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ORIGINAL ARTICLE

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The Critical Role of the Epidermal Growth Factor Receptor in Endochondral Ossification

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ABSTRACT

Loss of epidermal growth factor receptor (EGFR) activity in mice alters growth plate development, impairs endochondral ossification, and retards growth. However, the detailed mechanism by which EGFR regulates endochondral bone formation is unknown. Here, we show that administration of an EGFR-specific small-molecule inhibitor, gefitinib, into 1-month-old rats for 7 days produced profound defects in long bone growth plate cartilage characterized by epiphyseal growth plate thickening and massive accumulation of hypertrophic chondrocytes. Immunostaining demonstrated that growth plate chondrocytes express EGFR, but endothelial cells and osteoclasts show little to no expression. Gefitinib did not alter chondrocyte proliferation or differentiation and vascular invasion into the hypertrophic cartilage. However, osteoclast recruitment and differentiation at the chondro-osseous junction were attenuated owing to decreased RANKL expression in the growth plate. Moreover, gefitinib treatment inhibited the expression of matrix metalloproteinases (MMP-9, -13, and -14), increased the amount of collagen fibrils, and decreased degraded extracellular matrix products in the growth plate. In vitro, the EGFR ligand transforming growth factor α (TGF-α) strongly stimulated RANKL and MMPs expression and suppressed osteoprotegerin (OPG) expression in primary chondrocytes. In addition, a mouse model of cartilage-specific EGFR inactivation exhibited a similar phenotype of hypertrophic cartilage enlargement. Together our data demonstrate that EGFR signaling supports osteoclastogenesis at the chondro-osseous junction and promotes chondrogenic expression of MMPs in the growth plate. Therefore, we conclude that EGFR signaling plays an essential role in the remodeling of growth plate cartilage extracellular matrix into bone during endochondral ossification. © 2011 American Society for Bone and Mineral Research.

KEY WORDS: EGFR; ENDOCHONDRAL OSSIFICATION; GROWTH PLATE; CHONDROCYTES; MMP

Introduction

The majority of the mammalian skeleton, except for most of the craniofacial skeleton, forms through the process of endochondral ossification, in which a cartilage template is replaced by bone. In long bones, this process occurs at the primary and secondary ossification centers separated by the growth plate. The growth plate consists of a distinct polarized layer of chondrocytes. To achieve longitudinal growth, growth plate chondrocytes go through several stages, including proliferation, differentiation, hypertrophy, mineralization, and apoptosis. At the chondro-osseous junction (COJ), the invasion of hypertrophic cartilage by blood vessels, osteoclasts, and osteoblast precursor cells, together with terminally differentiated hypertrophic chondrocytes, leads to degradation and remodeling of the hypertrophic cartilage extracellular matrix (ECM) into trabecular bone.

Endochondral ossification is tightly controlled by circulating systemic hormones and locally produced signaling factors. These include Indian hedgehog (Ihh), parathyroid hormone (PTH) and parathyroid hormone–related protein (PTHrP) and their receptor PTH1R, fibroblast growth factor 18 (FGF-18) and its receptor FGFR3, vascular endothelial growth factor (VEGF), connective tissue growth factor (CTGF), bone morphogenetic proteins (BMPs), and Wnt proteins. In addition, the transcription factors *Sox9* and *Runx2/Cbfa1* play major roles in growth plate chondrocyte proliferation and differentiation.[1,2]

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The epidermal growth factor receptor (EGFR) belongs to a tyrosine kinase receptor family that also contains ErbB2, ErbB3, and ErbB4. Its ligands include EGF, amphiregulin, and transforming growth factor α (TGF-α), which only bind to EGFR, and heparin-binding EGF (HB-EGF), betacellulin, and epiregulin, which bind to both EGFR and ErbB4. Upon ligand binding, EGFR either homodimerizes or heterodimerizes with other ErbBs. The dimerized receptors then undergo auto- or transphosphorylation on tyrosine residues in the intracellular domain, thus activating several important intracellular signal-transduction pathways, including Ras-Raf-MAP-kinase and PI-3-kinase-Akt. ErbB2 is the preferred partner for EGFR, and the signals mediated by EGFR/ErbB2 are thought to account for most of EGFR's biologic activities. EGFR signaling modulates a variety of cell functions, such as proliferation, survival, adhesion, migration, and differentiation.[3]

Egfr null mice usually die at midgestation, birth, or within 20 postnatal days depending on genetic background owing to severe developmental abnormalities in placental, neural, and epithelial tissues.[4–6] A few surviving *Egfr* null pups displayed craniofacial alterations and cleft palates.[7] They also had delayed primary endochondral ossification, an enlarged hypertrophic zone in the growth plate, and impaired trabecular bone formation during embryonic development.[8] Similarly, mice expressing humanized EGFR (by replacement of the endogenous mouse *Egfr* gene with human *EGFR* cDNA) exhibited low EGFR activity in the skeleton and had a greatly enlarged hypertrophic chondrocyte zone in the growth plate.[9] Overexpression of herstatin, a soluble ErbB2 receptor that acts in a dominant-negative fashion to inhibit EGFR signaling, under the limb-specific Prx1 promoter in mice resulted in shortened limbs and an expanded hypertrophic zone.[10] In contrast, mice ubiquitously overexpressing the EGFR ligand betacellulin had a smaller hypertrophic zone regardless of age and sex.[11] In another transgenic mouse model where human EGF was ubiquitously expressed under the β-actin promoter, the proximal tibial growth plate retained columns of prehypertrophic chondrocytes that was not seen in control animals at 6 months of age.[12] Taken together, these data clearly indicate that EGFR signaling plays an important role in long bone development and endochondral ossification, but the underlying mechanism is largely unknown.

Gefitinib is a Food and Drug Administration–approved small-molecule EGFR inhibitor that blocks EGFR activity by competing with ATP binding to the receptor's kinase pocket.[13] In this study, we treated young growing rats with gefitinib to investigate the effects of blocking EGFR activity on endochondral ossification. Using histologic analyses, immunohistochemistry, quantitative measurement of gene and protein expression, and primary chondrocyte cultures, we demonstrate that EGFR signaling plays an essential role in the remodeling of growth plate cartilage ECM into bone during endochondral ossification.

Materials and Methods

Animals

One-month-old male Sprague-Dawley rats (Taconic, Hudson, NY, USA) were administered either vehicle (0.5% methyl cellulose) or gefitinib (100 mg/kg/d; LC Laboratories, Woburn, MA, USA) daily by oral gavage for 7 days. There was no significant body weight loss after treatment. After euthanization, blood was collected by cardiac puncture to measure serum calcium ion concentration (Calcium Reagent Set; Pointe Scientific, Canton, MI, USA). Femurs and tibias were harvested and processed for growth plate tissue, histologic analysis, micro–computed tomography (μCT), and immunohistochemisty.

Egfr$^{f/f}$,[14] *Egfr*$^{Wa5/+}$,[15] and *Col2a1-Cre*[16] mouse strains were used as described previously. To generate *Col2a1-Cre Egfr*$^{Wa5/f}$ mice, we first bred *Col2a1-Cre* mice with *Egfr*$^{Wa5/+}$ mice to obtain *Col2a1-Cre Egfr*$^{Wa5/+}$ mice, which were then crossed with *Egfr*$^{f/f}$ mice to generate *Col2a1-Cre Egfr*$^{Wa5/f}$ mice and their siblings, *Col2a1-Cre Egfr*$^{f/+}$, *Egfr*$^{Wa5/f}$, and *Egfr*$^{f/+}$ mice. *Col2a1-Cre Egfr*$^{Wa5/f}$ mice were identified by their wavy coat appearance and PCR genotyping of the *Cre* gene using primers 5′-GAG TGA TGA GGT TCG CAA GA-3′ and 5′-CTA CAC CAG AGA CGG AAA TC-3′. All animal work performed in this study was approved by the Institutional Animal Care and Use Committee (IACUC) at the University of Pennsylvania.

