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Surviving Endoplasmic Reticulum Stress Is Coupled to Altered Chondrocyte Differentiation and Function

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In protein folding and secretion disorders, activation of endoplasmic reticulum (ER) stress signaling (ERSS) protects cells, alleviating stress that would otherwise trigger apoptosis. Whether the stress-surviving cells resume normal function is not known. We studied the in vivo impact of ER stress in terminally differentiating hypertrophic chondrocytes (HCs) during endochondral bone formation. In transgenic mice expressing mutant collagen X as a consequence of a 13-base pair deletion in Col10a1 (13del), misfolded α1(X) chains accumulate in HCs and elicit ERSS. Histological and gene expression analyses showed that these chondrocytes survived ER stress, but terminal differentiation is interrupted, and endochondral bone formation is delayed, producing a chondrodysplasia phenotype. This altered differentiation involves cell-cycle re-entry, the re-expression of genes characteristic of a prehypertrophic-like state, and is cell-autonomous. Concomitantly, expression of Col10a1 and 13del mRNAs are reduced, and ER stress is alleviated. ERSS, abnormal chondrocyte differentiation, and altered growth plate architecture also occur in mice expressing mutant collagen II and aggrecan. Alteration of the differentiation program in chondrocytes expressing unfolded or misfolded proteins may be part of an adaptive response that facilitates survival and recovery from the ensuing ER stress. However, the altered differentiation disrupts the highly coordinated events of endochondral ossification culminating in chondrodysplasia.


Introduction

Development and growth require the ability to detect, respond to, and survive stresses that compromise the normal state. Accumulation of misfolded or unfolded mutant proteins in the endoplasmic reticulum (ER) induces ER stress and may seriously affect the viability of cells. To cope with ER stress, ER-resident sensors detect misfolded or unfolded proteins and elicit the ER stress signaling (ERSS), which includes the induction of the highly conserved “unfolded protein response” (UPR). ERSS may lead to cytoprotection or death, depending on the nature of the stress and the cellular context. ERSS involves the activation of at least three independent ER stress sensors: inositol-requiring 1 (IRE1), PKR-like ER kinase (PERK), and membrane-tethered activating transcription factor 6 (ATF6) [1]. Their activation represses protein synthesis via phosphorylation of the translation initiation factor eIF2α and activates signaling pathways that up-regulate the expression of ER-resident molecular chaperones and translation regulators. Activation of IRE1, PERK, and ATF6 depends on their dissociation from the molecular chaperone, binding Ig protein (BiP), a master regulator of ERSS. BiP ensures high-fidelity protein folding and prevents the accumulation of unfolded or aggregated proteins. Upon stress, unfolded proteins bind BiP and sequester it from interaction with IRE1, PERK, and ATF6. The released ATF6 and IRE1 activate the transcription factor XBP1 via production of its spliced form, XBP1s [2,3]. In an auto-regulatory loop, BiP activity increases further, since BiP up-regulation is partially dependent on XBP1s [4]. Induction of ERSS means that the amount of new protein translocated into the ER

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Author Summary

The assembly and folding of secreted proteins in the endoplasmic reticulum (ER) is quintessentially regulated by a complex mechanism that maintains an equilibrium between folded and unfolded proteins. Perturbation of this homeostasis induces ER stress, which, if not alleviated, interdicts collagen X trimer assembly in vitro by cell-free translation of wild-type (wt) and 13del mRNAs. Consistent with previous findings [24], we tested the effect of the 13del mutation on collagen X trimer assembly in vitro by cell-free translation of wild-type (wt) and 13del mRNAs. Consistent with previous findings [24], we tested the effect of the 13del mutation on collagen X trimer assembly in vitro by cell-free translation of wild-type (wt) and 13del mRNAs. Consistent with previous findings [24], we tested the effect of the 13del mutation on collagen X trimer assembly in vitro by cell-free translation of wild-type (wt) and 13del mRNAs. Consistent with previous findings [24], we tested the effect of the 13del mutation on collagen X trimer assembly in vitro by cell-free translation of wild-type (wt) and 13del mRNAs.

Results

The Col10a1 13del Mutation Results in Impaired Collagen X Assembly

Trimer assembly of collagen X α-chains via the NC1 domain is critical for triple helix formation and for secretion [24]. We tested the effect of the 13del mutation on collagen X trimer assembly in vitro by cell-free translation of wild-type (wt) and 13del mRNAs. Consistent with previous findings [21,22], the mutation resulted in collagen X α-chains that were unable to assemble into trimers (Figure 1A). Cotranslation of wt Col10a1 and 13del mRNAs resulted in fewer as the cartilage matrix mineralizes and is being replaced with bone. This program is regulated by a complex network of molecules such as Indian hedgehog (IHH), parathyroid hormone-related peptide (PTHrP), bone morphogenetic proteins, fibroblast growth factors (FGFs), their respective receptors, and interaction between the cells and the extracellular matrix (ECM) [12,13].

Perturbation of this differentiation program results in a malformed skeleton (chondrodysplasia). Distension of the ER is a hallmark of cells undergoing ER stress [14,15]. Disorganization of growth plate chondrocytes and distended ER are characteristics of several chondrodysplasias [16–18], many of which are caused by mutations in genes encoding ECM proteins, such as collagens II, IX, XI, cartilage oligomeric matrix protein (COMP), and aggrecan (reviewed in [19]) and that result in the synthesis of abnormal proteins. Cultured pseudochondroplastic chondrocytes or cells transfected with mutant COMP retain ECM proteins and chaperones intracellularly and have an increased capacity for apoptosis [14,16,20]. Collagen X is an ECM protein synthesized specifically by HCs. Mutations in the human COL10A1 gene interfere with collagen X trimer assembly and secretion, with retention of mutant chains in the ER [21–23], resulting in metaphyseal chondrodysplasia type Schmid (MCDS) (reviewed in [24,25]). Abnormal organization of chondrocytes and an expanded hypertrophic zone (HZ) have been observed in the growth plate of a swine model for MCDS [26].

