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The identification of a gain-of-function mutation in *CACNA1C* as the cause of Timothy Syndrome (TS), a rare disorder characterized by cardiac arrhythmias and syndactyly, highlighted unexpected roles for the L-type voltage-gated Ca\textsuperscript{2+} channel Ca\textsubscript{v}1.2 in nonexcitable cells. How abnormal Ca\textsuperscript{2+} influx through Ca\textsubscript{v}1.2 underlies phenotypes such as the accompanying syndactyly or craniofacial abnormalities in the majority of affected individuals is not readily explained by established Ca\textsubscript{v}1.2 roles. Here, we show that Ca\textsubscript{v}1.2 is expressed in the first and second pharyngeal arches within the subset of cells that give rise to jaw primordia. Gain-of-function and loss-of-function studies in mouse, in concert with knockdown/rescue and pharmacological approaches in zebrafish, demonstrated that Ca\textsuperscript{2+} influx through Ca\textsubscript{v}1.2 regulates jaw development. Cranial neural crest migration was unaffected by Ca\textsubscript{v}1.2 knockdown, suggesting a role for Ca\textsubscript{v}1.2 later in development. Focusing on the mandible, we observed that cellular hypertrophy and hyperplasia depended upon Ca\textsuperscript{2+} signals through Ca\textsubscript{v}1.2, including those that activated the calcineurin signaling pathway. Together, these results provide new insights into the role of voltage-gated Ca\textsuperscript{2+} channels in nonexcitable cells during development.

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Calcium influx through L-type CaV1.2 Ca2+ channels regulates mandibular development

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The identification of a gain-of-function mutation in CACNA1C as the cause of Timothy Syndrome (TS), a rare disorder characterized by cardiac arrhythmias and syndactyly, highlighted unexpected roles for the L-type voltage-gated Ca2+ channel CaV1.2 in nonexcitable cells. How abnormal Ca2+ influx through CaV1.2 underlies phenotypes such as the accompanying syndactyly or craniofacial abnormalities in the majority of affected individuals is not readily explained by established CaV1.2 roles. Here, we show that CaV1.2 is expressed in the first and second pharyngeal arches within the subset of cells that give rise to jaw primordia. Gain-of-function and loss-of-function studies in mouse, in concert with knockdown/rescue and pharmacological approaches in zebrafish, demonstrated that Ca2+ influx through CaV1.2 regulates jaw development. Cranial neural crest migration was unaffected by CaV1.2 knockdown, suggesting a role for CaV1.2 later in development. Focusing on the mandible, we observed that cellular hypertrophy and hyperplasia depended upon Ca2+ signals through CaV1.2, including those that activated the calcineurin signaling pathway. Together, these results provide new insights into the role of voltage-gated Ca2+ channels in nonexcitable cells during development.

Introduction
Voltage-gated Ca2+ channels are the sine qua non of excitable cells—translating electrical activity into the cytoplasmic Ca2+ changes that regulate cellular responses such as neuronal activity, muscle contraction, and hormone release. Nonexcitable cells generally employ different means to increase cytoplasmic Ca2+, such as receptor-operated Ca2+ channels or release from intracellular stores. Although expression of certain voltage-gated Ca2+ channels, mainly the CaV1.2 L-type Ca2+ channel, has been documented in certain nonexcitable cells, the physiologic roles of voltage-gated Ca2+ channels in these cells have been enigmatic and largely unexplored.

The broad array of abnormalities within nonexcitable tissues in Timothy Syndrome (TS) patients (1), however, revealed that CaV1.2 controls critical, yet previously unknown, roles in multiple nonexcitable tissues. Identified as a novel cardiac arrhythmia syndrome associated with syndactyly and dysmorphic facial features (2), the TS defect was discovered to be a specific gain-of-function mutation (G406R) in CACNA1C, the gene encoding CaV1.2. The mutation greatly slows channel inactivation, and thereby prolongs cellular repolarization in cardiac myocytes, which provided a clear rationale for the cardiac arrhythmias. Yet how CaV1.2 affects nonexcitable cells, as indicated by additional phenotypes documented in TS, such as small teeth, baldness at birth, and dysmorphic facial features, is unclear. These phenotypes were not consistent with previously understood roles for CaV1.2. Here, we exploited both mouse and zebrafish models to define how Ca2+ influx through CaV1.2 affects craniofacial development.

