Conformational dynamics in TRPV1 channels reported by an encoded coumarin amino acid

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Abstract TRPV1 channels support the detection of noxious and nociceptive input. Currently available functional and structural data suggest that TRPV1 channels have two gates within their permeation pathway: one formed by a ‘bundle-crossing’ at the intracellular entrance and a second constriction at the selectivity filter. To describe conformational changes associated with channel gating, the fluorescent non-canonical amino acid coumarin-tyrosine was genetically encoded at Y671, a residue proximal to the selectivity filter. Total internal reflection fluorescence microscopy was performed to image the conformational dynamics of the channels in live cells. Photon counts and optical fluctuations from coumarin encoded within TRPV1 tetramers correlates with channel activation by capsaicin, providing an optical marker of conformational dynamics at the selectivity filter. In agreement with the fluorescence data, molecular dynamics simulations display alternating solvent exposure of Y671 in the closed and open states. Overall, the data point to a dynamic selectivity filter that may serve as a gate for permeation.

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Introduction Cation channels from the TRPV family are functional tetramers with a central pore domain that is shaped by TM5 and TM6 transmembrane segments from each of the four subunits (Ramsey et al., 2006) (Figure 1a). As in Shaker-related tetrameric ion channels, the pore domain houses the ion selectivity filter and an intracellular ‘bundle crossing’ formed by the α-helical S6 segments. Functional and structural data suggest that the selectivity filter and inner bundle crossing have the potential to control the flux of ions according to the electrochemical gradient (Cao et al., 2013; Gao et al., 2016; Salazar et al., 2009). The lower constriction is highly conserved (Palovcak et al., 2015) and associated to the canonical gate (Cao et al., 2013; Steinberg et al., 2014), but less is known about the putative role of the upper constriction at the ion selectivity filter, possibly due to the functionally sensitive nature of this region to side-chain mutagenesis. Nevertheless, high-resolution structures of TRPV1 suggest that the upper constriction undergoes structural changes in the presence of DkTx (Gao et al., 2016), a spider toxin that increases the open probability of the channel (Siemens et al., 2006). Moreover, the inhibition of the unitary conductance of TRPV1 channels...
by protons suggests that the selectivity filter region is flexible and is capable of adopting multiple, functionally distinct conformational states (Liu et al., 2009; Wen et al., 2016). However, it is not known if such conformational dynamics at the selectivity filter might be coupled to channel activation by agonists, such as capsaicin, and if filter gating is sufficient or acts in concert with the lower bundle crossing to control the ionic conductance.

Researchers have a number of unanswered questions about how TRP channels work. Where in the channels are gates located? How do the channels control the flow of ions, and how do they communicate with each other? And which regions of the protein sense environmental cues? As a result, new technologies are being developed to make it easier to study the types of rearrangements that TRP channels experience when they activate.

Steinberg, Kasimova et al. have used total internal reflection microscopy – a method that images fluorescent molecules – to measure the conformational change of a single TRP channel in a living cell. This channel, called TRPV1, senses external heat and plays an important role in pain perception. Its gate can also be opened by the pungent compound of chili pepper, capsaicin.

The results of the experiments suggest that a selectivity filter region in TRPV1 channels changes its shape when the channel opens in response to capsaicin. Then, this selectivity filter appears to do double duty – it controls which types of ions pass through the channels as well as controlling their flow rate.

Because of its role in pain perception, having a better understanding of how TRPV1 works will be valuable for researchers who are trying to develop new pain relief treatments. The so-called ‘seeing is believing’ method used by Steinberg, Kasimova et al. could also be used to study other membrane proteins, both to guide drug development and to improve our understanding of how cells interact with their environment.

