

## SYMPOSIUM REPORT

# Excitation–transcription coupling in smooth muscle

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Calcium ( $\text{Ca}^{2+}$ ) signals affect virtually every biological process, including both contraction and gene transcription in smooth muscle.  $\text{Ca}^{2+}$ -regulated gene transcription is known to be important for both physiological and pathological responses in smooth muscle. The aim of this review is to discuss the current understanding of gene transcription regulated by excitation through  $\text{Ca}^{2+}$  signalling using a comparison of the two most characterized  $\text{Ca}^{2+}$ -regulated transcription factors in smooth muscle,  $\text{Ca}^{2+}$ -cyclic AMP response element binding protein (CREB) and nuclear factor of activated T-cells (NFAT). Recent studies have shown commonalities and differences in the regulation of CREB and NFAT through both voltage- and non-voltage-gated  $\text{Ca}^{2+}$  channels that lead to expression of smooth muscle cell specific differentiation markers as well as markers of proliferation. New insights into the regulation of specific genes through companion elements on the promoters of  $\text{Ca}^{2+}$ -regulated genes have led to new models for transcriptional regulation by  $\text{Ca}^{2+}$  that are defined both by the source and duration of the  $\text{Ca}^{2+}$  signal and the composition of enhancer elements found within the regulatory regions of specific genes. Thus the combination of signalling pathways elicited by particular  $\text{Ca}^{2+}$  signals affect selective promoter elements that are key to the ultimate pattern of gene transcription.

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Excitation–contraction coupling in smooth muscle cells (SMCs) is tightly controlled by spatio-temporal  $\text{Ca}^{2+}$  events that involve both influx of extracellular  $\text{Ca}^{2+}$  and release from selective intracellular  $\text{Ca}^{2+}$  stores (reviewed in Bolton *et al.* 2004). Recent findings have revealed that the  $\text{Ca}^{2+}$ -regulated transcription factors CREB and NFAT have selective  $\text{Ca}^{2+}$  source requirements and are influenced by transcriptional coactivators and cofactors for CREB and NFAT. Excitation–transcription coupling is thus clearly relevant to both normal physiological responses and to the pathogenesis of vascular diseases that are known to include altered  $\text{Ca}^{2+}$  handling and changes in gene expression.

## $\text{Ca}^{2+}$ regulation of CREB and gene transcription in smooth muscle

CREB ( $\text{Ca}^{2+}$ -cyclic AMP response element binding protein) regulates transcription through recognition and binding to  $\text{Ca}^{2+}$ -cyclic AMP (cAMP)-response elements

(CREs) in the promoter of many genes (Shaywitz & Greenberg, 1999). Stimulus-induced CREB activation requires phosphorylation of  $^{133}\text{S}$ erine to promote recruitment of CREB binding protein (CBP300) and other cofactors to form an active transcriptional complex (Gonzalez *et al.* 1989; Mayr & Montminy, 2001).  $\text{Ca}^{2+}$  from many sources can activate CREB-induced transcription through the  $\text{Ca}^{2+}$  calmodulin-dependent protein kinase (CaMK), growth factor/MAPK, and cAMP-dependent protein kinase pathways (Shaywitz & Greenberg, 1999) (Fig. 1). Inactivation of CREB through phosphatase activity can also be regulated by  $\text{Ca}^{2+}$  through  $\text{Ca}^{2+}$ -CaM activation of the protein phosphatase calcineurin which indirectly leads to dephosphorylation of CREB (Alberts *et al.* 1994).

CREB activation elicited by membrane depolarization and  $\text{Ca}^{2+}$  entry through voltage-dependent calcium channels (VDCCs) has been confirmed in both cultured SMCs and intact cerebral arteries (Cartin *et al.* 2000; Stevenson *et al.* 2001a). Depolarization-mediated CREB phosphorylation correlates with an increase in transcription of the CRE-containing immediate early gene, *c-fos*, and is sensitive to inhibitors of VDCCs.

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Although CREB is predominantly nuclear, it has been shown to accumulate in the cytoplasm of vascular SMCs when nuclear import is blocked prior to membrane depolarization (Stevenson *et al.* 2001a). While the relevance of nuclear shuttling of CREB has not been established, it could explain CREB interactions with multiple kinases that do not cross the nuclear membrane and the perceived loss of CREB from the nucleus following ischaemia (Klemm *et al.* 2001).

