

## Gating and permeation of Orai channels

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## 1. ABSTRACT

$\text{Ca}^{2+}$  release-activated  $\text{Ca}^{2+}$  channels mediate a sustained  $\text{Ca}^{2+}$  influx following depletion of endoplasmic reticulum stores. This signalling cascade that triggers T-cell activation or mast cell degranulation involves STIM1, the  $\text{Ca}^{2+}$  sensor in the endoplasmic reticulum, and the  $\text{Ca}^{2+}$  selective Orai channel in the plasma membrane. This review describes the molecular mechanism (s) governing the STIM1/Orai signalling machinery. Moreover, we provide an overview on additional proteins modulating or interacting with the STIM1/Orai1 system. A structure-function relationship highlights regions within STIM1/Orai proteins contributing to activation, permeation and inactivation of CRAC currents.

## 2. STORE-OPERATED $\text{Ca}^{2+}$ CHANNELS

Changes in cytosolic  $\text{Ca}^{2+}$  levels control a variety of cellular processes ranging from short-term to long-term responses of immune cells, like mast cells, T-, B-cells and lymphocytes (1). Activation of immune receptors such as T-, B-cell- or Fc-receptors initiates robust  $\text{Ca}^{2+}$  influx into the cell. A main calcium entry pathway is represented by the so called store-operated calcium channels (SOCs) among which the calcium release-activated  $\text{Ca}^{2+}$  (CRAC) channel is best characterized (1-5). The CRAC channel is activated by depletion of intracellular  $\text{Ca}^{2+}$  stores which is caused by the second messenger inositol 1,4,5-trisphosphate ( $\text{IP}_3$ ) (2-6). Biophysical properties of the CRAC channels include a high  $\text{Ca}^{2+}$  selectivity, very low

single channel conductance and a pronounced inwardly rectifying current/voltage relationship (2). Function-based genetic screens by systematic RNA interference (RNAi) has revealed solid evidence that the stromal interaction molecule (STIM) and the Orai (also termed CRACM) family are key components of the CRAC channels (7-11).

### 2.1. STIM1, the $\text{Ca}^{2+}$ sensor in the ER membrane

STIM1 has been identified as an ER-located  $\text{Ca}^{2+}$  sensor (7, 8) containing a pair of luminal EF-hands and a sterile- $\alpha$  motif (SAM) in its N-terminus followed by a single transmembrane domain (12). The cytosolic C-terminus includes three coiled-coil domains (13), a CRAC modulatory domain (CMD) and a serine-/proline- and lysine-rich region (7, 14-17). Within the STIM1 C-terminus, a region including the second coiled-coil domain and the following ~55 amino acids has been recently identified as the smallest fragment binding to and activating Orai1 (18-21). The second STIM protein, i.e. STIM2, is structurally 61% homologous to STIM1. The sequences of both proteins diverge significantly in their short N-terminal region (22) and their C-terminus subsequent to the ERM/coiled-coil region (23).

### 2.2. Orai proteins, the pore forming subunits of CRAC channels

RNAi based screens and analysis of single nucleotide polymorphism arrays of patients with severe combined immune deficiency (SCID) syndrome who exhibit a defect in CRAC channel function, have led to the identification of Orai1 (9-11). Orai1 is located in the plasma membrane and functions as a  $\text{Ca}^{2+}$ -selective ion channel (9-11). Since co-expression of STIM1 and Orai1 has revealed currents with biophysical and pharmacological properties similar to endogenous CRAC currents in RBL mast or Jurkat T cells (24), both proteins are supposed to manifest the main components of CRAC channels. The Orai family includes two further human homologs, Orai2 and Orai3, all of which contain four transmembrane segments and cytosolic N- and C-termini (10). While a proline-/arginine-rich region is only present in the Orai1 N-terminus (25), a cluster of positively charged amino acids close to the first transmembrane region is fully conserved within all three Orai channels. The C-terminus of each Orai protein contains a putative coiled-coil domain (26-28). All three Orai channels are highly selective for  $\text{Ca}^{2+}$  over monovalent ions and can be activated following store depletion via coupling to STIM1. Furthermore the respective Orai channels exhibit distinct inactivation profiles and 2-aminoethyl-diphenyl borate (2-APB) sensitivities (29).

### 2.3. Stoichiometry of Orai channels and their assembly

Orai proteins display no known homology to other calcium channels which led to speculations concerning the subunit stoichiometry of the channel. Primarily biochemical assays have revealed the existence of Orai1 dimers; while tetramers have been found after addition of a chemical cross-linking agent (30). By applying disulfide cross-linking assays Orai1 assembles as a tetramer or as a higher order oligomer (31). Electron microscopy studies have determined a tetrameric

stoichiometry of purified Orai1 proteins (32). In functional assays, currents derived from a tetrameric Orai1 concatamer remained unaffected by co-expression with dominant-negative Orai1 monomers indicating the Orai channels represent a tetrameric assembly (33). Single molecule imaging approaches (34, 35) have allowed for monitoring single molecule photo-bleaching to measure the stoichiometry of each CRAC channel complex formed by co-localized GFP-tagged Orai1 subunits. While Ji *et al.* (34) have observed exclusively Orai1 tetramers in fixed HEK-293 cells, Penna *et al.* (35) have demonstrated Orai dimers in resting *Xenopus laevis* oocytes that associate to tetramers only upon co-expression of the STIM1 C-terminus. The latter data may argue for a stimulatory role of STIM1 in the tetrameric assembly of Orai proteins. A constraint of these two studies may arise from analysis to only immobile or immobilized proteins. Orai proteins are expected less mobile upon potential pre-association with STIM1. We have recently focused on the mobile fraction of Orai1 proteins from resting cells, and primarily tetrameric assemblies have been observed (36).

In addition to the homomeric assembly of Orai proteins, they are also able to form heteromeric channels (29, 30, 37). Besides tetrameric Orai protein aggregation, Shuttleworth's lab has reported that Orai1 and Orai3 subunits are able to form pentameric aggregates which function as arachidonate regulated  $\text{Ca}^{2+}$  (ARC) channels. A multimer including three Orai1 and two Orai3 subunits represents the functional ARC channel pore (33, 38-40). It has been shown that the Orai3 N-terminal domain accounts for the switch from a predominantly store-operated to an exclusively arachidonic acid activated channel (41).

Orai subunits oligomerize mainly via their transmembrane regions as deletion of the cytosolic strands does not impair aggregation of Orai proteins (28, 42). Nevertheless Orai1 N-terminus has still been suggested to play a role in Orai assembly as it acts in a dominant negative manner on SOC (25) in line with our results (43) (R. Schindl, C. Romanin, unpublished results). However, a detailed analysis of domains relevant for Orai subunit multimerization is still lacking.

## 3. SIGNALLING MACHINERY OF STIM AND ORAI

STIM1 and Orai1 represent the two pivotal molecular components that link  $\text{Ca}^{2+}$  store-depletion of the ER with CRAC channel activation (7-12, 44). STIM1 proteins are diffusely located in the ER membrane and sense with their N-terminal EF-hands the luminal  $\text{Ca}^{2+}$  content (7, 8). Store-depletion triggers oligomerization of the STIM1 proteins which redistribute into puncta at junctional ER sites close to the plasma membrane (20nm) (7, 14, 44-48). Thereby STIM1 couples to Orai channels in the plasma membrane forming co-clustered puncta (7, 45, 48, 49). Orai channels are activated by this association and  $\text{Ca}^{2+}$  flows into the cell. Recently, Korzeniowski *et al.* (50) have demonstrated that a basic amino acid stretch within the second coiled-coil domain of STIM1 interacts with an acidic domain in the first coiled-coil domain. This intramolecular clamp is abrogated upon store-depletion and

allows the coupling of the basic segment in the second coiled-coil domain of STIM1 with acidic residues within the C-terminal coiled-coil region of Orai1 (50). Furthermore, Muik *et al* have (51) visualized the intramolecular transition switching the cytosolic portion of STIM1 into an extended conformation and revealed the additional involvement of hydrophobic amino acids contributing to this conformational rearrangement. The stoichiometry of STIM1 proteins required for Orai1 channel opening has been recently estimated with eight STIM1 molecules interacting with one CRAC channel to induced maximal activation (52). Thus, CRAC channel activation is not mediated in an “all-or-one” fashion but occurs via a graded process involving up to eight STIM1 molecules (52). Overall, these findings delineate a complex signaling cascade with the co-clustering of STIM1 and Orai1 thereby activating CRAC channels. Within this signaling process a series of interaction domains that mediate STIM1 oligomerization, Orai multimerization as well as STIM1/Orai coupling are involved.

