**Report**

**Alternative Mechanisms for Fast Na\(^+\)/Ca\(^{2+}\) Signaling in Eukaryotes via a Novel Class of Single-Domain Voltage-Gated Channels**

**Graphical Abstract**

i. Diatoms exhibit fast animal-like action potentials but the underlying molecular mechanisms are unknown

![Phaeodactylum tricornutum](image)

ii. Diatoms encode novel 1D voltage-gated channels (EukCatAs)

![Single-domain EukCatA channels](image)

iii. EukCatAs are fast Na\(^+\) & Ca\(^{2+}\) channels & provide alternative mechanisms for rapid signalling in eukaryotes

![Mutants also exhibit motility defects](image)

**Highlights**

- Novel class of single-domain, voltage-gated channels (EukCatAs) identified in diatoms
- EukCatAs are fast voltage-gated Na\(^+\)- and Ca\(^{2+}\)-permeable channels
- EukCatAs underpin voltage-activated Ca\(^{2+}\) signaling and membrane excitability
- EukCatAs may have functionally replaced 4D-Ca\(_v\)/Na\(_v\) channels in pennate diatoms

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**In Brief**

Diatoms exhibit fast animal-like action potentials, but many species lack 4D-Ca\(_v\)/Na\(_v\) channels that underpin membrane excitability in animals. Diatoms do encode novel 1D voltage-gated channels (EukCatAs). Helliwell, Chrachri et al. show that EukCatAs are fast Na\(^+\) and Ca\(^{2+}\) channels that provide alternative mechanisms for rapid signaling in eukaryotes.

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Alternative Mechanisms for Fast Na\(^+\)/Ca\(^{2+}\) Signaling in Eukaryotes via a Novel Class of Single-Domain Voltage-Gated Channels

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SUMMARY

Rapid Na\(^{+}\)/Ca\(^{2+}\)-based action potentials govern essential cellular functions in eukaryotes, from the motile responses of unicellular protists, such as *Paramecium* [1, 2], to complex animal neuromuscular activity [3]. A key innovation underpinning this fundamental signaling process has been the evolution of four-domain voltage-gated Na\(^+\)/Ca\(^{2+}\) channels (4D-Ca\(_{v}\)/Navs). These channels are widely distributed across eukaryote diversity [4], albeit several eukaryotes, including land plants and fungi, have lost voltage-sensitive 4D-Ca\(_{v}\)/Navs [5–7]. Because these lineages appear to lack rapid Na\(^{+}\)/Ca\(^{2+}\)-based action potentials, 4D-Ca\(_{v}\)/Navs are generally considered necessary for fast Na\(^{+}\)/Ca\(^{2+}\)-based signaling [7]. However, the cellular mechanisms underpinning the membrane physiology of many eukaryotes remain unexamined. Eukaryotic phytoplankton critically influence our climate as major primary producers and sophisticated signaling mechanisms most likely contribute to their ecological success [12]. The centric diatom *Odontella sinensis* exhibits spontaneous action potentials resembling those produced by 4D-Ca\(_{v}\)/Navs [10, 13](Figures 1A and 1B). However, the molecular basis and functional roles of action potentials in these non-motile phytoplankton cells are unknown. Our previous surveys of diatom genomes identified that the centric diatom *Thalassiosira pseudonana*, but not the model pennate *Phaeodactylum tricornutum*, encodes a 4D-Ca\(_{v}\)/Navs gene homolog [4]. In contrast, both genomes contain uncharacterized single-domain channels resembling prokaryote BacNa\(_{v}\) channels [4]. Here, we show that single-domain channels are actually broadly distributed across major eukaryote phytoplankton lineages and represent three novel classes of single-domain channels, which we refer collectively to as EukCats. Functional characterization of diatom EukCatAs indicates that they are voltage-gated Na\(^{+}\)- and Ca\(^{2+}\)-permeable channels, with rapid kinetics resembling metazoan 4D-Ca\(_{v}\)/Navs. In *Phaeodactylum tricornutum*, which lacks 4D-Ca\(_{v}\)/Navs, EukCatAs underpin voltage-activated Ca\(^{2+}\) signaling important for membrane excitability, and mutants exhibit impaired motility. EukCatAs therefore provide alternative mechanisms for rapid Na\(^{+}\)/Ca\(^{2+}\) signaling in eukaryotes and may functionally replace 4D-Ca\(_{v}\)/Navs in pennate diatoms. Marine phytoplankton thus possess unique signaling mechanisms that may be key to environmental sensing in the oceans.