Results
CaV1.2 is expressed in the developing jaw. To determine how CaV1.2 might contribute to craniofacial development, we started by investigating whether CaV1.2 was present in jaw primordia during the appropriate developmental stages. We used a CaV1.2 reporter mouse (CaV1.2+/lacZ) in which lacZ disrupted one allele of Cacna1c, thereby marking CaV1.2-expressing cells. Although CaV1.2−/− mice die in utero, CaV1.2+/− mice are viable and fertile without any obvious differences in any aspect of morphology or development (3). Thus, analysis of β-gal expression in CaV1.2+/lacZ reporter embryos should approximate CaV1.2 temporal expression and accurately reflect CaV1.2 spatial expression. Examination of β-gal activity in CaV1.2+/lacZ E9.5 embryos revealed intense staining mainly in the developing heart (Figure 1A), as expected. By E11.5, however, we observed extensive activity in the first and second pharyngeal arches (Figure 1, B–D), as well as in the limb buds. Coronal sections through the first arch in E11.5 embryos showed that the β-gal activity was mainly in the periphery (Figure 1, E and F), where a subset of cranial neural crest–derived cartilage progenitors resides and from which jaw structures such as the mandible develop (4, 5); the identification of β-gal–positive cells in this region suggests that they are of neural crest lineage. Thus, the presence of CaV1.2-expressing cells in these structures provides a basis for the syndactyly and craniofacial abnormalities seen in TS patients.

Altered CaV1.2 activity affects jaw development in mice. To test whether abnormal signaling through CaV1.2 in the developing jaw causes craniofacial abnormalities, we exploited a mouse model in which a floxed STOP TS mutant CaV1.2 (CaV1.2T5) allele for the pore-forming α1C subunit of CaV1.2 (or CaV1.2WT as a control) had been knocked into the Rosa26 locus (6). To examine the effects of
Cav1.2 in mandibular development uncomplicated by effects in other tissues, we expressed Cav1.2WT or Cav1.2TS in a subset of craniofacial mesenchyme by breeding these mice with a Prx1-Cre transgenic mouse. Within the branchial arches, Prx1 drives Cre recombinase expression starting around E11.5 in the ventral surfaces (7), where we observed endogenous Cav1.2 expression (Figure 1, C and D). Prx1 also drives expression in limb bud mesenchyme (7), in both chondrocytes and osteoblasts (8), which allowed us to obtain material to test whether expression levels of Cav1.2WT and Cav1.2TS were comparable in tissues in which Prx1 is active. We isolated articular chondrocytes from the femur and tibia of Prx1-Cav1.2TS, Prx1-Cav1.2WT, and Prx1-Cav1.2TS mice and performed immunocytochemistry for α1C. An experimenter blinded to the genotypes used identical exposure settings for representative images from all three genotypes and observed that transgenic expression of α1C was elevated in Prx1-Cav1.2TS compared with Prx1-Cav1.2TS mice, but was equivalent to Prx1-Cav1.2WT mice (Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI66903DS1). Having established a similar expression of Cav1.2TS and Cav1.2WT driven by Prx1, we obtained radiographs of skulls to ascertain the effect of Cav1.2TS on jaw development. We observed that radiographs of skulls from mice expressing Cav1.2WT (Prx1+ or Prx-Cav1.2WT) were not different from those of their Prx1 littermate controls (Figure 2A) or wild-type animals (not shown). In contrast, the tip of the mandible (lower jaw) extended anteriorly as far as, or beyond, the tip of the maxilla (upper jaw) in 6 of 7 mice in which Prx1 drove Cav1.2TS expression (Figure 2B). In Prx1 littermates, the maxilla extended beyond the mandible (3 of 3 animals), as in the wild-type animals (Figure 2B). The relatively larger mandible in Prx1-Cav1.2TS mice recapitulated the phenotype reported in TS patients (Figure 2C and ref. 1). Together, these data demonstrate that expression of the TS mutant Cav1.2, and not just overexpression of Cav1.2WT, is necessary to recapitulate this TS phenotype.

Based on these results with the gain-of-function Cav1.2TS, we hypothesized that Cav1.2 haploinsufficiency might affect mandible size in the opposite manner. Although previous examination of Cav1.2+/− mice revealed no differences (compared with wild-type mice) in morphology or development (3) — and we also found that overall mouse size, weight, and tibial length were not different between the 2 genotypes — subtle extracardiac phenotypes might have been missed in that original study. Indeed, in a blinded analysis, we found that the normalized intracoronoid width was smaller in Cav1.2+/− mice (0.40 ± 0.00, n = 6) compared with wild-type littermate controls (0.48 ± 0.01, n = 6, P < 0.001) (Figure 2D). Together, these data suggest that altered Ca2+ influx through Cav1.2 in a tissue-specific manner can affect craniofacial development.