### 3.1. Domains mediating STIM1 oligomerization

At resting state, STIM1 is uniformly distributed within the ER (28, 47) and exhibits tubular structures. It binds to the microtubule-plus-end-tracking protein EB1 at those sites where microtubule ends come in close contact with the ER (53). Moreover, STIM1 co-localizes with endogenous  $\alpha$ -tubulin (54). The STIM1 EF-hand senses the decrease in  $\text{Ca}^{2+}$  concentrations in the ER lumen which under resting cell conditions is approximately 300–500  $\mu\text{M}$  (55, 56). Subsequently, STIM1 forms oligomers before it redistributes at an  $\text{EC}_{50}$  of 210  $\mu\text{M}$   $\text{Ca}^{2+}$  (57) into punctuate clusters close to the plasma-membrane (7, 14, 44–48). STIM1 oligomerization has been reported to be sufficient to drive puncta formation and CRAC channel activation (58). STIM1 redistribution and CRAC activation share a steep dependence on the  $\text{Ca}^{2+}$  level in the ER and defines input-output relationship of the CRAC channel (58). The initial trigger for STIM1 oligomerization is represented by its N-terminal EF-hand. Upon store-depletion the EF-hand looses bound  $\text{Ca}^{2+}$  and consequently allows for aggregation of STIM1 proteins. In line, an N-terminal STIM1 fragment including the EF-hand and the SAM domain oligomerizes in the absence of  $\text{Ca}^{2+}$  (59, 60). In between the EF-hand and the SAM domain lies a “hidden” EF-hand that is unable to bind  $\text{Ca}^{2+}$  (59). Both EF-hands together mediate interactions via hydrophobic residues with the SAM domain (59). Specific mutations of these residues disrupt  $\text{Ca}^{2+}$  sensitivity and oligomerization via destabilization of the entire EF-SAM entity consequently resulting in puncta formation and constitutive activation of SOC (59). In accordance, a STIM1 deletion mutant lacking the whole C-terminus also oligomerizes via the N-terminal EF-SAM domain, but forms unstable aggregates (61). However, a functional EF-hand-SAM domain is not sufficient to trigger, via oligomerization, the activation of Orai channels. Therefore, STIM1 cytosolic regions are indispensable for CRAC channel activation as described in the following passage.

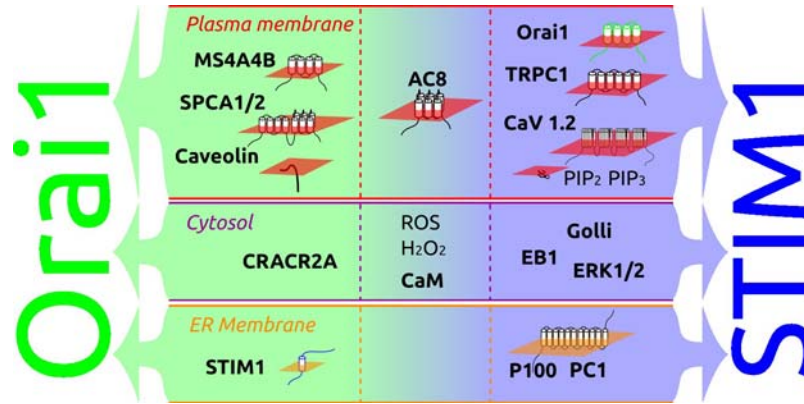
Within the cytosolic region of STIM1, the first coiled-coil domain has been reported to support formation

of resting STIM1 oligomers (61). However, complexes formed by the interaction of the first coiled-coil domain are still unstable as observed by STIM1 C-terminal deletion mutants truncated after this region (61). A short C-terminal STIM1 fragment (233–420) which includes only the first and second coiled-coil domains and lacks the STIM1 N-terminus and the transmembrane domain are also unable to form higher order aggregates than monomers (18). The formation of stable store-dependent oligomers is enabled when the first coiled-coil domain together with the Orai1 activation domain (CAD, 342–448) is present within the STIM1 protein (61). Similarly, STIM1 C-terminal fragments (233–450, 233–474) including the first, second and third coiled-coil domains together with  $\sim 30$  additional amino acids are sufficient for aggregation (18). Within CAD, the second and third coiled-coil domains as well as  $\sim 20$  C-terminal residues have been suggested to contribute to oligomer formation (61). Employing short STIM1 C-terminal fragment, Muik *et al* (18, 43) have narrowed down the domain contributing to STIM1 oligomerization to the region between amino acid 420–450, located C-terminal to the coiled-coil regions.

### 3.2. Domains mediating STIM1/Orai coupling

Among the STIM1 C-terminal coiled-coil domains, the second is indispensable for the coupling to Orai1 (27). Short STIM1 C-terminal fragments (CAD (aa342–448), SOAR (aa344–442), OASF (aa233–450), Ccb9 (aa339–444)) including mainly the second and third coiled-coil domains together with some additional residues downstream have emerged as sufficient for coupling to and activation of Orai proteins (18–21). Park *et al.* (20) have further demonstrated that the GST-tagged 107 residue STIM1 C-terminal fragment CAD co-precipitates and co-elutes with Orai1.

The potential coupling site for the second coiled-coil domain of STIM1 is the coiled-coil domain in the C-terminus of Orai proteins. All Orai proteins contain a single, putative coiled-coil domain in their C-terminus, estimated with a 15–17 fold higher probability in Orai2 and Orai3 compared to Orai1 (27). While a coiled-coil single point mutation in Orai1 C-terminus (L273S, L276D) has abrogated communication with STIM1 C-terminus (27, 28, 62), the analogous exchange in Orai2 and Orai3 still allows for moderate STIM1 C-terminal coupling and current activation (27). Introduction of a second point mutation in the C-terminus of either Orai2 or Orai3 fully disrupts coupling to STIM1. Decreasing the probability of the putative, second coiled-coil domain of STIM1 C-terminus by a single mutation retained partial stimulation of Orai2 and Orai3 channels while Orai1 currents are inhibited. A double mutation within the second coiled-coil motif of STIM1 C-terminus fully disrupts communication with all three Orai channels. Thus, coiled-coil domains represent pivotal structures mediating coupling of STIM1 and Orai (27). The coiled-coil domain of Orai1 includes a series of acidic residues, while the second coiled-coil domain of STIM1 overlaps with a highly conserved cluster of basic



**Figure 1.** Structure-function relationship of the STIM1/Orai1 proteins depicting regions contributing to activation (yellow), permeation (pink) and inactivation (blue) of Orai1/CRAC channels. Activation: STIM1 – CAD/SOAR, Orai – C-terminus, N-terminus; Permeation: Orai – E106 in TM1, negative residues in the first loop, 2-APB and Orai3; Inactivation: STIM1 – negative residues 474-485; Orai – negative residues in C-terminus, second. intracellular loop, N-terminus/CaM/Ca<sup>2+</sup>.

residues (KIKKKR – aa 382-387 of human STIM1; KLRKKR – aa 380-385 of BmSTIM1). Recent publications (63-65) have demonstrated that these charged amino acids enable STIM1/Orai coupling. However, a charge swap within coiled-coil domains of STIM1 and Orai C-termini disrupted coupling of these mutants (64). Hence, additional structural features have been hypothesized to be involved in the coupling process. Besides the requirement of hydrophobic amino acids for lipophilic interactions within a coiled-coil structure, charged residues additionally contribute to stable coiled-coil formation or heteromerization (66, 67). Thus, deletion or mutation of these charged amino acids might disrupt coiled-coil structure or heteromerization and consequently impair STIM1/Orai coupling.