RESULTS AND DISCUSSION

Diatoms are a diverse group of unicellular algae characterized by their ability to produce a silicified cell wall (frustule). They are abundant primary producers in marine and freshwater ecosys-

tems, particularly in coastal waters [11]. Diatoms are typified by their ability to divide rapidly when they encounter favorable conditions, and sophisticated signaling mechanisms most likely contribute to their ecological success [12]. The centric diatom *Odontella sinensis* exhibits spontaneous action potentials resembling those produced by 4D-Ca\(_{v}\)/Navs [10, 13](Figures 1A and 1B). However, the molecular basis and functional roles of action potentials in these non-motile phytoplankton cells are unknown. Our previous surveys of diatom genomes identified that the centric diatom *Thalassiosira pseudonana*, but not the model pennate *Phaeodactylum tricornutum*, encodes a 4D-Ca\(_{v}\)/Navs gene homolog [4]. In contrast, both genomes contain uncharacterized single-domain channels resembling prokaryote BacNa\(_{v}\) channels, first characterized from *Bacillus halodurans* (NaChBac) [14]. NaChBac yields voltage-gated, Na\(^{+}\) selective currents, with activation and inactivation kinetics typically 10–100 times slower than those of mammalian 4D-Na\(_{v}\)s [14], although representatives from marine bacteria (e.g., Na\(_{v}\)Shep from *Shewanella putrefaciens*) are considerably faster [15]. We therefore reasoned that the single-domain channels identified in diatom genomes could contribute to membrane...
excitability if they are strongly voltage gated and exhibit appropriate activation and inactivation kinetics.

To further examine the mechanisms underpinning membrane excitability in diatoms, we determined the broader distribution of 4D-Ca\textsubscript{v}/Na\textsubscript{s} in available diatom genome and transcriptome databases. 4D-Ca\textsubscript{v}/Na\textsubscript{s} were present in only 6/24 species surveyed (Figure 1C; Data S1), and these were confined to centrics, indicating that pennate diatoms have most likely lost 4D-Ca\textsubscript{v}/Na\textsubscript{s}. Moreover, although two sequenced centric diatom genomes contain a 4D-Ca\textsubscript{v}/Na\textsubscript{s} homolog (Figure 1C), a patchy distribution was seen in centric transcriptomes, indicating absence or poor expression. Notably, 4D-Ca\textsubscript{v}/Na\textsubscript{s} are absent from the transcriptome of *O. sinensis* and several other mediophyte diatoms. Thus, alternative channels may underpin the fast Na\textsuperscript{+}/Ca\textsuperscript{2+} action potentials of *O. sinensis*.

In contrast, single-domain channels were present in 6/6 of diatom genomes and 17/18 of transcriptomes examined, spanning all major classes (Figure 1C). We also identified similar
channels in several other important eukaryotic phytoplankton (including haptophytes, dinoflagellates, cryptophytes, and pelagophytes). Notably, these represent some of the most ecologically significant marine phytoplankton taxa [16] (Data S1). Phylogenetic analyses reveal that the single-domain channels group into three strongly supported clades (Figure 1D). Clade A includes diatoms; clade B representatives of the haptophytes, cryptophytes, and pelagophytes; and clade C dinoflagellates. These clades were phylogenetically distinct from BacNa,s and CatSpers (a specialized family of weakly voltage-gated, single-domain channels present in mammalian sperm) [17, 18]. We have thus collectively termed these novel, single-domain eukaryote channels 1D-EukGats. Our findings highlight that single-domain, voltage-gated channels are far more prevalent in eukaryotes than previously recognized and thus warrant further attention.

*O. sinensis* action potentials arise from rapid Na⁺- and Ca²⁺-based, depolarization-activated currents with activation and inactivation kinetics strongly resembling animal 4D-Nav/Ca,s [10]. Furthermore, the anesthetic lidocaine significantly inhibited these currents, but not tetrodotoxin (TTX), the mammalian 4D-Nav,1 blocker [3]. Diatom EukCatAs exhibit the typical organization of voltage-gated channel sub-units, with six predicted transmembrane segments (S1–S6), including the conserved arginine-rich S4 segment associated with voltage activation (Figures 1D and S1A) and a selectivity filter motif (SF) (Figure S1B) [14]. A coiled-coil domain is also present, which in BacNa,s is involved in tetramerization and gating [19]. We generated codon-optimized constructs for heterologous expression in human HEK293 cells. We chose representative sequences from the genetically tractable diatom *Phaeodactylum tricornutum* [20] (PtEUKCATA1) and from *O. sinensis* (OsEUKCATA1) (Figures 1E, S1A, and S1B; Methods S1). These were expressed as C-terminal GFP fusions. To confirm PtEUKCATA1 and OsEUKCATA1 expression, we detected very rapid depolarization events resembling action potentials (average delay to maximal fluorescence: 33.4 ± 4.77 s; Figures 2B and 3C). The observed variability in the timing of this response (94% of cells; n = 54) that typically initiated after a short delay (average delay to maximal fluorescence: 33.4 ± 4.77 s; Figures 3B and 3C). The observed variability in the timing of this response is most likely due to differences in resting potential and/or the threshold for depolarization between cells. Direct imaging of membrane potential in PR1 cells indicated that action potentials, when observed, directly preceded the [Ca²⁺]ₜₜₑₜ elevations in aequorin expressing *P. tricornutum* [12]. Treatment with 90% artificial seawater (ASW; diluted with deionized water) resulted in a single large transient increase in R-GECO fluorescence (average maximum intensity 2.53 ± 0.844; n = 12; SEM), which was dependent on external Ca²⁺ (Figure S2) [28].

