Sphingosine-1-Phosphate Receptor-2 Regulates Expression of Smooth Muscle Alpha-Actin After Arterial Injury

Allison D. Grabski, Takuya Shimizu, Jessie Deou, William M. Mahoney Jr, Michael A. Reidy, Guenter Daum

Objective—This study tests the hypothesis that S1P2R regulates expression of SMC differentiation genes after arterial injury. Methods and Results—Carotid ligation injury was performed in wild-type and S1P2R-null mice. At various time points after injury, expression of multiple SMC differentiation genes, myocardin, and S1P receptors (S1P1R, S1P2R, and S1P3R) was measured by quantitative PCR. These experiments demonstrate that at day 7 after injury, S1P2R specifically regulates expression of smooth muscle α-actin (SMA) and that this is not mediated by changes in expression of myocardin or any of the S1PRs. In vitro studies using carotid SMCs prepared from wild-type and S1P2R-null mice show that S1P stimulates expression of all SMC-differentiation genes tested, but S1P2R significantly regulates expression of SMA and SM22α only. Chromatin immunoprecipitation assays suggest that S1P-induced recruitment of serum response factor to the SMA promoter and enhancer largely depends on S1P2R. S1P-stimulated SMA expression requires S1P2R-dependent activation of RhoA and mobilization of calcium from intracellular stores. Chelation of calcium does not affect the activation of RhoA by S1P, whereas blockade of Rho by C3 exotoxin partially inhibits the mobilization of calcium by S1P.

Conclusions—The results of this study support the hypothesis that S1P2R regulates expression of SMA after injury. We further conclude that transcriptional regulation of SMA by S1P in vitro requires S1P2R-dependent activation of RhoA and mobilization of calcium from intracellular calcium stores. (Arterioscler Thromb Vasc Biol. 2009;29:00-00.)

Key Words: sphingosine-1-phosphate ■ S1P2R ■ smooth muscle actin ■ Rho ■ calcium

Restenosis is a major complication of surgical procedures performed to restore arterial blood flow. Despite all efforts, pharmacological inhibition of restenosis has not yet been achieved. In normal arteries, smooth muscle cells (SMCs) are quiescent and regulate vascular tone. After arterial injury, medial SMCs proliferate and lose expression of genes encoding the contractile apparatus, a process referred to as phenotypic modulation. It is generally believed that decreased expression of these “differentiation genes” is instrumental for the increased proliferative potential of SMCs after injury, although the exact molecular mechanisms remain to be defined. In this study, we test the hypothesis that one of the pathways regulating phenotypic modulation after arterial injury involves the sphingosine-1-phosphate receptor-2 (S1P2R).

The bioactive sphingolipid S1P is best known for its regulation of lymphocyte egress from lymphatic organs and its requirement for vessel formation in development. Both processes are mediated by S1P1R, one of the 5 G protein–coupled receptors that bind S1P. SMCs express 3 S1P receptors (S1P1R, S1P2R and S1P3R). Concomitant pharmacological blockade of S1P1R and S1P3R inhibits neointimal growth in balloon-injured rat carotid arteries, suggesting a lesion-promoting role for S1P. Consistent with this conclusion, increased S1P concentrations in human serum were found to be highly predictive for the onset and progression of coronary artery disease. In contrast, we have recently suggested an inhibitory role for S1P in arterial lesion growth based on our observation that S1P2R-null mice but not their wild-type littermates develop large intimal lesions after carotid injury. In this study, medial proliferation was increased in S1P2R-null arteries compared to wild-type arteries, indicating that S1P2R prevents SMC proliferation. In addition to SMC migration and proliferation, S1P has been shown to induce expression of SMC differentiation genes such as smooth muscle α-actin (SMA), and this effect has been ascribed to activation of Rho. Activation of most promoters of SMC differentiation genes require binding of the transcription factor serum response factor (SRF) in combination with myocardin or a myocardin-related-transcription factor (MRTF) as a cofactor. On activation of Rho and stimulation of actin polymerization, cytosolic MRTF is released from G-actin and translocates into the nucleus. The physiological relevance of this process has been shown in proepicardial cells in which blockade of Rho kinase prevents their differentiation to coronary SMCs. Recently, a role for voltage-gated calcium channels (VGCCs) in the expression of...
SMC differentiation genes in rat SMCs has been suggested. In KCl-treated cells, blockade of VGCCs by nifedipine attenuated SMA expression. Moreover, S1P-induced membrane translocation of RhoA was decreased by pretreatment of SMCs with nifedipine.