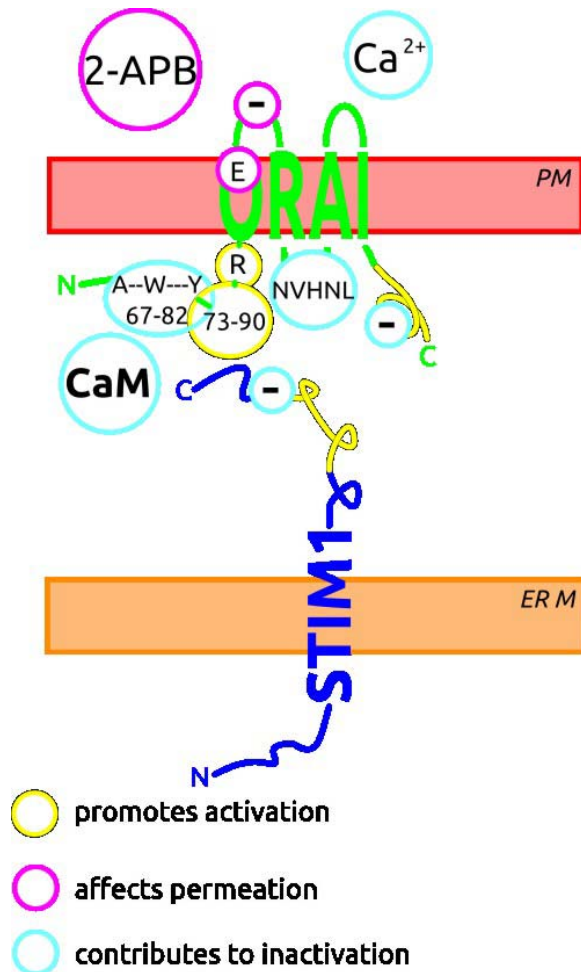
### 3.3. Regions modulating STIM1-Orai coupling

While coiled-coiled domains are indispensable for STIM1/Orai coupling, several regions within both proteins exhibit a modulatory role on Orai activation. The coupling of STIM1 to Orai1 does not only include the C-terminal coiled-coil domain but also the N-terminal region of Orai1 (20, 28, 42). The CAD fragment interacts with Orai1 C-terminus and to a weaker extent with the N-terminus (20). Park *et al.* (20) as well as Hogan *et al.* have shown direct binding of STIM1 C-terminal fragments to both N- and C-terminus of Orai1, thereby triggering channel gating. Deletion of the whole N-terminus of Orai1 abolishes SOCE, while its partial truncation up to amino acid 73, with the conserved region retained, preserves Orai1 channel activity (42, 68). This observation suggests that the Orai1 N-terminal region between amino acid 74 and 90 conserved among all Orai proteins (Figure 1) is indispensable for Orai activation. Within this region a CaM binding domain has been predicted (69). Mutation of specific amino acids, i.e. A73, W76 and Y80, results in the loss of CaM binding which is accompanied by elimination of fast inactivation (see below section on inactivation). Besides hydrophobic residues, it contains five positively charged amino acids. This series of basic residues see whether PIP<sub>2</sub> depletion modulates processes of the STIM1/Orai

signaling machinery. In any case, this N-terminal polybasic region, which is fully conserved in all Orai proteins, is expected to play an important role in the activation by STIM1. While all Orai proteins exhibit this polybasic domain within the N-terminus, an arginine-/proline-rich region occurs only in Orai1 (43). A series of Orai1 mutants lacking the proline-/arginine-rich region, i.e. Orai1  $\Delta$ N<sub>1-73</sub> (19, 42), an Orai1 chimera with the N-terminus of Orai2 (25) or Orai1 P3,5A and Orai1 P39,40A (19) exhibit significantly reduced store-operated Ca<sup>2+</sup> currents upon store depletion. Together these observations suggest that the extent of maximum current density of Orai channels is at least partially determined by the presence of these prolines within the N-terminus. This region partially resembles the consensus sequence of a PH-domain (66), suggesting that it binds PIP<sub>2</sub>. Thus, it will be interesting to

Recently, a point mutation approach has revealed that a highly conserved amino acid (K85 in CRACM1 and K60 in CRACM3) in the N-terminal region close to the first transmembrane domain represents a critical element for STIM1-dependent gating of CRAC channels (68). These respective single point mutations (K85E and K60E) have abolished store-dependent currents and have diminished store-independent gating by 2-APB (68). Nevertheless, co-immunoprecipitation studies have shown still retained but weaker binding of CAD to an N-terminal peptide of Orai3 K60E N-terminus (68). In aggregate, these results have revealed a single amino acid in the N terminus of CRAC channels essential for their store-operated gating.

A polybasic cluster at the very end of the STIM1 C-terminus - the lysine-rich domain - represents another regulatory region. It is required for the redistribution of STIM1 as its deletion eliminates puncta formation despite preserved STIM1 homomerization (7, 20). Nevertheless, this deletion mutant is still able to activate Orai1 channels in a store-operated manner, yet with a slightly delayed response (42). The polybasic region represents a putative



**Figure 2.** Overview on proteins and lipids interacting with STIM1/Orai1

phosphoinositide binding domain. Hence, it has been assumed that puncta formation is forced by phosphoinositides in the plasma membrane (47). The role of phosphoinositides will be further discussed below.

While STIM1 aggregation is influenced by the lysine-rich region, STIM1/Orai coupling is regulated by the CRAC modulatory domain, termed CMD (aa 474-485). This region comprises seven negatively charged residues and is located in the C-terminus of STIM1. Mutation of at least four of these amino acids or their deletion leads to a strongly enhanced coupling to Orai1 together with 2-3 fold increased  $\text{Ca}^{2+}$  inward currents (17, 69, 70). These enhanced  $\text{Ca}^{2+}$  currents are accompanied by a loss of fast inactivation, as detailed below. In aggregate, it may be assumed that CMD acts as an inhibitory region on STIM1/Orai coupling, current activation as well as inactivation.

### 3.4. Direct interaction of STIM1 and Orai1 and modulatory proteins

Whether the coupling of STIM1 and Orai1 occurs directly or requires additional components has been a

controversial issue for a long time. While Yeromin *et al.* (71) have first observed STIM1-Orai1 co-immunoprecipitation, this has not been observed by Gwack *et al.* (30). Chemically inducible bridge formation between the plasma and ER membranes to estimate the distance of the STIM1/Orai1 has revealed that Orai1 is part of a much larger complex than represented solely by coupled STIM1 and Orai1 (49). One hypothesis favors a  $\text{Ca}^{2+}$  influx factor (CIF), which may be generated via ER store depletion to activate STIM1/Orai1 signaling machinery (72). However, a number of laboratories have demonstrated that STIM1 and Orai1 couple close to each other upon store-depletion employing fluorescence resonance energy transfer as well as biochemistry (20, 28, 62, 63, 73) as mentioned in detail in a previous chapter (19-21, 27, 28). Employing a yeast expression system and purified STIM1 proteins, Zhou *et al.* (74) have demonstrated that STIM1 and Orai1 are sufficient for CRAC channel activation without the requirement of additional proteins. Hence, there is clear evidence that STIM1 and Orai1 represent the key proteins for Orai1 current activation. Additional components within the CRAC channel signaling complex may function in a modulatory manner on CRAC current regulation. These proteins/lipids comprise (overview in Figure 2): CaM (69, 75), CRACR2A/B (76), MS4A4B (77), Golli (78), adenylyl cyclase type 8 (AC8) (79), the polycystin-1 cleavage product P100 (80), caveolin (81), SPCA2 (82) and the L-type  $\text{Ca}^{2+}$  channel (Cav1.2) (83, 84) or the phospholipids  $\text{PIP}_2$  and  $\text{PIP}_3$  (85-87) which have been recently identified to be involved in the STIM1/Orai complex.

CaM represents an ubiquitous signaling molecule playing an essential role in diverse cellular processes ranging from muscle contraction by gene expression to cell growth as well as apoptosis (88). Employing bioinformatics (<http://calcium.uhnres.utoronto.ca/ctdb/ctdb/sequence.html>) a putative CaM binding domain has been identified within the C-terminus of STIM1 as well as the N-terminus of all Orai proteins. While the role of CaM on STIM1 has not been investigated so far, STIM2 mediated CRAC currents are inhibited by CaM (75). This blockage only occurs when intracellular  $\text{Ca}^{2+}$  levels are elevated, suggesting that only  $\text{Ca}^{2+}$ -bound CaM but not apo-CaM is required (75). Yet, functional effects coupled to a direct interaction of CaM with one of the pivotal players of CRAC channel signaling machinery have only been reported for Orai1 (69). (see section on inactivation).