We therefore developed tools for Ca²⁺ imaging in single *P. tricornutum* cells because EukCatAs are Ca²⁺ permeable and [Ca²⁺]ₜₜₑₜ elevations are routinely used as measurements of neuronal membrane excitability [26]. We generated a transgenic strain of *P. tricornutum* stably expressing the intensometric fluorescent Ca²⁺ indicator R-GECO (line PR1; Figure 3A). Perfusion of *P. tricornutum* with elevated K⁺ (100 mM), which depolarizes the plasma membrane in other diatoms [25], resulted in a gradual depolarization in the majority of cells (84%; n = 37 cells; Figure 3A). In addition, we detected very rapid depolarization events resembling action potentials in 23% of cells (n = 35 cells; 12.5 fps; 15 replicate experiments). This indicates that *P. tricornutum* cells exhibit membrane excitability, although it is likely that limitations in imaged acquisition speed and/or sensitivity resulted in under-sampling of action potentials using voltage imaging [26, 27].

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reported for *O. sinensis* when Ca²⁺ is removed [29]. Moreover, multiple action potentials were more frequently observed in the absence of Ca²⁺ (7/10 cells exhibited multiple action potentials, compared to 1/8 cells in the presence of Ca²⁺). In contrast, K⁺-mediated Ca²⁺ elevations were not observed in PtR1 cells in the absence of Ca²⁺ (Figure S3E), indicating that external Ca²⁺ is necessary for depolarization-activated Ca²⁺ signaling in *P. tricornutum*. Together, these results suggest that a Ca²⁺-dependent negative feedback mechanism may regulate *P. tricornutum* membrane excitability. Thus, despite lacking 4D-Ca²⁺/Na⁺ channels, plasma membrane depolarization in *P. tricornutum* leads to rapid action-potential-like depolarization events and [Ca²⁺]_{cyt} elevations.

In addition to *PtEUKCATA1*, the *P. tricornutum* genome contains two further *EukCatA* isoforms that share 49.7% and 50.0% amino acid sequence identity (JGI protein IDs 54164 and 43828, respectively; Figure S1). Transcriptome data indicate that *PtEUKCATA1* is expressed in *P. tricornutum* cells in standard liquid culture [30], and we confirmed its expression using RT-PCR. To examine the role of *PtEUKCATA1* in
generating depolarization-activated Ca\(^{2+}\) elevations, we employed CRISPR-Cas9 gene editing to generate bi-allelic knockout mutants in the PtR1 line (Figures S4A and S4B; STAR Methods). PtR1-eukcatA1 mutants exhibited only a modest reduction in specific growth rate in liquid culture (Figure S4C). However, four mutants were unable to generate depolarization-activated Ca\(^{2+}\) elevations (Figures 3D and 3E). In contrast, the PtR1-eukcatA1 mutants showed no defect in their response to hypo-osmotic stress when compared to WT PtR1 cells (Figures S4D–S4F). This indicates that the Ca\(^{2+}\) signaling phenotype in PtR1-eukcatA1 mutants is due to specific defects in depolarization-activated Ca\(^{2+}\) signaling, rather
than broader defects in cellular Ca\(^{2+}\) signaling. The results are consistent with a role for voltage-dependent EukCataA channels in generation of action potentials and initiating Ca\(^{2+}\) elevations. Because two of the PtR1-eukcatA1 mutants (A3 and E3) did not retain the Cas9 gene (Figure S4A), we reintroduced the WT PtEUKCATA1 gene into mutant A3 under its native promoter and confirmed expression of the WT PtEUKCATA1 transcript in these lines (Figure S4G). This resulted in partial or complete complementation of the defective phenotype (n = 3; Figures 3F–3H). These data provide conclusive evidence that

Figure 4. Gliding Motility, but Not Growth, Is Impaired in PtR1-eukcatA1 Mutants

(A) Cumulative movement of *P. tricornutum* cells on solid agar. *P. tricornutum* cells on agar plates adopt the oval morphotype and exhibit gliding motility (demonstrated by a diffuse “halo” around colonies spotted onto an agar plate—inset). % increase in spot area is shown after 27 days. The area of the halo is reduced in PtR1-eukcatA1 mutants compared to PtR1. Error bars indicate SEM; n = 4; p values (Student's t test): *p < 0.05; **p < 0.01; ***p < 0.001. No statistical difference was evident between WT and PtR1 (R).

(B) Time-lapse video microscopy of gliding oval *P. tricornutum* cells. Oval morphotypes cells (numbered) were placed onto a thin agarose layer and covered with ASW. Gliding cells leave tracks in the agar, indicating their path. The starting position of the cells is indicated in the final image (white oval). In the images shown, cells either exhibit constant forward motility (cell 4), multiple reversals of direction (cell 5), or no motility (cell 2). Scale bar represents 50 \( \mu \)m.

(C) Percentage of motile cells for WT, PtR1, and four PtR1-eukcatA1 mutant lines over 10-min experiments. p values (Fisher’s exact test): *p < 0.05; **p < 0.01; ***p < 0.001.

(D) Description of metrics used to quantify gliding motility in oval *P. tricornutum* cells. Linear velocity indicates the displacement from the starting position. Curvilinear velocity is the total distance traveled.