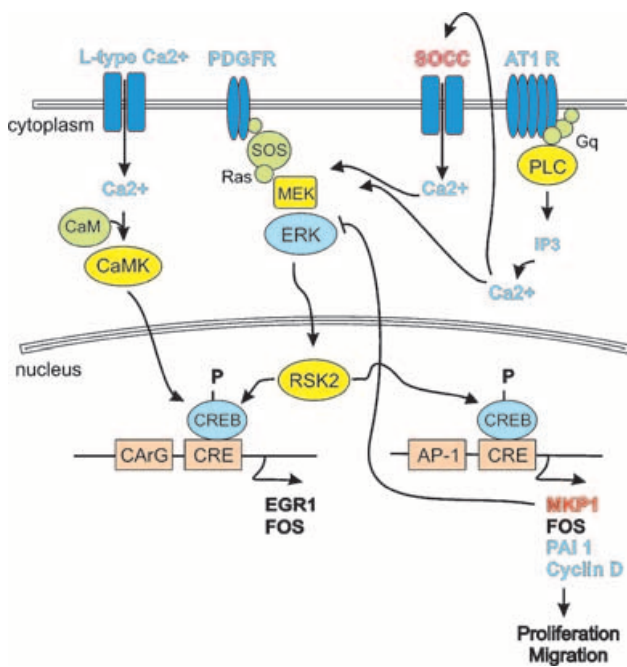
A role for SR  $\text{Ca}^{2+}$  in signalling to CREB in SMCs has been demonstrated both in response to  $\text{Ca}^{2+}$  release from inositol 1,4,5-trisphosphate ( $\text{IP}_3$ ) receptors and through store-operated  $\text{Ca}^{2+}$  entry. Endothelin-1, platelet-derived growth factor (PDGF), sphingosine-1-phosphate, aldosterone, low-density lipoprotein (LDL) and ischaemia have all been shown to induce CREB phosphorylation in SMCs through an  $\text{IP}_3$ -dependent mechanism (Christ *et al.* 1999; Stevenson *et al.* 2001a; Coussin *et al.* 2003; Egan & Nixon, 2004; Rius *et al.* 2004; Meller *et al.* 2005). The majority of these pathways are also influenced by MAPK signalling, and a link between  $\text{Ca}^{2+}$  and MAPK signalling to CREB has been observed for noradrenaline (norepinephrine)-induced CREB signalling (Hu *et al.* 1999). Store-operated  $\text{Ca}^{2+}$  entry (SOCE), in response to SR  $\text{Ca}^{2+}$  depletion, has also been shown to stimulate CREB

phosphorylation in both cultured and intact vascular SMCs (Fig. 2), and a role for SOCE has been reported in CREB activation stimulated by angiotensin II (Pulver *et al.* 2004). Determinations of the relevance of SOCE activation by other  $\text{IP}_3$  mediators and its importance in MAPK signalling are important targets of future investigations related to CREB signalling.

Not all  $\text{Ca}^{2+}$  signals lead to activation of CREB. Release of  $\text{Ca}^{2+}$  from ryanodine receptors (RyR) in the form of  $\text{Ca}^{2+}$  sparks has been shown to have an inhibitory effect on CREB activation, probably through membrane hyperpolarization (Cartin *et al.* 2000). These results stress the importance that the nature of the  $\text{Ca}^{2+}$  signal has on the downstream changes in gene transcription mediated by CREB.