Genetic and pharmacological manipulation shows that Cav1.2 regulates mandibular development in zebrafish. We exploited zebrafish to begin dissection of the molecular mechanisms by which Cav1.2 regulates craniofacial development. Among the advantages of this model system is that, due to oxygen diffusion, embryos do not require heart function until approximately 5 days post fertilization, a developmental stage significantly beyond when a functioning heart is nec-

Figure 1
Cav1.2 is expressed in developing jaw. (A–D) Whole-mount β-gal staining of Cav1.2ΔlacZ embryos. Cav1.2 is highly expressed in the developing heart around E9.5 (A). By E11.5 intense staining is present in the first (arrowhead) and second (arrow) pharyngeal arches (B–D). (E and F) β-gal staining of a coronal section through the first mandibular arch. F is a magnified section of the boxed area shown in E.

Figure 2
Cav1.2 expression in pharyngeal arches affects craniofacial development. (A) X-rays of a Prx-Cav1.2WT skull and a Prx1-littermate skull. Note that the upper jaw extends anteriorly to the mandible (arrows), (B) X-rays of a Prx1-Cav1.2TS skull and a Prx1-littermate skull. When Cav1.2TS is expressed (in the Prx1 animal), the mandible extends more anteriorly, as is also seen in TS patients. (C) Image showing patient phenotype (arrow points to mandible). Image in C is reproduced with permission from the authors and publisher (1). (D) Mandibles from adult Cav1.2ΔlacZ or wild-type (littermates). Note reduced width between coronoid processes in Cav1.2ΔlacZ compared with wild-type mice. Scale bars: 5 mm.
Ca^{2+} influx through CaV1.2 regulates size of mandible in zebrafish. (A) Alcian blue–stained embryos at 72 hpf. CON, uninjected control; CMO, control morpholino; MO, CaV1.2 morpholinos; MO + WT, CaV1.2 morpholinos coinjected with rabbit CaV1.2WT cRNA; MO + 4EQ, CaV1.2 morpholinos coinjected with rabbit CaV1.2 cRNA with mutations in the 4-pore glutamates (non-Ca^{2+} permeant); MO + TS, CaV1.2 morpholinos coinjected with rabbit CaV1.2TS cRNA. (B) Mandibular area (as outlined for CON in A normalized to the area in CMO (n = 20 for each). *P < 0.001 versus CMO. (C) Mandibular area normalized to the area in MO (n = 20 for each). *P < 0.001 versus MO. (D) Alcian blue–stained embryos at 72 hpf after treatment with DMSO or nisoldipine. (E) Mandibular area normalized to the area in DMSO (n = 20 for each). *P < 0.001 versus DMSO.
in both groups. As shown in Supplemental Figure 5, the absence of cardiac activity (in the wea\textsuperscript{haf} homozygotes) did not reduce mandible size, suggesting that the specific knockdown of Ca\textsubscript{V}1.2 by morpholinos affected mandible size independent of effects upon cardiac function.

We were therefore able to query the effects of rescue with informative mutants. Like Ca\textsubscript{V}1.2\textsuperscript{WT} cRNA, coinjection of a Ca\textsubscript{V}1.2\textsuperscript{TS} cRNA also doubled mandible size. Although Ca\textsubscript{V}1.2\textsuperscript{TS} cRNA did not increase the mandible size more than Ca\textsubscript{V}1.2\textsuperscript{WT} cRNA, it did affect chondrocyte size and pattern within the developing mandible.
We next tested whether jaw development depended upon Ca\(^{2+}\) influx through Ca\(_{\text{v}}\)\(_{1.2}\) with a Ca\(^{2+}\)-impermeant rabbit CaV1.2, in which 4 key aspartate residues in the channel’s pore-forming \(\alpha_1C\) subunit were mutated to glutamine. This 4EQ mutant (CaV1.2\(_{\text{4EQ}}\)) retains its ability to scaffold other signaling proteins (e.g., auxiliary subunits) and to conduct ions, but completely blocks Ca\(^{2+}\) permeation (11). Unlike CaV1.2\(_{\text{WT}}\) or CaV1.2\(_{\text{TS}}\), CaV1.2\(_{\text{4EQ}}\) did not restore mandible size when coinjected with the CaV1.2 knockdown morpholino cocktail (Figure 3, A and C).