(E) Live-cell imaging of oval cells shows that mean linear velocity is significantly reduced in PtR1-eukcatA1 mutants compared to the PtR1 line. n, total number of cells quantified across 4 independent experiments; error bars indicate SEM; p values (Student’s t test): *p < 0.05; **p < 0.01; ***p < 0.001.

(F) Comparison of curvilinear velocity of the same lines. Error bars indicate SEM; p values (Student’s t test): *p < 0.05; **p < 0.01; ***p < 0.001.

(G) Gliding locomotion in *P. tricornutum* cells is inhibited in the absence of Ca\(^{2+}\). Cells were prewashed with either ASW or ASW-Ca\(^{2+}\) + 200 \( \mu \)M EGTA prior to motility assay (*Fisher’s exact test: ***p < 0.001).

(H) Mean linear velocity of PtR1-eukcatA1 mutant A3 compared to PtR1 (R) and three independent complemented lines: C1; C2; and C3. Error bars indicate SEM; p values (Student’s t test): *p < 0.05; **p < 0.01; ***p < 0.001.

See also Figure S4.
**STAR METHODS**

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**SUPPLEMENTAL INFORMATION**

Supplemental Information can be found online at https://doi.org/10.1016/j.cub.2019.03.041.
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AUTHOR CONTRIBUTIONS


DECLARATION OF INTERESTS

The authors declare no competing interests.

REFERENCES


## STAR★METHODS

### KEY RESOURCES TABLE

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Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Colin Brownlee (cbr@mba.ac.uk).

### EXPERIMENTAL MODEL AND SUBJECT DETAILS

#### Strains and culturing

**Algal strains**

*Phaeodactyllum tricornutum* strain CCAP1055/1 was obtained from the Culture Collection of Algae and Protozoa (SAMS limited, Scottish Marine Institute (Oban, UK)) (Key Resources Table). *P. tricornutum* cells were maintained in either filtered seawater (FSW) or artificial seawater, ASW (450 mM NaCl, 30 mM MgCl₂, 16 mM MgSO₄, 8 mM KCl, 10 mM CaCl₂, 2 mM NaHCO₃, and 97 μM H₂BO₃), supplemented with f/2 nutrients [50], with 100 μM Na₂SiO₃·5H₂O, but not vitamins. Cultures were grown routinely in FSW, but were acclimated to ASW for 1-2 weeks prior to Ca²⁺ imaging experiments that required defined media. Cultures were maintained at 18°C with 50–80 μmol m⁻² s⁻¹ light on a 16:8 h light:dark cycle.

**Cell lines**

HEK293 cells (ATCC CRL-1573) were grown in a humidified incubator at 37°C in 5% CO₂ and 95% O₂. Growth medium consisted of high glucose DMEM–Dulbecco’s Modified Eagle Medium with Antibiotic Antimycotic (GIBCO), and 10% FBS (GIBCO). Cells were passaged every 3–4 days at 1:6 or 1:12 dilutions (cell/mm²).

### METHOD DETAILS

#### Bioinformatics analysis

Sequence similarity searches were carried out to survey a broad range of eukaryote genomes and transcriptomes for single and four-domain voltage-gated ion channels (Data S1; Figure 1). Query sequences from *Bacillus halodurans* C-125 NaChBac (protein id: BAB05220.1) and BacNa⁺-like sequences previously identified in diatom (*P. tricornutum* protein id: 43878) [4, 51], in addition to the 4D-Ca/VNa⁺ sequence of *T. pseudonana* (protein id: 22071) were used. Transcriptome databases surveyed were obtained...

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from the Marine Microbial Eukaryote Sequencing Project (MMETSP, https://www.imicrobe.us/#/projects/104) [52]. The MMETSP databases provide transcriptome sequencing resources for ecologically significant marine microbial eukaryotes spanning the breadth of the eukaryotic tree of life (with representatives from all the major eukaryote super groups including the Archaeplastida, Alveolates, Stramenopiles, Rhizaria, Opisthokonts, Amoebozoa and Excavata). Eukaryote genomes from a range of sources were also used. The genomes of *E. huxleyi* [51], *T. pseudonana* [53], *P. tricornutum* [54], *Pavlova* sp. CCMP2436, * Aureococcus anophagefferens* clone 1984, *Volvox carteri* f. nagariensis EVE [55], *Coccomyxa subellipsoidea C-169* [56], *Ostreococcus lucimarinus* CCMP2514, *Ostreococcus tauri* OTH95 [57], *Micromonas* sp. RCC299 [58], *Porphyra umbilicalis* [59], Pelagophyceae sp. CCMP2097, *Pseudo-Nitzschia multiseries* CLN-47, *Guillardia theta* CCMP2712, and *Bigelowia natans* CCMP2755 were obtained from Joint Genome Institute http://genome.jgi.doe.gov/. Further searches were performed at NCBI (http://blast.ncbi.nlm.nih.gov/). 