These observations raise the possibility that in chondrodysplasias caused by mutations that affect protein assembly and secretion, ERSS disrupts chondrocyte differentiation and thereby chondrocyte organization in the growth plate. In this study, we present evidence that when unfolded collagen X encoded by a murine Col10a1-equivalent of an MCDS mutation, a 13-base pair (bp) deletion within the NC1encoding domain [27], is expressed in transgenic mice (13del), ERSS is triggered in the growth plate. Concomitantly, HC fate and terminal differentiation are perturbed, but apoptosis is not increased. The normal terminal differentiation program is disrupted. The 13del HCs in the lower part of the HZ re-enter the cell cycle and express markers more typical of preHCs, accompanied by down-regulation of Col10a1-13del gene (hereafter referred to as 13del) expression, suggesting an alteration in their cellular identity. This alteration of 13del HCs is cell autonomous, implying an association with activation of the ERSS. These findings reveal for the first time that HCs undergoing ER stress in vivo adapt, altering their differentiation status to a less-mature state in which expression of 13del is reduced, thereby alleviating the unfolded protein load.
collagen X trimers, suggesting 13del α-chains reduced trimer assembly (Figure 1A). Thus, this mutation would be expected to impair collagen X folding/assembly in vivo.

Abnormal Chondrocyte Differentiation in 13del Transgenic Mice

To assess the impact of unfolded collagen X α-chains on the differentiation of the chondrocyte layers in vivo, we generated transgenic mice carrying the 13del (Figure 1B). Five independent lines carrying the 13del transgene all exhibited disproportionate dwarfism with shorter limbs (Figure 1C). Histologic and morphometric analyses revealed altered proportional organization of the growth plate with a significant expansion specifically of the HZ (Figure 1D). This expansion was detectable in 13del growth plates at late fetal stage, peaking on about day 10 ($p = 0.015$, $n = 6$), and diminishing by 4 wk ($p < 0.001$, $n = 13$). By 10 wk, the height was normal and corresponded to the cessation of transgene expression (see below). Longitudinal bone growth as measured by calcein labeling was significantly reduced in 13del mice at 5- to 10-d-old (Figure 1E). At 10 wk, 13del tibiae were 15% shorter than that of the wt ($n = 12$, $p = 4 \times 10^{-14}$). These results indicated that the phenotypic changes were associated with disturbed endochondral ossification.

Transgenic mice overexpressing wt Col10a1 in HCs under the identical regulatory sequences are phenotypically normal (unpublished data). Hence, the observed expansion in the HZ is consistent with a defect induced by the expression of the
transgene. RNase protection assays confirmed the expression of the 13del transgene (Figure 1F). The expansion of the HZ was relatively greater in another 13del line showing higher transgene expression and was less in yet another line with lower 13del expression (Figure S1), indicating a dosage-dependent effect. In situ hybridization using Col10a1- and 13del-specific riboprobes revealed co-expression of 13del mRNA with endogenous Col10a1 specifically in the 13del HCs (Figure 2A). In wt littermates, Col10a1 expression was largely restricted to, and maintained at a high level in the HZ (Figure 2A). By contrast, the expression of both Col10a1 and the 13del transgene in 13del mice was down-regulated toward the lower portion of the hypertrophic zone (LHZ) (Figure 2A), indicating an alteration in the differentiation program of HCs.

13del HCs Retain 13del Proteins Intracellularly and Survive ER Stress

Immunostaining with a 13del-specific antibody showed 13del proteins were restricted to the HCs in the growth plate. The 13del proteins were intracellular, with little or no staining in the ECM (Figure 2B, 13del panels), and co-localized with concanavalin A, which binds to carbohydrate moieties in the ER (Figure 2B, middle panels). Endogenous wt collagen X was secreted to the ECM in mutant as in wt mice (Figure 2B, insets). The 13del protein level varied both temporally and spatially: just before birth at 18.5 d post coitum (dpc), when the HZ expansion had not yet reached its maximum, mutant proteins appeared to be evenly present in the HZ (Figure 2C). By contrast, there was reduced amounts of mutant protein in the LHZ of 3-wk-old 13del mice (Figure 2C), a time point at which the degree of expansion of the HZ relative to wt was less than for 10-d-old mice.

Ultrastructural analysis revealed distended and fragmented ER in 13del HCs, but not in other growth plate zones (Figure 3A), raising the possibility that they were experiencing ER stress. We tested for expression of alternatively spliced Xbp1 mRNA (Xbp1s), a major transducer of the ER stress signal. Both the spliced and unspliced isoforms of Xbp1 were expressed in growth plate cartilage mRNA from 13del mice (Figure 3B), whereas only the unspliced form was found in wt littermates. Immunostaining revealed a strong induction of XBP1s protein in HCs expressing 13del protein in 13del upper HZ (UHZ) compared with wt littermates (Figure 3C, Figure S3A). Expression of Edem, a direct downstream target gene of XBP1s [28, 29], was also induced in 13del HZ, but not in the wt littermates (Figure S2).

The mRNA for the molecular chaperone BiP is strongly expressed in the UHZ in 13del mice (Figure 3D), concomitant with the expression of the 13del transgene (Figure 2A), and gradually less so in cells toward the LHZ. This is consistent with the higher level of unfolded proteins and induction of ERSS in 13del UHZ. Immunostaining revealed markedly higher levels of BiP in HCs of the LHZ than in wt littermates (Figure 3E). Immunoblot analysis of proteins extracted from hypertrophic cartilage confirmed this up-regulation of BiP in 13del mice (unpublished data).

Another bZIP transcription factor, ATF4, regulates ER stress by inducing the apoptosis-associated gene Chop [30]. Quantitative RT-PCR showed marked up-regulation of Chop transcript (unpublished data), and immunostaining showed elevation of CHOP protein in 13del HCs (Figure 3F).

Figure 2. Intracellular Accumulation of 13del Proteins

(A) In situ hybridization for wt Col10a1 or 13del transcripts at 10-d-old proximal tibial growth plates.

(B) Immunofluorescence of cryosections immunostained with a 13del-specific antibody (13del Ab, green fluorescence). Absence of staining in the HZ of wt littermates showed the antibody is specific for 13del protein (Figure 1G, wt panel). Red fluorescence signal marks concanavalin A (ConA) in the ER. Localization of 13del proteins within the ER (yellow) is shown by the overlapping green and red fluorescence signals. Insets show extracellular immunostaining for normal collagen X in wt and 13del mice.

(C) Immunohistochemistry using 13del-specific antibody on paraffin-embedded proximal tibial growth plate sections. Specific staining (brown) was seen only in 13del HZ. The sections were not counterstained in order to access the intensity of staining more easily. Bar indicates 100 μm.

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compared to wt mice, but not of apoptosis as determined by terminal transference dUTP nick end labeling (TUNEL) assays (Figure S4). Cytoplasmic localization of p53 is a molecular consequence of preventing apoptosis during ER stress [31], and we observed this in 13del HCs in the LHZ (Figure 3G). The ER-stressed HCs survived, which is consistent with an expansion of the HZ.

