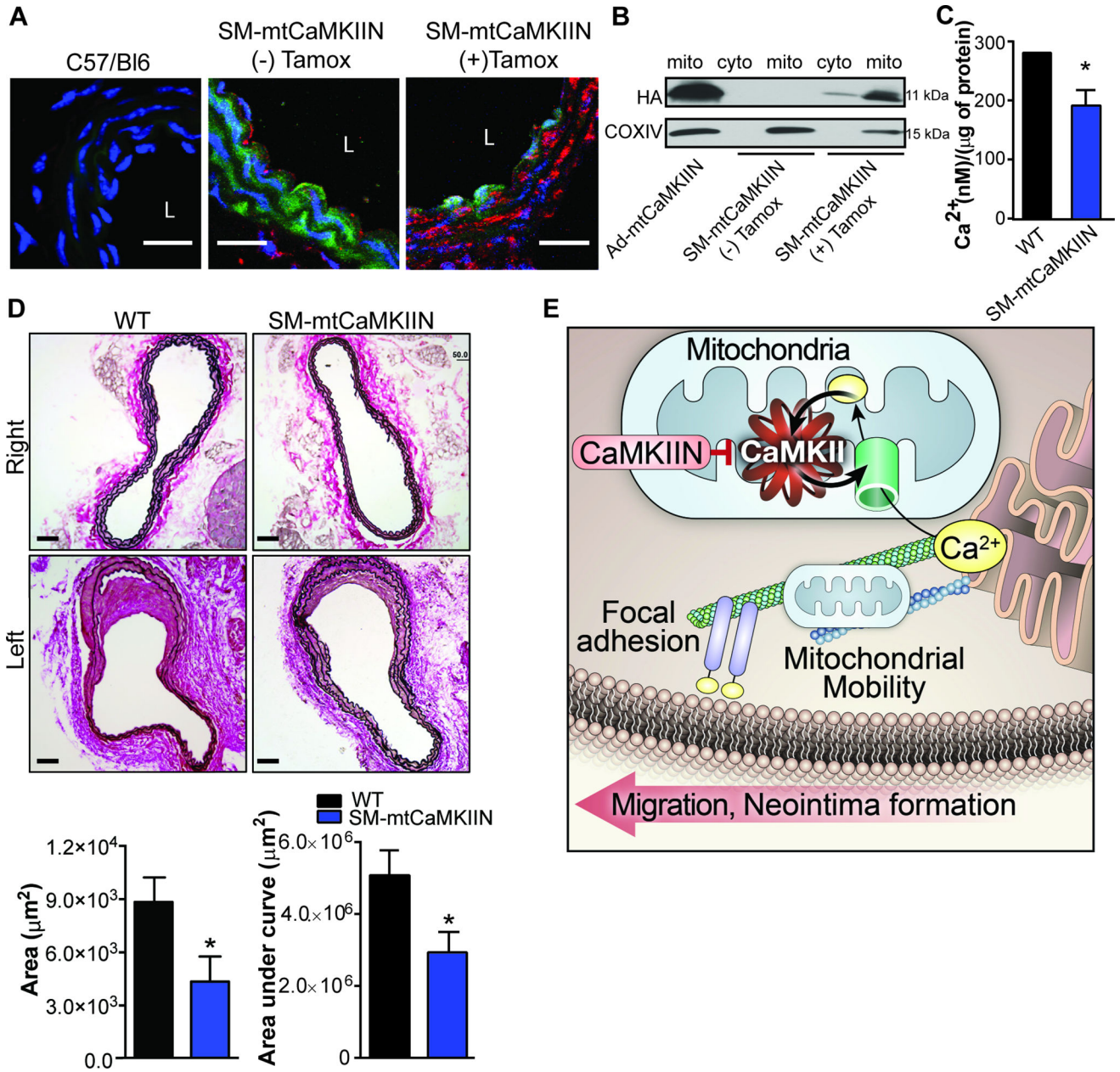


Figure 6. Mitochondrial CaMKII inhibition in vivo blocks neointimal hyperplasia following endothelial injury

A) Representative images of carotid arteries from C57/B16 (WT) and SMmtCaMKIIN mice with and without tamoxifen (Tamox) treatment, which induces cre recombination. Green: ubiquitously expressed GFP; red: mtCaMKIIN; blue: Nuclei. “L” indicates arterial lumen; scale bar= 20 μm. B) Immunoblots for hemagglutinin (HA)-tagged CaMKIIN in mitochondrial or cytosolic fractions isolated from aortas of SM-mtCaMKIIN mice with and without tamoxifen treatment. VSMC infected with Ad-mtCaMKIIN as positive control; Cox IV: mitochondrial marker. C) Ca²⁺ concentration by o-cresolphthalein assay in mitochondria isolated from aortas of SM-mtCaMKIIN or WT littermate controls (SM-Cre mice). Data were normalized to total mitochondrial protein measured by BCA assay (n=5 mice per

genotype). D) Representative images of Verhoeff's Van Gieson staining of left common carotid arteries at 28 days after endothelial injury in WT or SM-mtCaMKIIN mice. Contralateral (right) common carotid artery serves as uninjured control with quantification of neointimal area at 200 μm from the carotid bifurcation and neointimal volume calculated from all neointimal areas within 500 μm from carotid bifurcation; scale bar= 50 μm , n=12 mice per genotype. * $p < 0.05$ versus WT by Student's T-test. E) Graphic representation of the proposed pathway by which mitochondrial CaMKII regulation of mitochondrial Ca^{2+} , mobility, and VSMC migration. mtCaMKII regulates a feed-forward circuit that promotes mitochondrial Ca^{2+} uptake. Inhibition of mtCaMKII leads to decreased mitochondrial Ca^{2+} uptake, leading to decreased Ca^{2+} clearance in the cytosol and mitochondrial arrest. This prevents mitochondria from translocating to focal adhesions, thus inhibiting VSMC migration and neointima formation.