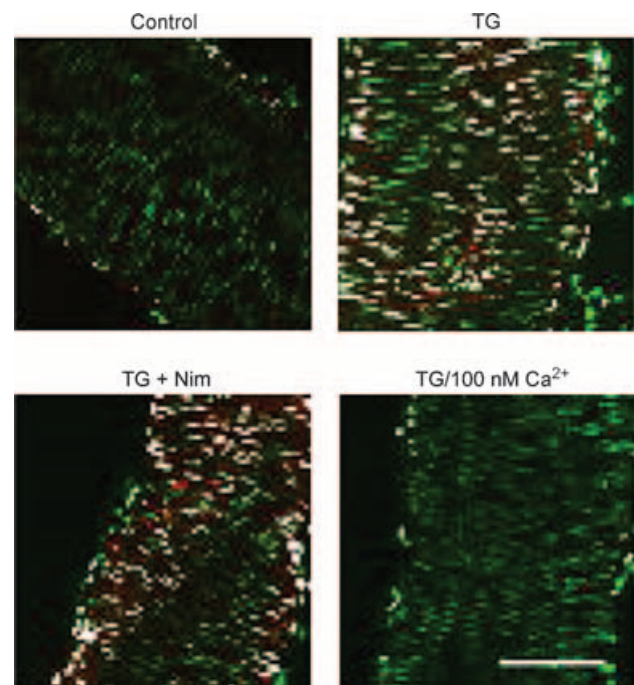
### $\text{Ca}^{2+}$ regulation of NFAT in smooth muscle

Nuclear factor of activated T cells (NFAT) has recently been shown to play an important role in regulating  $\text{Ca}^{2+}$ -dependent gene transcription in SMCs.



**Figure 1. Regulation of CREB activation through multiple signalling cascades in SMCs.**

Store-operated  $\text{Ca}^{2+}$  channel (SOCC), phospholipase C (PLC), son of sevenless (SOS), platelet-derived growth receptor (PDGFR), GTPase binding protein q (Gq), extracellular-signal regulated kinase (ERK), MAPK/ERK kinase (MEK), receptor signal kinase (RSK), angiotensin II type 1 receptor (AT1R), serum response element (CARG), plasminogen activator 1 inhibitor (PAI1).



**Figure 2. CREB is activated by SOCE in intact vascular smooth muscle**

From Pulver *et al.* (2004), used with permission. Rat cerebral arteries were isolated and incubated in HEPES-buffered saline (HBS) with normal  $\text{Ca}^{2+}$  ( $2 \text{ mmol l}^{-1}$ ),  $100 \text{ nmol l}^{-1}$   $\text{Ca}^{2+}$ , or  $100 \text{ nmol l}^{-1}$  nimodipine (Nim) for 15 min. Arteries were then exposed to  $100 \text{ nmol l}^{-1}$  thapsigargin (TG) for 15 min or  $60 \text{ mM K}^+$  for 10 min. CREB phosphorylation was detected by anti-P-CREB immunofluorescence. Shown are confocal images representing P-CREB (red), YOYO-1 DNA nuclear stain (green) and overlap of P-CREB and YOYO-1 DNA (white). Bar represents  $100 \mu\text{m}$ .

The activation of NFAT is regulated through its subcellular localization, which reflects the intensity of  $\text{Ca}^{2+}$ –calcineurin signalling and the activities of several nuclear protein kinases (Fig. 3) (Hogan *et al.* 2003). Upon elevation of intracellular  $\text{Ca}^{2+}$  levels, the  $\text{Ca}^{2+}$ –CaM-dependent phosphatase, calcineurin, dephosphorylates NFAT, allowing for the translocation of the NFAT–calcineurin complex into the nucleus. Because of its dependence on  $\text{Ca}^{2+}$ –calcineurin signalling, NFAT has the ability to sense dynamic changes in  $[\text{Ca}^{2+}]_i$  and frequencies of  $\text{Ca}^{2+}$  oscillations (Dolmetsch *et al.* 1997; Li *et al.* 1998).

NFAT translocation and transcriptional activity has been clearly demonstrated in both cultured and native SMCs (Boss *et al.* 1998; Stevenson *et al.* 2001*b*). In cerebral SMCs, the vasoconstrictor UTP, and other  $G_{q/11}$ -coupled receptor agonists induce NFAT4 nuclear accumulation. This induction is dependent on release of  $\text{Ca}^{2+}$  from intracellular stores and requires function of VDCCs (Stevenson *et al.* 2001*b*; Gomez *et al.* 2002). However, counter to expectations, a sustained increase in  $[\text{Ca}^{2+}]_i$  induced by membrane depolarization is not sufficient to achieve NFAT4 nuclear accumulation in vascular SMCs (Stevenson *et al.* 2001*b*).