Normal Rate of Chondrocyte Hypertrophy in 13del Proliferating Chondrocytes

To determine whether the accumulation of HCs was due to increased rate of chondrocyte hypertrophy, we performed in vivo pulse-labeling experiments using 5-bromo-2'-deoxyuridine (BrdU). Two hours after BrdU injection, only proliferating chondrocytes were labeled in both 13del and wt mice (Figure 4A). There was no difference between wt and 13del in the proportion of labeled proliferating cells in the proliferating zone (PZ) (11.17% and 10.65%; \( p = 0.116; n = 3 \) for each genotype). After a 48-h chase, the position of the most distally located BrdU-labeled HCs relative to the PH was similar in 13del and wt mice, indicating that the transition to hypertrophy was unaffected (Figure 4A). The percentage of BrdU-labeled HCs relative to total number of BrdU-labeled chondrocytes in the PZ and HZ was also similar (\( p = 0.53 \)) in 13del (31.9 ± 3.8%; \( n = 4 \)) and wt mice (30.7 ± 4.4%; \( n = 4 \)), indicating that the rate of chondrocyte progression to the
hypertrophic state is normal in 13del. This suggests that the 13del-induced defect arises within the HZ.

**Altered Cell-Cycle Regulation in 13del HCs**

\(p57^{Kip2}\) regulates cell-cycle exit and postmitotic hypertrophic differentiation in chondrocytes \([32,33]\). Expression of \(p57^{Kip2}\) in the UHZ was up-regulated to a similar degree in wt and 13del mice (Figure 4B), which indicates that 13del cells had exited the cell cycle and entered the hypertrophic program. However, \(p57^{Kip2}\) was significantly down-regulated in the mid to lower 13del HZ (Figure 4B), which suggests that the cells could have re-entered the cell cycle.

The 13del expressing HCs in the mid to lower HZ, but not wt cells, were also found to express cyclin D1, a marker for the G1 phase (Figure 4C, Figure S3B). Proliferating cell nuclear antigen (PCNA), a marker for proliferating cells, was also expressed specifically by cells of the 13del HZ, but not wt (Figure 4D). Together, these data suggest that in 13del mice, hypertrophic differentiation was initiated, but HCs in the mid to lower HZ re-entered the cell cycle. However, given that BrdU-labeled HCs were not detectable in the 13del HZ after 2 h (Figure 4A), 13del HCs did not appear to have progressed through the G1/S checkpoint. Thus, expansion of the HZ cannot be attributed to the proliferation of HCs by mitotic division.
Re-expression of Gene Markers for Earlier Chondrocytic Lineages by 13del HCs

We observed that some chondrocytes within the 13del LHZ acquired a more flattened and elongated cell shape with condensed nuclei (Figure 4B–4D). Moreover, we found that there were increased numbers of smaller chondrocytes in the 13del LHZ close to the chondro-osseous junction (29.5% ± 6.42%) compared to wt LHZ (17.8% ± 7.49%) (p = 0.04 by t-test; see Materials and Methods), indicating a change in identity. Thus, we hypothesized that the differentiation status of HCs in the HZ had been altered, contributing to the

Figure 5. Altered Differentiation of HCs to “PreHC-Like” Cells

Analyses of the proximal tibial growth plate of 10-day-old mice. (A–D and F) In situ hybridization using specific markers for resting, proliferating chondrocytes, and preHCs (Col2a1) (A), preHCs (Ppr) (B), preHCs and HCs (Ihh) (C), proliferating chondrocytes (Ptc) (D), and terminal HCs (Opn) (F). The chondro-osseous junction is depicted by a yellow line). (E) To show that altered differentiation took place after the initiation of hypertrophy, X-gal staining was performed on 10-d-old Col10a1-Cre/ROSA26 Cre reporter (R26R) mice with or without the 13del transgene. Positive staining appears as pink under dark field. The inset in the 13del panel shows co-localized X-gal staining (pink) and Ppr in situ hybridization signal (white dots) in mid-lower HZ of the triple mutant. (G) In situ hybridization for Opn and Ppr in consecutive sections. In some HCs of 13del mice, Opn and Ppr are co-expressed (yellow-circled cells). In wt mice, the expression profiles of Opn and Ppr are mutually exclusive (see red- and green-circled cells). Bar indicates 100 μm.

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expansion of the HZ. The different subpopulations of chondrocytes display characteristic expression profiles of many genes encoding transcription factors (e.g., Sox9), signaling/growth factors (e.g., Ihh, Pthrp, and Igf2), receptors (e.g., patched [Ptc] and PTH/PTHrP receptor [Ppr]), cell-cycle regulators (e.g., p57kip2 and cyclin D1), and ECM components (Col2a1, Col10a1, and Agl1).

As wt proliferating chondrocytes undergo hypertrophy, several genes are down-regulated in preparation for replacement of cartilage by bone. Col2a1 is normally expressed throughout the growth plate with the highest levels in the resting zone (RZ), PZ, and PH, and the lowest in the HZ (Figure 5A). Sox9 expression parallels that of its transcriptional target Col2a1, except in the HZ, where it is absent (Figure S5A). Igf2 is expressed at high levels in proliferating chondrocytes and at lower levels in preHCS, and is down-regulated in HCs (Figure S5B). Consistent with the finding that entry into the hypertrophic phase was not affected in 13del mice, the expression of Col2a1, Sox9, and Igf2 was down-regulated in the UHZ. However, 13del chondrocytes in the mid- and lower portions of the HZ re-expressed Sox9, Col2a1, and Igf2 (Figures 5A, S5A, and S5B). The α1-chain of collagen I (Col1a1), a marker of osteoblasts, was not expressed in 13del HCs (Figure S5C). Because HCs in the LHZ have normally progressed to the terminal stages of differentiation, our data indicate 13del LHZ chondrocytes had reverted to a “preHC-like” status.

Re-Activation of the IHH and PPR Signaling Pathways in 13del HCs

To further characterize the abnormality in terminal chondrocyte differentiation, we focused on two pathways, IHH/PTC and PTHrP/PPR, which cooperate to regulate chondrocyte proliferation and hypertrophy [34]. In 10-d-old wt mice, expression of Ppr (encoding PTH/PTHrP receptor) and Ihh was found predominately in both preHCS and upper HCs (Figure 5B and 5C), and Ihh mRNA was diminished in the LHZ and absent from cells bordering the chondro-osseous junction. Expression of Ptc, which encodes for IHH receptor and a target gene of IHH per se, flanked the Ihh-expressing domain proximally and distally, just adjacent to the preHCS and within the osteogenic cells at the chondro-osseous junction (Figure 5D). In 10-d-old mice, Ihh, Ptc, and Ppr were expressed in similar regions in both 13del and wt; but in 13del mice, these genes were re-expressed in some cells in the LHZ (Figure 5B–5D). The strong activation of Ptc transcription and re-expression of Ppr indicate that cells in the 13del LHZ are receiving and responding to IHH signal. Overall, 13del cells in the LHZ expressed markers that are more characteristic of preHCS.