The genomes of *Alveolates, Stramenopiles, Rhizaria, Opisthokonts, Amoebozoa* and *Excavata*. Eukaryote genomes from a range of sources were used to investigate the breadth of the eukaryotic tree of life (with representatives from all the major eukaryote super groups including the * Archaeplastida*, *Rhizaria*, *Opisthokonts*, *Amoebozoa*, and *Excavata*). Eukaryote genomes from a range of sources were also used. The genomes of *E. huxleyi* [51], *T. pseudonana* [53], *P. tricornutum* [54], *Pavlova* sp. CCMP2436, *Aureococcus anophagefferens* clone 1984, *Volvox carteri* f. nagariensis EVE [55], *Coccomyxa subellipsoidea C-169* [56], *Ostreococcus lucimarinus* CCMP2514, *Ostreococcus tauri* OTH95 [57], *Micromonas* sp. RCC299 [58], *Porphyra umbilicalis* [59], Pelagophyceae sp. CCMP2097, *Pseudo-Nitzschia multiseries* CLN-47, *Guillardia theta* CCMP2712, and *Bigelowia natans* CCMP2755 were obtained from Joint Genome Institute [52]. Further searches were performed at NCBI (http://blast.ncbi.nlm.nih.gov/). 

Databases were searched using BLASTP and TBLASTN with an E-value cut off score of 1E-10. Each hit was inspected manually for relevant protein domains using Interpro [64], looking specifically for voltage-sensing domain (IPR005821), ion transport domain (IPR027359) and EF hands (IPR011992). The presence of a minimum of three pore domains was used as a threshold for candidate 4D-Cav/Navs in order to distinguish them from other voltage-gated cation channels. Protein hits of all ids reported in this study are given in Data S1.

Phylogenetic analyses of EukCat, Catsper and BacNa sequences were performed using MUSCLE via the Molecular Evolutionary Genetics Analysis (MEGA7) software [47]. After manual refinement, GBLOCKS0.91B was employed to remove poorly aligned residues, using the least stringent parameters [65], resulting in an alignment of 172 amino acid residues. Maximum likelihood trees were generated using MEGA7 with 100 bootstraps. Model analysis was performed in MEGA7 to determine an appropriate substitution model (WAG+G+I). Bayesian posterior probabilities were additionally calculated using BEAST v1.8.4 [48] running for 10000000 generations.

**Synthesis of heterologous expression plasmids for HEK293 cells**

Amino acid sequences of proteins used for heterologous expression are described in Methods S1. Coding sequences for OsEUKCATA1 were obtained from MMETSP transcriptomic datasets: *O. sinensis* (protein id: CAMPEP_0183296650; transcriptome database id: MMETSP0160). To confirm these sequences we amplified the open reading frame (ORF) from cDNA made from liquid cultures of *O. sinensis* (using the primers: Osinensis_F1: ATGAAGGACGGAACAGCATCCC, Osinensis_R1: AGAAT CAGTCTGGTGTGGTGAAGATGCAC). The coding sequence for PIUEKCAT1 (protein id: 43878) was predicted from the JGI genome project for *P. tricornutum*. To confirm correct prediction of intron/exon boundaries for this gene model, the predicted ORF of PIUEKCAT1 was amplified from a liquid culture of *P. tricornutum* CCAP1055/1 (using the primers: Pt43878_F: GCCATCCGATGATGCAAGGAATCGTGGAG and Pt43878_R: AAACATTCTCGGGGACTTCTC). cDNA was synthesized using SuperScript III reverse transcriptase from RNA extracted using ISOLATE II RNA Mini Kit (Bioline) following the manufacturer’s instructions. Codon-optimized versions of the transcripts were then synthesized (GenScript, Piscataway, NJ) for characterization in human expression systems, and sub-cloned into pcDNA3.1-C-eGFP using HindIII and BamHI. A 6 bp Kozak sequence (GCCACC) was included upstream of the ATG, and the stop codon removed.

**Transfection of HEK293 cells**

HEK293 cells were plated for transfection onto glass-bottom (35mm) Petri-dishes coated with poly-L-lysine (ibidi GmbH, Germany) to help with cell adhesion. Transfections of HEK293 were performed with 4 μL Lipofectamine 2000 (Invitrogen) and 1-2.5 μg plasmid DNA per 35 mm², each prepared separately with Opti-MEM (GIBCO). The lipofectamine and DNA were mixed and allowed to rest for 5 min. before 200 μL of the mixture was added to each plate. After 12-30 h of incubation, cells were rinsed and maintained with fresh growth media and kept in the incubator at 37°C with 5% CO₂/95% O₂ until used for electrophysiologic experiments. Expression of the transgene was confirmed by fluorescence microscopy.