The present study tests the hypothesis that S1P2R regulates expression of SMC differentiation genes after arterial injury and investigates the potential signaling pathways involved.

Methods

Materials

S1P was purchased from Cayman and thrombin from American Diagnostica Inc. Antibodies were from Abcam (SM22α, β-actin), Cell Signaling (β-tubulin), Santa Cruz (SRF, Pol II, rabbit IgG), and Sigma (SMA, mouse IgG-1, IgG-2a, rabbit IgG, and Sigma (SMA, mouse IgG-1, IgG-2a, rabbit IgG). The ECL-kit, horseradish peroxidase (HRP)-coupled antimouse antibody, and HRP-coupled protein A, and protein A sepharose beads were from GE Healthcare. C3 exotoxin was from Cytoskeleton, BAPTA-AM and thapsigargin from Calbiochem, and nifedipine from Sigma. Custom primers and probes were purchased from Invitrogen or Integrated DNA Technologies. All primer and probe sequences are shown in supplemental Table I (available online at http://atvb.ahajournals.org).

Animals, Surgical Procedures, and Isolation of Carotid SMCs

S1P2R-null mice and wild-type mice were kindly provided by Dr Richard L. Proia (National Institutes of Health, Bethesda, Md.). Heterozygous mice were bred to generate S1P2R-null and wild-type littermates. Genotypes were verified by polymerase chain reaction analysis using specific primers. The left common carotid artery of male mice (8 to 10 weeks old) was dissected and ligated near the carotid bifurcation as previously described. At the indicated time points, carotid arteries were excised and immediately frozen in liquid nitrogen or transferred to RNALater (Ambion). Carotid SMCs were isolated as previously described and maintained in DMEM supplemented with antibiotics (200 U/mL penicillin, 0.2 mg/mL streptomycin, 0.1 mg/mL amphotericin, 10% fetal bovine serum (Atlantic Biologics), and 2% ITS supplement (HyClone), and 10% fetal bovine serum (Invitrogen) for 30 minutes and rinsed with Tyrode solution. SMCs were stimulated with S1P (1 μmol/L) or KCl (60 mmol/L), and changes in fluorescence were imaged once every second for 150 seconds using confocal microscopy (LSM-510, Carl Zeiss; excitation: 488 nm; emission: 505 to 570 nm). The pixel intensities were quantified using NIH ImageJ software.

Analysis of Gene Expression by Real-Time PCR and Western Blot Analysis

Standard protocols were used to analyze gene expression by real-time PCR and Western blot analysis using preparations of total RNA and protein, respectively. Please see the supplemental materials for detailed methods, including primer sequences (supplemental Table I).

Chromatin Immunoprecipitation Assay

Chromatin Immunoprecipitation (ChIP) assays were performed with minor adjustments as recently described. Please see the supplemental materials for detailed methods including primer sequences (supplemental Table II).

RhoA Assay

Rho activity was measured using a commercially available kit as to the manufacturer’s instructions (Cytoskeleton).

Calcium Measurement

Serum-starved SMCs were loaded with 3 μmol/L Fluo4 calcium indicator dye (Molecular Probes, Invitrogen) for 30 minutes and rinsed with Tyrode solution. SMCs were stimulated with S1P (1 μmol/L) or KCl (60 mmol/L), and changes in fluorescence were imaged once every second for 150 seconds using confocal microscopy (LSM-510, Carl Zeiss; excitation: 488 nm; emission: 505 to 570 nm). The pixel intensities were quantified using NIH ImageJ software.