Altered Terminal Differentiation in 13del HCs

To confirm that 13del HCs had initiated hypertrophic differentiation normally, we created Col10a1-Cre/ROSA26 CRE reporter mice that expressed CRE recombinase and β-galactosidase specifically in HCs and crossed them with 13del mice. In the compound mutant mice with or without 13del transgene, all the HCs expressed β-galactosidase as shown by X-gal staining (Figure 5E). Some 13del HCs in the mid-lower HZ exhibited both Ppr-re-expression and positive X-gal staining (Figure 5E, inset in 13del panel). Because the Cre gene had been inserted into the Col10a1 gene by homologous recombination, its expression is under the control of the endogenous Col10a1 promoter. Therefore, the induction of β-galactosidase expression indicated that differentiation of 13del HCs was disrupted after they have initiated hypertrophy.

As HCs attain the terminal stages of differentiation at the chondro-osseous junction, they express osteopontin (Opn) and matrix metalloproteinase 13 (Mmp13). In wt mice, these genes were expressed exclusively in HCs at the chondro-osseous junction, whereas in 13del mice, expression of Opn and Mmp13 (Figure 5F and Figure S5D) were delayed and scattered throughout the LHZ. In situ hybridization of consecutive sections through 13del growth plates revealed that some ectopic Opn-expressing HCs also expressed Ppr, manifesting the characteristics of both preHC and terminally differentiated chondrocytes (Figure 5G). This co-expression of Opn and Ppr was not observed in wt growth plates (Figure 5G).

Altered Differentiation and Function of 13del HCs Is Cell Autonomous

To determine whether the altered differentiation program was intrinsic to 13del chondrocytes, we created mouse chimeras by aggregating morulae from 13del mice and from mice ubiquitously expressing the enhanced green fluorescent protein (EGFP). Wt cells were detected by immunostaining for EGFP (Figure 6A–6C); 13del cells were detected by in situ hybridization using the 13del-specific riboprobe (Figure 6D–6F). Mice with different degrees of EGFP/13del chimism, as well as EGFP/wt chimeras, were studied and expression of BiP (Figure 6G–6l), p57kip2 (Figure 6j–6l) and Ppr (Figure 6M–6O) were analyzed.

As anticipated, the growth plates of EGFP/wt chimeras were indistinguishable from wt (Figure 6A). In EGFP/13del chimeras, the most noticeable changes were variations in the height of the HZ and an undulating chondro-osseous junction in the growth plate (Figure 6B). Where the contribution of 13del cells was higher, the degree of expansion of HCs was likewise higher and the undulation of the chondro-osseous junction generally correlated well with the relative contribution of 13del cells. This correlation suggests that the defect in 13del HCs is a cell-autonomous one, since their abnormal differentiation could not be overcome by the presence of wt HCs.

Key marker for ERSS (BiP) (Figure 6H), for cell-cycle progression (p57kip2) (Figure 6K), and for chondrocyte differentiation (Ppr) (Figure 6N) were expressed abnormally in regions containing 13del cells. 13del HCs in the LHZ of chimeras re-expressed Ppr (Figure 6N). Thus, the presence of wt cells did not “rescue” the 13del cells, and the signal for altering differentiation program is most likely cell autonomous.

13del Expression Correlates with the Levels of ER Stress and Alteration in Differentiation

To understand the relationship between 13del transgene expression, ERSS, and the alteration in differentiation in fetal and postnatal growth, expression of the 13del transgene, the endogenous Col10a1 gene, BiP, and Ppr was followed over fetal and postnatal stages. Interestingly, at 14.5 dpc, although expression of endogenous Col10a1 (Figure 7A1) can be seen in the HZ of 13del mice, little or no 13del transgene expression was detected (Figure 7A2), and BiP expression was not...
induced in the HZ (Figure 7A3). Similar to wt mice, expression of Ppr was restricted to the PH and upper HZ in 13del mice and no expansion of HZ was detected (Figure 7A4 and 7A5). In addition, Opn expression was restricted to the last layer of HCs and the primary ossification center in both genotypes (Figure 7A5 and 7A5'). 13del transgene expression in HCs could be detected at 15.5 dpc (Figure 7B2), with a concomitant induction of strong expression of BiP in the HZ (Figure 7B3; in contrast to Figure 7B3'). At this stage, the HZ in 13del was not expanded, and Ppr and Opn expression patterns were normal (Figure 7B4 and 7B4', and 7B5 and 7B5'). At 17.5 dpc, the expression pattern of these key genes remained similar; however, a slight expansion of the HZ and punctate Opn expression in the LHZ could be detected in 13del mice (Figure 7C1-7C5). Re-expression of Ppr in the LHZ was detectable at 18.5 dpc (unpublished data), and most obvious at 10 d old (Figure 8A4) that correlated with the greatest HZ expansion (Figure 8A1-8A5) and induction of BiP expression (Figure 8A3). The 13del transgene, Col10a1, and BiP expression were down-regulated in the LHZ of 13del mice at 10 day old, when Ppr was re-expressed (Figure 8A1-8A5) and Opn showed punctate expression (Figure 8A1-8A5). A similar pattern for these markers was also observed in 3-wk-old 13del mice, although the degree of HZ expansion was reduced in terms of the number of cell layers in the HZ (Figure 8B1-8B5).

In 4-wk-old 13del mice, expression of the 13del transgene was relatively weaker than endogenous Col10a1 and was distributed through the middle to lower HZ (Figure 8C2 and 8C2'). Expansion of HZ was further diminished; strong expression of BiP persisted only in the middle to lower HZ (Figure 8C3), and there were much fewer cells expressing Ppr in the LHZ (Figure 8C4). By 6 wk and 10 wk, 13del transgene expression continued to diminish, being undetectable by 10 wk (Figure 8D2 and unpublished data), although robust levels of the endogenous Col10a1 gene were found (Figure 8D1). Induction of BiP was barely detectable at 6 wk and was absent at 10 wk (Figure 8D3 and unpublished data). These were accompanied with return to normal height of HZ and normal Ppr and Opn expression pattern similar to wt (Figure 8D4 and 8D5 and unpublished data).