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Figure 1. Functional expression of coumarin-containing TRPV1 channels at the membrane of HEK-293T cells.
(a) Top-down and lateral view of the pore region of rTRPV1 tetramers. Dashed lines denote the positions of putative gates, a canonical gate at I679 and a secondary constriction within the pore at Y671 (green shade). The different subunits are shown in different colors. (b) Epifluorescence images obtained from transiently transfected HEK-293T cells. Cells were co-transfected with wild-type rTRPV1-YPF and with rTRPV1-Y671coum. The scale bar corresponds to 10 μm. Images correspond to the average of 50 frames. (c) Representative traces obtained from transiently transfected HEK-293T cells subjected to voltage steps from −180 mV to +180 mV, in 20 mV increments, Figure 1 continued on next page.
The f-ncAA coumarin has potential for the study of expressed protein conformational dynamics because of its small size and its exquisite sensitivity to environmental polarity (Liu et al., 2015; Wagner, 2009; Wang et al., 2006). This sensitivity can be exploited to report on variations (i.e. dielectric changes) in the surroundings of the incorporated f-ncAA and, in turn, it can be interpreted as a signature of a protein conformational change. Notable examples include the use of coumarin and the amber codon suppression technique to report on peptide binding to viral proteins (Ugwumba et al., 2011), on the photoregulation of firefly luciferase and on the subcellular localization of proteins in living mammalian cells (Luo et al., 2014), as well as on structural rearrangements in isolated NaK channels (Liu et al., 2015).

Here, the spectral dynamics of an encoded hydroxy-coumarin were determined in individual live cells with total internal reflection (TIRF) microscopy and rapid imaging of single emitters to study the conformational changes occurring within the pore of the capsaicin receptor TRPV1 during activation.

**Results**

**Expression of Tyr-coumarin at genetically encoded positions**

Previous cysteine accessibility experiments showed that Y671C residues define the boundary for both silver (Ag+) state-dependent accessibility and disulphide bond formation in the closed state (Salazar et al., 2009). Thus, we reasoned that a genetically encoded coumarin residue at position Y671 (Y671Coum) would be functionally tolerated and if so, could potentially be well positioned to report on local structural rearrangements occurring within the pore during gating (Figure 1a). As expected for cells containing an encoded fluorescent probe, HEK-293T cells heterologously expressing both TRPV1–YFP and amber codon-containing TRPV1 mutants (TRPV1–YFP/ TRPV1Tag) exhibit coumarin–YFP colocalization (Figure 1b; Figure 1—figure supplement 1) consistent with the presence of coumarin and YFP co-fluorescence. Whole-cell patch-clamp electrophysiological recordings performed at room temperature (22°C) demonstrate the functional expression of the coumarin-containing TRPV1 channels (TRPV1Tag) when expressed alone or at 1:7 molar ratio (TRPV1Tag:TRPV1–YFP) (Figure 1c). The later condition was chosen to simplify the imaging of single emitters (i.e. one coumarin molecule per channel tetramer or cluster of tetramers). Both macroscopic channel kinetics and the conductance-voltage (G-V) relationship were similar between wild type (WT) and coumarin-containing channels (Figure 1c). The G-V relationship from wild type and coumarin channels were well fit by a Boltzmann function with a half-maximal activation voltage (V0.5) near +100 mV (Figure 1d).

Thus, the data suggest that position Y671 in TRPV1 is amenable to nonsense suppression and encoding of f-ncAA coumarin.
Optical recordings of capsaicin-induced changes in solvation

In order to demonstrate the ability of the genetically encoded hydroxy-coumarin side chain to act as a reporter for protein activity in live cells, HEK Y671-coumarin TRPV1 expressing cells were imaged within the evanescent field in total internal reflection fluorescence (TIRF) microscopy, with a single-photon counting avalanche diode (SPAD) camera (64 × 32 pixels array with in-pixel counters) (Bronzi et al., 2014; Michalet et al., 2013). Specifically, photon counts of the emission signal were examined to determine the effect of capsaicin, the canonical agonist of the TRPV1 channel (Figure 1e and f; Figure 1—figure supplement 2). The photon count distribution showed clear differences between pixels representing background and pixels from fluorescent spots, which presumably arise from fluorescent channel subunits (Figure 1f). Further, when the cell is exposed to a maximal concentration of capsaicin (3 μM), the photon counting rate further shifted to higher values (Figure 1f). The modes observed for these populations showed significant differences (n = 4; p<0.05). One interpretation of the capsaicin-induced increase in photon emission counts is that it stems from local changes in the immediate environment of the dye. To simplify the analysis and interpretation of the optical data, we set out to measure the fluctuations of the fluorescence signal emitted from a single diffraction-limited emitter directly. Given the large pixel size and the low fill-factor of the SPAD array used (Bronzi et al., 2014; Michalet et al., 2013), the precise localization of a diffraction-limited signal is not possible under the condition of overexpression of membrane proteins in living cells. Therefore, steady state fluctuations of fluorescence were recorded by an electron-multiplying charge coupled device (EM-CCD) camera to resolve changes in the optical properties of the dye (Blunch et al., 2008).