Another EF-hand-containing protein, CRACR2A (76), has been recently reported to stabilize the interaction between STIM1 and Orai1. These proteins are suggested to form a ternary complex which dissociates at higher  $\text{Ca}^{2+}$  concentrations. A mutation in the EF hand of CRACR2A leads to enhanced STIM1 clustering and elevated cytoplasmic  $\text{Ca}^{2+}$  concentrations causing cell death in T-cells. CRACR2A interacts with the N-terminus of Orai1, and requires the positively charged amino acids K85 and K87 in the conserved region close to the first transmembrane domain (76). The homologue CRACR2B seems to have a distinct role to that of CRACR2A. Although its knock-down by siRNA has reduced SOC in HEK and Jurkat cells, its co-expression with Orai1 does not

increase the store-operated  $\text{Ca}^{2+}$  entry to a similar extent as in the presence of CRACR2A. Additionally, an interaction of CRACR2B with Orai1 N-terminus is lacking. Functional electrophysiological studies demonstrating an effect of CRACR2A on CRAC channel currents are not yet available.

MS4A4B is a GITR (glucocorticoid-induced TNFR- (Tumor Necrosis Factor Receptor) related protein) associated membrane adapter which is expressed in regulatory T cells and modulates T cell activation. It has been demonstrated to interact in addition to GITR with diverse surface proteins, and also with Orai1 (77).

Golli, a member of the myelin basic protein (MBP) family has been discovered to directly interact with the STIM1 C-terminus, which is modulated by intracellular  $\text{Ca}^{2+}$  concentrations. An over-expression of Golli reduces SOCE in HeLa cells which can be overcome by additional over-expression of STIM1 (78).

AC8, which generates cAMP via  $\text{Ca}^{2+}$ -bound CaM, has been found to co-localize with STIM1 and Orai1 in lipid rafts (79). A cytosolic FRET-based cAMP sensor has enabled monitoring the increased cAMP production upon elevation of  $\text{Ca}^{2+}$  levels via STIM1/Orai1 coupling. Interference with STIM1 translocation markedly suppresses  $\text{Ca}^{2+}$ -dependent cAMP formation (79). Thus, AC8 forms aggregates with STIM1 and Orai proteins and stimulates down-stream processes following the  $\text{Ca}^{2+}$  influx.

The protein polycystin 1 (PC1), a member of the TRP ion channel family represents an essential regulator of intracellular  $\text{Ca}^{2+}$  in renal tubules of the kidney (80). The cleavage product P100 of PC1 is a 100 kDa fragment that down-regulates store-operated  $\text{Ca}^{2+}$  entry by physical interaction with STIM1 and interference with STIM1 puncta formation. A disease-caused mutation in PC1, has been demonstrated not to inhibit SOCE. Thus, store-dependent  $\text{Ca}^{2+}$  entry might play a role in kidney diseases.

Cav, a member of integral membrane proteins has been shown to bind to an Orai1 Cav consensus-binding site in the Orai1 N-terminus (81). This interaction together with a dynamin-dependent endocytic pathway has been shown to mediate internalization of Orai1 during meiosis in oocytes. At resting state, a significant amount of total Orai1 localizes to intracellular compartments while store depletion completely shifts endosomal Orai1 to the cell membrane. Thus a vesicular trafficking mechanisms controls Orai1 subcellular localization in the oocyte at steady-state, during meiosis, and after store depletion.

SPCA2, a member of the secretory pathway  $\text{Ca}^{2+}$ -ATPases (SPCA), has been reported to constitutively activate  $\text{Ca}^{2+}$  entry (82). This process is dependent on Orai1, however, independent of store-depletion, STIM1 and STIM2. Moreover, it is uncoupled from the  $\text{Ca}^{2+}$ -ATPase activity of SPCA2. The amino terminus of SPCA2 binds to the C-terminus of Orai1, which then enables SPCA2 C-terminus to activate  $\text{Ca}^{2+}$  influx. In this context,

SPC2 and Orai1 have been suggested to promote tumorigenesis of breast cancer derived cells.

Besides SOC channels, voltage-gated  $\text{Ca}^{2+}$  channels provide another major  $\text{Ca}^{2+}$  entry pathway into the cell. Two laboratories (83, 84) have recently shown that STIM1 suppresses  $\text{Ca}^{2+}$  currents of the L-type  $\text{Ca}^{2+}$  channel  $\text{Ca}_v1.2$ . This inhibition is similarly seen with the short STIM-Orai activating region (SOAR) of STIM1 (84). The C-terminus of  $\text{Ca}_v1.2$  interacts with STIM1 leading to an internalization of  $\text{Ca}_v1.2$  (83). STIM1 co-localizes with both  $\text{Ca}_v1.2$  and Orai1 channels in discrete endoplasmic reticulum/plasma membrane junctions (84). Thus, STIM1 interacts with and reciprocally regulates two major calcium channels hitherto thought to operate independently (84).

In summary, STIM1/Orai mediated  $\text{Ca}^{2+}$  entry is apparently fine-tuned by the expression of the above proteins in different tissues (see Figure 2).

### 3.5. STIM1/Orai and lipid rafts

Lipid raft domains have been reported to provide an adequate environment for the interaction of different SOCE-associated proteins (89-91). They contain twice the amount of cholesterol than the surrounding bilayer (92). Due to the rigid nature of the sterol groups, cholesterol partitions preferentially into the lipid rafts where acyl chains of the lipids tend to be more rigid and in a less fluid state (93). One of the first studies focused particularly on the role of lipid rafts in the clustering of STIM1 as well as co-regulation of STIM1 with TRPC1, a member of the canonical transient receptor (TRPC) potential channels (94). Upon sequestration of membrane cholesterol in human salivary gland and HEK293 cells, thapsigargin-induced clustering and puncta formation of STIM1 is significantly attenuated. Both STIM1 and TRPC1 partition to plasma membrane lipid raft domains and their degree of association is dynamically regulated by the status of the ER  $\text{Ca}^{2+}$  content. Disruption of lipid raft domains has decreased plasma membrane recruitment and association with TRPC1 as well as activation of SOC. Together these results suggest that a functional interaction of STIM1 with TRPC1 is facilitated by intact lipid raft domains (90).

Further evidence that STIM1 and Orai1 co-localize in lipid rafts has been obtained of studies on AC8 and TRP as well as Orai channels. Both proteins have been identified in lipid rafts together with STIM1 and Orai1 (79, 94, 95). Disturbance of lipid rafts, employing methyl-beta-cyclodextrin, has reduced association of endogenously expressed Orai1 and both STIM1 and TRPC1 upon depletion of the intracellular  $\text{Ca}^{2+}$  stores and has attenuated thapsigargin-evoked  $\text{Ca}^{2+}$  entry (96). Galan *et al.* have additionally shown that disturbance of lipid rafts, employing methyl-beta-cyclodextrin, reduces association of endogenously expressed Orai1 and both STIM1 and TRPC1 upon depletion of the intracellular  $\text{Ca}^{2+}$  stores and attenuates thapsigargin-evoked  $\text{Ca}^{2+}$  entry (96). Moreover, cholesterol sequestration by methyl-beta-cyclodextrin prevents store-operated  $\text{Ca}^{2+}$  influx (96). In contrast, cholesterol depletion after store-depletion has further

enhanced thapsigargin-induced  $\text{Ca}^{2+}$  entry. Hence, it has been hypothesized that lipid rafts are important for the activation but not for the maintenance of SOCE.

In summary, TRPC1 and AC8, etc have been identified to co-localize with STIM1 and Orai1 in lipid rafts, even if they are not necessarily required for CRAC current activation. However, they might act in a modulatory manner and lipid rafts probably facilitate their interplay.