The close correlation between Col10a1 and 13del expression with BiP was further shown by quantitative RT-PCR using serial transverse sections of the tibial growth plates. In the wt, levels of Col10a1 were high throughout the HZ, decreasing sharply across the chondro-osseous junction (Figure 9A, fraction 19–18). This reduction in expression is normally accompanied by an up-regulation of Mmp9, a marker for terminally differentiated HCs (Figure 9A, fraction 19–18). BiP expression was low throughout, and the levels showed only mild fluctuation. In the 13del HZ, Col10a1 and 13del levels were high in the UHZ. The up-regulation of Col10a1 and 13del expression was closely correlated with strong induction of BiP and Chop expression (Figure 9B, Fraction 34–30; unpublished data for Chop). In the 13del LHZ, Col10a1 and 13del expression was down-regulated some distance away from the chondro-osseous junction, which is marked by Mmp9 up-regulation (Figure 9B, fraction 31–29). This down-regulation was accompanied by reduced BiP and Chop expression in the LHZ, indicating ER stress was alleviated (Figure 9B, fraction 31–30). These data suggest that ER stress and its alleviation are closely associated with the altered terminal differentiation in 13del HCs.

Together, these data demonstrated that in 13del mice, transgene expression activated ERSS in the first instance, followed by Ppr re-expression in the LHZ, leading to an expanded HZ. From weaning age (3 wk) onwards, transgene expression level steadily diminished together with attenuation of ERSS.
ER Stress in Other Mouse Models of Chondrodysplasia

To assess whether the ERSS can be induced in chondrocytes at a different stage of differentiation and is, therefore, potentially implicated in other forms of chondrodysplasia, we tested whether ER stress was triggered in the chondrocytes of growth plates of two other mouse models of chondrodysplasia, cmd/cmd mutants express a severely truncated aggrecan core protein because of a premature stop codon in exon 5 [35]. Col2a1G904C transgenic mice express procollagen II with a glycine to cysteine mutation (G904C) [36]. Both mutants show a fragmented ER in chondrocytes (Col2a1G904C, Figure S6; cmd/cmd mice [37]). The normal chondrocyte columns were disorganized, and immunostaining for BiP was enhanced in both mutants, indicating induction of ERSS (Figure 10A, Figure S6). There was no distinct zone of proliferating chondrocytes in the cmd/cmd mutant, with only a very small portion of cells progressing to hypertrophy, indicated by the region of the growth plate stained for collagen X (Figure 10A).

CHOP expression was elevated, but there was no increase in apoptotic cells (unpublished data). There was also increased ectopic expression of cell-cycle markers such as p57Kip2 and PCNA (Figure 10A), indicating these cells are trapped in an abnormal state of cell-cycle progression.

Discussion

Many studies have shown that factors influencing cell fate and/or differentiation are activated in ERSS, but how such changes impact differentiation programs in vivo is poorly understood. We have shown that HCs in the murine growth plate expressing unfolded collagen X experience ER stress but do not undergo apoptosis. The normal terminal differentiation process is interrupted; HCs adapt and survive via cell-autonomous reversion to a preHC-like state that results in delayed endochondral ossification and chondrodysplasia.

Expression of Unfolded Collagen X Triggers ER Stress

In vitro translation assays suggest that 13del mutant collagen X proteins are unable to assemble into trimers, and thus are poorly secreted. The accumulation of the 13del proteins in the ER and the low to undetectable level in the ECM of the HZs of 13del mice confirmed the secretion defect. Poor secretion is also seen with collagen X containing other MCDS mutations that prohibit subunit folding and assembly [23,38].

The 13del mice reveal that misfolding of mutant collagen X occurs in vivo. High-level expression of Col10a1 is characteristic of chondrocyte hypertrophy. 13del HCs transcribed both endogenous Col10a1 and 13del transgene. Intracellular accumulation of 13del proteins suggested that the endogenous degradation machinery could not clear all the mutant protein. The distended, fragmented ER indicates that ER stress was induced in HCs expressing 13del proteins, leading to activation of ERSS. Up-regulation of BiP, CHOP, expression of Xbp1s, Edem, and cytoplasmic localization of p53 in 13del HCs are all indicators that ERSS was triggered. The co-expression of both XBP1s protein and 13del in the same cells suggests that expression of the mutant collagen directly induced ERSS.

Interestingly, in contrast to the expanded HZ in 13del mice, expression of chicken collagen X chains containing a deletion within the helical domain in transgenic mice results in chondrodysplasia and a compressed HZ [39]. The underlying molecular mechanism is not clear, and there are no mutations reported in the helical domain of collagen X in humans for comparison. Trimerization of the mutant chicken...
collagen X was not affected and homo- and hetero-trimers formed efficiently in vitro [40]. Furthermore, mutant collagen X is detected in the extracellular matrix in growth plate cartilage of the transgenic mice, with little evidence for intracellular accumulation [40]. Thus, the molecular consequence to 13del mice is likely to be different, and the compression may be related to the presence of mutant chicken collagen X mixed with wt mouse collagen X or hybrid mouse–mutant chicken collagen X in the growth plate matrix, impairing the supramolecular structure of extracellular collagen X and hence tissue integrity.

Visualizing Induction and Progression of ERSS in the 13del Growth Plate In Situ

A single histological section of the growth plate provides a continuous snapshot of the different phases of chondrocyte differentiation as they progress from a resting state to the proliferative state, become prehypertrophic, and then enter the final stages of hypertrophy and terminal differentiation at the chondro-osseous junction. Thus, our analyses of molecular changes in 13del chondrocytes using longitudinal sections taken through the growth plate provide an in vivo picture of ER stress induction. The response of the HCs to ER stress, indicated by induction of BiP expression, can then be monitored as the HCs approach the chondro-osseous junction. In cultured cells, induction of ERSS is characterized by a rapid increase of BiP mRNAs [41,42].

In 13del, strong induction of BiP mRNA in the UHZ was observed in pre-weaning age, suggesting that HCs are experiencing ER stress soon after hypertrophy. In contrast, by 4 wk postpartum, in UHZ chondrocytes, 13del transgene expression was diminishing, whereas BiP mRNA was more abundant in the LHZ where cells were expressing a higher level of the transgene and ER stress is maintained in these cells. Therefore, the stress level in 13del HCs varied during growth according to transgene expression level, and the stress response is dosage dependent.

It is interesting to note that the 13del transgene did not fully recapitulate the expression of the endogenous Col10a1 gene in fetal and postnatal growth. It is turned on later (between 14.5 and 15.5 dpc) and turned off earlier (between 6–10 wk postpartum) when compared to the endogenous Col10a1, probably because the transgene did not contain the full complement of Col10a1 regulatory elements; for example, the lack of a conserved enhancer element upstream of the transgene ([43] and unpublished data). When normal Col10a1 alone was expressed (14.5 dpc and at 10 wk postpartum), induction of BiP expression was not detected. This asynchrony in timing of expression between 13del and the endogenous Col10a1 and the qRT-PCR data serves to high-
light the close association between 13del expression and BiP up-regulation, further supporting the notion that 13del proteins induced ERSS directly.