As in the electrophysiological experiments, cDNAs encoding for both wild-type channels (TRPV1) and amber-codon-containing mutants were mixed in 7:1 ratio to promote the formation of uneven channel tetramers. This strategy results in a small yet discrete number of diffraction-limited coumarin-emitting spots as observed by TIRF microscopy (Figure 2a). The coumarin signal colocalizes well with the YFP signal corresponding to wild-type YFP-tagged channel subunits (Figure 2a).

Close examination of these fluorescent spots by photobleaching showed a stepwise behavior allowing for ex-post identification of spots containing a single emitter (Figure 2b). A clear change in fluorescence was evidenced by the ensemble average of several diffraction-limited spots once the cell is exposed to capsaicin (3 μM; Figure 2c). The ensemble recording showed not only an increase of fluorescence after agonist treatment but also increases in the standard deviation of the signal’s mean value (Figure 2c).

Activation kinetics obtained from the optical signal

Given the Y671 position within the TRPV1 selectivity filter, we reasoned that the environmental sensitivity of coumarin may well provide kinetic information on channel gating. Stationary noise analysis was performed on the basis of the autocorrelation (C(t)) of the fluorescence signal (Figure 3a). The autocovariance function can be used to calculate the correlation between values of a noisy signal taken at increasing time intervals, Δt. In this regard, C(t) will be higher for small values of Δt (i.e. for data points close to each other) and this function rapidly decays as Δt become larger. In the present example, this analysis allows for the identification of a characteristic time constant (τ) of the exponential decay, which describes the autocorrelation of the fluorescent signal originating from single emitters. The obtained τ has an inverse relationship to the rates defining the equilibrium of the reaction between open and closed states (Anderson et al., 1973; Zingsheim and Neher, 1974). The calculated autocorrelation function discriminates well between the three conditions tested (i.e. background, no capsaicin, and capsaicin present in the media). The background signal is obtained from cells that have the coumarin amino acid but lack the expressed TRPV1 TAG cDNA. This condition generated noise with a single, fast time constant (τ = 8.5 ms) that was easily separated from the double exponential decay time constants observed in the signal originating from the encoded coumarin conditions. In the absence of capsaicin, the coumarin signal autocorrelation had two time constants with corresponding values of 12 ± 6 ms and 78 ± 22 ms. Incubations with saturating capsaicin concentrations (3 μM) changed these time constants to 13 ± 4 ms and 148 ± 38 ms (n = 7; Figure 3a), consistent with the possibility that the encoded coumarin is reporting on an agonist-induced increase in τ. Such a result can be interpreted as an stabilization of the bright state after ligand binding (i.e. longer bursts of activity) either alone or in combination with the destabilization of
the dark or non-emitting state, a possibility consistent with the previously determined distribution of closed and open states in TRPV1 channels when activated by capsaicin (Hui et al., 2003).

In order to begin to distinguish between these possibilities, we examined unitary transitions in the optical data (Figure 3b; see Materials and methods). To do so, we inferred that the signal minima (i.e. \( L_0 \)) would correspond to the magnitude of background signal and would corroborate that fluorescence transitions drop from a given maxima (\( L_1 \)) to the observed minima (\( L_0 \)) as expected (Figure 3b, inset). We analyzed the signal in the presence of capsaicin using a threshold-crossing criterion, where the threshold was chosen as 2.5 times the standard deviation of the mean amplitude of background fluctuations (see Materials and methods). This strategy produced an idealized recording, similar to the analysis of single ion channel current idealization trace (Figure 3b). An analysis of this record shows that the agonist does not affect the amplitude of the fluorescence fluctuations, but rather it promotes a shortening of the mean dwell-time of the bright state, which we defined as \( L_1 \), going from 398 ± 133 ms to 156 ± 52 ms (n = 5; Figure 3c and d). On the other hand, capsaicin increases the probability of being in the bright state (Figure 3). Taken together, these two observations support the notion that capsaicin increases the burst length of transitions to the bright state.