Histologic analyses, immunohistochemistry, and in situ hybridization

To study growth plate morphology and calcification of rat bones, tibias were dissected, fixed in 70% ethanol, processed for methyl methacrylate (MMA) embedding, and cut into 5-μm longitudinal sections using a Reichert-Jung Polycut-S motorized microtome. Consecutive sections were processed for Goldner's trichrome and von Kossa staining. Proliferative and hypertrophic zones of the growth plate were measured on Goldner's trichrome–stained sections under the microscope at $\times$100 magnification and calculated as an average of three measurements of the left, middle, and right regions of the growth plate. All sections were collected from the centers of tibias. The *proliferative zone* is defined as the area that contains flattened cells in a longitudinal and columnar arrangement. The *hypertrophic zone* is defined as the area at which the cell size starts to increase to the area where cartilage becomes bone.[17,18]

For histologic staining, tartrate-resistant acid phosphatase (TRAP) staining, and immunohistochemistry of rat bones, femurs or tibias were fixed in 10% neutral buffered formalin overnight, washed under tap water, and then decalcified in 0.5 M EDTA (pH 7.4) for 3 weeks prior to processing and embedding in paraffin. Then 6-μm-thick sections were cut for analysis. For safranin O staining, sections were stained with hematoxylin, followed by 0.001% (wt/vol) fast green and 0.1% (wt/vol) safranin O. For TRAP staining, sections were stained using a leukocyte acid phosphatase kit (Sigma-Aldrich, St Louis, MO, USA). TRAP$^+$ cells at the COJ and in the primary spongiosa were counted under the microscope at $\times$100 magnification. For immunohistochemistry, sections were deparaffinized and washed in PBS. After antigen retrieval, endogenous peroxidase activity was quenched in 3% H_2O_2 for 15 minutes and washed in PBS. Sections then were blocked in blocking serum at room temperature for 1 hour and incubated with a primary antibody at 4 °C overnight. After washing in PBS, sections were incubated with a biotinylated secondary antibody and then with an avidin-biotinylated

horseradish peroxidase complex (Vectastain ABC Kit, Vector Laboratories, Burlingame, CA, USA) according to the manufacturer's directions. Finally, peroxidase activity was revealed by immersion in DAB (Dako, Glostrup, Denmark). The following primary antibodies were used: rabbit anti-Ki67 antibody (Santa Cruz Biotechnology, Santa Cruz, CA, USA), rabbit anti-p57 antibody (Abcam, Cambridge, MA, USA), rabbit anti-EGFR antibody (Abcam), rabbit anti-type II collagen antibody (Abcam), and rabbit anti-Col2-3/4C (MMP-13-generated type 2 collagen cleavage fragment) antibody (a gift from Dr John S Mort). For bromodeoxyuridine (BrdU) staining, rats were injected intraperitoneally with BrdU at a dose of 100 μg/g of body weight 2 hours before euthanization. The staining was carried out on paraffin sections using a BrdU staining kit (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's directions.

In situ hybridization of paraffin sections processed from rat tibias was performed as described previously.[19] Highly conserved regions between mouse and rat cDNA (over 93% homology) were used as templates to generate probes: a 515 bp mouse *collagen 10a1* (1302–1816, NM _009925) and a 734-bp mouse *Mmp13* (11–744, BC125320).

To study mouse growth plate morphology, tibias were dissected from P_5 pups of *Col2a1-Cre* $Egfr^{Wa5/f}$ mice and their siblings and processed for paraffin sections. Sections were stained with hematoxylin and eosin (H&E) and measured for lengths of proliferative and hypertrophic zones, as described earlier.

μCT measurement

The femurs were subjected to ex vivo μCT analysis (Skyscan1172 High-Resolution μCT; Skyscan, Aartselaar, Belgium). To study the trabecular architecture of the distal femoral metaphysis, primary and secondary spongiosa areas, corresponding to 0.5 to 2.3 and 2.3 to 3.8 mm, respectively, below the lowest point of growth plate, were scanned at 10-μm resolution and analyzed using 3D analysis.

Growth plate tissue harvest, RNA and protein analyses

Rat tibias were dissected free of soft tissue, and their proximal ends, containing the growth plate, were cut longitudinally into approximately 0.5-mm-thick sections using a no. 22 surgical scalpel blade. Only sections obtained from the centers of tibias (approximately three to four sections per tibia) were used for the microdissection. Under a dissection microscope, perichondrum and epiphyseal bone were removed first from these sections, and growth plate cartilage then was carefully dissected out from the metaphyseal bone at the area just above the COJ (a fine red line) with a no. 15 surgical scalpel blade. As shown in Supplemental Fig. S1, cartilage harvested by this method contained only chondrocytes and excluded cells located in the COJ and bone. Growth plate tissues from the same bone were combined and processed for the following analyses.

To obtain RNA, growth plate tissue was homogenized in Tri Reagent (Sigma-Aldrich), followed by total RNA isolation and purification. A Taqman Reverse Transcription Kit (Applied BioSystems, Inc., Foster City, CA, USA) was used to reverse transcribe mRNA into cDNA. Following this, quantitative real-time PCR (qRT-PCR) was performed using a Power SYBR Green PCR Master Mix Kit (Applied BioSystems, Inc). The primer sequences for the genes used in this study are listed in Supplemental Table S1. Relative expression was calculated for each gene by the $2^{-\Delta\Delta CT}$ method with β-actin for normalization.

To obtain protein, growth plate tissue was ground in a liquid nitrogen–cooled pestle with a mortar and then dissolved in RIPA buffer (Santa Cruz Biotechnology). Equal amounts of protein lysates (30 μg/lane) were resolved by SDS-PAGE on 10% polyacrylamide gels, transferred to polyvinylidene difluoride membranes (Hybone-P; Amersham Biosciences, Pittsburgh, PA, USA), and blotted with rabbit anti-MMP-9, anti-MMP-13, or anti-MMP-14 antibodies (Abcam), anti-CGGVDIPEN (MMP-generated aggrecan cleavage fragment) antibody (a gift from Dr John S Mort), or mouse anti-β-actin antibody (Santa Cruz Biotechnology) at 4 °C overnight. After incubation with horseradish peroxidase–conjugated secondary antibody, blots were developed by enhanced chemiluminescence (ECL; GE Healthcare, Piscataway, NJ, USA) following the manufacturer's protocol and visualized by exposure to X-ray film (Eastman Kodak, Rochester, NY, USA).

Alternatively, total protein lysates (15 μg) were mixed with 2 × sample buffer (4% SDS, 25% glycerol, 0.01% bromophenol blue, and 62.5 mM Tris, pH 6.8) and loaded without boiling onto a 10% acrylamide gel copolymerized with 1 mg/mL of gelatin (Sigma-Aldrich). After running at 100 V for 1.5 hours at 4 °C under nonreducing conditions, the gel was washed twice in 2.5% Triton X-100 for 30 minutes to allow enzyme renaturation and then incubated in development buffer (Bio-Rad, Hercules, CA, USA) at 37 °C for 5 hours. The gel was stained with 0.5% Coomassie blue R-250 (Thermo Scientific, Waltham, MA, USA) for 1 hour and destained in 40% methanol, 10% acetic acid solution until evidence of proteolytic activity appeared as clear bands against the blue background.

Primary chondrocytes

Primary epiphyseal chondrocytes were isolated from the distal femoral and proximal and distal tibial condyles of 1- to 3-day-old Sprague-Dawley rats. Briefly, epiphyseal condyles were dissected, cleaned of connective tissue, and digested in type 2 collagenase solution (2.2 mg/mL in PBS; Invitrogen) at 37 °C with gentle agitation for 30 minutes. The condyles were collected and further digested for 4 hours. The supernatant was filtered and centrifuged to collect chondrocytes. Cells were plated at a density of $4 \times 10^4/cm^2$ in 24-well plates in chondrogenic medium (DMEM/F12 medium with 5% fetal bovine serum, 50 μg/mL of L-ascorbic acid, 1% glutamine, 100 μg/mL of streptomycin, and 100 U/mL of penicillin). Two to three days later, when cells reached 90% confluence, cultures were given fresh medium. The following day, cells were treated with 50 ng/mL of recombinant human TGF-α (Pepro-Tech, Rocky Hill, NJ, USA), and RNA and protein were harvested at indicated times for analysis.

