A NOTCH3-Mediated Squamous Cell Differentiation Program Limits Expansion of EMT-Competent Cells That Express the ZEB Transcription Factors

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Abstract

Zinc finger E-box–binding (ZEB) proteins ZEB1 and ZEB2 are transcription factors essential in TGF-β–mediated senescence, epithelial-to-mesenchymal transition (EMT), and cancer stem cell functions. ZEBs are negatively regulated by members of the miR-200 microRNA family, but precisely how tumor cells expressing ZEBs emerge during invasive growth remains unknown. Here, we report that NOTCH3-mediated signaling prevents expansion of a unique subset of ZEB-expressing cells. ZEB expression was associated with the lack of cellular capability of undergoing NOTCH3-mediated squamous differentiation in human esophageal cells. Genetic inhibition of the Notch-mediated transcriptional activity by dominant-negative Mastermind-like 1 (DNMAML1) prevented squamous differentiation and induction of Notch target genes including NOTCH3. Moreover, DNMAML1-enriched EMT-competent cells exhibited robust upregulation of ZEBs, downregulation of the miR-200 family, and enhanced anchorage-independent growth and tumor formation in nude mice. RNA interference experiments suggested the involvement of ZEBs in anchorage-independent colony formation, invasion, and TGF-β–mediated EMT. Invasive growth and impaired squamous differentiation were recapitulated upon Notch inhibition by DNMAML1 in organotypic three-dimensional culture, a form of human tissue engineering. Together, our findings indicate that NOTCH3 is a key factor limiting the expansion of ZEB-expressing cells, providing novel mechanistic insights into the role of Notch signaling in the cell fate regulation and disease progression of esophageal squamous cancers. Cancer Res; 71(21); 6836–47. ©2011 AACR.

Introduction

The stratified squamous epithelium of the esophagus is regulated at an exquisite level. Exiting from the cell cycle, basal keratinocytes migrate toward the luminal surface. They undergo terminal differentiation in the suprabasal layer, expressing Involucrin (IVL) and cytokeratins, such as CK13, and eventually desquamated into the lumen to complete epithelial renewal. Esophageal squamous cell carcinoma (ESCC) is one of the most aggressive forms of squamous cell carcinomas (SCC; ref. 1) and is a paradigm for the investigation for all types of SCCs. Squamous differentiation contributes to tumor heterogeneity in SCCs. An individual tumor often consists of both well-differentiated cell nests with central keratinization (i.e., keratin pearl) and poorly differentiated cell nests. The Notch pathway regulates cell fate and differentiation through cell–cell communication. Ligand binding triggers a series of enzymatic cleavages of 1 of 4 Notch receptor paralogues (NOTCH1–4), resulting in nuclear translocation of the intracellular domain of Notch (ICN). ICN forms a transcriptional activation complex containing a common transcription factor CSL. [CBF-1/RBP-Jκ, Su(H), Lag-1] and the coactivator Mastermind-like (MAML; ref. 2). Notch target genes include the HES/HEY family of transcription factors. CSL-dependent canonical Notch signaling regulates squamous differentiation and epidermal barrier functions (3). Loss of Notch receptors or γ-secretase, a key Notch-processing enzyme, or inhibition of the CSL-dependent activity by dominant-negative MAML1 (DNMAML1) impairs squamous differentiation and causes...
Epithelial-to-mesenchymal transition (EMT) is marked by loss of epithelial characteristics (e.g., cell polarity and cell–cell junctions) and gain of mesenchymal characteristics (e.g., fibroblastic spindle-shaped morphology and an increased motility). EMT occurs during cancer cell invasion and metastasis (11–13). In a mouse xenograft model using viral oncogene–transformed human esophageal cells, we have documented EMT in vivo (14). In primary ESCCs, EMT markers are upregulated at the invasive front (15–19). TGF-β is a potent EMT inducer in the tumor microenvironment (20) and expressed by both tumor and stromal cells in ESCC (21). EMT occurs during the early stages of carcinogenesis to bypass oncogene-induced senescence (19, 22). We have found recently that malignant transformation of human esophageal cells by epidermal growth factor receptor (EGFR) oncogene causes enrichment of EMT-competent cells negating oncogene-induced senescence through transcriptional repression of the INK4 locus by zinc finger E-box–binding (ZEB) proteins ZEB1 and ZEB2 (23), transcription factors essential in TGF-β–mediated EMT, senescence, and maintenance of cancer stem cells (24, 25). ZEBs are subjected to negative regulation by the microRNA (miR)-200 family members (26). However, neither the status of ZEBs nor their regulation in ESCCs is known to date.