### 3.6. STIM1/Orai1 and plasma membrane phosphoinositides

STIM1 contains a lysine-rich domain at the very end of its C-terminus which resembles a  $\text{PIP}_2$  binding domain. An interaction with  $\text{PIP}_2$  has been hypothesized to modulate STIM1 puncta formation (47). Various recent studies have focused on the role of phosphoinositides on STIM1 localization as well as SOC activation. ATP depletion which is accompanied by decrease in plasma membrane  $\text{PIP}_2$  has been reported to induce puncta formation of STIM1-Orai1 clusters (85). However, ATP also affects a series of other proteins and signaling cascades within the cell. Walsh *et al.* (86) have reported that  $\text{PIP}_2$  or  $\text{PIP}_3$  depletion alone hardly reduce STIM1 puncta formation, whereas depletion of both phospholipids  $\text{PIP}_2$  and  $\text{PIP}_3$  together significantly reduces targeting of STIM1 to ER-PM junctions (86). Concerning the effect of  $\text{PIP}_2$  on SOCE contradictory results have been obtained (86, 87). Korzeniowski *et al.* (87) have reported that endogenous as well as STIM1/Orai1 mediated SOCE remained unaffected upon  $\text{PIP}_2$  depletion. In contrast, Walsh *et al.* (78) have observed that  $\text{PIP}_2$  depletion reduces endogenous SOCE by about 60%, while over-expression of Orai1 partially reversed this  $\text{Ca}^{2+}$  entry. Moreover it has been reported that  $\text{PIP}_2$  contributes to the stabilization of STIM1-PM interaction rather than to STIM1 translocation (87). One reason for these distinct findings may be seen in the fact that depletion of phosphoinositides is carried out before (78) or after (87) stimulation of puncta formation. Ecran *et al.* (97) have demonstrated preferential binding of STIM1 to liposomes containing  $\text{PIP}_2$  suggesting a specific contribution of  $\text{PIP}_2$  for recruitment of STIM1 C-terminus to the plasma membrane.

Contrary to the phosphoinositides, down-regulation of phosphatidylinositol-4-kinases ( $\text{PI}_4\text{K}$ ) under conditions in which  $\text{PIP}_2$  levels remained constant has not affected STIM1 movements, although STIM1/Orai1-mediated or CRAC currents are strongly inhibited (87).

In summary, phosphoinositides exhibit a regulatory impact on the STIM1/Orai1 signaling cascade, however, other components besides STIM1 might be additionally involved.

### 3.7. Phosphorylation sites in STIM1 and Orai proteins

STIM1 has been defined as a phosphor-protein as it contains a series of phosphorylation sites in its C-terminus (98). Recently, Smyth *et al.* (99) have identified that STIM1 phosphorylation suppresses store-operated  $\text{Ca}^{2+}$  entry during mitosis in accordance to earlier findings (100). Here, two serines S486 and S668 represent the mitosis-

specific phosphorylation sites, and their mutation to alanines rescues mitotic SOCE (99). Additionally STIM1 has been found to function as a probable target of the extracellular-signal-regulated kinase 1 and 2 (ERK1/2) (101). Phosphorylation of ERK1/2 target sites on STIM1 has been shown to modulate store-operated calcium entry. Mutation of these specific sites S575A/S608A/S621A does not alter thapsigargin-induced aggregation or re-localization of STIM1 but does decrease the binding to Orai1. Hence, the authors suggest that the decreased STIM1/Orai1 coupling is responsible for reduced SOC entry.

Store-operated currents are inactive during meiosis, due to an internalization of Orai1 proteins, and diminished STIM1 cluster formation in response to store-depletion (102). Similarly, store-operated currents are suppressed during mitosis which underlies the inability of STIM1 to form puncta near the plasma membrane upon store-depletion. Two residues Ser 486 and Ser 668 have been identified as mitosis-specific phosphorylation sites with their mutation significantly rescuing store-operated  $\text{Ca}^{2+}$  entry (99).

Orai1 is also phosphorylated at N-terminal residues S27 and S30 by PKC (103). Substitution of these serines by alanines has enhanced store-operated  $\text{Ca}^{2+}$  entry as well as CRAC channel currents suggesting that PKC suppresses SOC and CRAC channel function by phosphorylation of Orai1 at these residues.

Thus, phosphorylation of the two pivotal players of the STIM1/Orai1 signaling cascade exerts a modulatory role on CRAC channels.

### 3.8. Regulation of STIM1/Orai1 signaling by oxidative stress

Reactive oxygen species (ROS) are important mediators of many physiological and patho-physiological processes (104, 105) and are generated in the intracellular as well as extracellular space by redox-active proteins (104, 106, 107). Antioxidants clear ROS and preserve the physiological redox state of cells (104, 108). Among the ~20 types of ROS, hydrogen peroxide ( $\text{H}_2\text{O}_2$ ) appears biologically most relevant (104).  $\text{H}_2\text{O}_2$  is relatively stable and can diffuse across the cell membrane. It primarily acts by oxidizing cysteine residues in target proteins (104). In several recent studies a molecular link between oxidative stress and STIM1/Orai1 regulation has been reported (109-111).

Two independent studies have recently shown that native CRAC currents are stimulated by oxidative stress employing micromolar concentrations of  $\text{H}_2\text{O}_2$  (110, 111). Grupe *et al.* (110) have suggested that STIM1 is required for activation of CRAC currents by oxidant stress. Another study has attributed the stimulating effect of oxidative stress on CRAC currents to a decrease in the  $\text{Ca}^{2+}$ -binding affinity of STIM1. The cysteine 56 near the EF-hand within STIM1 N-terminus is S-glutathionylated upon addition of ROS which then triggers STIM1 oligomerization (111). Hence, CRAC channels are



## Gating and permeation of Orai channels

constitutively activated which facilitates an enhancement in  $\text{Ca}^{2+}$  levels.

In contrast, Niemeyer's lab (109) has demonstrated that Orai1 channels are inhibited by oxidation via  $\text{H}_2\text{O}_2$ . Contrary to Orai1, Orai3 remained unaffected upon oxidative stress. The differential redox sensitivity of Orai1 and Orai3 channels depends mainly on an extracellularly located reactive cysteine, which is absent in Orai3. The authors hypothesize that oxidation of cysteines may lock the pore in the closed conformation. Moreover redox sensitivity in  $\text{T}_\text{H}$  cells depends on their differentiation state. CRAC currents in naïve cells are blocked by  $\text{H}_2\text{O}_2$ , while those in effector cells remain unaffected. This difference has been attributed to an enhanced level of Orai3 expression. Thus, the controversial stimulatory or inhibitory effect of oxidative stress on CRAC currents may occur due to a distinct expression ratio of the three Orai homologues compared to the sole Orai1 expression in HEK cells. Moreover, different concentrations of  $\text{H}_2\text{O}_2$  have been employed in these studies (109-111). Alternatively, these results may indicate several target sites on STIM1 and Orai proteins within the CRAC channel signaling cascade.

These findings demonstrate the influence of oxidative stress on STIM1/Orai activation reveal new perspectives of a cross talk between  $\text{Ca}^{2+}$  homeostasis and ROS.

## 4. PERMEATION OF ORAI AND CRAC CHANNELS

The discovery of the three Orai proteins has enabled comparison of their electrophysiological properties with those of endogenous, expressed CRAC currents. Whole cell recordings of CRAC currents with  $\text{Ca}^{2+}$  as a charge carrier yield a current-voltage relationship with a prominent inward rectification and a high reversal potential of  $> +60\text{mV}$  (112). The  $\text{Ca}^{2+}$  selectivity of CRAC channels has been estimated more than 1000 times higher for  $\text{Ca}^{2+}$  over  $\text{Na}^+$  at physiological conditions (113). Hence CRAC channels conduct one of the most  $\text{Ca}^{2+}$  selective currents, and all three Orai channels exhibit similar permeation properties (29, 114). Currents of CRAC and Orai1 channels are transiently increased when  $\text{Ba}^{2+}$  is substituted for  $\text{Ca}^{2+}$  as charge carrier, suggesting a preferred conductance for  $\text{Ba}^{2+}$  over  $\text{Ca}^{2+}$  (115-117). Subsequent steady-state  $\text{Ba}^{2+}$  currents are diminished (29, 118). Omission of  $\text{Ca}^{2+}$  in the presence of extracellular  $\text{Na}^+$  and  $\text{Mg}^{2+}$  abolishes inward current (24, 112). However, in the absence of divalent ions, CRAC and Orai channels become permeable for monovalent ions, like  $\text{Na}^+$  and  $\text{Li}^+$  (29, 113, 118, 119). A  $\text{Na}^+$  divalent-free solution yields increased currents due to a removal of  $\text{Ca}^{2+}$  from a binding site within the pore (117, 120).  $\text{Na}^+$  currents of CRAC channels, Orai1 and Orai2 subsequently depotentiate (121), while Orai3 channels exhibit a significantly slower depotentiation (118). The monovalent cesium ion is almost impermeant for both CRAC and Orai channels, while other  $\text{Ca}^{2+}$  selective channels, such as TRPV6 or L-type  $\text{Ca}^{2+}$  channels are highly  $\text{Cs}^+$  permeable in a divalent-free solution (122, 123). The diameter of a cesium ion covered by a hydration shell

in solution is 3.8 Å. To estimate the pore size of CRAC/Orai channels, methylated derivatives of ammonium with known diameters have been analysed. The size of these ions has been calculated with the Corey-Pauling-Koltun space-filling models (124). The narrowest region of the pore of CRAC/Orai channels has been determined as ~ 3.8 to 3.9 Å (117, 125, 126), suggesting that  $\text{Cs}^+$  ions are small enough to enter the selectivity filter but may be sterically hindered. In addition, CRAC and Orai channels exhibit an extremely small unitary conductance of 9-24 fS, and 6 fS respectively, in a 2-110 mM  $\text{Ca}^{2+}$  solution (117, 121, 127).