Statistical analysis

All data were analyzed by independent Student's *t* test assuming equal variances in each group or two-way ANOVA with a

Bonferroni post-test. Animal number per group varied from three to six. For cell culture experiments, all results are derived from experiments being repeated independently at least three times. A value of $p < 0.05$ was considered significant. All data are expressed as mean ± SEM.

Results

Inhibition of EGFR activity altered growth plate architecture

To study the role of EGFR in postnatal growth plate development, we administered an EGFR-specific inhibitor, gefitinib, to 1-month-old rats for 7 days. Gefitinib-treated rats developed profound changes in the growth plate cartilage in both femurs and tibias that were characterized by epiphyseal growth plate thickening and accumulation of hypertrophic chondrocytes (Fig. 1*A*, *B*). In these animals, we observed an overall 2.0-fold increase in the tibial growth plate length. This is due mainly to a striking increase in the length of the hypertrophic zone (2.3-fold). There was no significant change in the length of the proliferative zone (1.2-fold increase, $p = 0.07$; Fig. 1*C*, *D*, *G*). The enlargement of the hypertrophic zone is due mainly to an increase in the number of chondrocytes but not an increase in cell size because the cell number per length remains the same (Fig. 1*H*). The expansion of the hypertrophic zone also was confirmed by safranin O staining, which showed less staining intensity in the hypertrophic zone than in the proliferative zone (Fig. 1*E*, *F*). In addition, immunostaining for Ki67, a marker for replicating cells, and p57, a marker for cell cycle exit, as well as in situ hybridization for Col10a1, a hypertrophic zone marker, further demonstrated that elongation of the growth plate in gefitinib-treated rats was due mainly to expansion of the hypertropic zone (Supplemental Fig. S2). This change in the growth plate was reversible because the length of the growth plate returned to normal 1 week after withdrawal of the EGFR inhibitor (data not shown). A similar phenotype also was noticed with rats treated with another EGFR-specific inhibitor, erlotinib (data not shown), confirming that this growth plate phenotype results from the loss of EGFR activity. In addition, we observed a small but significant decrease in the long bone length (for tibia, vehicle 22.3 ± 0.2 mm versus gefitinib 20.5 ± 0.3 mm, $p = 0.02$; for femur, vehicle 25.7 ± 0.4 mm versus gefitinib 24.1 ± 0.3 mm, $p = 0.03$, $n = 3$ to 6/group) after 7 days of treatment.

The primary spongiosa of metaphyseal bone underneath the growth plate is derived directly from the hypertrophic zone through a bone-modeling process. In normal rats, bone spicules in this area were extended from the chondrocyte columns and parallel to each other. However, gefitinib-treated rats had shorter bone spicules with irregular shapes (Fig. 2*A*, *B*). Interestingly, we noticed that there were more cartilage remnants in the bone spicules (*light blue areas* in Fig. 2*A*) in gefitinib-treated rats than in vehicle-treated rats, implying that gefitinib delays the conversion of cartilage matrix into bone matrix.

μCT imaging further confirmed this phenomenon and the expansion of the growth plate (Fig. 2*B*). Quantitative analyses showed that the bone volume in the primary spongiosa was decreased significantly by 14% in gefitinib-treated rats (Fig. 2*C*). This was due mainly to an elevation in trabecular separation (22%) and a reduction in trabecular number (14%). The trabecular thickness was not changed in this area. In the secondary spongiosa, where bone remodeling occurs, we observed a larger decrease in bone volume (36%) with similar changes in trabecular separation (19% increase; not significant) and trabecular number (36%; Fig. 2*D*). This result is consistent with our recent finding that gefitinib treatment decreases bone volume and inhibits bone formation in young mice.[20] Overall, these data indicate that postnatal long bone growth is affected by the loss of EGFR activity.

Gefitinib treatment delayed cartilage mineralization.

Next, we investigated whether cartilage mineralization was altered in the growth plates of gefitinib-treated rats. In agreement with numerous reports, von Kossa staining revealed that about one-half to two-thirds of the hypertrophic zones in the growth plates of normal rats were calcified (Supplemental Fig. S3*A*, *B*). However, after gefitinib treatment, only the last two to three rows of chondrocytes in the hypertrophic zones were mineralized (Supplemental Fig. S3*C*, *D*). This enlargement of growth plate and delayed mineralization are reminiscent of osteomalacia, a disease caused by the depletion of calcium. However, we did not observe any changes in the serum calcium ion level (vehicle 12.2 ± 0.7 mg/dL versus gefitinib 12.5 ± 0.2 mm, $p = 0.87$, $n = 6$/group). Moreover, no expanded osteoid was observed in the trabecular bone of gefitinib-treated animals (Fig. 1*A*, *B* and Fig. 2*A*), suggesting that this phenomenon is not a result of altered calcium homeostasis.

Growth plate chondrocytes express EGFR

We performed immunohistochemistry to identify the cells that express EGFR protein in the growth plate. As shown in Supplemental Fig. S4*A*, *B*, strong EGFR expression was detected in all chondrocytes within the growth plate, suggesting that growth plate chondrocytes are the primary target for gefitinib. In addition, we observed very weak to no EGFR staining in the endothelial cells (Supplemental Fig. S4*C*) and multinucleated osteoclasts (Supplemental Fig. S4*D*) and strong staining in osteoblasts (Supplemental Fig. S4*C*) in the primary spongiosa. These data are in agreement with our previous report that osteoblasts express EGFR but that osteoclast progenitors and mature osteoclasts do not bind EGF ligand and do not possess functional EGFR.[21]

Chondrocyte proliferation and differentiation are unchanged in gefitinib-treated rats

The expansion of the growth plate in gefitinib-treated rats could be the result of increased chondrocyte cell proliferation or altered differentiation. The aforementioned data demonstrating that gefitinib expands the hypertrophic zone but has no effect on the length of the proliferative zone provided the first hint that gefitinib does not change the proliferation and differentiation of chondrocytes in vivo. To further test this, we labeled rats with BrdU. Tibias harvested from gefitinib-treated rats contained a similar percentage of $BrdU^+$ cells in the proliferative zone (vehicle 22.6% ± 1.7% versus gefitinib 22.4% ± 2.3%, $n = 3$/