Statistics

As indicated in figure legends, data are presented as mean±SD or SEM. Significance of differences between 2 groups was calculated using Student t test, and Bonferroni adjustments were used for multiple variant analyses. Multiple isolations of SMCs were used in all in vitro experiments.

Results

S1P2R Regulates Expression of SMA After Arterial Injury

We recently reported that S1P2R-deficient arteries respond to injury with the formation of a large neointima, whereas wild-type arteries do not. In agreement with this observation, we observed increased medial proliferation in injured S1P2R-null arteries compared to wild-type arteries. To test the possibility that S1P2R regulates expression of SMC differentiation genes thereby controlling injury-induced phenotypic modulation, we measured mRNA of SMA, SM22α, calponin-1 (CNN1), and smooth muscle-myosin heavy chain (SM-MHC) in carotid arteries of S1P2R-null and wild-type mice at day 0, 2, 4, and 7 after injury. Expression of each gene tested decreased with injury (Figure 1A). At day 7, however, only SMA was significantly lower expressed in S1P2R-null arteries compared to wild-type arteries. Neither myocardin, S1P1R, nor S1P3R were differentially expressed between wild-type and S1P2R-null arteries after injury (Figure 1A). Neither myocardin, S1P1R, nor S1P3R were differentially expressed between wild-type and S1P2R-null arteries after injury (Figure 1A and 1B), and therefore none of these genes is likely to mediate S1P2R-dependent SMA expression after injury. To confirm RNA expression data, we measured SMA and SM22α protein as well. Whereas SMA is present at similar levels in uninjured wild-type and S1P2R-null arteries, its expression at day 7 and 14 after injury decreased significantly in S1P2R-null arteries only (by 30%, at day 7; supplemental Figure I). Such differences were not observed for SM22α (supplemental Figure I).

S1P2R Regulates Expression of SMA in Response to S1P

In vitro, S1P has previously been shown to stimulate SMA expression in SMCs, and a role for S1P2R and possibly S1P3R in this process has been suggested. Using wild-type and S1P2R-null SMCs in vitro, we found that expression of SMA, SM22α, CNN1, and SM-MHC, but not myocardin, is induced by S1P (Figure 2A). A significant difference between wild-type and S1P2R-null SMCs, however, was observed with SMA and SM22α only, both of which were more strongly induced in wild-type SMCs (Figure 2A). The same difference, although less pronounced, was observed for SMA and SM22α protein (Figure 2B). As SMA expression is regulated by SRF, we performed ChIP assays to investigate whether SRF enrichment at the promoter or the enhancer region in the first intron of the SMA gene are regulated by S1P2R. In wild-type SMCs, S1P increased enrichment of SRF at both sites by approximately 5-fold (Figure 3A). In S1P2R-null SMCs, enrichment of SRF before or after S1P stimulation was significantly less (Figure 3A). To demonstrate that S1P also stimulates transcription of the SMA gene, we determined binding of RNA polymerase II (Pol II) to the promoter and enhancer region. Binding of Pol II to either region...
was stimulated by S1P in both cell types but markedly decreased in S1P2R-null SMCs compared to wild-type SMCs (Figure 3B).

S1P-Induced SMA Expression Requires Rho Activation and Calcium Release From Intracellular Stores

It is known that S1P activates Rho and causes an increase in intracellular calcium.19–22 We tested a role for Rho and calcium in S1P2R-dependent SMA expression by using various inhibitors. Treatment of wild-type SMCs with C3 exotoxin (a Rho inhibitor23), BAPTA-AM (calcium chelator), or thapsigargin (an inhibitor of the sarco-endoplasmic reticulum Ca\(^{2+}\)/ATPase, SERCA) all prevented the S1P-dependent induction of SMA message and protein expression (Figure 4). In contrast, blockade of L-type VGCCs with nifedipine had no effect on SMA expression by S1P.