Hence, these permeation properties and the amino acid sequence of the Orai proteins which is unrelated to other ion channels suggest a unique selectivity filter for these channels. The CRAC channel is formed by a tetrameric assembly of Orai proteins (33-35) that either contains the same isoforms or any other heteromeric combination (29, 30, 37).  $\text{Ca}^{2+}$  selectivity is expected to be mediated by negatively charged amino acids within or close to the transmembrane regions that interact with and partially dehydrate  $\text{Ca}^{2+}$  ions. Analysis of negatively charged residues reveals altered permeation profiles when glutamates/aspartates within the first and third transmembrane (TM) segment and the first loop (71, 117, 126, 128, 129) are mutated. Orai1 or Orai3 point mutants with a glutamate to aspartate substitution in TM1 (human: E106 in Orai1, E80 in Orai2, E81 in Orai3, drosophila: E180 Orai) results in a strongly reduced  $\text{Ca}^{2+}$  selectivity, but increased monovalent cation permeability (71, 117, 126, 128, 129). E106 substitution to a glutamine or alanine in Orai1 produces a non-permeant channel that acts in a dominant negative manner on all three Orai-mediated (29, 71, 129) and native CRAC currents in T-cells (30, 128). Within TM3 (human: E190 in Orai1, E164 in Orai2, E165 in Orai3 and drosophila: E262 Orai), the glutamate to glutamine substitution affects  $\text{Ca}^{2+}$  selectivity while mutation to an aspartate or alanine retains pore properties of Orai1 and Orai3 (126, 128, 129). The reduced  $\text{Ca}^{2+}$  selectivity of Orai1-E106D and Orai1-E190Q correlates with an increase of the minimum pore size to 5.3 and 7 Å, respectively (117). The enlargement of the narrow Orai1 channel pore comes along with further relief of the steric hindrance for  $\text{Cs}^+$  permeation (117).

In an alternative approach, single residues within the first and third transmembrane segments were systematically substituted to cysteines (130, 131). Hence, accessible cysteine residues are able to interact with applied thiol-specific reagents or  $\text{Cd}^{2+}$ , leading to a rapid channel block.  $\text{Cd}^{2+}$  with a similar size as  $\text{Ca}^{2+}$  ions, strongly blocks several of the mutants with a cysteine introduced in the first TM1 domain, in contrast to methanethiosulfate (MTS) derived reagents. Hence, the bulky MTS reagents are unable to access the deep pore regions (130). Cross-linking of Orai1 mutants in TM1 with cysteines at position 88, 95, 102 and 106 results in dimerisation, demonstrating that TM1 is centrally located between or among Orai1 subunits (31). A weaker dimerization has been observed with several other positions in the N-terminal half of TM1, but not in the C-terminal half (131). The close packing of the



N-terminal segment of TM1 may contribute to the low single-channel conductance and help to coordinate  $\text{Ca}^{2+}$  binding of E106 in Orai1. This glutamate side-chain contributes to limit the maximum size of ions up to 3.8 Å, allowing only small cations such as  $\text{Na}^+$  or  $\text{Ca}^{2+}$  to pass. In line, this constriction is reduced by a substitution to an aspartate that includes a shorter side-chain in comparison to the glutamate.

All cysteine mutants in the third transmembrane domain and especially Orai1-E190C lack any significant changes in ion-selectivity, thus excluding it as a high affinity  $\text{Ca}^{2+}$  binding site (130). These mutants also fail to crosslink, suggesting that TM3 helices are distant from each other in the Orai1 channel (31). Hence, these results have been taken as indication that the TM3 segment with the E190 therein do not flank the ion-conduction pathway (130), suggesting an allosteric effect of E190Q mutant on the pore.

A second important site in the permeation pathway is formed by the first extracellular loop. In contrast to the conserved glutamates in the TM segments of all three Orai proteins, key residues within this loop consist either of glutamates, glutamines, aspartates or asparagines (D110/112/114 for Orai1; E84/Q86/Q88 for Orai2; E85/D87/E89 for Orai3, D182/D184/N186 for *Drosophila* Orai). None of the aspartate to alanine single point mutations in the first loop of Orai1 alters  $\text{Ca}^{2+}$  selectivity. Moreover, a systematic substitution of single amino acids to cysteins within the first loop retained the high  $\text{Ca}^{2+}$  selectivity of wild-type Orai1 (130). However, channel block by lanthanides is reduced for each of the aspartate to alanine loop mutants as well as the Orai1-Q108C mutant in comparison to wild-type Orai1 (71, 130). Alanine substitutions of two aspartates in the first loop of Orai1 (Orai1-D110A-D112A) drastically increase outward currents, while inward currents remain preserved (10). Therefore, at least these two acidic residues together are required to attract  $\text{Ca}^{2+}$  ions towards the pore (71), while a single substitution is silent and probably compensated by the other two aspartates. Alternatively, these mutants allosterically affect the pore and modulate the channels' selectivity. A triple alanine mutant (Orai1-D110A-D112A-D114A) increases  $\text{Cs}^+$  permeability concomitant with an increased minimum pore size of 4.4 Å (117). The cysteine scanning methods reveals several additional properties. Application of 6 to > 8 Å large MTS reagents blocked several of the cysteine loop mutants, suggesting that these residues flank a wide outer vestibule (130). However, it is of note that several cysteine mutants form spontaneous disulfide bonds, suggesting close proximity of residues in the first loops of two Orai1 proteins. These findings can be reconciled if the first loop behaves more like a flexible domain (130) that undergoes a conformational change.

In a heteromeric Orai channel the first loops of different proteins apparently get in close contact during  $\text{Ca}^{2+}$  permeation and may affect pore properties. Indeed, co-expression of Orai1 and Orai3 or an Orai1/Orai3 tandem construct result in a diminished  $\text{Ca}^{2+}$  selectivity and robust  $\text{Cs}^+$  permeation in contrast to homomeric isoforms (132). Substituting glutamates to aspartates in the first loop of

Orai3 mimicking the outer vestibule of Orai1 yield highly  $\text{Ca}^{2+}$  selective currents similar to wild-type Orai channels. However, co-expression with either wild-type Orai3 or Orai1 decreases or recovers  $\text{Ca}^{2+}$  selectivity (132). These experiments suggest that an asymmetric arrangement of aspartate/glutamate within the first loops result in altered pore conformation, probably via an allosteric mechanism. Other reports have presented heteromeric Orai1/Orai3 channels as the molecular basis of the ARC channel that responds to arachidonic acid rather than store-depletion (39, 133). Hence, analysis of native heteromeric Orai1/Orai3 channels (134-136) may help to determine the intrinsic function of the proteins.

Summarizing, the  $\text{Ca}^{2+}$  ions initially enter through a flexible outer pore vestibule and permeate through the narrow pore that is surrounded by residues of helical first transmembrane segments (130). The  $\text{Ca}^{2+}$  ions need to pass the selectivity filter mainly formed by glutamate residues within TM1. A second constriction site arises through the smaller N-terminal packing of TM1 segment. The hydrophilic side-chain of arginine 91 in Orai1, directly located at the interface between TM1 and the N-terminus, is required to allow  $\text{Ca}^{2+}$  passage into the cytosol (137), which is inhibited by mutations to hydrophobic residues.