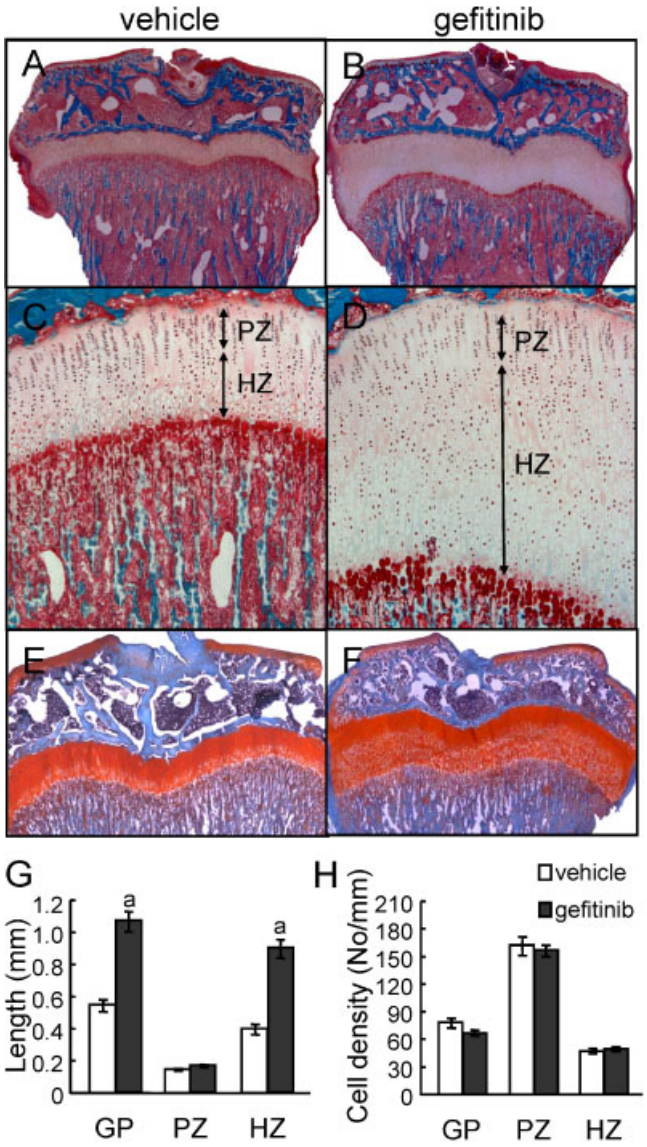

Fig. 1. In vivo inhibition of EGFR activity expands the long bone growth plates. One-month-old rats were treated with either vehicle (*A*, *C*, *E*) or gefitinib (*B*, *D*, *F*) for 7 days, and their tibias were processed for MMA sections (*A*–*D*) or paraffin sections (*E*, *F*) for histologic examination. Staining of the bone with Goldner's trichrome showed a striking enlargement of the growth plate, particularly the hypertrophic zone, in the gefitinib-treated animals (the whole bone at low magnification [*A*, *B*] and the growth plate region at high magnification [*C*, *D*]). PZ = proliferative zone; HZ = hypertrophic zone. (*E*, *F*) Safranin O staining confirms the increase in the length of the hypertrophic zone. (*G*) Quantification of the lengths of the whole growth plate (GP) and each zone. $n = 5$/group. $^{a}p < 0.001$ versus vehicle. (*H*) Quantification of chondrocyte number along the longitudinal length of cartilage.

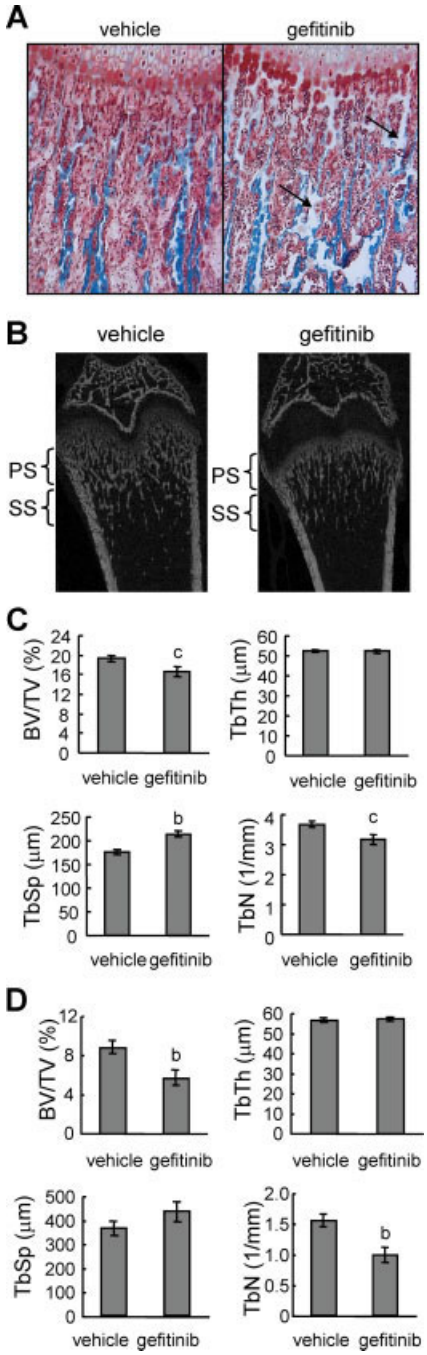

Fig. 2. Gefitinib treatment expands the growth plate and decreases bone volume in the primary spongiosa (PS) and secondary spongiosa (SS) of rat long bones. (*A*) Magnified image of the COJ and primary spongiosa in Goldner's trichrome–stained rat tibias with or without gefitinib treatment. Arrows indicate cartilage remnants (*light blue*) in the bone spicules. (*B*) μCT images of longitudinal sections of distal femurs of vehicle- and gefitinib-treated rats. (*C*) Structural parameters of trabecular bone in the primary spongiosa. (*D*) Structural parameters of trabecular bone in the secondary spongiosa. BV/TV = trabecular bone volume/tissue volume; TbTh = trabecular thickness; TbSp = trabecular separation; TbN = trabecular number. $n = 6$/group. $^{b}p < 0.01$; $^{c}p < 0.05$ versus vehicle.

group) and a similar length of BrdU-labeled area as vehicle-treated rats (Fig. 3*A*), indicating that enlargement of the growth plate is not due to an increased proliferative capacity of chondrocytes.

We then examined chondrocyte differentiation by measuring the mRNA expression of stage-specific differentiation markers in the growth plate. Note that growth plate tissue was dissected from tibias free of perichondrum and bone contamination, as described under "Materials and Methods." The genes for *aggrecan* and *type 2 collagen* (*Col2a1*), *Ihh*, and *type 10 collagen* (*Col10a1*) are specifically expressed in the proliferative, pre-hypertrophic, and hypertrophic zones, respectively. We found

that while the expression levels of *aggrecan*, *Col2a1*, and *Ihh* were not changed, *Col10a1* increased about twofold in gefitinib-treated rats (Fig. 3*B*), which is consistent with the enlarged hypertrophic zone in gefitinib-treated rats and in agreement with the in situ data detecting *Col10a1* mRNA expression in the growth plate (Supplemental Fig. S2). *Sox9* and *Runx2* are two master transcription factors that are essential for growth plate development. *Sox9* is expressed in proliferative and prehypertrophic zones[22] and is important for determination of chondrocyte fate and maintenance of chondrocyte proliferation,[23] whereas *Runx2* is required for chondrocyte maturation and terminal differentiation.[23] We found that gefitinib-treated rats expressed similar levels of *Sox9* and *Runx2* mRNA in the growth plate as vehicle-treated animals (Fig. 3*B*). Taken together, our data strongly suggest that chondrocyte differentiation is not affected by EGFR inhibition.

Gefitinib-treated rats have normal angiogenesis at the COJ

Previous reports have shown that suppressing the expression or activity of VEGFa, an important regulator of angiogenesis during endochondral ossification, inhibits blood vessel invasion into the hypertrophic zone of long bone growth plates and results in expansion of the hypertrophic zone.[24] To test whether vascularization is impaired in our animal model, we used H&E staining to identify red blood cells and their associated blood vessels along the COJ. As shown in Fig. 3*C*, we did not observe any overt difference in the number, location, orientation, or morphology of blood vessels underneath the growth plate in gefitinib-treated rats compared with vehicle-treated rats. This is consistent with our immunohistochemistry results that endothelial cells do not express EGFR (Supplemental Fig. S4*C*) and suggests that angiogenesis is not directly impaired by gefitinib. qRT-PCR revealed that the mRNA expression of *Vegfa*, along with another angiogenesis factor, *transferrin*,[25] was increased about 5.3- and 4.8-fold, respectively, in the growth plate after gefitinib treatment (data not shown), which is consistent with expansion of the hypertrophic zone.

Gefitinib treatment suppresses the ability of chondrocytes to support osteoclastogenesis at the COJ

Osteoclasts at the COJ play an essential role in endochondral ossification by secreting various proteinases to digest cartilage ECM for vascular invasion and conversion from cartilage matrix into bone matrix. Mice that are unable to generate osteoclasts also develop enlarged hypertrophic zones in their growth plates.[26] We therefore assessed the number of osteoclasts along the COJ using TRAP staining. Notably, we observed a significant decrease in the number of $TRAP^+$ cells located just below the last row of terminally differentiated chondrocytes in the gefitinib group compared with the vehicle group (vehicle 10.9 ± 1.0 cells/mm versus gefitinib 5.5 ± 0.7 cells/mm, $p = 0.01$, $n = 6$/group). However, the number of $TRAP^+$ cells in the area directly below the COJ to 0.64 mm below the COJ was similar between these two groups (vehicle 59.4 ± 5.4 cells/mm^2 versus gefitinib 58.0 ± 5.6 cells/mm^2, $n = 6$ /group; Fig. 4*A*).