Herein, we show that ZEB1 is induced in ESCCs at the invasive front undergoing EMT-like dedifferentiation. Loss of the NOTCH3-mediated CSL-dependent transcriptional activity allows expansion of EMT-competent cells expressing ZEBs, providing a novel mechanistic link between the Notch pathway and cell fate regulatory transcription factors during cancer progression.

Materials and Methods

Tissue samples
Paraffin blocks containing primary ESCCs and adjacent normal tissues were procured via surgery as described previously (n = 31; ref. 27) and at the Hospital of the University of Fukui (n = 20). All of the clinical materials were obtained from informed consent patients in accordance with Institutional Review Board standards and guidelines.

Cell lines, treatment, and organotypic three-dimensional culture

HCE7 and other (TE series) ESCC cell lines were described previously (28). EPC2-hTERT and derivatives transformed by either SV40 Large T antigen and Ha-RasV12 (T-TeRAS) or EGFR, p53R175H, and cyclin D1 (EPC2-T) were described (27, 29, 30). EPC2-hTERT derivatives stably expressing short hairpin RNA (shRNA) directed against NOTCH3 (2 cell lines Notch3-A and Notch3-B expressing independent shRNA sequences V2LHS_229748 and N3-B, V2LHS_93017, respectively) or a nonsilencing control sequence (Open Biosystems) was described previously (10). Cells were treated with 0.6 mmol/L calcium chloride (Ca2+), compound E, a γ-secretase inhibitor (GSI), or 5 ng/mL TGF-β1 as described (10, 14, 23). Phase-contrast images were acquired to score spindle-shaped cells by counting at least 100 cells per hpf (n = 6) as described (14, 23). Organotypic three-dimensional (3D) culture was done as described previously (10, 14, 31).

Retrovirus- and lentivirus-mediated gene transfer and RNA interference

Retroviruses expressing ICN1 or DNMAML1 (10) and tetracycline-inducible lentiviruses (Open Biosystems) expressing shRNA directed against ZEB1 (clone V2THS_116663 and V2THS_116659), ZEB2 (clone V2THS_95420 and V3THS_373827), or a nonsilencing control sequence (clone RHS4743) were produced and transduced as described (10, 14, 23). Cells were labeled with tdTomato for xenograft transplantation experiments as described (32). Cells transduced with green fluorescent protein (for DNMAML1) or tdTomato were selected for the brightest level of fluorescence (top 20%) by flow sorting. siRNA directed against NOTCH1 (2 independent sequences Notch1-A, HSS181550 and Notch1-B, HSS107249), or a nonsilencing scramble control sequence (12935-300; Invitrogen) was transfected transiently using the Lipofectamine RNAiMAX reagent (Invitrogen) as described previously (10).

Soft agar colony formation assays
Soft agar colony formation assays were done as described previously (33). In brief, 2.5 × 104 cells were suspended in 0.67% agarose containing media and overlaid on top of a 1% agarose containing the medium per well and grown for 2 weeks.