### 4.1. Distinct effects of 2-APB on the three Orai isoforms

Several compounds that block CRAC currents have been re-examined for their effects on STIM1/Orai mediated channels as recently reviewed (138, 139). The best pharmacologically characterised modulator of CRAC/Orai currents is 2-aminoethoxydiphenyl borate (2-APB). The effects of 2-APB are complex and depend on the Orai isoform. Orai1 and Orai2, when co-expressed with STIM1, are stimulated by low concentration of 2-APB and inhibited by high concentrations, while Orai3 currents are exclusively increased (140). The stimulatory effect of 2-APB is attributed to an increased association of STIM1 with Orai channels as monitored by FRET microscopy (62, 141). The inhibitory effect of 2-APB may result from a reversal of STIM1 puncta formation in store-depleted cells (114, 140). However, co-expression of STIM1 and Orai1 diminishes this effect (114). Alternatively, 2-APB alters the FRET between two labelled Orai proteins, pointing to a conformational change within the channel (62).

In addition, 2-APB is able to modulate the permeation profile of Orai3 channels, suggesting an interaction with the channels' pore. Independent of STIM1 or store-depletion, Orai3 is robustly stimulated by 2-APB (37, 118, 126, 140) and Orai1 to a minor extent (140). While store-operated Orai3 channels exhibit a  $\text{Ca}^{2+}$ -selective inward-rectifying current, those stimulated by 2-APB permeate both  $\text{Ca}^{2+}$  and monovalent cations, yielding a double-rectifying current-voltage relationship (126, 140). A decrease in  $\text{Ca}^{2+}$  selectivity correlates with an increase in pore dimension to more than 5 Å (126). Interaction of 2-APB is mapped to the second as well as third transmembrane segment and the second loop of Orai3 (37). Consistently, we have observed a dramatically decreased sensitivity to 2-APB for an Orai3 chimera with a

substituted 2<sup>nd</sup> loop of Orai1 (unpublished results; R. Schindl, I. Frischauf, C. Romanin). In addition, heteromeric Orai1/Orai3 concatemers, which have been established by direct linkage of the two proteins exhibit substantially reduced 2-APB activation (132). Hence, the homomeric Orai3 channel architecture contains unique structures for 2-APB sensitivity (37). Surprisingly, 2-APB stimulated Orai3 currents represent a similar current-voltage profile as a glutamate to glutamine single point mutant within of the third TM in either Orai1 (Orai1-E190Q) or Orai3 (Orai3-E165Q) (126, 128, 129). Therefore these mutants may adopt a similar conformation in the selectivity filter as Orai3 in the presence of 2-APB. Indeed, store-operated Orai3-E165Q currents are only marginally stimulated by 2-APB (126), suggesting that 2-APB is unable to further enhance currents in this altered pore configuration. An alanine point mutation at a corresponding site in Orai1 (Orai1-E190A) robustly but transiently activated currents upon 2-APB addition, yielding a similar double-rectifying current-voltage relationship (140). Hence, this glutamate located in the third transmembrane domain of Orai3 together with the Orai3 subtype-specific regions is involved in 2-APB interaction.

### 4.2. The Orai1 R91W mutant linked to Severe Combined Immune Deficiency (SCID)

SCID represents a subgroup of immune disorders leading to defective T cell signaling and arises amongst other gene defects by the single point mutation R91W in Orai1 (142-144). This Orai1 R91W mutant displays complete loss of function upon store depletion (9, 137, 145). The arginine at position 91 in Orai1 is fully conserved in Orai2 and Orai3, located at the beginning of the first transmembrane domain (146). Point mutations at respective positions R65W in Orai2 and R66W in Orai3 cause analogous loss of function as with Orai1 R91W (126, 137). Whether the Orai SCID mutant acts in a dominant negative manner has so far remained controversial. While Muik *et al* (28) have reported that Orai1 R91W causes a noticeable delay of activation but no significant reduction of maximum STIM1/Orai1 currents, other studies (147, 148) have determined a dominant negative effect of Orai1 R91W on SOCE in HEK cells. A series of concatenated tetramers of Orai1 proteins that contain increasing numbers of mutant Orai1 R91W linked to wild-type Orai1 proteins exhibit a gradual reduction of Ca<sup>2+</sup> currents (40). Hence the diverse observations may arise from distinct channel stoichiometries due to different expression levels of wild-type Orai1 and its R91W mutant.

Despite a functional defect of Orai1 R91W its coupling to STIM1 is still largely preserved. A series of point mutants substituting the arginine at position 91 by various other amino acids ranging from charged to hydrophobic residues, has revealed that the increase in hydrophobicity at the N-terminus/transmembrane interface represents the major cause for yielding non-functional Orai channels (137). Structurally, this enhanced hydrophobicity may alter Orai channel conformation by altering the orientation of the first transmembrane helix in the plasma membrane thus resulting in loss of channel function. As Orai channels with an increased pore size (117) such as

Orai1 E106D or Orai3 in the presence of 2-APB (126) that additionally include the R91W or R66W mutation, respectively, also remain non-functional, we have suggested a markedly disrupted permeation/gating for the Orai1 R91W mutant (137).

Navarro-Borelly *et al* (62) report that store depletion triggers molecular rearrangements in Orai1 which are possibly reflected by a decline in Orai1–Orai1 homomeric FRET. Such a reduction has been similarly detected for Orai1 R91W–Orai1 R91W homomers. They attributed this decrease in FRET to a conformational coupling induced by the coupling of STIM1, which occurs both for wild-type Orai1 as well as its R91W mutant. Hence, these authors (62) suggest a defect in permeation rather than channel gating of Orai1 R91W. Nevertheless, a potential constriction or collapse of the pore appears unlikely, as Orai mutants with increased pore sizes do not recover function. As permeation is somehow coupled to gating (117), both processes are probably defective in the Orai1 R91W mutant. The findings that an increased hydrophobicity at the N-terminus/transmembrane interface leads to disrupted channel function by disturbed permeation/gating offers a mechanistic interpretation of SCID-linked Orai1 R91W non-functionality. However, an ultimate proof for the suggested defect in permeation / gating structures awaits resolution at the atomic level by crystallizing the respective Orai1 proteins.

## 5. INACTIVATION OF ORAI AND CRAC CHANNELS

Accurate control of activation and inactivation of Ca<sup>2+</sup> channels is a prerequisite for correct cell function. Fast inactivation of CRAC channels limits Ca<sup>2+</sup> influx into the cell and thus represents an important feedback mechanism. It occurs over tens of milliseconds during hyperpolarizing voltage steps and results from feedback inhibition of channel activity by high cytoplasmic Ca<sup>2+</sup> concentrations close to the channels pore mouth (113, 149). However, the resolution of the underlying mechanisms of rapid inactivation is only starting to emerge.

All store-operated Orai channels display fast inactivation within the first 100 ms of a voltage step, with that of Orai3 three times stronger compared to Orai1 or Orai2 (29, 70, 132). Subsequently Orai1 channels reactivate, while Orai2 and Orai3 currents exhibit a slow inactivation phase over 1 second (29, 132).

For native CRAC channels, Zweifach *et al.* (149) have demonstrated that fast inactivation is strongly reduced in the presence of Ba<sup>2+</sup> compared to Ca<sup>2+</sup>. It is of note that inactivation of native CRAC currents in RBL cells (17) as well as Jurkat T lymphocytes (149) is much more pronounced than that observed for Orai1 currents in HEK 293 cells. Moreover the characteristic reactivation phase of Orai1 currents is lacking for native CRAC currents. Apparently, additional factors contribute to inactivation of native CRAC currents, among which a potential involvement of other Orai proteins may be considered. Orai2 and Orai3 proteins when expressed together with

STIM1 in HEK293 cells exhibit indeed a stronger, fast inactivation than Orai1, and at least Orai2 expression is reported for RBL cells (29). Thus heteromeric assemblies with Orai1 possibly increasing the extent of inactivation are conceivable. Alternatively the distinct amount of inactivation in native tissue compared to over-expression systems might result from a distinct stoichiometry within a STIM1-Orai1 complex (150). Recently it has been reported that low Orai1 to STIM1 ratios produce CRAC currents with strong fast  $\text{Ca}^{2+}$ -dependent inactivation, while cells expressing high ratios yield attenuated inactivation (150). The results suggest that several key properties of  $\text{Ca}^{2+}$  channels formed by Orai1 depend on its interaction with STIM1. Consequently, the stoichiometry of this interaction may vary depending on the relative expression levels of these proteins and thus result in varying fast inactivation.