**HEK293 whole cell patch-clamp electrophysiology**

Electrophysiological recordings were carried out at room temperature with an Axopatch 200B or MultiClamp 700B amplifier (Molecular Devices, Sunnyvale, California) through a PC computer equipped with a Digidata 1322 analog-to-digital converter in conjunction with pClamp 9.2 or pClamp10.1 software (Molecular Devices, Sunnyvale, California). Patch electrodes were pulled from filamented borosilicate glass (1.5 mm OD, 0.86mm ID) using a P-97 puller (Sutter Instruments, Novato, CA, USA) to resistances of 2-5 MΩ. For analysis of OsEUKCATA1, unpolished electrode tips were coated with beeswax to minimize pipette capacitance. Voltage errors incurred from the liquid junction potentials (LJPs) and series resistance (recorded from the amplifier) were corrected by subtraction post hoc. These corrected voltages were used to plot IV curves and in all subsequent investigations. The amplitudes of the currents were measured from the baseline to the peak value and were normalized for cell capacitance as whole-cell current densities (pA/pF). Activation curves were derived by plotting normalized sodium conductance (GNa) as a function of test potential and fitted with the Boltzmann equation:

\[ G_{Na} = \frac{G_{Na\ max}}{1 + e^{\left(\frac{V_m - V_0}{\Delta V}\right)}} \]
for selection (see ‘Biolistic Transformation of P. tricornutum’).

P. tricornutum

Biolistic transformation of P. tricornutum to the antibiotic zeocin [67] via EcoR1 and BamH1. The construct was transformed into WT O. sinensis.

Native phytoplankton cell patch-clamp recording and analysis

O. sinensis single electrode voltage clamp recordings were obtained as previously described [10, 13]. Briefly, cells were plated into coverslip dishes in ASW consisting of: 450 mM NaCl, 30 mM MgCl2, 16 mM MgSO4, 8 mM KCl, 10 mM CaCl2, 2 mM NaHCO3 pH 8.0. Cells were imaged through the girdle band with a sharp microelectrode filled with 1 M KCl (resistance 10 MΩ) mounted on the head-stage of an Axoclamp 900A amplifier (Molecular Devices), controlled with a Sutter MP285 motorized micromanipulator (Sutter Instruments, Petaluma, CA). Current and voltage signals were pre-amplified 5-10× before being acquired using a Digidata 1200 with Clampex 10.2 acquisition software (Molecular Devices, Sunnyvale, CA). The gain for the switch clamp was between 5-10 and switching frequency > 13 kHz for the data presented.

Generation of P. tricornutum constructs

We employed the CRISPR-Cas9 vector developed by Nymark et al., (2016) for editing the PIEUKCATA1 gene (protein id: 43878) in P. tricornutum [20]. We designed two sgRNAs targeted to generate a short deletion, which has proven efficient for high-throughput screening for bi-allelic mutants via PCR in diatoms [66]. A library of candidate sgRNAs was generated using the PHYTOCRISPEX [49] web tool with default parameters (NGG PAM, and CRISPR start from ‘G’). The Broad Institute sgRNA design program (https://portals.broadinstitute.org/gpp/public/analysis-tools/sgrna-design) was used subsequently to obtain ‘on-target’ efficiency scores. Two 20 bp guide RNAs (ccPt43878A: GATGATGACATTGGAATGGG and ccPt43878B: GGAGGAATACTACTGGGCTC) that passed the PHYTOCRISPEX OFF-target criteria were chosen based on their ON-target scores (0.45 and 0.51, respectively) and position within the gene. Target sgRNAs were predicted to disrupt the region encoding the pore domain of the protein in order to maximize disruption of channel function. Complementary oligos containing flanking overhang sequences corresponding to the pKS diaCas9_sgRNA plasmid (Addgene: 74923) were then synthesized. One μg of complementary oligos for ccPt43878A (ccPt43878A_F: TCGAGATGAT GACATTGGAATGGG and ccPt43878A_R: AAACCCATCCATTGACATCTACATC) and ccPt43878B (ccPt43878B_F: TCGAGG AGAATCTAGGGCTC and ccPt43878B_R: AAACCCATCCATTGACATCTACATC) were annealed in a reaction mix containing 1 × 4 Ligase Buffer (NEB) in a total volume of 50 μl, incubated for 10 min at 85°C and allowed to cool to room temperature. The resulting annealed oligos were ligated into pKS diaCas9_sgRNA using a molar vector to insert ratio of 1:20, and a T4 DNA ligase (Fermentas). Plasmids were verified via Sanger sequencing.

For the PIEUKCATA1 complementation construct, we amplified the PIEUKCATA1 gene from 747 bp upstream of the ATG up to, but not including, the stop codon (TGA) using primers: PIEUKCATA1_comp_F-AACCAATGCATTGGCTGCAGGTCGACTAGGGC CACAGGTA and PIEUKCATA1_comp_R-AACCAATTTCTGGGACTTCCTC. The forward primer includes a flanking PstI site, for downstream cloning into a derivative of the pPha-T1 vector (accession AF219942): pPha-T1-Venus vector, using PstI and Stul sites. To make the pPha-T1-Venus vector we synthesized a codon-optimized Venus sequence (accession AJN91098.1) incorporating an EcoRI and Stul site upstream of the ATG, and a 3′ BamH1 site (GenScript, Piscataway, NJ). The codon optimized Venus construct was then sub-cloned into the pPha-T1 (accession AF219942) vector using EcoRI and BamH1 sites.