Finally, we validated the morpholino knockdown effects and confirmed the requirement for Ca\(^{2+}\) influx by two additional approaches. First, we measured mandible size in the offspring of heterozygotes of the CaV1.2 null mutant \(\text{cacna1c m231}\) zebrafish (12). Embryos without ventricular contraction (\(\text{isl}\) phenotype) and mandible size was calculated at 72 hpf. The size of mandibles from embryos with the \(\text{isl}\) phenotype was reduced by more than 50% (Supplemental Figure 6). Second, we applied the Ca V1.2 antagonist nisoldipine, which reduced mandible size compared with the DMSO control treatment (Figure 3, D and E). Together, these data suggest that Ca\(^{2+}\) influx through CaV1.2 is necessary for regulating mandible size during development.

(Figures Continued...)

(see Figure 4F). Ca\(^{2+}\) influx through CaV1.2 regulates mandibular chondrocyte hypertrophy and hyperplasia. CaV1.2 affected cell hypertrophy and/or hyperplasia. To determine if CaV1.2 affected cell hypertrophy, we measured cell size in the developing mandible. After staining embryos at 72 hpf with Alcian blue, flat-mounted images of the lateral aspect of Meckel’s cartilage (Figure 4A) provided an unobstructed view of individual chondrocytes,
which assumed a regular and linear pattern that we exploited to quantify the individual cell area (Figure 4B). Pharmacological blockade of CaV1.2 with nisoldipine reduced cell size (Figure 4, B and C), consistent with the effects on the mandible (Figure 3D) and also affected the linear organized pattern. Cell area was also restored by CaV1.2 knockdown morpholinos compared with embryos injected with a control morpholino or noninjected controls. As with overall mandible size, cell size was restored by coinjection of a morpholino-sensitive CaV1.2WT but not by the CaV1.2-impermeant mutant CaV1.24E60Q (Figure 4, D–G). Interestingly, after coinjection of CaV1.2TS, cell size was not only restored (and even larger than rescue with CaV1.2WT), but also this region of the Meckel’s cartilage appeared to be crowded with additional cells (Figure 4F). This suggests that CaV1.2 influx through CaV1.2 might also regulate cellular hyperplasia in the developing mandible. We measured cell proliferation in developing mandibles of transgenic zebrafish embryos in which GFP is driven by the sox10 promoter, a marker of the cranial neural crest (13). In these embryos, the developing mandible is GFP+ by 72 hpf, at which point we labeled embryos (treated with control morpholin or CaV1.2 morpholinos) with BrdU and calculated the percentage of cells that were both GFP+ and BrdU+ compared with the total number of GFP+ cells in the section. There was a significantly lower percentage of both BrdU+ and double-labeled cells in the CaV1.2 morpholino–treated embryos within the mandible (Figure 4H). Together, these data suggest that CaV1.2 controls chondrocyte hypertrophy and hyperplasia during mandibular development.

Calcineurin lies downstream of CaV1.2 in regulating size and hypertrophy in mandibular chondrocytes. The regulation of cellular hypertrophy (Figure 4) suggested to us that the CaV1.2-dependent phosphatase calcineurin, which regulates the nuclear factor of activated T cells (NFAT) signaling pathway, might be one candidate for a regulator downstream of CaV1.2, as this pathway regulates hypertrophy in several cell types, such as cardiac myocytes (14). We tested this hypothesis with two independent approaches. First, we inhibited calcineurin activity with FK506 and cyclosporine with doses previously used in zebrafish (15). Mandibular area and cell size were reduced compared with a DMSO control treatment (Figure 5, A and B), reminiscent of the effects after loss of Ca2+ influx through CaV1.2 (see Figures 3 and 4). To query whether calcineurin might be downstream of CaV1.2, we then bypassed the requirement for Ca2+ influx through CaV1.2 by coinjecting cRNA for a constitutively active, CaV1.2-insensitive calcineurin (caCN) (16) with CaV1.2 morpholinos. This treatment partially restored mandible size and cell size (Figure 5, C and D). This second approach also helped confirm that the CaV1.2-dependent effects on mandibular development were independent of cardiac function, since the rescue of mandible and cell size did not correlate with the restoration of cardiac function in CaV1.2 morpholino–treated embryos (Supplemental Video 3). We also examined whether calcineurin affected cell size. Using analyses similar to those shown in Figure 4, we demonstrated that calcineurin inhibition with FK506 and cyclosporine reduced cell size compared with DMSO (Figure 5, E and F). On the other hand, coinjection of cRNA for a constitutively active, CaV1.2-insensitive calcineurin markedly increased cell size (Figure 5, G and H).