Further molecular determinants for inactivation of Orai channels are represented by cytosolic regions of the Orai channels as well as C-terminal regions within STIM1 (for an overview see Figure 1).

Regarding the role of Orai N-terminus in fast inactivation, an interaction of calmodulin (CaM) with a membrane proximal N-terminal domain in Orai1 has been identified (69). Specific mutations within this CaM binding domain (A73E, W76E, Y80E) which abrogate CaM binding have reduced fast inactivation (69). However, further detailed analysis is still required to elucidate how STIM1, Orai and CaM interplay. A potential effect of other Orai N-terminal regions like the arginine-/proline-rich domain within Orai1 or the conserved region close to the first transmembrane sequence on inactivation is still unresolved.

Transfer of the C-terminus of Orai1 onto Orai2 or Orai3 results in chimeric channels exhibiting diminished Orai1-type fast inactivation (70). Fast inactivation of Orai2 and Orai3 channels has been attributed to three conserved glutamates in their C-termini (70). Moreover a central region within the intracellular loop of Orai1 between TM2 and TM3 is essential for fast inactivation of Orai1 (151). Mutations within this loop region have decreased fast inactivation. Since fast inactivation of a concatamer containing three loop mutants and one wild-type Orai1 subunit is still present, it has been concluded that a single functional loop domain is sufficient for inactivation probably by blocking the pore. Expression of a peptide comprising the second loop inhibited Orai1 channel activity, suggesting a key role of the second loop as inactivation particle (151).

Yamashita *et al.* (117) have demonstrated that fast inactivation is additionally controlled by negatively charged residues within the outer pore vestibule of Orai1 channels. Their mutation to alanines has diminished  $\text{Ca}^{2+}$ -mediated fast inactivation concomitant to an alteration of ion permeation properties.

Hence, multiple domains within Orai channels have been identified contributing to current inactivation.

Within STIM1, an acidic cluster (aa 475-483) is indispensable for fast inactivation of all Orai channels (17, 69, 70). Mutations of all the negatively charged residues within this CRAC modulatory domain (CMD) to alanines inhibited or reduced fast inactivation of all Orai1-3 channels. Interestingly, partial D/E to alanine mutations revealed that four negative residues (aa475, 476, 478, 479) within CMD are sufficient for Orai1 (17) but not Orai3 (70) to accomplish fast inactivation. Since Orai1 displays besides fast inactivation, a unique slow reactivation phase, we further examined if it is influenced by the negative residues. However, CMD mutations or deletions in full-length STIM1 as well as STIM1 C-terminal fragments did not affect the extent of reactivation (data not shown). Similarly, fast inactivation of CRAC currents in RBL cells was reduced by over-expressing STIM1 C-terminus with the seven negatively charged residues mutated to alanines (STIM1 C-terminus 7xA) (17) compared to those expressing wild-type STIM1 C-terminus while the second phase of the inactivation profile remained unaffected.

As mutation of negative residues within Orai2 and Orai3 C-termini have been additionally shown to inhibit fast inactivation, Muallem's group has proposed a model where the negative residues of both STIM1 and Orai C-termini act as  $\text{Ca}^{2+}$  sensor to reduce channel activity (70). Concomitant mutations of anionic amino acids in either C-terminus substantially but not fully inhibited fast inactivation. Hence, additional domains/components may contribute to this negative feedback mechanism.

### 5.1. 2-APB alters inactivation of Orai/CRAC channels

The dual 2-APB action on native CRAC currents of T-lymphocytes is also accompanied by alterations in the kinetics of fast  $\text{Ca}^{2+}$ -dependent inactivation. Activation of these currents by concentrations of 1-5  $\mu\text{M}$  2-APB enhances the extent of fast inactivation. In contrast, inhibition by high concentrations of 2-APB is accompanied by the loss of fast  $\text{Ca}^{2+}$ -dependent inactivation (115, 125, 149, 152). Based on the concomitant reduction of both CRAC current amplitude and inactivation, it has been hypothesized that these effects are possibly linked (125). Prakriya *et al.* (125) have hypothesized that 2-APB may interrupt the coupling between the CRAC channel and components mediating activation and fast inactivation. The hypothesized component mediating inactivation of CRAC currents (125) may be represented by STIM1. Whether 2-APB disrupts coupling of STIM1 to Orai is still a matter of debate. It seems that the mechanism of inhibition is more complex than simple pore blockade, particularly with the Orai3 isoform. The intriguing strong activation of Orai3 currents by high concentrations of 2-APB occurs along with a loss of fast inactivation and the induction of a robust reactivation phase (data not shown). In this case, 2-APB affects both activation and inactivation, but also the selectivity of the pore. Based on the findings that 2-APB stimulated Orai3 channels display an increased pore size, it appears likely that the pore is somewhat linked to the inactivation gate.

## 6. CONCLUSIONS

Store-operated  $\text{Ca}^{2+}$  channels have been extensively studied over the last 20 years before Orai1 and STIM1 has been identified as the two pivotal key players in the CRAC channel signaling machinery of T-cells (9). They are involved in a broad range of cellular processes together with their pharmacological, physiological and pathophysiological roles and an important role in autoimmune and inflammatory immune disorders (2). The identification of STIM1 and Orai1-3 and their role in calcium signaling through SOC/CRAC channels opens the repertoire for targeting immune diseases, like rheumatoid arthritis, inflammatory disorders, allograft rejection (138). In lymphocytes, mast cells as well as platelets, novel drug development is additionally clear in light of the uniquely important roles of the Orai proteins (138).

Various proteins have been already identified which additionally couple to and/or modulate the STIM1/Orai signaling machinery (Figure 2). Their overall interplay expected to be tissue-specific awaits detailed characterization. Although these additional proteins are dispensable for basic STIM1/Orai function, they may still have a modulatory impact fine-tuning the CRAC channel machinery.

The identification of STIM1 and Orai proteins has further allowed characterizing molecular events and structure-function relationships governing CRAC current activation, permeation and inactivation (Figure 1). However, within this signaling cascade various processes still require more detailed elucidation. Particularly, the activation step (s) transforming STIM1 interaction with Orai1 into the opening of CRAC channels is only partially understood. FRET microscopy studies have provided evidence for a conformational change of the intracellular N- and C-termini of Orai1 upon binding to STIM1 (62). These changes may be coupled to movements of the gate and provide the energy required for CRAC channel opening. This process may be similarly mirrored in conformational rearrangement within STIM1 which has been recently suggested to involve an intramolecular switching mechanism (50).

While the Orai1 C-terminus is an essential region for coupling to the CAD/SOAR domain in STIM1, an important role of the Orai1 N-terminus for the gating has recently been reported (153). The proposed bridging of Orai N- and C-termini via STIM1 together with the identification of the respective interactions sites on both proteins has still to be demonstrated.

While several Orai domains contribute to the in-/reactivation behaviour, those that are responsible for the distinct subtype-specific gating profiles have so far remained elusive. A chimeric approach with single to multiple domain exchange may reveal a potential interdependence of domains in controlling inactivation/reactivation.

A 3D atomic resolution of Orai and STIM1 proteins, preferentially as complex, will reveal ultimate insight not only in the gating process, but also on the unusual selectivity filter of this ligand-gated  $\text{Ca}^{2+}$  channel, and pave the way for rational drug design.

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**Abbreviations:** ARC: arachidonate regulated  $\text{Ca}^{2+}$ , 2-APB: 2-aminoethyldiphenyl borate, CIF:  $\text{Ca}^{2+}$  influx factor, CMD: CRAC modulatory domain, CRAC:  $\text{Ca}^{2+}$  release activated  $\text{Ca}^{2+}$ ,  $\text{IP}_3$ : inositol 1,4,5-triphosphate, MTS: methanethiosulfate, RBL: rat basophilic leucemia; ROS: reactive oxygen species, SAM: sterile alpha motif, SCID: severe combined immune deficiency, SOC: store-operated  $\text{Ca}^{2+}$ , SOCE: store-operated  $\text{Ca}^{2+}$  entry, TRPC: canonical transient receptor potential

**Key Words:** STIM1, Orai, CRAC, Activation, Permeation, Gating, Inactivation, Review

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