The aforementioned immunohistochemisty data (Supplemental Fig. S4*D*) and our previous report[21] demonstrate that osteoclasts are not direct targets for gefitinib. To understand how gefitinib treatment reduced the number of osteoclasts along the COJ, we compared the mRNA levels of receptor activator of nuclear factor κB ligand (RANKL), a major determinant for osteoclastogenesis, and osteoprotegerin (OPG), a decoy receptor for RANKL, in the growth plate using qRT-PCR. Interestingly, we observed a 3.6-fold decrease in RANKL expression but no significant change in OPG expression ($p = 0.17$) in the gefitinib group compared with control. These changes result in an overall 60% decrease in the RANKL/OPG ratio after gefitinib treatment (Fig. 4*B*). To determine whether these changes were due to the direct action of gefitinib on chondrocytes, we treated primary chondrocytes with TGF-α to activate EGFR. qRT-PCR revealed that TGF-α upregulated RANKL expression but suppressed OPG expression, resulting in 1.8-, 5.0-, and 16.6-fold increases in the ratio of RANKL/OPG after 8, 24, and 48 hours of treatment, respectively (Fig. 4*C*). Moreover, this regulation was completely abolished by inhibition of EGFR activity (Fig. 4*D*). These data demonstrate that EGFR signaling is important for chondrocytes to support osteoclastogenesis at the COJ.

Inhibition of EGFR activity decreases matrix metalloproteinase (MMP-9, -13, and -14) expression and ECM degradation

MMPs are members of a family of zinc-dependent proteolytic enzymes. Several of them are expressed at high levels in bone and cartilage and essential for the cleavage of cartilage ECM and remodeling of cartilage into bone. Blocking MMP activity either by a broad-spectrum inhibitor[27] or by knocking down specific MMP genes, such as *Mmp9*,[28] *Mmp13*,[29,30] and *Mmp14*,[31] diminishes matrix degradation and expands the growth plate. Interestingly, we found that the mRNA levels of these MMPs were significantly suppressed three- to fourfold in the growth plate of gefitinib-treated rats (Fig. 5*A*). Western blotting confirmed strong decreases at the protein level (Fig. 5*B*). Moreover, gelatin zymography showed that the activity of MMP-9 (gelatinase B), in both pro and mature forms, was attenuated, whereas MMP-2 (gelatinase A) activity was not affected (Fig. 5*C*). In situ hybridization further revealed that *Mmp13* gene expression in the terminally differentiated chondrocytes was suppressed dramatically by gefitinib (Fig. 5*D*).

To test whether the decrease in MMP expression led to accumulation of intact collagen fibers, polarized light microscopy was used to quantify the intensity of birefringent collagen in the growth plate. In the vehicle group, we observed strong type 1 collagen birefringence in the primary spongiosa, most of which was aligned with bone spicules. However, the birefringence in the growth plate was weak and existed mostly in the longitudinal septa between columns of chondrocytes (Fig. 5*E*). Quantitative imaging analysis revealed that there was a significant 2.2-fold increase in the intensity of birefringence in the growth plate of gefitinib-treated rats. Moreover, picrosirius red staining for collagen showed a similar increase in collagen birefringent intensity in the gefitinib group (data not shown). Type 2 collagen

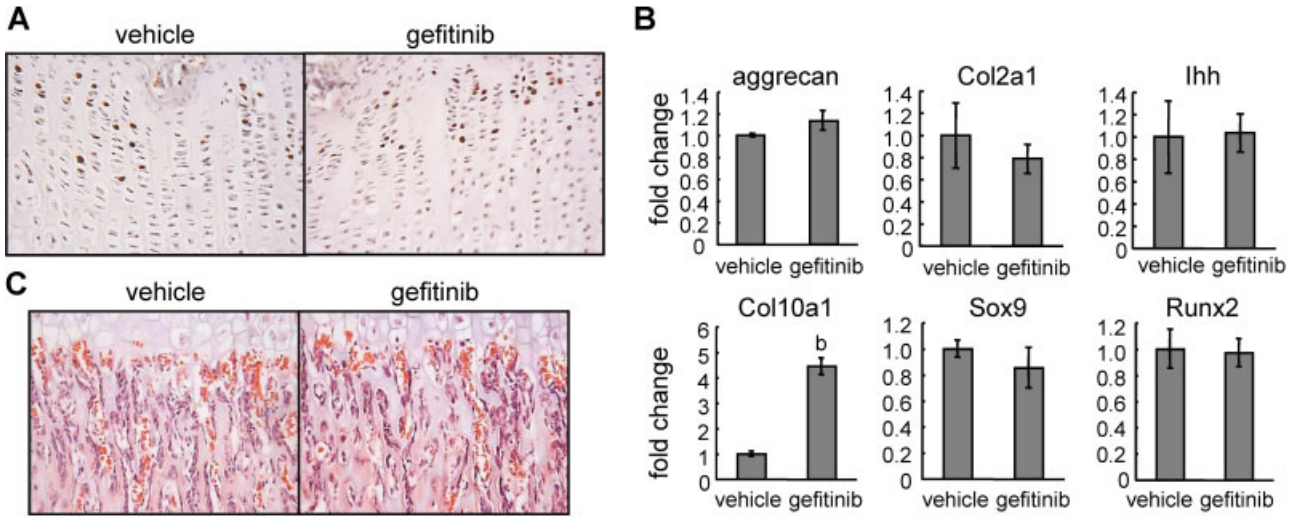

Fig. 3. Gefitinib treatment does not alter chondrocyte proliferation, differentiation, and vascular invasion. (*A*) BrdU incorporation (*brown staining*) in the proliferative zone of growth plates from vehicle- and gefitinib-treated rats. (*B*) qRT-PCR analysis of gene expression of stage-specific chondrocyte markers (*aggrecan*, *Col2a1*, *Ihh*, and *Col10a1*) and transcription factors (*Sox9* and *Runx2*). $^{b}p < 0.01$ versus vehicle. (*C*) H&E staining of rat tibias shows that there is no overt difference in localization, size, or morphology of blood vessels in the gefitinib-treated rats compared with the vehicle-treated rats. Red blood cells are stained red with no blue nuclei.

is the major collagen in the growth plate. Immunohistochemical staining showed an increase in type 2 collagen in the gefitinib-treated growth plate compared with control (Fig. 5*F*). This increase is not due to an increase in gene expression because the mRNA level of *Col2a1* was not changed (Fig. 3*B*).

Accumulation of ECM proteins owing to decreases in MMP levels should be accompanied by reduced ECM degradation. Immunostaining for a neoepitope in the collagenase cleavage site in the 3/4 fragment of type 2 collagen indicated that there was decreased degraded type 2 collagen in the perilacunar