Surviving ER Stress Is Coupled with Altered Terminal Differentiation

ERSS is primarily a response to relieve ER stress for cell survival. However, ER stress can lead to cell death as shown in various systems. In the Akita diabetic mouse, ER stress led to apoptosis via CHOP induction. In the absence of CHOP, apoptosis was reduced and the onset of diabetes was delayed [15,44]. CHOP is also implicated for anti-apoptotic activity. In a mouse model of human Pelizaeus-Merzbacher disease experiencing ER stress, CHOP protects oligodendrocytes from apoptosis [7]. These contradictory results may be explained by the dependence of concurrent signaling events during ER stress. Indeed, signals both upstream and downstream of CHOP (i.e., the PERK signaling cascade) have been shown to have opposite effects on cell survival [45–47]. In 13del, despite raised CHOP expression in the UHZ, apoptosis was not triggered and the HCs survived. In this situation, ERSS may play a cytoprotective role. It is known that growth plate chondrocytes are destined to survive hypoxic stress during development [48]. This implies that they are pre-conditioned to survive hypoxic conditions before becoming terminally differentiated, probably through the cytoprotective actions of HIF-1α PERK, and eIF2α [6,49,50]. Chondrocytes may have additional adaptive mechanisms that protect against stress-induced apoptosis or have a high stress tolerance or threshold before cell death can be triggered. One may speculate that cells that are not preconditioned to survive stress (e.g., neurons) may be much more susceptible to ER stress-induced death. Paradoxically, the cytoprotective effect of ERSS may interfere with the normal apoptotic fate of HCs, contributing to the abnormal terminal differentiation of 13del HCs.

Survival of 13del HCs was associated with signs of stress alleviation. The diminished expression of Col10a1/13del in the LHZ indicates that production of the mutant collagen X chains in those chondrocytes was reduced, and ER stress was correspondingly alleviated, as revealed by the down-regulation of BiP and Chop transcript in the LHZ. The outcome of alleviation of ER stress is the reduction in synthesis of 13del proteins. In 13del, a reduction in Col10a1 and 13del mRNAs occurred that must contribute towards alleviation of ER stress. Such reduction could occur by nonsense-mediated decay, as suggested for MCDS caused by the nonsense mutations [51,52] or by IRE1-mediated mRNA degradation recently identified to occur during the UPR [53] or by regulating transcription.

It is notable that the reduction in Col10a1/13del expression also correlated with the change in cell-cycle control and differentiation state of the chondrocytes in the LHZ (summarized in Figure 10B). These changes point to more complex modes of alleviating ER stress. In the 13del UHZ, the strong transcription of both wt and 13del Col10a1, up-

Figure 9. Correlation of Altered Differentiation of HCs and ERSS

Serial transverse sections of 10-d-old tibiae were collected for quantitative RT-PCR analyses. A section between each fraction of 20 sections was stained with safranin-O and the von Kossa stain to identify the bony or cartilaginous nature of each fraction. The section around the chondro-osseous junction is shown from wt (A) and 13del (B) mice. Mineralized tissues stained dark brown and cartilaginous tissues stained orange. Relative transcript abundance was quantified for Col10a1 and 13del, BiP, and Mmp9 in wt (A) and 13del (B). The Col10a1 primers also recognize 13del transcripts. Fractions are numbered from the bone shaft towards the growth plate cartilage for reference only, and there is no correlation between wt and 13del fractions. The position of the fractions relative to the bone and HZ of the growth plate is indicated. The HZ is delineated by a pair of dotted line in each graph; PZ and RZ are on the right-hand side of the HZ. Error bars represent ±1 standard deviation (SD).

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regulated expression of p57Kip2, and extent of BrdU labeling in pulse-chase experiments indicated that 13del preHCs had exited the cell cycle and progressed into hypertrophy normally. Normal entry into hypertrophy is further confirmed by the expression of Col10a1-Cre and β-galactosidase activity in all HCs in the 13del expanded HZ. However, down-regulation of both Col10a1 and 13del transcripts in advance of expression of Mmp9, and delayed expression of Mmp13 and

Figure 10. ERSS in cmd/cmd Mutant and a Model for Surviving ER Stress
(A) ERSS and disrupted chondrocyte differentiation in the growth plate of the cmd/cmd mutant. Immunohistochemical detection of BIP, p57Kip2, PCNA, and collagen X (ColX) in the tibial growth plates of 18.5 dpc fetus. Color contrast of these images was adjusted as described in Materials and Methods. Bar indicates 100 μm.
(B) Comparative summary of expression pattern for molecular markers in the growth plate in wt and 13del mice.
(C) Model for the reprogramming of HCs in 13del transgenic mice expressing unfolded collagen X.
AC, zone containing abnormal chondrocytes; p53(c), cytoplasmic localized p53.
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PTHrP suppresses cell-cycle re-entry. This is a novel finding since HCs are terminally differentiated and are not expected to return to the cell cycle. PTHrP suppresses p57Kip2 expression [33], IGF2 antagonizes p57Kip2 [54], and cyclin D1 is a target of IHH [55] and IGF2 [56] signaling. Igf2, Ppr, and Ihh show highest expression level in wt proliferating chondrocytes or preHCS, and are down-regulated in HZ. Their re-expression in the 13del LHZ suggests a link to the observed cell-cycle re-entry. Activated PTHrP and IGF2 signaling may down-regulate p57Kip2 expression, whereas activated IHH and IGF2 signaling could up-regulate cyclin D1 expression, stimulating cell-cycle re-entry. Cell-cycle re-entry for 13del LHZ chondrocytes is most likely a secondary effect due to the re-activation of signaling pathways that regulate chondrocyte proliferation and hypertrophy.

Cells in the 13del LHZ were asynchronized in terms of their differentiation state: some of them expressed preHC markers (e.g., Ppr), some expressed markers for terminally differentiated HCs (e.g., Opn), and some expressed both Ppr and Opn. The latter can be interpreted as cells captured in a “reprogramming” process. Because, as indicated in wt mice, expression of Opn marks HCs that have progressed to the terminal status, and for Ppr to be expressed in the same 13del HCs suggests a reversion process has occurred. However, the reversal of differentiation is not absolute, as endochondral ossification does occur, albeit delayed. Therefore, the co-expression of Ppr and Opn could also indicate stress-alleliated HCs resuming terminal differentiation. These cells may bypass the intermediate hypertrophic state to avoid expressing high level of mutant collagen X.