One possibility for this finding is that NFAT nuclear accumulation is further regulated by serine/threonine protein kinases, which promote the nuclear export of NFAT. Recent work examining the role of c-Jun amino-terminal kinase (JNK) using JNK knockout animals suggest that although elevated  $\text{Ca}^{2+}$  levels are sufficient to promote NFAT nuclear import, suppression of NFAT nuclear export activity is also required. Specifically, nuclear JNK2 has been shown to selectively promote the nuclear export of NFAT4 in both transfection studies (Chow *et al.* 1997) and native isolated cerebral arteries (Gomez *et al.* 2003). These data suggest that although  $\text{Ca}^{2+}$  elevation is necessary, it may not be the rate-limiting step in NFAT nuclear accumulation in SMCs.

In intact arteries, NFAT translocates to the nucleus in response to physiological intraluminal pressure. Translocation is dependent on  $\text{Ca}^{2+}$  influx through VDCCs, requires the nitric oxide/protein kinase G pathway, and correlates with an inhibition of JNK-dependent nuclear export (Gonzalez Bosc *et al.* 2004). These results implicate a potential role for endothelial-derived nitric oxide in the regulation of NFAT activity and suggest that physiological pressure changes are sufficient to induce transcriptional activity through NFAT.

### $\text{Ca}^{2+}$ and smooth muscle-specific gene expression

Many vascular disease states are characterized by changes in gene expression that inhibit differentiation and promote the proliferative phenotype. The serum response factor

(SRF) DNA binding site or CarG box ( $\text{CC[A/T]}_6\text{GG}$ ) plays an important role in regulating SMC-specific genes (Kumar & Owens, 2003). Evidence is now emerging that suggests a complex interaction between  $\text{Ca}^{2+}$  signalling, regulatory elements and cofactors that affect SRF binding and/or transcriptional activity. Wamhoff *et al.* (2004) found that  $\text{Ca}^{2+}$  influx through VDCCs stimulates expression of SRF-dependent SMC differentiation markers through a mechanism requiring Rho kinase and the SRF coactivator myocardin. In addition,  $\text{Ca}^{2+}$ -dependent CRE elements have been found adjacent to CarG elements in several SRF-regulated SMC genes (Sekiguchi *et al.* 2001; Najwer & Lilly, 2005). Furthermore,  $\text{Ca}^{2+}$ -dependent NFAT activation has been shown to cooperatively regulate the activity of an intronic CarG enhancer of smooth muscle  $\alpha$ -actin (Gonzalez Bosc *et al.* 2005). Thus, co-activators as well as CREB and NFAT have the capacity to direct expression of SRF-regulated genes in response to  $\text{Ca}^{2+}$  signalling in SMCs.

The paradox that remains is the existence of CarG elements in genes that promote de-differentiation as well as differentiation. What mechanisms underlie this distinction? New evidence supports the hypothesis that growth and developmental signals modulate SRF-dependent gene expression by regulating repressive cofactors that compete for SRF binding (Wamhoff *et al.* 2004; Wang *et al.* 2004). In light of the complexities regulating SRF function, future experiments are warranted

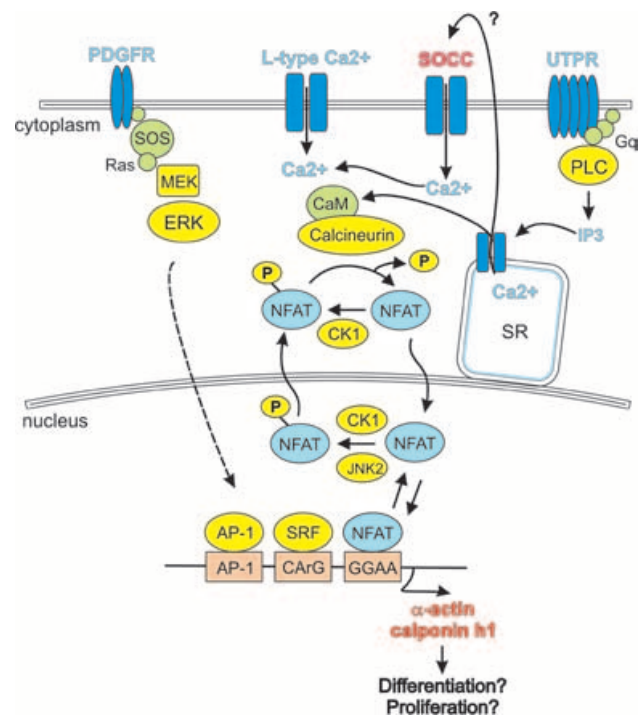


Figure 3. Regulation of NFAT via nuclear translocation in SMCs

to explore these and other potential requirements for SRF-dependent progression to distinct SMC phenotypes.