We next determined the contribution of S1P2R to activation of Rho and release of calcium by S1P. Based on the
literature, S1P2R is the dominant S1P receptor to activate Rho but S1P3R might also contribute.\textsuperscript{19–22,24} In contrast, S1P3R is generally considered the primary S1P receptor responsible for the increase of intracellular calcium in response to S1P.\textsuperscript{24} In comparison to wild-type SMCs, activation of RhoA by S1P in S1P2R-null SMCs is insignificant (Figure 5A). As L-type VGCC-mediated calcium influx has recently been suggested to contribute to RhoA activation,\textsuperscript{6} we tested
whether a calcium-dependent event is upstream of S1P-mediated activation of RhoA. This is not the case as chelating calcium does not affect activation of RhoA by S1P (Figure 5B). Further, blockade of either SERCA by thapsigargin or L-type VGCCs by nifedipine had no effect on RhoA activity following S1P stimulation (Figure 5B).

To assess the contribution of S1P2R to the increase in intracellular calcium induced by S1P, we measured calcium transients in wild-type and S1P2R-null SMCs. In average, S1P2R-null cells reached only 25% of the S1P-mediated calcium increase observed in wild-type cells (Figure 6A), whereas, as expected, wild-type and S1P2R-null SMCs responded similarly to thrombin (Figure 6A). The S1P-induced calcium transients were abolished by BAPTA-AM and thapsigargin but not affected by nifedipine (Figure 6B), which is consistent with our observation that thapsigargin but not nifedipine inhibits S1P-induced expression of SMA (Figure 4). The effects of these drugs on KCl-stimulated calcium transients in SMCs have been investigated in control experiments, which confirmed the efficacy of nifedipine (supplemental Figure I). Further, we found that C3 exotoxin reduced the S1P-stimulated calcium release by approximately 60% suggesting that C3 exotoxin reduced the inhibitory effect of S1P2R on neointimal formation, at least in part, calcium transients induced by S1P (Figure 6B).

**Discussion**

We previously demonstrated that S1P2R-null carotid arteries respond to ligation injury with the formation of large neointimal lesions, whereas their wild-type littermates do not, suggesting that S1P2R inhibits neointimal growth.8 S1P2R blocks SMC migration by inhibiting activation of Rac25,26 Although this mechanism is likely to contribute to the inhibitory effect of S1P2R on neointimal formation, it does not explain our finding that medial proliferation is much higher in injured S1P2R-null carotid arteries compared to wild-type arteries.8 An inhibitory effect of S1P2R on SMC proliferation in vitro has recently been demonstrated using the S1P2R antagonist, JTE-013.8 Given the previous observations in vitro that S1P induces expression of SMC differentiation genes via a Rho-dependent pathway9,10 and that S1P2R is the major contributor to Rho activation in response to S1P,19–22 we tested the hypothesis that S1P2R regulates expression of SMC differentiation genes after arterial injury. We measured mRNA expression of CNN1, SM22α, SM-MHC, and SMA after carotid injury in wild-type and S1P2R-null mice and found that at 2 days after injury, expression of all genes was decreased by approximately 50% in both animals. The only difference between wild-type and S1P2R-null animals was that reexpression of SMA at day 7 after injury only occurred in wild-type arteries (Figure 1A and supplemental Figure I). This was unexpected given our assumption that all SMC differentiation genes tested are similarly regulated by SRF and its cofactors of the myocardin/MRTF family. In vitro, S1P induces expression of SMA, SM22α, CNN1, and SM-MHC to different extent, and S1P2R seems to only promote the expression of SMA and SM22α.
(Figure 2). Clearly, these genes are regulated by multiple pathways that are differentially activated by S1P. We do not know why SM22α is strongly induced by S1P/S1P2R in vitro, but its expression does not differ between injured wild-type and S1P2R-null arteries (compare Figure 1A with Figure 2). It is possible that differences emerge later after injury.