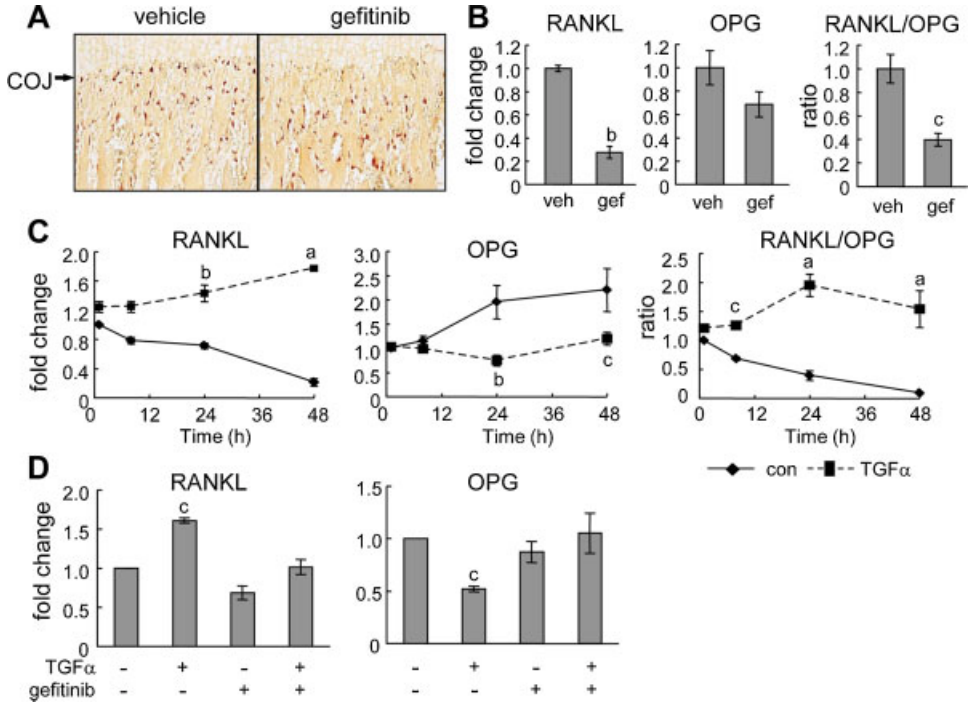

Fig. 4. Osteoclast differentiation at the COJ is delayed in gefitinib-treated rats. (*A*) TRAP staining (*red*) of rat tibias reveals that gefitinib-treated rats have fewer osteoclasts at the COJ but comparable osteoclast number in the primary spongiosa underneath the junction. (*B*) qRT-PCR measurement of mRNA expression of *RANKL* and *OPG* in the growth plate dissected from vehicle- and gefitinib-treated rats. (*C*) qRT-PCR measurement of mRNA expression of *RANKL* and *OPG* in primary chondrocytes treated with TGF-α for indicated time points. The mRNA level of the control group at 1 hour was set to 1. (*D*) qRT-PCR demonstrates that 5 μM gefitinib abolishes the effects of 24 hours of TGF-α treatment on *RANKL* and *OPG* expression in primary chondrocytes. $^{a}p < 0.001$; $^{b}p < 0.01$; $^{c}p < 0.05$ versus control.

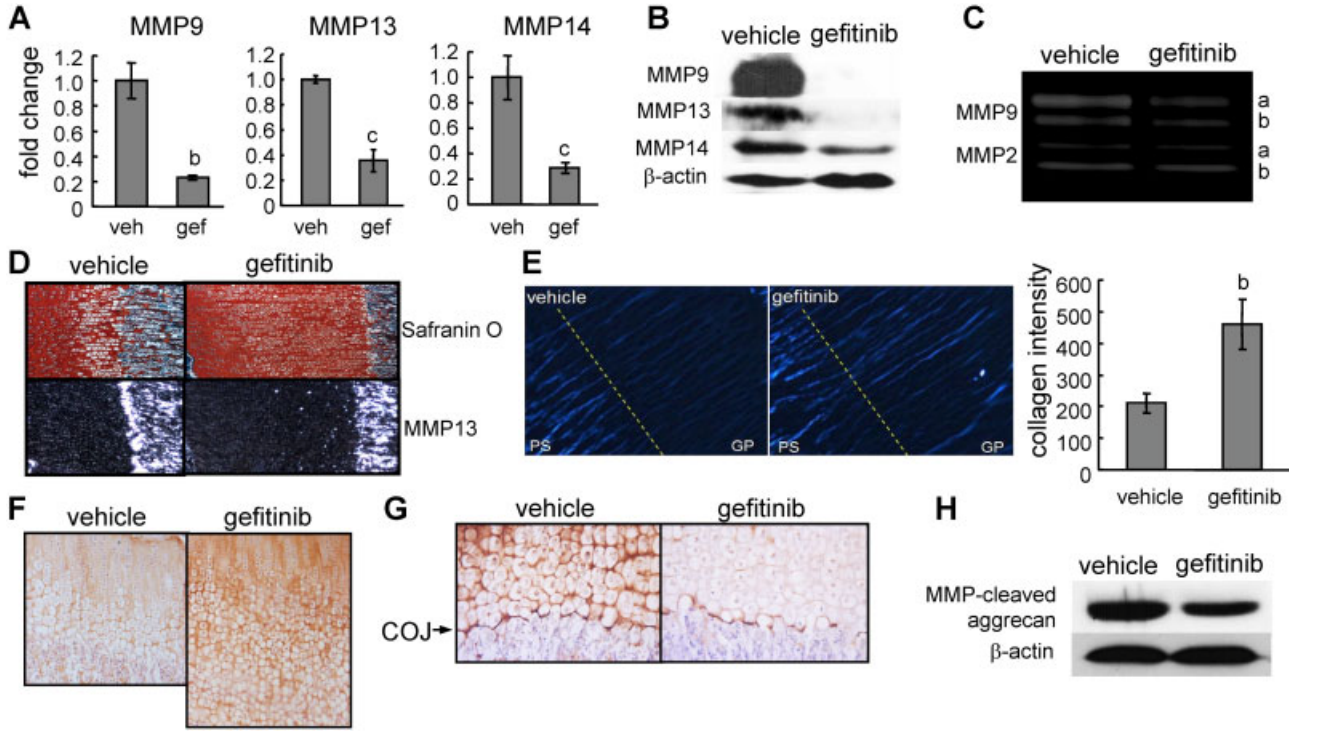

Fig. 5. Blocking EGFR activity suppresses the expression of MMPs and ECM degradation in the growth plate. (*A*) qRT-PCR analyses of *Mmp* mRNA expression in the growth plate tissues from vehicle- and gefitinib-treated rats. $^{b}p < 0.01$; $^{c}p < 0.05$ versus vehicle. (*B*) Western blotting shows that the protein levels of MMP-9, -13, and -14 in the growth plates from gefitinib-treated rats were decreased to 7.9% ± 2.1%, 14.0% ± 12.6%, and 39.2% ± 10.5%, respectively, of those from the vehicle-treated group, as measured by densitometric analysis. (*C*) Gelatin zymographic analysis of protein lysates from the growth plate further confirms the decrease in MMP-9 activity in gefitinib-treated animals. The activity of MMP-2 was shown here as an internal control. The amounts of pro (*a*) and mature (*b*) MMP-9 in the gefitinib-treated group decreased to 30% and 47% of that in vehicle-treated group, as measured by densitometric analysis. (*D*) In situ hybridization reveals a decrease of MMP13 expression in the gefitinib-treated tibial growth plate. (*E*) Polarized light microscopy of unstained tibial paraffin sections from vehicle- and gefitinib-treated rats. The sections were oriented with maximum birefringence (*white blue*). The COJ is depicted as a dashed line separating the growth plate (GP) and the primary spongiosa (PS) areas. The intensity of birefringence then was analyzed and quantified by ImageJ. $n = 6$/group. $^{b}p < 0.01$ versus vehicle. (*F*) Immunostaining of type 2 collagen in the growth plate. (*G*) Immunostaining of collagenase-produced 3/4 cleavage fragment of type 2 collagen. (*H*) Western blot of protein lysates from growth plate tissues using an antibody to the MMP-cleaved aggrecan product.

surrounding of hypertrophic chondrocytes and at the COJ in the gefitinib-treated group compared with the vehicle group (Fig. 5*G*). As shown in Fig. 5*H*, Western blotting indicated that the amount of MMP-cleaved aggrecan fragments also was decreased in the gefitinib-treated growth plate. Taken together, these data strongly suggest that ECM degradation is partially blunted by EGFR inhibition.

EGFR signaling stimulates MMP expression in primary chondrocytes

We next determined whether the decrease in MMP expression was due to a direct effect of gefitinib on the EGFR in chondrocytes. Primary chondrocytes were treated with TGF-α to activate EGFR. qRT-PCR revealed that TGF-α increased *Mmp9* mRNA 1.9-, 3.8-, and 12.8-fold at 8, 24, and 48 hours, respectively, and increased *Mmp13* mRNA 1.7-, 3.3-, and 23.9-fold at 8, 24, and 48 hours, respectively (Fig. 6*A*). However, *Mmp14* mRNA was increased only 1.6-fold at 48 hours. Western blot analyses confirmed that the expression levels of MMP-9, -13, and -14 were upregulated at the protein level. This stimulation was completely abolished by gefitinib (Fig. 6*B*), indicating that TGF-α regulation of MMPs is EGFR-dependent.