Mandibular progenitor cells express functional CaV1.2 channels. The identification of CaV1.2 expression in cranial neural crest–derived cells (Figure 1, E and F) and the developmental effects observed after perturbing CaV1.2 (Figures 2–4), prompted us to test whether cranial neural crest cells express functional CaV1.2 channels. Previously, voltage-gated L-type CaV2 channels have been hypothesized to regulate neural crest migration and differentiation (17), yet the contributions of specific L-type CaV2 channels have not been identified, and analysis by electrophysiologic methods has not yet been performed. We did not find that CaV1.2 regulated cranial neural crest cell migration. Using the sox10-GFP transgenic zebrafish embryos to visualize the cranial neural crest cells that migrate dorsolaterally in distinct streams from the neural tube to form craniofacial structures, we found that cranial neural crest migration was unaffected in embryos treated with CaV1.2 morpholinos (Figure 6A). The development of a grossly intact, albeit smaller, jaw in embryos treated with CaV1.2 morpholinos (Figure 3) also suggested that cranial neural crest migration does not depend upon CaV1.2. We queried the presence of CaV1.2 CaV2 channels in cranial neural crest cells by comparing voltage-gated Ca2+ currents in cells isolated from morpholino-treated and wild-type embryos. We isolated single GFP+ cells from decapitated heads obtained from sox10-GFP zebrafish embryos at 64 to 66 hpf (Figure 6, A and B).
Cells without processes were chosen for electrophysiologic analysis to reduce the chance of recording from neuron precursors. The cells were small (average cell capacitance was 1.55 ± 0.3 pF). Resting membrane potential was −35.9 ± 2.7 mV, consistent with what has previously been recorded in cranial neural crest cells (18). Using the whole-cell patch-clamp technique, a ramp protocol in the presence of 15 mM Ba2+ elicited small inward currents in cells isolated from wild-type embryos, but never in cells isolated from embryos treated with the CaV1.2 morpholinos, which always displayed outward currents under these conditions (Figure 6, C and D).

**Discussion**

Although identification of CACNA1C as the TS locus revealed unexpected roles for CaV1.2 in nonexcitable cells (1), CaV1.2 participation outside of neurons, muscle, and hormone-secreting cells has received little attention. Here, we provide to the best of our knowledge the first evidence for how CaV1.2 participates in mandibular development and thereby contributes to the dysmorphic facial features that have been reported in more than half of TS patients. Using a combination of mouse and zebrafish models, we demonstrated that Ca2+ influx through CaV1.2 is necessary for proper mandibular development.

Regulation of Ca2+ influx is the best-characterized role for CaV1.2, but voltage-gated CaV1.2 channels anchor large macromolecular complexes (19) and could therefore control cellular processes independent of Ca2+ influx. Indeed, the CaV1.2 channel auxiliary subunit β4 controls epiboly in zebrafish through a CaV1.2-independent manner (20). The inability of the CaV1.2βRE channel to rescue the CaV1.2 morpholino effects (Figure 3, A and C) and the smaller jaws observed after pharmacologic blockade of CaV1.2 with nisoldipine (Figure 3, D and E) provide additional evidence that mandibular development depends directly on Ca2+ influx through CaV1.2. Dihydropyridines have not been shown to disrupt the CaV1.2 macromolecular complex, and the CaV1.2βRE channel remains a voltage-sensitive cation channel—though one that is not able to permeate Ca2+ due to loss of the high-affinity binding site in the pore (11). Thus, we conclude that functions other than Ca2+ permeation are unlikely to contribute to the CaV1.2-dependent regulation of mandibular development.

Our hypothesis is further reinforced by the complementary effects on mandible size with gain-of-function and loss-of-function approaches in mice: CaV1.2 haploinsufficiency reduced mandible size, while expression of a CaV1.2TS mutant channel in the developing jaw and the accompanying augmented Ca2+ influx increased mandible size (Figure 2). While we observed an increase in mandible size in mice expressing CaV1.2TS, the original description in TS patients reported a small upper jaw (maxilla) (1). We suspect that the maxilla in TS patients appears relatively small in comparison with the abnormally large mandible, as shown in the x-rays from Prx1-CaV1.2TS mice (Figure 2B). In zebrafish, the inability of CaV1.2TS cRNA to increase mandible size more than CaV1.2WT cRNA did likely reflects that the zebrafish model is best suited to inform about earlier developmental events. The cRNA was injected into a single-cell embryo along with cau1c morpholinos. As the embryo increases in size and cell number, both the amount of morpholino and CaV1.2TS cRNA per cell become diluted. Endogenous CaV1.2 expression increases (as shown in Supplemental Figure 3D) and likely dominates the phenotype. Nevertheless, that both CaV1.2WT and CaV1.2TS cRNA can rescue cau1c morphants provides powerful evidence that our morpholinos are on target. The cells expressing CaV1.2 that are responsible for these developmental effects likely include the early chondrocytes of the mandible. Using a CaV1.2 reporter mouse, we first identified CaV1.2 at E11.5 within the periphery of the first branchial arch, which contains cranial neural crest–derived cells (see Figure 1). Consistent with these data, we recorded inward Ca2+ currents from zebrafish cranial neural crest–derived (Sox10+) cells, but not after CaV1.2 morpholino knockdown (Figure 6). The Prx1-CaV1.2TS mouse model also suggests a role for developing chondrocytes, since the Prx1-Cre transgene is specifically active in the first pharyngeal arch (7) and in chondrocytes (8).