This is in agreement with the autocorrelation data, which show that capsaicin increases the time constant, and consistent with an increased burst length of bright events. The data from single emitters also supports previous data showing that the main gating effect of capsaicin is increasing the burst-length of openings by shortening the closed state, instead of prolonging the duration of the open state (Hui et al., 2003).

Overall, the fluorescence data is consistent with the possibility that coumarin at position Y671 reports on the transition between open and closed states of the channel. Further, given the physicochemical properties of coumarin (i.e. that it is quenched in an aqueous environment), the data
Figure 3. Optical studies of ion channel gating. (a) Stationary noise of single spots, with each curve corresponding to the averaged fitted curves for the indicated conditions (n = 7, paired). The autocorrelation function was obtained for background (gray), capsaicin free (blue), and 3 μM capsaicin (orange). (b) Analysis of fluorescence fluctuations. Superimposed traces of capsaicin (blue) and background (red). The threshold for level one is highlighted (2.5 standard deviations [SD], dotted line). The gray box indicates the zoomed-in portion of the recording presented in the inset below, with the dotted lines indicating background average. An idealization is shown in black. (c) Semi-log plot of the amplitude versus dwell-time shows a shortening of mean time $L_0$. (d) Plot summarizing datasets of amplitude versus dwell time at 0 and 3 μM capsaicin (n = 5, paired). Error bars correspond to SEM. (e) Dose–response curve showing changes in the probability of level 1 ($P_{L1}$), calculated from non-corrected fluorescence fluctuations, for the two positions tested for the indicated channel types expressing coumarin. (f) Normalized dose–response curves for background subtracted fluorescence fluctuations (orange) and whole-cell electrophysiological response (purple). The electrophysiological response was tested at $-70 \text{ mV}$ in the presence of the indicated concentrations of capsaicin. Error bars correspond to SEM.

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The following figure supplements are available for figure 3:

Figure supplement 1.
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Figure supplement 2. Distribution of the whole data set obtained from the fluctuation analysis of the fluorescence signal.
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suggest that position Y671 is more water-exposed and thus has decreased in fluorescent output, in
the closed state compared to the open state (Wagner, 2009). By comparison, the available TRPV1
structural data place W426 in an apparently invariant solvent-exposed region (Figure 3—figure sup-
plement 1a), thus, the open-closed transition would not be expected to induce evident changes in
local solvation (Gao et al., 2016). In order to investigate the specificity of the spectral effects mea-
sured at Y671 with coumarin, a second site, W426, was examined in parallel. Electrophysiological
analysis confirmed that W426coum is a functional channel (Figure 3—figure supplement 1b and c),
and the photon-count analysis suggests that the fluorescence signal from this position is insensitive
to capsaicin administration (Figure 3—figure supplement 1d and e). Further, the fluctuations of
coumarin fluorescence at 426coum are unresponsive to capsaicin treatment, as determined by the cal-
culated bright state probability, P11 (Figure 3e; Figure 3—figure supplement 1f and g). Conversely,
the P11 of position 671coum reported capsaicin dose-dependent fluorescent changes which are well
fitted by the capsaicin dose-response curve obtained from capsaicin-activated currents at ~70 mV
(Figure 3e; Figure 3—figure supplement 2). Lastly, when the fluorescence data from Y671coum
was normalized and compared with the electrophysiological data taken from whole-cell macroscopic
recordings, we observed a close match between the calculated EC50 for optical and electrophysi-
ological data, 0.33 μM versus 0.43 μM, respectively (Figure 3f). Taken together, the data and bio-
physical analysis suggest a continuum of coordinated motions within the pore, with the Y671coum
optical data reporting on a transition to the open conducting conformation in the selectivity filter.

Rearrangements of tyrosine 671 during closed-open transition

To relate the changes in coumarin fluorescence to possible structural transitions experienced by the
channel during gating, we analyzed the molecular dynamics (MD) trajectories of wild-type and
671coum TRPV1 channels in the closed and open states (about 750 ns each). First, we compared the
conformations that Y671 adopts in the closed and open states of TRPV1 (Figure 4a and b).