RNA isolation, cDNA synthesis, real-time reverse transcription PCR, and microarray analysis
RNA isolation, cDNA synthesis, and real-time reverse transcription PCR (RT-PCR) were done as described (10, 23) using TaqMan Gene Expression and MicroRNA assays (Applied Biosystems; Supplementary Table S1). Gene array experiments were done using an Affymetrix gene chip (U133 2.0 Plus) as described previously (27, 34). Data were deposited at the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo; accession no.: GSE27424).

Western blot analysis
Western blotting was done as described (10, 23). Supplementary Table S2 lists primary antibodies and the titers used for Western blotting.

Flow cytometry
Flow cytometry was done using the FACSCalibur (BD Biosciences). In brief, cells were fixed and permeabilized in cold acetone at −20°C for 10 minutes and washed twice, followed by incubation on ice for 30 minutes with primary rabbit monoclonal anti-ZEB1 antibody (1:200; Cell Signaling Technology;
considered to be statistically significant.

**Immunofluorescence and immunohistochemistry**

Immunofluorescence and immunohistochemistry (IHC) were done as described previously (10, 23, 27, 35). Supplementary Table S2 summarizes antibodies, titers, and specific conditions. Stained objects were examined with a Nikon Microphot microscope and imaged with a digital camera. The immunohistochemical staining was assessed independently (S. Naganuma, H. Itoh, and A.J. Klein-Szanto), and the intensity was expressed as negative (−), weakly positive (+), or moderately positive (+++).

**Xenograft transplantation experiments and in vivo fluorescence imaging**

Xenograft transplantation experiments were done as described previously. In brief, 3 × 10^6 cells were suspended in 50% Matrigel and implanted subcutaneously into the dorsal skin of athymic nu/nu mice (4–6 weeks old; Charles River Breeding Laboratories). Tumor growth was monitored by in vivo fluorescence imaging of tdTomato using Maestro instrumentation (Cambridge Research and Instrumentation) with DsRed filter settings. Anesthetized mice were scanned (550–700 nm) using a 5-nm step, and background fluorescence was eliminated by using the spectral unmixing capability. Tumor volumes were also measured. All experiments were done under approved protocols from the University of Pennsylvania Institutional Animal Care and Use Committee and NIH guidelines.

**Statistical analyses**

Data from triplicate and hexaduplicate experiments in real-time RT-PCR, luciferase assays, soft agar colony formation assays, and xenograft transplantation were presented as mean ± SE and analyzed by the 2-tailed Student t test. P < 0.05 was considered to be statistically significant.

**Results**

**ZEB1 is localized to the invasive fronts exhibiting downregulation of the miR-200 family**

The expression status of ZEB1 in primary ESCC remains unknown. IHC revealed nuclear expression of ZEB1 in ESCC tumor cells in 17 of 51 cases (33%). ZEB1-positive tumor cells were found focally either within a cord-like invasive small nest (Fig. 1A and Supplementary Fig. S1) or at the periphery, but not the center, of well-differentiated tumor nests forming a keratin pearl (Fig. 1B). ZEB1-positive tumor cells were of basoloid type or less differentiated (dedifferentiated) and often displaying spindle cell shape, reminiscent of EMT. ZEB1 was not detected in the normal adult esophageal epithelium. However, it was detectable in early lesions such as carcinoma in situ (Supplementary Fig. S1), albeit infrequently (16%, 3 of 19 informative cases). Quantitative RT-PCR coupled with laser capture microdissection documented downregulation of the miR-200 family, a chief negative regulator of ZEBs at the invasive fronts of tumors showing ZEB1 upregulation (Supplementary Fig. S2 and not shown). ZEB1 was not detected in well-differentiated tumor nests expressing IVL along with NOTCH1 and NOTCH3 (Supplementary Fig. S3). On the basis of these observations, we hypothesized that ZEB1 is induced in dedifferentiated ESCC cells at the interface of the microenvironment and that EMT may occur upon loss of the commitment toward Notch-mediated squamous differentiation.