**Relationship between ER Stress and Altered Terminal Differentiation**

The inability of wt HCs to rescue the delayed terminal differentiation, and the altered gene expression of 13del cells in chimeras, suggest that these changes are dominant and cell autonomous. The normal terminal differentiation of HCs in collagen X null mice [57] and identical expansion of HZ in compound 13del; Col10a1 null mutants (unpublished data) are consistent with such a dominant effect. Given that there is normal entry into hypertrophy and a clear demarcation region of fully differentiated HCs in the UHZ, as shown by the β-galactosidase activity in all HCs in Col10a1-Cre–Rosa26 reporter mice, the reversion of cells in the LHZ to a preHC-like status must be due to altered terminal differentiation of the stressed HCs.

The concomitant onset of ERSS in the 13del UHZ with disruption of terminal differentiation provides visual evidence for a possible link between these two processes, and is consistent with the latter occurring as a consequence of ERSS. The correlation between levels of 13del expression with degree of HZ expansion in independent lines of mice suggests a direct link between level of ER stress and the altered differentiation. In addition, the gradual loss of preHC-like cells after weaning age correlates with the down-regulation of 13del and delayed BIP induction, suggesting a causal relationship between ER stress and altered HC differentiation. Co-expression in the same cells of 13del with XBP1s and with cyclin D1 proteins provides molecular evidence for a direct link.

Reverting to a preHC-like state may be an adaptive or fortuitous response by which the 13del HCs alleviate and survive ER stress. This is interesting, since by reverting to a preHC-like state, both wt and 13del Col10a1 transcription would be down-regulated, thereby reducing the source of the ER stress (13del proteins) to a more acceptable level. Consistent with this hypothesis, expression of 13del, Col10a1, and BIP was reduced in the LHZ at 10 d and 3 wk postpartum.

Chondrocytes in culture are able to re-differentiate after dedifferentiation to a fibroblastic/osteoblastic state [58,59]. This plasticity involves changes in transcriptional profile and may be retained in HCs. The altered terminal differentiation of 13del HCs is the first in vivo demonstration of the phenotypic plasticity and capacity to revert to a preHC-like state. Unlike in cell culture, none of the 13del HCs expressed Col11a1, the osteoblast marker, suggesting that reprogrammed differentiation to a preHC-like state occurred rather than transdifferentiation to osteoblasts. This inherent plasticity may be exploited by HCs to adapt and survive ER stress in vivo.

Our findings provide novel mechanistic insight into how chondrocytes overcome ER stress in vivo. Until now, it is generally accepted from in vitro studies that cells respond to ER stress either by undergoing apoptosis or by a general down-regulation of protein synthesis and up-regulation of protein-folding-degradation capacity and thereby relieve the load of unfolded proteins in the ER. However, there is no information on the impact of ER stress on the differentiation program of chondrocytes either in vitro or in vivo.

We propose a model (Figure 10C) in which, in addition to the alleviation mechanisms mediated by the UPR, 13del HCs cope with ER stress through a “reprogram, recover, and survive” adaptive mechanism. Initially, 13del protein expression induces ERSS, but not apoptosis. The differentiation program of the HCs is altered in which they “revert” or “reprogram” to a preHC-like state in which collagen X expression is reduced. The “reprogramming” involves re-activation of signaling pathways that may stimulate re-entry into the cell cycle. However, p57Kip2 restricts cell-cycle progression. By reprogramming, the 13del HCs finally down-regulate endogenous Col10a1 and 13del mRNA levels, thereby alleviating the load of mutant protein and ER stress, providing the means to survive and complete differentiation, albeit with delayed endochondral ossification.

The exact mechanisms that mediate the reversion of the differentiation pathway in 13del HCs are not known. It is conceivable that the ER stress response takes control over gene expression and protein metabolism to such a significant extent that it interferes with normal differentiation processes, which may involve complex alteration in signal transduction and transcription factors recruitment and interaction, as well as epigenetic changes upon ER stress [60]. Identifying and understanding the underlying mechanisms are important and issues for further study.

**Implications for the Pathogenesis of Chondrodysplasias**

Our data have broad implications for the mechanism of disrupted chondrocyte differentiation in MCDS and other chondrodysplasias caused by mutations that impair protein
assembly and secretion. Although ER stress-induced apoptosis may provide a major route for pathogenesis, our study raises the possibility that chondrocytes can survive ER stress in a process that changes the normal differentiation program. Changes in the pattern of markers that characterize the differentiation status of chondrocytes have been noted in chondrodysplastic models. Mutations in collagen II that interfere with assembly and secretion, leading to chondrodysplasia, are associated with distension of the ER [61,62]. In Col2a1<sup>13del</sup> mice, the fragmented ER, as well as the increased levels of BiP and CHOP in growth plate chondrocytes, indicate that ERSS is induced; abnormal terminal differentiation of HCs is indicated by the up-regulation of Col2a1 and Agel expression [36]. Transgenic mice expressing collagen II with a 36 amino acid deletion showed disorganized chondrocytes and fragmented ER, and there was loss of expression of the cell-cycle regulator Cdkn1a and the key differentiation markers Ihh, Col10a1, and Fgfr3 [62]. In endochondral tissue, the distributions and co-expression patterns of several chondrocyte differentiation markers [63] and regulators of the cell cycle (p57Kip2 and PCNA) were altered. The abnormal gene expression in these models and 13del suggest that alteration of the normal progression of differentiation, cell-cycle control, and fate change may be a common consequence of ER stress in chondrocytes. However, the phenotypic consequence in terms of differentiation pathway and growth plate architecture may differ depending on the nature of the mutation and the expressing cell type.

The 13del mouse has also provided insight into the adaptive mechanisms that facilitate survival of chondrocytes in vivo in the face of ER stress. But survival is not without cost; the changes in HC differentiation do result in delayed endochondral ossification. We postulate that the change in differentiation program contributes to the disorganization of chondrocytes in the growth plate that occurs in many chondrodysplasias. Whether this strategy is peculiar to chondrocytes or can be adopted by other cell types affected in protein-folding disorders is an important issue to address in the future.

Materials and Methods

Generation of constructs and transgenic mice. Thirteen nucleotides (residues 6058–6070) of the murine Col10a1 gene were excised by overlapping PCR [22]. The resultant PCR product was cloned to generate the Col10a1<sub>13del</sub> transgene. This transgene is a 10.5-kilobase (kb) fragment of the murine Col10a1 gene containing 2 kb of the 5′ and 1.3 kb of 3′ flanking sequence after exon 3 (Figure 1B).