### CREB and NFAT in smooth muscle pathologies

The pathogenesis of vascular diseases such as hypertension includes altered  $\text{Ca}^{2+}$  handling that triggers changes in gene expression, and these changes are probably attributed to the ability of mature smooth muscle cells to de-differentiate and proliferate (Somlyo & Somlyo, 1994). Although proliferation is important in recovering from vascular injury, arterial intervention procedures such as angioplasty result in abnormal proliferation and restenosis.

Cerebral arteries from hypertensive animals exhibit elevated SMC  $\text{Ca}^{2+}$ , phospho-CREB and c-fos mRNA (Wellman *et al.* 2001). Interestingly, these effects are readily reversed by *in situ* inhibition of VDCCs, suggesting a defect in the 'off' mechanism of CREB activation. These findings provide an important link between altered gene regulation through CREB and de-regulation of  $\text{Ca}^{2+}$  signalling in a disease state. In pulmonary artery SMCs CREB is necessary and sufficient for induction of transient receptor potential cation channel 4 (TRPC4), that has been linked to the development of pulmonary hypertension (Landsberg & Yuan, 2004; Zhang *et al.* 2004).

Increased levels of phospho-CREB have also been correlated with the proliferative response associated with arteriolar injury including angiotensin II-induced hypertension, chronic nicotine administration and oxidative endothelial injury (Gerzanich *et al.* 2003). In addition, expression of dominant negative CREB constructs suppresses neointimal formation and increases apoptosis following balloon injury (Tokunou *et al.* 2003). Transient ischaemia also leads to CREB phosphorylation and increased CRE-mediated Bcl-2 expression (Meller *et al.* 2005). Together, these results suggest a role for CREB in both survival and proliferation of SMCs following injury. The role of CREB in the proliferative response to disease is clearly complex, however, in that SMC proliferation induced by *in vivo* hypoxia correlates with a reduction in CREB content (Klemm *et al.* 2001).

Although NFAT has also been shown to regulate genes related to cell cycle progression and cell differentiation in T cells and neurones, the functions of NFAT in SMCs are largely unknown. In aortic SMCs, NFAT2 nuclear translocation has been correlated with differentiation and found to be important for driving transcription of the smooth muscle-specific Sm-myosin heavy chain (MHC) promoter in a  $\text{Ca}^{2+}$ - and calcineurin-dependent manner (Wada *et al.* 2002). However, NFAT also plays a role in vascular SMC (VSMC) proliferation and motility induced by both receptor tyrosine kinase (RTK) and G protein-coupled receptor agonists (GPCR), PDGF and

thrombin, respectively (Yellaturu *et al.* 2002; Liu *et al.* 2004). Taken together these findings reveal that NFAT, like CREB, is a likely candidate for mediating both differentiation and mitogenic effects in SMCs.

Few studies have directly compared NFAT and CREB signalling in SMCs. In a model of VLDL-induced SMC proliferation, NFAT activation correlates with a decrease in phospho-CREB, suggesting that the proliferative effect of VLDL increases NFAT activity while reducing CREB activity (Lipskaia *et al.* 2003). One caveat to these experiments is that in this model CREB is phosphorylated under basal conditions, an observation that has not been detected in other SMC culture cell systems or in intact arteries (Cartin *et al.* 2000; Pulver *et al.* 2004; Meller *et al.* 2005).

Overall, the evidence suggests that physiological or pathological alterations in  $\text{Ca}^{2+}$  signalling pathways are likely to have effects on both CREB and NFAT function and have the potential to disrupt normal patterns of gene transcription in SMCs. Future studies focused on CREB- and/or NFAT-dependent transcription patterns hold the promise of better understanding the role of excitation–transcription coupling as it relates to genomic effects on smooth muscle phenotype.

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