**Upregulation of ZEBs and reciprocal downregulation of the miR-200 family are associated with suppression of Notch signaling and squamous differentiation**

Next, we determined ZEBs and other markers for EMT as well as squamous differentiation in ESCC cell lines. As controls, we used immortalized human esophageal cell line EPC2-hTERT and its transformed derivative T-TeRAS. EPC2-hTERT cells express low levels of ZEBs consistent with its minimal capability of undergoing EMT (14, 23). In contrast, ZEBs were upregulated in T-TeRAS and HCE7 cells, exhibiting a fibroblastic morphology and changes in EMT indicators such as loss of CDH1 (E-cadherin) and upregulation of CDH2 (N-cadherin; Fig. 2A and Supplementary Fig. S4). Reciprocally, the miR-200 family members were suppressed sharply in these cell lines (Supplementary Fig. S5). Calcium induces squamous differentiation in keratinocytes. EPC2-hTERT cells are maintained in medium containing low Ca^2+ concentration (0.09 mmol/L). Addition of calcium (0.6 mmol/L) induced mRNA for CK13 and IVL, markers for squamous differentiation (Fig. 2A). Calcium induced concurrently mRNA and ICN for NOTCH1 and NOTCH3, indicating activation of Notch signaling (Fig. 2) as described previously (10). Interestingly, ZEBs were suppressed in EPC2-hTERT cells upon calcium-induced squamous differentiation (Fig. 2A). Unlike EPC2-hTERT, T-TeRAS and ESCC cell lines grow in the presence of high concentrations of Ca^2+ (0.95 and 1.8 mmol/L, respectively). Nonetheless, they expressed relatively low levels of IVL (Fig. 2A), implying restricted capability of undergoing squamous differentiation. In T-TeRAS and HCE7, there were inverse relationships between the levels of ZEBs and NOTCH1, NOTCH3, and CK13 (Fig. 2A). Given low levels of ICN1 and ICN3 in HCE7 and T-TeRAS (Fig. 2B and data not shown), we hypothesized that restriction in Notch-mediated squamous differentiation may alter ESCC cell fate through induction of ZEBs.

**Inhibition of Notch-mediated squamous differentiation increases malignant potential of transformed human esophageal cells**

To determine the roles of Notch signaling in cell fate switch in transformed esophageal epithelial cells, we transduced EPC2-T cells stably with DNMAML1, a genetic pan-Notch inhibitor (Supplementary Fig. S6A). We used EPC2-T because it maintains epithelial characteristics unlike T-TeRAS and HCE7 cells. DNMAML1 prevented ICN1, an active form of NOTCH1, from activating a CSL reporter and Notch target genes in EPC2-T cells (Supplementary Fig. S6B and S6C). DNMAML1 alone suppressed the basal level of CK13 and IVL (Supplementary Fig. S6D), suggesting an inhibited squamous differentiation status. Pharmacologic inhibition...
of Notch signaling by GSI induced similar inhibitory effects upon these Notch target genes (data not shown) as observed in the parental EPC2-hTERT cells (10). We assessed the biological impact of Notch inhibition in EPC2-T cells by carrying out organotypic 3D culture, a form of human tissue engineering. As observed with other transformed human esophageal cells (14, 31, 36), control EPC2-T cells not only formed a dysplastic stratified squamous epithelium but exhibited downward invasive growth into the matrix compartment to form cell nests resembling keratin pearls, a hallmark of well-differentiated SCCs (Fig. 3A, left). In contrast, DNMAML1 impaired epithelial stratification sharply as observed in nontransformed human esophageal cells (10).