Using ChIP assays, we demonstrate that S1P2R regulates SRF binding to the regulatory CArG domains in the SMA promoter and enhancer region (Figure 3A). A similar observation was made for Pol II which is consistent with the conclusion that S1P2R regulates SMA transcription. We do not believe that this process is regulated by changes in myocardin expression because there is no difference in myocardin mRNA levels between wild-type and S1P2R-null arteries at any time point after injury (0 to 7 days), and especially at day 7, when expression of SMA is significantly higher in wild-type arteries (Figure 1A). As has been previously suggested by in vitro experiments, a possible mechanism for S1P2R-dependent regulation of SMA expression is the Rho-dependent translocation of the SRF cofactors MRTF-A/B from the cytosol into the nucleus.9 Whether this mechanism also regulates SMA expression by S1P2R after injury in vivo remains to be investigated.

Given a recent report in balloon-injured rat carotid arteries demonstrating that injury regulates expression of S1PRs,6 we investigated whether differences in S1P1R and S1P3R expression in wild-type and S1P2R-null mice could account for the observation that S1P2R-null arteries but not wild-type arteries form intimal lesions after injury. In contrast to the rat model, we did not observe significant changes of S1P expression after injury (Figure 1B). At most, there is a trend that expression of S1P3R is slightly induced after injury, but this was observed in wild-type as well as in S1P2R-null arteries (Figure 1B). It is possible that differences between the rat and mouse model regarding expression of S1PRs after injury is attributable to the endothelium which is removed in the rat model but present in the mouse model. Taken together, our current hypothesis is that S1P2R regulates the reexpression of SMA after injury, thereby limiting the potential of the injured artery to form an intima, but we cannot rule out other mechanisms.

To elucidate S1P2R-dependent signaling pathways that regulate SMA expression, we compared the responses of wild-type and S1P2R-null SMCs to S1P. We confirmed previous suggestions that S1P2R activates RhoA, and that RhoA is critical for SMA expression by S1P (Figures 4 and 5). In addition, we determined that release of calcium from intracellular stores is stimulated by S1P and contributes to S1P-mediated SMA expression (Figure 4), whereas we used mouse carotid SMCs. The SERCA-inhibitor thapsigargin blocked S1P-mediated SMA expression (Figure 4) as well as the increase of intracellular calcium (Figure 6D), but not the activation of RhoA by S1P (Figure 5B). This apparent discrepancy in S1P using different calcium stores to express SMA may be attributable to cell-type-specific properties as the above mentioned study6 was performed in rat aortic SMCs, whereas we used mouse carotid SMCs.

The mechanism by which calcium regulates SMA expression in SMCs is unknown. SRF is phosphorylated by calcium-dependent calmodulin kinase (CaMK) at multiple sites,29 which may directly regulate its activity.30 In cardiac myocytes, calcium/CaMK inhibits the association between SRF and a histone deacetylase thereby derepressing SRF activity.31 Epigenetic regulation of the SMA promoter has been shown,32,33 and it is an attractive possibility that calcium regulates SRF activity by the recruitment of histone modifying enzymes.

In summary, we provide evidence that S1P/S1P2R regulates SMA expression in arteries after injury. In vitro, the extent of induction of other SRF-dependent SMC differentiation genes by S1P greatly varies, and in vivo, SMA is the only SMC differentiation gene we found regulated by S1P2R. Although more work is necessary to define the role for S1P2R in the injury response, we believe that induction of SMA, and potentially additional SMC differentiation genes,
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contributes to the inhibition of neointimal growth by S1P2R. We further demonstrate that S1P-mediated induction of SMA expression in vitro requires S1P2R-dependent activation of RhoA and release of calcium from intracellular stores.

Acknowledgments

We thank Richard Proia for the generous gift of S1P2R-null mice, Aesim Cho for mouse colony maintenance, L. Fernando Santana and Michael LaFlamme for their help with calcium measurements, Ron Seifert for his help with confocal microscopy, as well as Joel Nelson and Karol Bomsztyk for their expert advice concerning the FastChIP method.

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Disclosures

None.