Mice deficient in chondrogenic EGFR activity have an enlarged hypertropic zone

In the preceding experiments, oral administration of the EGFR inhibitor to rats suppressed EGFR activity ubiquitously. To exclude the possibility that gefitinib might act on cells other than chondrocytes to affect growth plate development, we initially generated *Col2a1* promoter–driven *Cre* (*Col2a1-Cre*) $Egfr^{flox/flox}$ mice. In neonatal mice, *Col2a1-Cre* was expressed in the chondrocytes of the long bone epiphysis.[16] However, genotyping and Western blotting with these mice revealed an incomplete deletion of *Egfr* alleles and no significant change in the amount of EGFR protein in the epiphyseal cartilage (Supplemental Fig. S5). To further reduce the remaining EGFR activity, we introduced an EGFR dominant-negative allele, *Wa5*,[15] and generated *Col2a1-Cre* $Egfr^{Wa5/f}$ mice. Previously, we have used this strategy successfully to characterize pre/osteoblast-specific *Egfr* null mice.[20] Analyzing the long bone

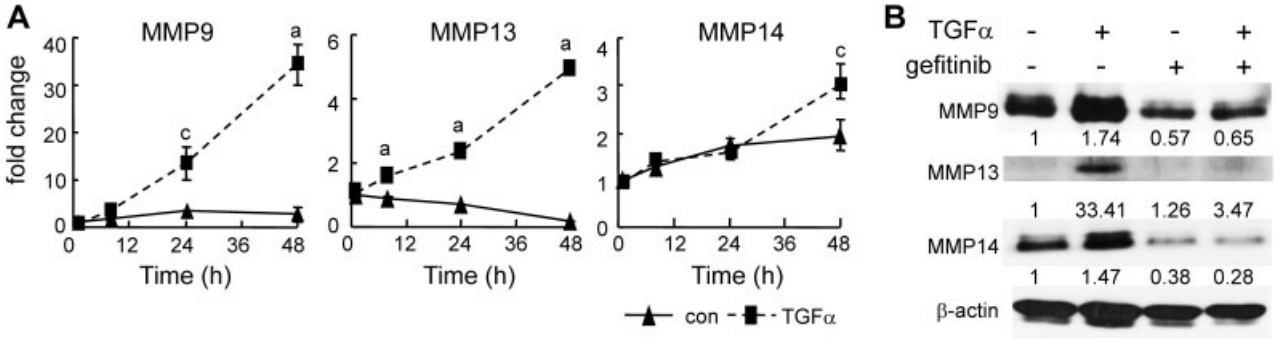

Fig. 6. EGFR signaling regulates MMP-9, -13, and -14 expression in primary chondrocytes. (*A*) Time course of TGF-α regulation of MMP expression. The mRNA levels were analyzed by qRT-PCR and adjusted to the mRNA level in the control harvested at 1 hour. $^{a}p < 0.001$; $^{c}p < 0.05$ versus control. (*B*) Western blots of MMP proteins in the primary chondrocytes after 4 days of TGF-α treatment. The medium was changed after 2 days, along with the addition of fresh TGF-α. In the gefitinib lanes, 5 μM gefitinib was added to the cells 1 hour prior to TGF-α treatment. The blots were quantified by densitometric measurement. The data were normalized against β-actin, and the corresponding values were shown underneath each blot.

growth plate at P_5 revealed that while the *Wa5* allele itself (*Egfr*$^{Wa5/f}$ mice) modestly increased the length of the hypertrophic zone (1.3-fold), introducing *Col2-Cre* further expanded the hypertrophic zone dramatically to 2.0-fold compared with *Egfr*$^{+/f}$ mice (Fig. 7*A*, *B*). These data strongly demonstrate that chondrogenic EGFR activity is essential for cartilage remodeling into bone. Consistent with the gefitinib-treated rat results, we did not observe any difference in the length of the proliferative zone in these mice (Fig. 7*B*), implying that the major reason for the expanded growth plate is also the delayed cartilage remodeling into bone.

Discussion

Significant skeletal defects have long been noticed in mouse models with abnormal EGFR activity. Recently, we reported that EGFR ligands stimulate osteoclastogenesis indirectly by suppressing OPG expression and enhancing monocyte chemotactic protein-1 (MCP1) expression in differentiating osteoblasts.[21] Furthermore, we demonstrated that EGFR is an anabolic regulator of bone formation that is important for the maintenance of a pool of mesenchymal stem cells and osteoprogenitors in bone.[20] In this report, we demonstrated that EGFR signaling is also an important regulator of postnatal growth plate development and endochondral ossification. Blocking EGFR activity specifically with small-molecule inhibitors dramatically expanded the length of the growth plate, particularly the hypertrophic zone, in rat long bones. While chondrocyte proliferation, differentiation, and angiogenesis at the COJ were relatively normal, the removal of hypertrophic cartilage matrix by osteoclasts and MMPs was suppressed. Interestingly, the effect of the EGFR inhibitor on the growth plate is reversible, suggesting that normal cartilage matrix degradation is restored rapidly after removal of EGFR inhibition. A similar growth plate phenomenon is also observed after chondrocyte-specific inactivation of the *Egfr* gene in mice and in *Tgfα* null mice (Usmani and colleagues, submitted), further confirming that EGFR signaling is critical for growth plate remodeling in long bones.

ECM degradation in the growth plate is an essential step in endochondral ossification. The growth plate contains an ECM mainly comprised of type 2 and type 10 collagens and the aggregating proteoglycan (aggrecan). To form new bone, hypertrophic chondrocytes and osteoclasts need to partially degrade the growth plate ECM at the COJ, generating space for osteoblasts to deposit bone matrix. MMPs, in particular MMP-9, -13, and -14, are key enzymes involved in this process. MMP-13, also named *collagenase 3*, is the major protease that degrades native type 2 collagen.[32] MMP-9 and -13 together are responsible for MMP-dependent aggrecan cleavage.[30] MMP-14, also named *membrane type 1 MMP* (MT1-MMP), functions as a potent pericellular collagenase capable of degrading both type 1 and type 2 collagen[33] and is important for the formation of the secondary ossification center.[31] Mice deficient in either MMP-9, -13, or -14 all have an expanded hypertrophic zone in the growth plate during early postnatal bone growth owing to impeded ECM degradation, a phenotype similar to our EGFR inhibitor–treated young rats. However, once *Mmp9* knockout or *Mmp13* knockout mice reach adulthood, the enlarged growth plate is no longer observed, likely owing to redundancy among the various proteases.

MMP9, -13, and -14 are expressed by cells in and surrounding the growth plate. MMP-13 is expressed mainly in hypertrophic chondrocytes and osteoblasts.[34] In situ hybridization and immunostaining indicate that cells with high MMP-9 expression are osteoclasts[28,35] and $TRAP^{-}$ cells of unknown lineage beneath the hypertrophic cartilage.[26] Meanwhile, MMP-9 expression also was identified in the hypertrophic chondrocytes of mouse cartilage by immunostaining[36] and throughout the growth plate in 4-week-old rats by in situ hybridization.[37] MMP-14 is expressed mainly in the resting and proliferative zones, whereas the hypertrophic zone showed little expression.[38] MMP-14 is also abundant in osteoclasts[39] and exhibits intense staining in the region beneath the COJ.[38] To avoid possible contamination of cells other than chondrocytes, we used a stereomicroscope to dissect out the growth plate tissue from rat tibias containing chondrocytes only but not osteoblasts, osteoclasts, and other cells at the COJ and confirmed the presence of only chondrocytes within our samples by histology.