Interestingly, DNMAML1 stimulated massive invasion of EPC2-T cells with loss of IVL expression and mislocalization of E-cadherin (Fig. 3A, right). DNMAML1 also enhanced cell migration and invasion in Boyden chamber assays (Supplementary Fig. S7). These findings indicate that the functional consequences of Notch inhibition in transformed cells may be not merely suppression of CSL-dependent squamous differentiation but activation of alternative cell fates such as EMT, thereby enhancing the malignant potential of cells. In agreement with such a premise, DNMAML1 increased anchorage-independent growth and tumorigenicity in immunodeficient mice (Fig. 3B and C and Supplementary Fig. S8). Interestingly, ZEB1 was upregulated also in the

Figure 1. ZEB1 upregulation at the invasive front of ESCCs. Representative images for hematoxylin and eosin (H&E) and corresponding IHC for ZEB1 in 2 primary ESCC cases featuring poorly differentiated invasive tumor nests (A) and tumor cells surrounding a well-differentiated lesion with keratin pearl formation (B). The selected areas were enlarged in the respective bottom panels. Note that ZEB1-positive tumor cells tend to show spindle cell differentiation (arrows). Stromal inflammatory cells and fibroblasts (arrowheads) are also positive for ZEB1. Scale bar, 100 μm.
invasive cells expressing DNMAML1 in organotypic 3D culture (Fig. 4A). Such findings prompted us to determine the roles of ZEBs in EPC2-T cells with altered Notch signaling by DNMAML1.

**Inhibition of Notch signaling promotes TGF-β-mediated EMT through ZEBs**

ZEBs were upregulated at the mRNA and protein levels in the presence of DNMAML1 (Fig. 4B and C). Moreover, the miR-200 family was downregulated reciprocally (Supplementary Fig. S9). We hypothesized that DNMAML1 may enrich a unique subset of cells expressing ZEBs with increased malignant potential. Flow cytometry revealed a significantly increased number of ZEB1-positive cells in the presence of DNMAML1 (Fig. 4D). However, a small number of ZEB1-positive cells were present in the control cells (Fig. 4D), suggesting that DNMAML may allow expansion of a preexisting ZEB1-positive cell population. Interestingly,
spindle-shaped cells were spontaneously induced in the presence of DNMAML1, which were augmented further by TGF-β stimulation (Fig. 5A). At least 60% of cells showed spindle-shaped cell morphology after TGF-β stimulation for 2 weeks although a subset of cells remained unchanged (Fig. 5A), implying cell heterogeneity. EMT was validated by an E-cadherin to N-cadherin class switch (Fig. 5B and Supplementary Fig. S10). TGF-β induced both ZEB1 and ZEB2, reinforcing their roles in EMT. To better define the specific functions of ZEBs, we conducted RNA interference (RNAi) experiments targeting either ZEB1 or ZEB2 using the tetracycline-inducible system. ZEB1 knockdown prevented TGF-β from inducing spindle-shaped cells and suppressing CDH1 (E-cadherin) more efficiently than ZEB2 knockdown (Fig. 5C–E). However, knockdown of either ZEB1 or ZEB2 had a limited impact upon TGF-β–induced N-cadherin expression (Fig. 5D and E), implying both ZEBs and/or other factors such as SNAI1 and TWIST1 in EMT (Supplementary Fig. S10). Interestingly, there was also a significant RNAi effect upon anchorage-independent growth of EPC2-T cells, where knockdown of ZEB1, but not ZEB2, reduced colony formation in soft agar by 35% (Supplementary Fig. S11). In addition, knockdown of ZEB1, but not ZEB2, restored the expression of miR-205 and miR-200b, yet only to a limited extent (Supplementary Fig. S12), consistent with the above described incomplete RNAi effect upon TGF-β-mediated EMT.

To confirm these findings in an independent cell line, we knocked down ZEBs in HCE7 cells. The RNAi effect upon E-cadherin and other EMT markers appeared to be similar to those observed in EPC2-T cells expressing DNMAML1 (Supplementary Fig. S13A). HCE7 cells remained mesenchymal morphologically despite highly efficient shRNA induction (Supplementary Fig. S13B). In addition, knockdown of ZEBs did not affect transcription factors such as SNAI1 and the miR-200 family (Supplementary Fig. S13C and data not shown). Nonetheless, knockdown of both ZEBs suppressed anchorage-independent growth and invasion in HCE7 cells (Supplementary Figs. S13D and S14).