To generate the PR-GECCO1 construct we synthesized (GenScript, Piscataway, NJ) the 1251 bp coding sequence (accession AEO16866.1), which was sub-cloned into the P. tricornutum shuttle vector pPha-T1 (accession AF219942) conferring resistance to the antibiotic zeocin [67] via EcoRI and BamH1. The construct was transformed into WT P. tricornutum strain CCAP1055/1, using zeocin for selection (see ‘Biolistic Transformation of P. tricornutum’).

Biolistic transformation of P. tricornutum

P. tricornutum cells were grown in liquid culture for 5 days. Cell density was adjusted to 1 × 10^9 cells/mL and 100 μL spread (in a 3 cm diameter circle) in the center of an 1/2 1% agar plate (made up with 50% diluted seawater without Si and vitamins), and left for 24 h in standard growth conditions prior to transformation. The plated cells were transformed via biolistic particle bombardment using the PDS-1000/He Particle Delivery System (Bio-Rad, Hercules, CA, USA). To prepare the DNA-loaded microparticles, 60 mg tungsten (0.6 μm in diameter) particles were washed 3 times in 100% ethanol and twice with sterile deionised water before being re-suspended in 1 mL sterile deionised water and distributed into 50 μL aliquots. A single aliquot of washed tungsten was then coated with 1.5 μg of the relevant plasmid DNA using 2.5 M CaCl2 and 20 mM spermidine (BioUltra, Sigma-Aldrich, cat no. 85558) with continuous vortexing. Coated particles were washed once in 100% ethanol and then re-suspended in 60 μL of 100% ethanol that was subsequently distributed between three macrocarrier disks for particle bombardment. The P. tricornutum agar plates were positioned on the second shelf of the PDS-1000/He Particle Delivery chamber, ~7.5 cm from the stopping screen. Helium supply with minimum pressure of
1600 psi (300 psi above the burst pressure of the 1350 psi rupture disk) and a vacuum of 23 inch Hg was used to fire the DNA-coated microparticles toward cells. Following particle bombardment cells were incubated for 24 h under standard culturing conditions before being transferred to selection plates (1% agar f/2 -Si and vitamins in 50% diluted seawater) with 300 μg mL\(^{-1}\) nourseothricin\(^{65}\) or 75 μg mL\(^{-1}\) zeocin depending on the plasmid. After three weeks colonies were re-streaked onto fresh selection plates.

To generate PIEUKCAT1 mutant lines we co-transformed PIR1 cells with pNAT\(^{66}\) and pKSdiaCas9_sgRNA constructs, using biolistic transformation selecting for nourseothricin resistant colonies. Putative PteukcatA1 mutants were screened via PCR using the Pheir Plant Direct PCR Kit (ThermoFisher Scientific) with primers designed to amplify Cas9 (Cas9-F: CTTCGACCTGCGGAAAGATG and Cas9_R: CCGGACGAGAGCTTTAAGGA) and then subsequently with primers flanking the target region for deletion (PTEUKCAT1_F: TTTGGTGCTATTTCTCTAGTC and PTEUKCAT1_R: TATCGTTCTTGGGTCTCCT) to identify bi-allelic polymorphisms in this region. The mutant line A3 was subsequently cotransformed with the PTEUKCAT1 complementation construct and a selection plasmid conferring resistance to Blasticidin \(^{68}\).

**Epifluorescence imaging in P. tricornutum**

*P. tricornutum* cells grown in liquid culture (ASW supplemented with f/2 nutrients \(^{50}\), with 100cM Na\(_2\)SiO\(_3\), 5H\(_2\)O, but not vitamins) for 72 h were placed in a 35 mm glass-bottomed dish (In Vitro Scientific, Sunnyvale, CA, USA) coated with 0.01% poly-L-lysine (Sigma-Aldrich, St Louis, MO, USA). Cells adhered to the bottom of the dish were imaged at 20°C using epifluorescence microscopy using a Nikon Eclipse Ti microscope with a 40 x, 1.30 NA oil immersion objective and detection with a Photometrics Evolve EM-CCD camera (Photometrics, Tucson, AZ, USA). Excitation of R-GECO (PtR1) cells was performed using a pE2 excitation system (CoolLED, Andover, UK) with 530-555 nm excitation and 575-630 nm emission filters. Images were captured using NIS-ELEMENTS v.3.1 software (Nikon, Japan) with a 300 ms camera exposure (frame rate of 3.33 frames s\(^{-1}\)). For membrane potential imaging cells were stained for 5 min with voltage-sensitive dye Annine-6-Plus (A-6-P; final concentration 0.8 μg/mL), centrifuged for 2 min at 10,000 rpm and resuspended in ASW without A-6-P to minimize background A-6-P fluorescence. Excitation of A-6-P cells was performed in the same manner as for the calcium imaging, using an excitation wavelength of 475-495 nm and emission wavelength of 575-615 nm. Images were recorded at 12.5 frames s\(^{-1}\) with 2 x 2 binning.