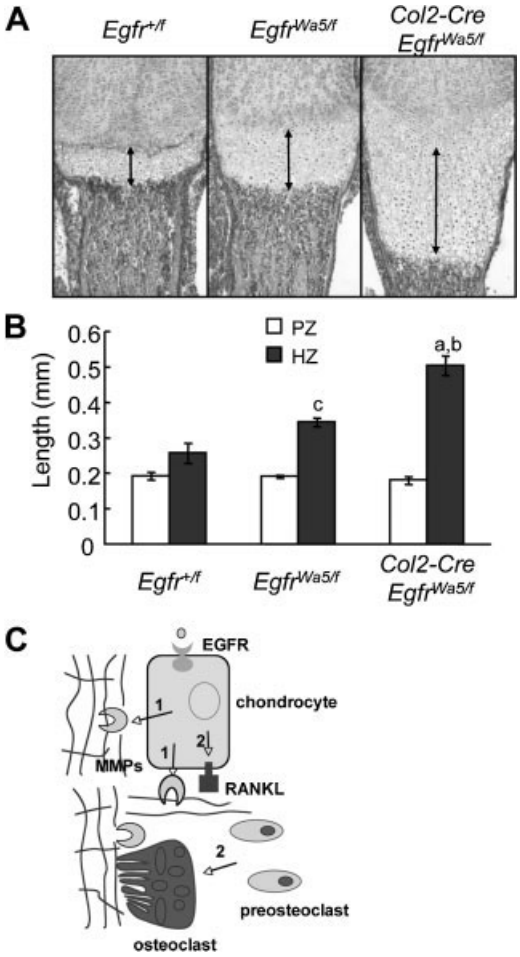

Fig. 7. Mice deficient in chondrogenic EGFR activity exhibit an enlarged hypertrophic zone. (*A*) H&E staining of tibial growth plates from *Col2-Cre Egfr$^{Wa5/f}$* mice and controls. Double-arrow lines indicate the hypertrophic zone. (*B*) Quantification of the lengths of proliferative (PZ) and hypertrophic (HZ) zones. $n = 4$ to 5/group. [a]$p < 0.001$ versus *Egfr$^{+/f}$*; [b]$p < 0.005$ versus *Egfr$^{Wa5/f}$*; [c]$p < 0.05$ versus *Egfr$^{+/f}$*. (*C*) A model of how EGFR signaling stimulates cartilage degradation. Two mechanisms contribute to this function of EGFR. First, EGFR signaling upregulates the expression of MMP-9, -13, and -14 in the growth plate and thus is responsible for cartilage ECM degradation. Second, EGFR signaling is important for RANKL expression in the growth plate and thus is responsible for osteoclastogenesis at the COJ.

We demonstrate that the growth plate samples do express *Mmp9*, *Mmp13*, and *Mmp14* mRNA and protein and that this expression was attenuated by blocking EGFR activity. This is consistent with a previous study that showed severe craniofacial defects in *Egfr* null mice and diminished MMP secretion from mandibular explants from these animals.[7] We show that the decreases in the amounts of MMP are correlated with the accumulation of collagen and decreases in degraded aggrecan and type 2 collagen products in the growth plate. Further in vitro experiments revealed that TGF-α stimulates MMP-9, -13, and -14 expression in primary chondrocytes via activation of EGFR. This result suggests that gefitinib acts directly on chondrocytes in vivo to block MMP expression. Taken together, these data demonstrate that EGFR signaling is critical for maintaining the expression of these three MMPs in the growth plate and subsequently promoting ECM degradation.

In addition to the diminished expression of MMPs, our data suggest that delayed osteoclast recruitment and differentiation at the COJ could be another mechanism for expansion of the growth plate after gefitinib treatment. We found that while the number of osteoclasts in the primary spongiosa was unchanged, the number of osteoclasts at the COJ was decreased significantly in gefitinib-treated rats. A previous report showed that *Egfr$^{-/-}$* mice have delayed endochondral ossification and an enlarged hypertrophic zone in the growth plate.[8] At E16.5, wild-type mice had already formed primary ossification centers, whereas *Egfr$^{-/-}$* mice still had a continuous cartilage anlage in the middle of the long bone. Wang and colleagues noticed that at that stage, the number of osteoclasts adjacent to the hypertrophic cartilage in *Egfr$^{-/-}$* mice was less than that in the bone marrow of wild-type mice and concluded that the impaired endochondral ossification in *Egfr$^{-/-}$* mice is due to the loss of EGFR signaling in osteoclasts. However, their conclusion cannot explain their observation that there was no difference in osteoclast number in the bone marrow at later stage (E18.5) when the primary ossification center was formed and the enlarged hypertrophic zone was still prominent in the *Egfr$^{-/-}$* mice. It also cannot explain why we did not observe any change in osteoclast number in the primary spongiosa after gefitinib treatment. In addition, our previous data showed that osteoclastic lineage cells do not express functional EGFR,[21] and our current immunostaining showed very weak EGFR staining in osteoclasts. Importantly, we also show that chondrocyte-specific inactivation of EGFR (*Col2a1-Cre Egfr$^{Wa5/f}$* mice) caused similar enlargement of the hypertrophic zone postnatally. All these data strongly suggest that an additional indirect mechanism may be responsible for mediating the effects of EGFR on osteoclasts.

Here we attribute the decrease in osteoclast number to a decrease in the RANKL/OPG ratio in the growth plate. RANKL and OPG are expressed by hypertrophic chondrocytes in the growth plate during embryonic development.[40] It is known that vitamin D_3 can regulate RANKL expression in chondrocytes to promote osteoclast formation in vivo.[41] In vitro coculture experiments demonstrate that chondrocytes are capable of supporting osteoclastogenesis directly.[42] Since RANKL/OPG are stimulated by TGF-α in primary chondrocytes, we conclude that hypertrophic chondrocytes are the major determinant of osteoclast formation at the COJ and that EGFR signaling in chondrocytes is essential for this process. Notably, *Tgfα* null mice also display reduced expression of RANKL and MMP13 in cartilage (Usmani and colleagues, submitted).

In vitro chondrocyte culture experiments have demonstrated that activation of EGFR signaling strongly stimulates chondrocyte proliferation,[43,44] inhibits chondrogenesis,[45] and suppresses the expression of chondrocyte matrix genes.[46] Surprisingly, we found that gefitinib treatment did not alter chondrocyte proliferation and differentiation in vivo. Since immunostaining shows EGFR expression throughout the growth plate, we reason that EGFR may be activated differentially within these zones. A previous study of growth plate in chickens suggested that EGF and TGF-α are expressed in the prehypertrophic and hypertrophic zones but not in the proliferative zone

during early postnatal growth.[47] Expression of EGF-like ligands only in mature chondrocytes can explain why inhibition of EGFR activity affects RANKL and MMP expression in hypertrophic chondrocytes but has no effect on chondrocyte proliferation and differentiation. Further analysis to locate the activated EGFR will be required to confirm this hypothesis.

In conclusion, our studies reveal a novel critical role of EGFR in growth plate cartilage ECM remodeling. We demonstrate that EGFR signaling regulates matrix degradation directly by stimulating growth plate chondrocytes to express MMPs and indirectly by supporting osteoclastogenesis at the COJ (Fig. 7*C*). These two mechanisms may be complementarily interplayed. It is possible that gefitinib-induced delay in growth plate mineralization is secondary to the defects in matrix degradation because MMP-9 and -13 are components of matrix vesicles[48] that are responsible for cartilage calcification, and MMP-13 activity is important for chondrocyte mineralization in vitro.[49] To date, no defects in human bone or cartilage growth have been linked to alterations in the EGFR pathway. However, in chickens, EGF may play a role in tibial dyschondroplasia, a chicken growth plate disorder that bears resemblance to human diseases such as osteochondrosis and metaphyseal chondroplasia. Chickens with this disorder show overexpression of EGF in the proliferating zone and diminished expression of EGF and TGF-α in the hypertrophic zone.[47] Future investigations are needed to understand how EGFR regulates endochondral ossification and whether alterations in this pathway lead to human long bone growth defects.

Disclosures

All the authors state that they have no conflicts of interest.

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Authors' roles: XZ and LQ designed the experiments and analyzed the data; XZ, VAS, SL, JZ, EK, HLD performed the experiments; LQ, ME, and FB supervised the experiments; LQ wrote the paper; XZ, VAS, FB and ME revised the paper.

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