13del transgenic mouse founders were generated by pronuclear injection into one-cell CBA/C57BL/F1 hybrid zygotes. Analyses were performed on 10- to 12-d-old littermates unless otherwise stated. Mice were genotyped by PCR using primers (5′-CCCGGGCATATATCATTCTCT-3′ and 5′-TAGCCCTTGTCTGATC-5′) flanking the 13-kb deletion.

Cell-free transcription and translation. Wt and 13del full-length cDNA constructs in pBluescript II Sk(−) (Stratagene, La Jolla, California, United States) were transcribed and translated using the TNT-T3 polynucleotide-coupled transcription and translation system (Promega, Madison, Wisconsin, United States), supplemented with canine microsomal membrane vesicles (Promega) as described previously [22]. For heterotrimer assembly, equal amounts of each of the normal and mutant plasmids were co-translated. Collagen X chains were analyzed on 7.5% (w/v) SDS-polyacrylamide gels.

Histological and immunohistochemical analyses. Limbs were fixed in 4% paraformaldehyde, and if necessary, were demineralized in 0.5 M EDTA (pH 8.0) containing 0.2% formaldehyde prior to embedding in paraffin. Immunohistochemistry was performed using antibodies for p57<sup>Kip2</sup>, p53, cyclin D1, CHOP, PCNA (Santa Cruz Biotechnology, Santa Cruz, California, United States), XBP1 (BioLegend, San Diego, California, United States), BiP (Stressgen, San Diego, California, United States), and green fluorescent protein (Abcam, Cambridge, United Kingdom). Signals were detected using the avidin-biotin-complex system (ABC; Vector Laboratories, Burlingame, California, United States) for p57<sup>Kip2</sup>, p53, and PCNA antibodies, or using the secondary antibody-HRP-anti-rabbit or anti-mouse antibodies (PerkinElmer, Wellesley, Massachusetts, United States).

Immunostaining for collagen X was performed as described [57]. The 13del antibody was raised in rabbits against a synthetic peptide, ATYPPLMSTPLSQDS, which corresponds to the C-terminus of the 13del protein. Goat anti-rabbit Alexa 488 (Molecular Probes, Eugene, Oregon, United States) was used for immunofluorescence on cryosections. Concanavalin A conjugated with Alexa 594 (Molecular Probes) was used to visualize the ER.

Histomorphometry and electron microscopy. The vertical height of RZ, PZ, and HZ in the tibial growth plate was measured on tissue sections using a test line grid as described previously [64]. Sizes of cells within the tibial LHZ were measured in wt and 13del mice as described [65]. Measurements were made in cells in which the plane of section was through the nucleus to avoid bias. Cells were defined as being “smaller” if the maximal height was equal to or less than that of the tallest cell in the height of cell section. At least five sections from each animal for three wt and three 13del mice were analyzed. For electron microscopy, growth plate cartilage was embedded in Epon 812 and ultra-thin (60 nm) sections were prepared for electron microscopy analysis as previously described [66].

BrdU incorporation. Mice were injected intraperitoneally with 200 μg per gram of body weight of BrdU per injection either 2 × 1 ml saline (injected 2 h later) or two doses 6 h apart (and sacrificed 48 h after the first injection). Following fixation, BrdU in paraffin sections of limbs was detected using a BrdU Staining Kit (Zymed Laboratories, South San Francisco, California, United States). To determine the rate of hypertrophy, digital photographs were taken, and the number of BrdU-labeled chondrocytes in the PZ and HZ of the growth plate was counted. Cells in three consecutive sections from four 13del and four wt mice were scored; differences were assessed using the Student t-test.

RNAse protection assay and RT-PCR. Total RNA was extracted from 10-d-old wt and 13del growth plate cartilage from 30 sections per fraction, on a Zeiss cryostat (Carl Zeiss, Oberkochen, Germany) and growth plates fractionated by collecting 5-mm sections, 20 sections per fraction, on a Zeiss cryostat (Carl Zeiss, Oberkochen, Germany). In between each fraction, a single section was mounted and subjected to von Kossa and Safranin-O staining to determine cell morphology of the tissue comprising the adjacent fractions. Total RNA was prepared from fractions using the Trizol reagent. cDNA was prepared from fractions by reverse transcription of 1 μg of total RNA using Superscript II reverse transcriptase and random hexamers. Quantitative PCR was carried out on an ABI 7700 real-time thermal cycler using a SYBR green qPCR kit from ABGene. Specific PCR primers designed with a melting temperature (Tm) of approximately 60 °C and to span at least one intron were used to determine gene expression profiles. The primers used are as follows: Col10a1, 5′-TTATCTCCATAGCCATAAAG and 5′-AGGTGGGC-GATTCCTCT; Bmp2, 5′-TGAAATCTGGAATGGGCAAGAG and 5′-GATCCATCAGCTCAGA; Mmp9, 5′-TTCTGGGCTTAG-GTCT and 5′-CTCCACTCCTCTGAGTCT; and Activin, 5′-GACGCGCCAGTCTCATCTAT; and 5′-GTACTTTGCGTCAGGAAG- GAG. Dissociation curves were collected for all PCR reactions to determine gene expression profiles. The primers used are as follows:

- Col2a1, 5′-TTCATCCCATACGCCATAAAG and 5′-AGGTGGGCGATTCCTCT; Bmp2, 5′-TGAAATCTGGAATGGGCAAGAG and 5′-GATCCATCAGCTCAGA; Mmp9, 5′-TTCTGGGCTTAG-GTCT and 5′-CTCCACTCCTCTGAGTCT; and Activin, 5′-GACGCGCCAGTCTCATCTAT; and 5′-GTACTTTGCGTCAGGAAG-GAG. Dissociation curves were collected for all PCR reactions to determine gene expression profiles.

In situ hybridization. In situ hybridization was performed as previously described [63], using 5′-[33P]UTP-labeled riboprobes for Dllh.
ER Stress in Hypertrophic Chondrocyte

Supporting Information

Figure S1. Degree of HZ Expansion Correlated with Transgene Expression Level

The transgene expression level for three independent 13del transgenic lines (13del-1, 13del-2, and 13del-3) was determined by RNase protection assay (see Materials and Methods for details), and the corresponding histology of proximal tibial growth plates shown. The transgene expression was normalized to 13del mice, the line on which we performed all our analyses. Three biological replicates were performed for each line and the relative expression indicated. The experiments. K. Y. Tsang, D. Chan, D. Cheslett, W. C. W. Chan, C. Yamada and J. F. Bateman contributed reagents/materials/analysis tools.

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Competing interests

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References