The resting membrane potential (approximately −35 mV) recorded from the isolated cranial neural crest cells expressing a CaV1.2-dependent, inward Ca2+ current suggests a mechanism by which the gain-of-function TS mutant channel could contribute to disease phenotypes in nonexcitable cells. At this voltage, steady-state inactivation curves for CaV1.2WT and CaV1.2TS channels begin to diverge, so the fraction of CaV1.2TS channels inactivated would be significantly smaller than that of CaV1.2WT channels (1). Thus, after CaV1.2 channels open to participate in the Ca2+ waves that accompany neural crest migration (17, 21), additional Ca2+ likely continues to flow through CaV1.2TS channels for some time, even after a return to more negative resting membrane potentials.

Knockdown of CaV1.2 by morpholinos resulted in a smaller jaw, but one that appeared to have all of its elements, suggesting that CaV1.2 exerts its effects after cranial neural crest migration. Consistent with that, we did not observe any defect in cranial neural crest migration after CaV1.2 knockdown (Figure 6A). Rather, CaV1.2 appears to participate in the subsequent hypertrophy and hyperplasia of the developing chondrocytes.

Calcineurin appears to be one Ca2+-dependent effector downstream of CaV1.2 based on two lines of evidence. First, inhibition of calcineurin produced a phenotype similar to pharmacological blockade of Ca2+ influx through CaV1.2 or CaV1.2 knockdown. Second, expression of a constitutively active calcineurin was able to bypass the requirement for Ca2+ influx through CaV1.2 (Figure 6). It is intriguing that calcineurin is a part of the CaV1.2 macromolecular complex, having been shown to interact either directly with CaV1.2 (22) or through an A-kinase anchoring protein (23). The most likely target of activated calcineurin is NFAT. The ability of constitutively active calcineurin to induce hypertrophy in developing chondrocytes is consistent with its well-documented roles in cardiac myocyte hypertrophy (24). Indeed, transgenic overexpression of NFAT, either in chondrocytes/osteoblasts or osteoclasts, leads to abnormal craniofacial development (25, 26). Since the rescue with constitutively active calcineurin was incomplete, additional Ca2+-sensitive pathways downstream of CaV1.2 are likely necessary.

The mechanisms by which CaV1.2 affects cellular processes in other nonexcitable tissues may be similar in some cases and different in others. For example, the baldness observed in all TS patients at birth could result from excessive activation of the calcineurin/NFAT pathway (via the mutant CaV1.2), as suggested by the hirsutism side effect commonly seen in patients treated with calcineurin inhibitors for immunosuppression. On the other hand, it is not readily obvious how the mutant CaV1.2 leads to the invariant syndactyly phenotype through a calcineurin/NFAT pathway. Interdigital apoptosis has been shown to be induced by BMPs, counterbalanced by noggin, a BMP antagonist, and survival signals from FGFs, all under the master control of the secreted morphogen Sonic hedgehog (Shh) (27), but not from an NFAT-dependent process.
Our findings provide a platform to specifically define the unexpected contributions of Cav1.2 to nonexcitable tissues and to explore more generally the roles of ion channels in these tissues. Loss-of-function mutations in GJAI, the gene coding for the gap-junction protein connexin43, underlie oculodentodigital dysplasia, which shares several features with TS, including craniofacial and tooth abnormalities, as well as syndactyly (28). This study provides additional support for the concept that ion channels are critical for multiple, unexpected processes in nonexcitable tissues.

**Methods**

**Mouse models.** Cav1.2^{−/−}\(×\)Cav1.3^{−/−} mice (B6.129P2-Caca1c^{tm1Dgen}/J) were obtained from The Jackson Laboratory. Cav1.2^{−/−} and Cav1.2^{−/−} mice, previously described (6), were crossed with Ptx1-Cre (B6.Cg-Tg[Prx1-cre]1Cjt/J; The Jackson Laboratory). Mandible and tibia measurements were performed at the times indicated either by dissection and isolation or by x-ray imaging on a Faxitron LX-60 Digital Radiography System acquired at a voltage of 26 kV and a 13-second acquisition time. All mouse experiments were approved by the Institutional Animal Care and Use Committee at Duke University.