In the closed state, the representative conformation shows that three out of four phenyl moieties
are approximately perpendicular to the membrane and do not contact each other (Figure 4a). In
this conformation, phenyl moieties create transient hydrogen bonds with the main-chain of F640 of
the selectivity filter. In the open state, the planar groups of the four tyrosine residues instead adopt
a parallel orientation to the membrane, forming a ring around the central pore (Figure 4b). These
opposing orientations in the closed and open conformations predicts an increase in the hydration of
the central pore, with the four Y671 moieties being more hydrated in the closed state (Figure 4c).
Surprisingly, the open state shows an intermittent occupancy by water molecules of the region sur-
rounded by the four Y671 side chains. Despite being somewhat counterintuitive, this observation is
not in contradiction with the conductive nature of the open state: even when devoid of
water molecules, the environment provided by the ring of hydroxyl groups from Y671 is highly polar
and does not impede ion permeation. In spite of these water density fluctuations, the pore is, on
average, continuously hydrated only in the open state (Figure 5a). Na+ permeation events in our
simulations (in the absence of any applied external field) were observed in the open state, but not in
the closed state.

An additional insight provided by the simulations is that the hydration of Y671 is different in the
two conformations: in the open channel, one face of the phenyl ring is exposed and the adjacent
ring is partially buried by F640 and M644, whereas in the closed state, both faces of the Y671 side
chain are exposed to water. To describe hydration of Y671 quantitatively, we calculated the corre-
spanding solvent accessible surface area (SASA) in the open and closed conformations. The evolu-
tion of the Y671 SASA reveals that the two MD trajectories start to diverge quite early: in particular,
in both conformations, the Y671 SASA drops down from ~35% to ~20% at the beginning of the
equilibration; then, after ~30 ns, in the closed and open states, respectively, the SASA either
increases up to ~30% or continues to decrease until it reaches an equilibrium value of ~15%
(Figure 4d). Further, it can be observed that although the open state displays the side chains of
Y671 residues engaged in mutual hydrogen bonding interactions, they establish vDW interactions
with nearby residues F640 and M644, whose side chains are in between the selectivity filter back-
bone groups of two adjacent subunits (Figure 4e). In the closed state, F640 and M644 residues still
interact with Y671 as in the open state; however, the different orientation of the side chain phenyl
groups allows for a rigid displacement of the pore helix toward the extracellular side of the pore,
narrowing the diameter of the selectivity filter (Figure 4a and e and Figure 5a and b).
Figure 4. Molecular dynamics simulations to calculate hydration of Y671. Molecular dynamics (MD) simulations of TRPV1 channels in the open (a) and closed (b) states. The upper and lower panels correspond to the side and top views of the S6 helices bundle (white), respectively. The pore helices (ph) are shown in blue. Y671 residues are represented as yellow sticks. In the open state, four Y671 residues create a ring oriented parallel to the membrane.

Figure 4 continued on next page
To explore the plausibility of this hypothetical gating mechanism, we performed additional simulations in which four coumarin moieties were modeled in the place of the side chains of Y671. The rationale for these additional calculations was to ascertain whether the bulkier coumarin moiety (as compared to tyrosine phenyl group) can accommodate configurations similar to those accommodated by the wild type. In particular, would the ‘ring configuration’ in the open state allow ion permeation in the case of coumarin? Is coumarin in the ‘vertical configuration’ able to establish H-bonds with and thus promote the displacement of the pore helix in the closed state? Although the length of the simulations performed on the coumarin mutant would need to be extended in order to establish a more quantitative comparison with the experimental data, these cursory calculations suggest that the proposed gating mechanism is not incompatible with the molecular size of the coumarin moiety (Figure 5c; Figure 5—figure supplement 1).