References

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Supplement Material

Analysis of gene expression by Real time PCR
Total RNA was prepared from wild-type and S1P2R-null SMCs (Qiagen Mini Kit). RNA (1 µg) was reverse transcribed using the MultiScribe reverse transcriptase system (Applied Biosystems). TaqMan (Applied Biosystems) or SYBR green (Quantace) incorporation were utilized to determine gene expression. For RT-PCR using TaqMan probes: 75 ng of cDNA was combined with SensiMix (Quantace), and TaqMan primer probe mix. For RT-PCR using SYBR green, 75 ng of cDNA was combined with a commercially available mix containing polymerase, buffer, nucleotides and internal control (Sensimix, Quantace), SYBR green (Quantace) and primers (Table I). Cycle threshold numbers were determined using an ABI 7500 thermocycler (Applied Biosystems). Specificity of primers was verified by dissociation curves, and gene expression was normalized to expression of 18S RNA or GAPDH, respectively.

<table>
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<tr>
<th>GENE</th>
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| S1P1R   | F - CTACTCCTTGTCACGGACTCGAA  
          | R - ACTCAAGCAGAATGATCCGCGCTT  
          | probe - 56-FAM/CGCCGCTGACCTCCGC/3IABkFQ                                  |
| S1P2R   | F - ATGTGACAAAGGCTGCCGAATG  
          | R - GCACGTAGTGGTTAGCATAGAGAG  
          | probe - 56-FAM/TCTGGGTGGCTTGGCCATCCTG/3IABkFQ                           |
| S1P3R   | F - ATGTACTTTTTTCATCGGCAAATTG  
          | R - ACGTCTTCTTCCTGGCGGACATA  
          | probe - 56-FAM/TGGCCGGCATAAGGTCATAAT/3IABkFQ                           |
| 18S     | F - CGGACAGGATTGACAGATTG  
          | R - CAAATCGCTCCAACAACTAA  
          | probe - 56-FAM/CACCACCACCCCGGAATCG/3IABkFQ                             |
| SMA     | F - TACATGGCGGGGACATGGA  
          | R - CGGATAGAACAAGGCGCATCATA  
          |                                            |
| CNN1    | F - ATGCCCAAGACCTGGCTCAAA  
          | R - ACTGCAATGGGCGACACAACA  
          |                                            |
| SM22α   | F - CAACAAGGGTCCATCTACAGG  
          | R - ATCTGGCGGGCTACATCA  
          |                                            |
| SM-MHC  | F - AAGCTGCGGCTAGAGGTCA  
          | R - CCCCTTTGAGATGGGCTAG  
          |                                            |
| myocardin | F - ACACTCCTGGGTCTGAA  
            | R - GCCGTATTAAGCCTGGTGG  
            |                                            |
| GAPDH   | F - GCCCAAGATGCGCCTTACGTG  
          | R - CATCCACTGGTGGCTGCAA  
          |                                            |

Table I: Primer and probe sequences for Real time PCR
Western blot analysis
Frozen arteries were pulverized using a mortar and pestle. Tissue powder was extracted in lysis buffer (Cytoskeleton). Extracts were cleared by centrifugation prior to determining protein concentration using Precision Red protein detection reagent (Cytoskeleton). SMCs were plated into 6-well plates (100,000 cells/well) and next day, media was changed to serum-free media. After 2-3 days, cells were extracted with SDS-polyacrylamide gel electrophoresis (SDS-PAGE) sample buffer. Equal amounts of protein were subjected to SDS-PAGE followed by Western blotting. Blots were probed with primary antibody overnight at 4°C and then developed with ECL (GE Healthcare). Equal loading of protein was confirmed by re-probing blots for β-actin or β-tubulin.

Chromatin immunoprecipitation (ChIP) assay

Cell Fixation and Lysis: Quiescent or stimulated (1 µmol/L S1P for 15 minutes) SMCs (10^6 cells) were fixed at room temperature by the addition of formaldehyde to the media (final concentration: 1.42%). After 45 min, formaldehyde was quenched with 125 mmol/L glycine for 5 minutes. Cells were harvested into ice-cold PBS, washed twice with PBS and lysed in ChIP immunoprecipitation (IP) buffer (150 mmol/L NaCl, 50 mmol/L Tris-HCl pH 7.5, 5 mmol/L EDTA, 0.5% v/v NP-40, 1% v/v Triton X-100, 1 mmol/L DTT, 10 µg/mL leupeptin, 10 mmol/L β-glycerophosphate, 10 mmol/L NaF, 0.1 mmol/L Na3VO4).