**Zebrafish embryo collection and preparation.** Zebrafish (Danio rerio) were maintained following published protocols (29) and various developmental stages were identified as described previously. loot and haf mutants (provided by Deborah Yelon, New York University School of Medicine, New York, New York, USA) were bred to generate loot/haf double heterozygotes. Wild-type Tubingen fish; loot/haf double heterozygotes; and loot (CaCac1c^{tm233}; provided by Calum MacRae, Harvard University, Cambridge, Massachusetts, USA); and transgenic fish expressing eGFP under control of the sox10 promoter (sox10:egfp), provided by Thomas Schilling, UC Irvine, Irvine California, USA) were used to obtain embryos where indicated in the text. All zebrafish experiments were approved by the Institutional Animal Care and Use Committee of Duke University.

**Whole-mount Alcian blue staining and whole-mount cell-size imaging.** At 72 hpf, fish were anesthetized with 1× tricaine and fixed in 2% paraformaldehyde and PBS (wt/vol) for 2 to 4 hours. After a graded rinse in ethanol, they were transferred into a solution of 0.1% Alcian blue (Sigma-Aldrich), 80% ethanol, and 20% acetic acid (wt/vol/vol) and incubated overnight at 4°C. After a series of graded ethanol-PBS rinses, embryos were bleached with 1% KOH and 3% H₂O₂ (vol/vol) for 2 hours, followed by a mild digestion overnight at 4°C with 0.05% trypsin, EDTA, saturated sodium tetraborate, and PBS (vol/vol). Stained embryos were preserved and imaged in 80% glycerol (vol/vol). Quantification on the whole mandible was performed with ImageJ software (NIH) with the observer blinded to the treatments. Following whole mandible imaging and quantification, embryos were decapitated and had excess tissue stripped before being flat-mounted between a slide and coverslip. Images were then taken on a Leica phase-contrast compound light microscope. Images were contrast and brightness enhanced. Data analysis was performed with OriginLab 8.5.

**Immunohistochemistry.** Embryos (sox10:egfp) at 76 hpf were treated with bromodeoxyuracil (BrdU) for 1 hour over ice and were allowed to recover for 1 hour at 27.8°C. Embryos were then anesthetized with 1× tricaine and fixed in 4% paraformaldehyde and PBS (wt/vol) for 2 hours. Fish were then washed gradually into 100% methanol for 3 days at 4°C. Subsequently, they were rehydrated into PBS, treated with 2N HCl at 42°C for 30 minutes. Following PBST (PBS and 0.1% Tween [vol/vol] washes), embryos were incubated with 1:200 mouse IgG anti-BrdU overnight at 4°C and then incubated with 1:200 goat anti-mouse IgG Alexa Fluor 488 overnight at 4°C. In order to visualize the jaw, embryos were incubated with 1:200 mouse IgG, anti-GFP overnight and then with a secondary rabbit anti-mouse IgG, Alexa Fluor 543 overnight. Embryo heads were removed, stabilized in methacryloxypropionate in the middle of a depression slide, and gently compressed by a coverslip before confocal microscopy. Quantification was performed using ImageJ software (NIH). A threshold was set and only cells containing GFP were examined for BrdU staining.

**Antisense morpholino knockdown and RNA rescue analysis.** Two morpholino oligonucleotides (Gene Tools) against caca1c were designed against the splice-site acceptor of exon 4 (CCCGTCTCTAGACAGACAAACAGA) and the splice-site donor of exon 4 (GGATCTTGCACCTACTACG-GACCA). Two scrambled 25-nt control morpholinos were designed by Gene Tools. Morpholinos were diluted and injected at 2 ng per embryo in a 2-nl bolus into single-cell zygotes. Efficacy of knockdown was assessed by quantitative PCR (qPCR) (Supplemental Figure 3) using qRT-PCR following protocols previously described. Primers used were as follows: Exon 3 forward, TTGCAACTCTGGTGGCCTTACCTG; Exon 3 forward, TCACACTAT-GCATACCTCGGGA; and Exon 5 reverse, TTGCTCCTCATTGGA-TACCACCA. Rabbit Caca1c cRNA (Caca1c^{−/−}) was prepared as described previously from pCARDH1 using 77 mMESSAGE mACHINE (Ambion, Life Technologies) (30). The Caca1c^{−/−} cRNA was prepared after mutating pCARDH1 (G436R) with QuikChange (Agilent). The Caca1c^{−/−} CACNA1C cRNA was provided by Paul Rosenberg (Duke University, Durham, North Carolina, USA) and cloned into pGHE for cRNA synthesis. Each construct was co-injected with the caca1c morpholino at 800 pg per embryo where indicated in the text.