Discussion
Ion channel gating occurs in the range of hundreds of μs and it is one of the fastest protein-dependent processes occurring within cells (Hille, 2001). This rapid time-frame imposes intrinsic technical barriers in the detection of a limited number of photons coming from few emitting molecules and a consequent low signal-to-noise ratio under these conditions (Ha, 2014). Given the design of our imaging setups and our experimental conditions (i.e. transient overexpression), we are bound to either the low (64 × 32 pixel) spatial resolution of the ns-time-scale sampling of the SPAD imager (which does not allow us to discriminate single emitters) or to a low signal-to-noise ratio restricting us to image at a maximum of 500 Hz (ms-time scale) for the individual diffraction-limited spots observed by an EM-CCD camera. As reported previously (Blunck et al., 2008), we observed that the latter approach is useful for conformational transitions in the order of 2–5 ms, thus barring optical access to the fast intra-burst channel activity that occurs in tens of μs. Therefore, the unitary transition analysis presented here was limited to the description of each burst as a single opening at the expense of missing activity during short openers. None the less, such an analysis, although lacking detail on unitary transitions, is a valid approach for estimating the duration of the mean open and closed state for a ligand-gated channel such as TRPV1, which has an open transition lasting for several hundreds of ms (Hui et al., 2003). The ideal experimental system would allow for sparse distribution (every ~1 micrometer) of the emitter-expressing receptors at the plasma membrane, so that the photon-count profile of individual molecules can be obtained with the SPAD imager with nanosecond resolution. However, in the absence of such technical advances, standard biophysical approaches are in place to provide insights on unitary gating events from an expressed population of channels. Interestingly, the similar rate constants obtained by noise analysis of the optical signal and from the subsequent modeling of the unitary transitions, suggest a strong internal consistency of data. Another limitation to consider in the analysis is the intrinsic blinking of the dye. In the
Figure 5. Structural changes resulting from rearrangements in the selectivity filter region. (a) Representation of the channel structures in the closed (left) and open (right) states. For clarity, only S6 (white) and pore helix (red) are shown for three subunits. The side chains of Y671 (at the upper gate) and I679, I675 (bottom gate) are highlighted using a stick representation and the permeant Na⁺ ions are shown as purple spheres. Blue shades show the average density of water molecules calculated along the MD trajectory. Note how the water density forms a continuum throughout the pore only Figure 5 continued on next page
present case, this represents roughly 12% of the P11 transitions and therefore obfuscates efforts to obtain absolute values for the open probability. Our solution to bypass this issue was to linearly sub-tract this 'background open probability' post-hoc and to normalize the data to its maximal theoreti-cal response. Still, even with this coarse approximation, the optical data is in surprising agreement with whole-cell electrophysiological recording of channel gating. Further, this approach allowed for the direct measurement of the steady-state activity of membrane receptors undergoing fast molecular rearrangements. Specifically, from our fluorescence recordings, we reasoned that Y671 could undergo three significant conforma-tional changes during the channel’s transition from the conducting to the non-conducting conforma-tion: (i) a side chain re-orientation with respect to the pore and pore helix, (ii) increased water exposure, and (iii) a reshaping of the H-bond interaction network. The spectral properties of coumarin are highly sensitive to changes in solvation and/or to changes in the coordination of the hydroxyl group of the dye (Wagner, 2009). Therefore, any of the modifications detected on MD simulations performed for the wild-type channel can potentially explain the observed changes in fluorescence. As a consequence, a detailed structural interpretation at the level of side-chain dynamics for the fluorescence fluctuations remains out of reach. Moreover, the data presented here do not prove a causal relationship between the motion of the aromatic side chain and the state of the pore helix.

Materials and methods

Cell culture

HEK293T cells (ATCC Cat# CRL-3216, RRID:CVCL_0063) were cultured in DMEM (Gibco Inc.) supplied with 10% FBS (Gibco Inc.). Plasmocin (Sigma) was used following the provider’s instructions to maintain the cell culture free of mycoplasma contamination. Cells were tested for mycoplasma by standard PCR. Cells were prepared at (60–70)% confluence and transfected with lipofectamine 2000, (Life technologies). The target gene was transfected 2–3 hr after the initial transfection of the pair tRNAtag/CoumRS. The ncAA was added to the cell culture to produce a final concentration of between 0.5 and 1 μM at the time of the second transfection procedure. Under these transfection conditions, the efficiency of incorporation of non-natural amino acid was as low as 12%, with read-through calculated to be about 4% (Steinberg et al., 2016). Imaging: to simplify the analysis of the optical data, we transfected a mixture of TRPV1FP/ TRPV1TAG in a 7:1 ratio in an attempt to drive the system to incorporate as few coumarin molecules per tetramer as possible. The ratio of expres-sion was not controlled as we concentrated efforts on single emitters identified ex-post. 24 hr after transfection of the target gene, cells were disaggregated and plated on poly-L-lysine treated glass covers. The f-ncAA-containing media was removed at least 12 hr prior to the experiment, allowing...
cells to clear the soluble ncAA. Generally, the cells were recorded 36–48 hr after the second transfection. Electrophysiology: cells were plated 2–3 hr before patching, and incubated with normal media lacking the supplemented coumarin.