Chromatin Preparation: The nuclear pellet was isolated by centrifugation and resuspended to the equivalent of 2 million cells per 100 µL of IP buffer and chromatin sheared using the Biorupter (a sealed-type sonicating water bath) set to medium intensity with 2 rounds of 15 minute sonication pulses. The remaining insoluble material was removed by centrifugation.

Immunoprecipitation: The supernatant was diluted to the equivalent of 5 million cells/mL with IP buffer. An aliquot of 0.2 mL was combined with antibody (2 µg SRF, 1.5 µg Pol II, 2 µg rabbit IgG or 1.5 µg normal mouse IgG-κ) and incubated at 4°C in an ultrasonic water bath (Branson) for 15 min. Following removal of non-specific aggregates by centrifugation, 40 µL of a 1:1 slurry of protein A sepharose beads and IP buffer without inhibitors (DTT, leupeptin, β-glycerophosphate, NaF, and Na3VO4) was added to samples. The mixture was incubated for 1 hr at 4°C with constant agitation, before the beads were collected by centrifugation and washed 5 times with IP buffer without inhibitors.

DNA isolation: Beads were mixed with 100 µL of 10% Chelex-100 (w/v in water, Bio-Rad), 20 µg of proteinase K (Qiagen), incubated at 60°C for 20 min in a thermal shaker (Eppendorf), and finally boiled for 10 minutes to elute DNA. The beads were removed by centrifugation and the supernatant subjected to qPCR analysis. See Table II for primer sequences.

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<th>REGION</th>
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<tr>
<td>promoter CArGs</td>
<td>F - TGGCCACCCAGATTAGAGAGTTT</td>
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<td></td>
<td>R - CCCACCTTCGCTTCCCCAAAAACAA</td>
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<tr>
<td>intronic CArG</td>
<td>F - CGGTGCAGTTCCAAAACAG</td>
</tr>
<tr>
<td></td>
<td>R - CCGCTGTGGTTTGCACAATCTTT</td>
</tr>
<tr>
<td>+6kB negative control</td>
<td>F - TTCCAGGACCTTTTGCATCC</td>
</tr>
<tr>
<td></td>
<td>R - CCGGTTAGGTTTCACTGTTG</td>
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Table II: Primer sequences for ChIP assays
S1P2R-null arteries express less SMA compared to wild-type arteries after injury (Figure I). S1P2R-null and wild-type mice underwent ligation injury of the left carotid artery. At the indicated time points, arteries were harvested; right arteries served as controls (0 days). (A) Protein was subjected to Western blotting analysis for expression of SMA, SM22α, and β-actin. This experiment was repeated with similar results. (B) SMA expression at day 7 after injury was quantified (mean ± S.E.M. (n=3). *P<0.05

Effect of nifedipine, BAPTA-AM and thapsigargin on KCl-induced calcium transients in SMCs (Figure II). As positive control for nifedipine, we confirmed that the drug blocks KCl-induced calcium transients. These control experiments included BAPTA-AM and thapsigargin. As expected, BAPTA-AM completely prevented KCl-mediated calcium transients, and as has been reported previously, thapsigargin was also inhibitory. Quiescent wild-type SMCs were loaded with Fluo4 calcium indicator dye and pretreated with BAPTA-AM, nifedipine and thapsigargin, as described for Figure 4, before stimulation with 60 mmol/L KCl. SMCs without pretreatment served as controls. Changes in intracellular calcium levels were recorded using confocal microscopy. Typical calcium transients are shown for nifedipine (A), BAPTA-AM (B) and thapsigargin (C). All experiments have been repeated with a different cell isolate and yielded similar results.

Figure II

A

Intracellular calcium [fold increase]

Time [s]

B

Intracellular calcium [fold increase]

Time [s]

C

Intracellular calcium [fold increase]

Time [s]

Nifedipine

Thapsigargin

BAPTA-AM

Figure II