**Pharmacology and drugs.** Nisoldipine, FK506, and cyclopamine were dissolved in DMSO (all from Sigma-Aldrich). Embryos (24 hpf) were chemically and manually dechorionated using pronase. Drugs were applied directly into embryo medium, which was supplemented with fresh medium every 24 hours. The following concentrations were used: 1% DMSO (vol/vol), 5 μM nisoldipine, 5 μM cyclopamine, and 1 μM FK506.

**Neural crest isolation and electrophysiology.** Embryos (sox10:egfp) at 64 to 66 hpf were anesthetized with 2× tricaine and then decapitated in HBSS without calcium or magnesium. Isolated heads were washed in HBSS, manually dissected, and then cells were enzymatically dissociated with a combination of collagenase and trypsin-EDTA in HBSS. Cells were spun down, washed, and resuspended in 10% FBS, 1% penicillin/streptomycin, and DMEM-F12 and incubated on glass coverslips coated with fibronectin, poly-D-lysine, and laminin. Ba²⁺ currents were recorded using the whole-cell patch-clamp technique. Patch pipettes were fabricated from borosilicate glass (Warner Instruments) by a P-97 Flaming-Brown micropipette puller (Sutter Instruments). Pipette resistance was between 6.0 and 8.0 MΩ. Voltage-clamp experiments were performed with an Axopatch 200b amplifier (Molecular Devices) at room temperature (20°C–22°C) 2 hours after plating. A Tyrode bath solution contained (in mM; Sigma-Aldrich) NaCl 140, KCl 5.4, CaCl₂ 1, MgCl₂ 1, HEPES 5, and glucose 10 (pH 7.3). Once the cell was ruptured, solution was quickly exchanged to a Ba²⁺ recording solution containing (in mM; Sigma-Aldrich) TEA-Cl 110, CsCl 15 mM, MgCl₂ 15 mM, HEPES 5, glucose 10, and 4-aminopyridine 2, pH 7.2, with CsOH. Isc was recorded using a ramp protocol from –80 to +60 over 500 milliseconds. Internal solution contained (in mM; Sigma-Aldrich) TEA-Cl 110, CsCl 15 mM, MgCl₂ 15 mM, HEPES 5, glucose 10, and 4-aminopyridine 2, pH 7.2, with CsOH. Isc was recorded using a ramp protocol from –80 to +60 over 500 milliseconds. Internal solution contained (in mM; Sigma-Aldrich) CsOH-H₂O 70, aspartic acid 80, CsCl 40, NaCl 10, HEPES 10, EGTA 10, MgATP 5, and Na₂GTP 4 (pH 7.2). Recordings were filtered at 2 kHz and digitally sampled at 25 kHz. Whole-cell membrane capacitance was calculated by integrating the capacitive transient elicited by a 5-mV pulse from –80 mV to 75 mV. Pipette capacitance was corrected and whole-cell capacitance and series resistance were at least 80% compensated. Peak negative currents were normalized to cell capacitance and reported as current density (pA/pF). To record resting membrane potential, a perforated patch with
400 nM amphotericin (Sigma-Aldrich) was performed using the following internal solution (in mM; Sigma-Aldrich): KCl 110, NaCl 5, MgATP 5, phosphocreatine 5, NaGTP 1, HEPES 10, pH 7.3, and Tyrode extracellular solution. Junction potential was measured to be 5.1 mV and not corrected. Data analysis was performed using Clampfit 10.2 software (Axon Instruments) and OriginPro 8.5 (OriginLab).

Chondrocyte isolation and immunocytochemistry. Chondrocytes were isolated from femurs and tibia as described (31). Cells were plated onto poly-D-lysine–coated coverslips and allowed to adhere for at least 24 hours. Cells were washed and fixed with 2% paraformaldehyde in PBS for 15 minutes at room temperature. After quenching with 10 mM glycine in PBS, cells were washed and fixed with 2% paraformaldehyde in PBS for 15 minutes at room temperature. Coverslips were washed and mounted in Vectashield (Vector Laboratories) containing DAPI and imaged on a Zeiss Axio Imager.

Expression times were kept constant for all images and the experimenter was blinded to the genotype. The Journal of Clinical Investigation 2001;1(2):265–275.

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