For simultaneous determination of membrane potential and [Ca\(^{2+}\)]\(_{cyt}\) we loaded PtR1 cells expressing R-GECO with A-6-P. Although there is some overlap in emission spectra of A-6-P and R-GECO, we were able to spatially distinguish between A-6-P localized to the membrane and R-GECO fluorescence in the cytosol. A-6-P fluorescence contributes to background fluorescence in the cytosol, but as A-6-P has a much lower dynamic range than R-GECO, this did not interfere with the detection of [Ca\(^{2+}\)]\(_{cyt}\) transients. Moreover, membrane depolarization results in a decrease in A-6-P fluorescence, whereas an increase in [Ca\(^{2+}\)]\(_{cyt}\) causes an increase in R-GECO fluorescence, allowing us to confirm that there was minimal interference between these fluorophores. An excitation wavelength of 475-495 nm and emission wavelength of 575-615 nm were used, with defined regions of interest within the cell.

During imaging, cells were continuously perfused with ASW (3 mL min\(^{-1}\)). Depolarization treatments were delivered by switching the perfusion from ASW to ASW with elevated K\(^{+}\) (100 mM) (358 mM NaCl, 30 mM MgCl\(_2\), 16 mM MgSO\(_4\), 100 mM KCl, 10 mM CaCl\(_2\), 2 mM NaHCO\(_3\), and 97μM H\(_2\)BO\(_3\)) supplemented with f/2 nutrients \(^{50}\), with 100cM Na\(_2\)SiO\(_3\), 5H\(_2\)O, but not vitamins) after 30 s for 90 s. For the hypoosmotic shock experiments multiple exposures to ASW diluted with deionised water were carried out. Cells exposed to hypoosmotic shock in the absence of Ca\(^{2+}\) were perfused with at least 50 mL Ca\(^{2+}\) free media (+200 μM EGTA) in order to minimize carryover of residual Ca\(^{2+}\) from the ASW growth medium.

Images were processed using NIS-ELEMENTS v.3.1 software. The mean fluorescence intensity within a region of interest over time was measured for each cell. Change in fluorescence intensity of R-GECO was calculated by normalizing each trace by the initial value \(F/F_0\). For membrane potential imaging, \(\Delta F/F\) was calculated by dividing the time varying fluorescence by the baseline fluorescence.

**P. tricornutum motility assays**

**Solid plate assays**

*P. tricornutum* cells grown in liquid culture (sub-cultured two times previously at 3 day intervals, to ensure maximal and uniform physiological health) under standard growth conditions for 48 h were diluted to uniform cell density (5 x 10\(^{5}\) cells/mL). Twenty μL of cells were then spotted on f/2 1% square agar plates, with each plate containing a spot for each of the six genotypic lines examined. To account for population variability the response was examined over cultures derived from four independent clones per cell line with six replicates per clone, and a total of 24 spots assayed for each genotypic line. Plates were positioned at alternating right angles toward the light source to minimize positional effects. After 27 days photographs were taken and ImageJ \(^{45}\) was used to quantify original spot area, spot spread and calculate percentage increase in area ((Total area - original spot area / original spot area) x 100).

**Video Microscopy**

Prior to the assay cells were passaged 3 times on solid agar (at 5 day intervals) to ensure maximal transition to oval morphology and uniform good physiological health between lines. On the third transition, 5 day old cells were scraped from the plate and resuspended into 5 μL f/2 medium before being spread on glass-bottomed dishes with 0.5 mL f/2 1% agar, and covered with liquid f/2 media. Care was taken to ensure that cells were only removed from controlled growth conditions just prior to the motility assay. Cells were then viewed by differential interference contrast microscopy using a Leica DMi8 microscope equipped with a 20 x objective and an environmental chamber to control temperature (18°C). The proportion of oval cells (compared to fusiform and triradiate morphotypes) in the populations used for the assay was calculated and did not vary significantly between lines (accounting for 94%, 95%, 93%, 92%, 95%, and 93%, respectively).
99% and 99% of cells for WT, PtR1, mutant A3, E3, B6, and B8 respectively (Figures 4E and 4F). For each analysis, 10 min videos were recorded at four frames/minute, with samples illuminated during image acquisition (camera exposure 200 ms). ImageJ [45] was used with the ImageJ plugin MTRACKJ [46] to track oval cell motility over the time-course of the experiment. Only tracks of oval cells that were not in contact with other cells at the beginning of the video and did not cross paths with other cells were quantified to avoid physical and biological interactions that might influence cell speed and/or path. Linear and curvilinear velocity were determined for each cell and the overall percentage of motile cells was calculated for each line totaling four independent videos for each line. Motility assays both carried out on plates and via video microscopy were done on well-established (at least 12 months old, sub-cultured weekly) transgenic lines (PtR1 and mutant lines A3, E3, B6, and B8) to ensure a stable and robust phenotype.

**QUANTIFICATION AND STATISTICAL ANALYSIS**

**Statistical Analyses**
Quantification of data are presented as mean ± standard error of the mean (SEM) with the precise number (n) indicated in the figure legends and where relevant the main text. Statistical analyses were performed using a Student's t test or a Fisher's exact test in SigmaPlot. Statistical differences are represented as p*, < 0.05; **, p < 0.01; ***, p < 0.001.

**DATA AND SOFTWARE AVAILABILITY**
The accession number for sequences/plasmids in GenBank or Fasta format from this study are given in the Key Resources Table.