In sum, inhibition of Notch-mediated squamous differentiation may divert the esophageal epithelial cell fate toward that of mesenchymal and raise cellular malignant potential in concert with ZEBs.

NOTCH3 contributes to esophageal cell fate decisions

Suppression of NOTCH1 and NOTCH3 was associated with lack of squamous differentiation markers and induction of ZEBs (Fig. 2). We have shown recently that NOTCH1 regulates squamous differentiation through NOTCH3 in normal esophageal epithelial cells (10). NOTCH1 knockdown did not have an immediate impact upon the basal expression of NOTCH3 (10) and ZEBs (Supplementary Fig. S15). DNMAML1 not only prevented ICN1 from inducing NOTCH3 mRNA but also suppressed the NOTCH3 basal level in EPC2-T cells.
Searching for NOTCH3-regulated genes, gene expression profiling was done using EPC2-hTERT cells stably expressing shRNA directed against NOTCH3 or a nonsilencing control shRNA (Supplementary Table S4). Interestingly, ZEBs were amongst the most highly upregulated genes along with N-cadherin, whereas E-cadherin was downregulated as validated by quantitative RT-PCR (Fig. 6A). Corroborating such observations was spontaneous emergence of spindle-shaped cells compatible with EMT in NOTCH3 knockdown cells (Fig. 6B). Furthermore, knockdown of NOTCH3 led to downregulation of the miR-200 family (Supplementary Fig. S16). Interestingly, there were changes in expression of transcription factors implicated in squamous epithelial biology and carcinogenesis. Among them were downregulation of KLF4 (required for squamous cell maturation; ref. 37) and upregulation of ID1 (inhibitor of differentiation; ref. 38) shown in Fig. 6A. These findings suggest that NOTCH3 may contribute to esophageal cell fate decision by promoting squamous cell differentiation while preventing dedifferentiation to mesenchymal cell lineages expressing ZEBs.

In aggregate, our data indicate that ZEB1 expression is associated with invasive growth of primary ESCCs. Suppression of Notch-mediated squamous cell differentiation may be associated with induction of ZEBs as implicated in ESCC cell lines. Inhibition of the CSL-dependent canonical Notch activities abrogates the squamous differentiation program, allowing expansion of cells expressing ZEBs with enhanced malignant potential. ZEBs contribute to EMT in response to TGF-β stimulation. NOTCH3 limits EMT competence and may have a role in cell fate decisions. Thus, we provide a novel mechanistic link between ZEBs and the Notch pathway in esophageal carcinogenesis and disease progression.
Discussion

ZEBs and the miR-200 family in esophageal carcinogenesis and disease progression

ZEBs and the miR-200 family have been linked to EMT, invasion, metastasis, chemotherapeutic drug resistance, and poor clinical outcomes in several cancers (26, 39). This is the first report about aberrant expression of ZEBs and the miR-200 family in SCCs including ESCCs. More importantly, however, we provide a novel link between ZEBs and Notch signaling which control a cell fate switch from squamous differentiation to EMT during tumor progression. Notch-mediated squamous differentiation may be suppressed at the tumor-invasive front where ZEBs facilitate a dedifferentiation process involving EMT in response to various stimuli, such as TGF-β, from the microenvironment as proposed in our model (Fig. 7). TGF-β, hypoxia, and inflammatory cytokines are among many factors known to induce ZEBs and EMT (26).