**Synthesis of TyrCoum**

L-(7-hydroxycoumarin-4-yl) ethylglycine was obtained as described before (Wang et al., 2006).

**Solutions**

Ringer solution for imaging experiments contained: 140 mM NaCl, 8 mM KCl, 8 mM HEPES, and 1 mM MgCl₂ at pH 7.4. External electrophysiology solutions contained 145 mM NaCl, 2 mM CaCl₂, 5 mM KCl, 10 mM HEPES and 10 mM glucose, pH 7.4; internal electrophysiology solutions contained 135 mM CsF, 5 mM KCl, 2 mM MgCl₂, 1 mM CaCl₂, 4 mM EGTA and 20 mM HEPES, pH 7.4.

**Molecular modeling**

To analyze Y671 hydration at the atomic level, we used the molecular dynamics trajectories obtained in our previous work (Kasimova et al., 2017). These trajectories were generated starting from the cryo-EM structure of the TRPV1 capsaicin-bound state (Cao et al., 2013). In one simulation, we initialized the system by inserting several water molecules (from 4 to 6) inside the channel peripheral cavities (located between the S4–S5 linker and the S6 C-terminus); in the second simulation, we left these cavities empty. During the equilibration (about 750 ns), the molecular structures converged, respectively, to the closed and open states. To estimate water density along the central pore, we implemented the following strategy. First, using HOLE software (Smart et al., 1996), we calculated the pore radius profile for each instantaneous configuration along the trajectory with a stride of 1 ns. Then, for the same set of frames, we calculated the three-dimensional histograms of water occupancy using the Volmap tool of VMD (RRID: SCR_001820) (Humphrey et al., 1996). Finally, we integrated the water occupancy in the XY plane (perpendicular to the channel central pore) using the pore radius profile as a boundary of the integration domain. The solvent accessible surface area (SASA) of Y671 in the closed and open states was estimated using the following procedure. From the MD trajectories, we extracted a set of sub-trajectories, each containing 10 frames taken with a stride of 0.2 ns. For each sub-trajectory, we computed the three-dimensional histogram of atomic occupancy (for all the atoms except water) using the Volmap tool of VMD (Humphrey et al., 1996). We then used this map to define a molecular surface. To this end, we first discretized the map by assigning a value of 1 or 0, depending on whether or not the local occupancy is larger than a preset threshold. We considered all the bins with a value of 1 and located 1.5 Å away from a bin with a value of 0. Finally, the Y671 SASA was calculated as the overlap between the solvent-accessible surface and the Y671 residue. Note that the SASA was normalized to the Y671 maximal surface area. Molecular dynamics simulations were performed in the open and closed states of the TRPV1 coumarin mutant. The force-field parameters for coumarin were obtained from the CHARMM general force field (Vanommeslaeghe and MacKerell, 2012). Simulations were performed using NAMD2.10 (RRID: SCR_014894) (Phillips et al., 2005) at constant temperature and pressure (one atm) using the Langevin piston approach. For the vDW interactions, we used a cutoff of 11 Å with a switching function between 8 Å and 11 Å. The long-range component of electrostatic interactions was calculated using the Particle Mesh Ewald approach using a cutoff for the short-range component of 11 Å. The equations of motion were integrated using a multiple time-step algorithm, with a time step of 2 fs and long-range interactions calculated every other step. Trajectories were collected for 100 ns.

**Optical recordings**

Cells were imaged using an inverted Olympus IX71 microscope main body and through-the-objective TIRF mode. Both 405 nm and 473 nm solid-state lasers (Coherent, Santa Clara, CA) were used to excite coumarin and YFP, respectively. Laser beams were focused to the backplane of a high-numerical aperture objective (Olympus 60X, N.A. 1.49, oil) by a combination of focusing lens. Fluorescence emission was collected by an Andor iXon™ + 860 EM-CCD camera (Andor/Oxford Instruments, Belfast, UK), after passing through an emission filter for each acquisition wavelength band of interest (coumarin: 450/70 nm; YFP:540/40 nm; Semrock, US). The light coming to the
Image analysis

For localization and co-localization, the set of frames was averaged to increase the signal-to-noise ratio (SNR=μ/σ), which is usually less than two for the single frame at 75% laser illumination. Noise analysis of the steady-state signal by autocorrelation was performed as employed in the past to investigate the kinetic properties of ion channel unitary events from recordings with low signal-to-noise ratios (Anderson et al., 1973; Zingsheim and Neher, 1974). For autocorrelation, a post-acquisition Gaussian digital filter was used at one fourth of the acquisition frequency. The background signal was averaged and the standard deviation (SD) calculated. Unitary fluctuation analysis: when analyzing the fluctuations of fluorescence, we aim to avoid false-positive signals and therefore defined 2.5 SD (μ ±2.5 σ = 0.987) of the background signal (or the equivalent base level) as a threshold to discriminate the two regimes (Peterson and Harris, 2010), basal level (L0) and higher signal level (L1). We reasoned that fluorescence fluctuations, intrinsic to the probe, might interfere with our calculations; Soluble coumarin deposited on a glass coverslip showed12% of positive transitions, a value we linearly subtracted from all the individual points taken from the recorded mutants (Y671 coum or W426 coum), so that a new corrected dataset having the apparent P L1 was obtained after subtraction. The fluorescence of the single emitter bleaches in less than 1 min of continuous illumination at 75% laser power. Normalization of optical data was performed by dividing signal amplitude by the maximal signal obtained (F/F max). Autocorrelation, idealization, and the analysis of unitary transitions was performed with pClamp 8.0 software (RRID:SCR_011323).

HEK-293T electrophysiology

Whole-cell currents were obtained from transiently transfected HEK-293T cells. Gigaseals were formed by using 2–4 MΩ borosilicate pipettes (Warner Instruments, Hamden, CT). Junction potentials (6–8 mV) were corrected for CsF/NaCl solutions. Seal resistance was 2–3 GΩ in all cases. Series resistance and cell capacitance were analogically compensated for directly on the amplifier. The mean maximum voltage drop was about 4 mV. Whole-cell voltage clamp was performed, and macroscopic currents from voltage steps were acquired at 20 kHz and filtered at 10 kHz. Ramp protocols were acquired at 10 kHz and filtered at 5 kHz. Currents are presented in terms of densities. Data were acquired using an Axopatch 200B and a digidata 1320 (Molecular Devices Inc., Sunnyvale, CA). The acquisition and basic analysis of the data were performed with pClamp 8.0 software.

Statistics

Single photon counting. Individual cells on one day of transfection contribute with several puncta, which are considered as replicates. Therefore the histogram presented in Figure 1g corresponds to n = 1 but comes from the average of several individual histograms (in this case, five on each curve). The final statistical procedure was done by comparing the mode of the different populations, n = 4 for each condition. A p-value of 0.05 was considered significant when comparing the modes of the photon count (Mann-Whitney test). Idealization and unitary transitions. The idealization was performed first by checking that the base level was similar to the background noise, then setting a
defined threshold on two standard deviations of background noise average. The comparison between the dwell times was performed in paired experiments (0 versus 3 μM, n = 11). The full data set for the dose-response curve was analyzed using one-way ANOVA. In general, when averaged, data are shown with the correspondent SEM. The statistical analysis was computed in Microcal OriginPro ver9 (OriginLab) (RRID:SCR_002815). Figures were prepared using Microcal OriginPro ver9, VMD (structural data), and ImageJ (RRID:SCR_003070). Source data is available through the Dryad repository (https://doi.org/10.5061/dryad.1kc2c).

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Additional information

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The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

Author contributions

Ximena Steinberg, Conceptualization, Formal analysis, Investigation; Marina A Kasimova, Jason D Galpin, Investigation, Methodology; Deny Cabezas-Bratesco, Ernesto Ladrón-de-Guevara, Formal analysis, Investigation; Federica Villa, Resources, Software, Methodology; Vincenzo Carnevale, Conceptualization, Resources, Formal analysis, Supervision, Funding acquisition, Investigation, Methodology, Writing—original draft, Project administration, Writing—review and editing; Leon Islas, Conceptualization, Formal analysis, Supervision, Funding acquisition, Investigation, Methodology, Writing—original draft, Writing—review and editing; Christopher A Ahern, Conceptualization, Resources, Supervision, Funding acquisition, Methodology, Writing—original draft, Project administration, Writing—review and editing; Sebastian E Brauchi, Conceptualization, Formal analysis,
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