ZEB1 is focally expressed in invasive ESCC (Fig. 1 and Supplementary Fig. S1) as observed in breast, colorectal, and pancreatic carcinomas (25, 40). In addition, we detected ZEB1 in early lesions comprising spindle-shaped tumor cells (Supplementary Fig. S1), implying ZEBs in early stages of carcinogenesis. ZEB1 plays a critical role in senescence as well as EMT. ZEB1 mouse embryonic fibroblasts undergo premature senescence and ectopic E-cadherin induction (24). ZEBs are induced during malignant transformation of esophageal cells to negate EGFR oncogene–induced senescence in concert with mutant p53 (23). Thus, our data reinforce the roles of EMT as a fail-safe mechanism against oncogene-induced senescence at early stages of carcinogenesis (19). In addition, transformed human esophageal cells undergo EMT at the invasive front in organotypic 3D culture (14, 41). Importantly, EMT has been implicated in generation of migratory cancer stem cells (42), which may be subjected to regulation by the ZEB1-miR-200 feedback loop (25). Because the miR-200 family regulates tumor cell plasticity, invasiveness, and metastasis (43), downregulation of the miR-200 family in invasive primary ESCC tumors (Supplementary Fig. S2) and cell culture (Fig. 2 and Supplementary Fig. S5) implicates their roles in the pathogenesis of ESCC. Although ZEB2 was detectable in culture (Figs. 2 and 4–6), IHC failed to localize ZEB2 in ESCCs with primary antibodies tested. Both ZEBs repress E-cadherin (39). Our RNAi data suggest that ZEB1 may have a predominant role over ZEB2 in EMT, especially in E-cadherin repression (Fig. 5 and Supplementary Fig. S13). However, both ZEBs had inhibitory effects upon colony formation and invasion in HCE7 cells (Supplementary Figs. S13 and S14). ZEB1 knockdown had

Figure 5. ZEBs mediate EMT in the transformed human esophageal cells expressing DNAML1. EPC2-T cells expressing either DNAML1 or GFP (control) were stimulated with TGF-β1 for 2 weeks (A–E). C–E, cells expressing tetracycline-inducible (Tet-On) shRNA directed against ZEB1, ZEB2, or a nonsilence control sequence (Scramble) were subjected to TGF-β1 stimulation along with or without 1 μg/mL of doxycycline (DOX) for 2 weeks. Representative data are shown using 2 independent shRNA sequences. A and C, phase-contrast images were taken to score spindle-shaped cells (arrows) as shown in the histrogram. Scale bar, 50 μm. In A, #, P < 0.01 versus GFP plus TGF-β1 (+); # P < 0.05 versus GFP plus TGF-β1 (-); n = 6. In C, *P < 0.01 versus TGF-β1 only (n = 6). B and E, Western blotting indicated indicated molecules with β-actin as a loading control. D, real-time RT-PCR determined mRNA for indicated genes with β-actin as an internal control. CDH1, E-cadherin; CDH2, N-cadherin; *, P < 0.01 versus TGF-β1 only (n = 3).
indirect effects upon ZEB2 expression as described previously (23, 44, 45). Thus, it is plausible that both ZEBs contribute to EMT and other biological processes. In addition, ZEB1 knock-down had limited RNAi effects. In particular, the failure of full restoration of the miR-200 family may suggest involvement of both ZEBs and/or other transcription factors induced by TGF-β (Supplementary Fig. S10). Recent studies show that TWIST1 and SNAI1 may repress the miR-200 family directly (13, 46). Further studies are required to address their roles by RNAi designed to target simultaneously both ZEBs and/or other factors. Moreover, a subset of cells did not express detectable ZEB1 (Fig. 4D) and failed to undergo EMT in response to TGF-β stimulation (Fig. 5A). Thus, they may be refractory to RNAi directed against ZEBs. We are currently characterizing such cell populations.

**Induction of EMT as a novel consequence of Notch inhibition in ESCCs**

Cancer invasion may involve a dedifferentiation process which was implicated in ESCC cells exhibiting mesenchymal characteristics with concomitant downregulation of NOTCH receptor paralogues (Fig. 2). Inhibition of canonical Notch signaling impaired squamous differentiation in transformed human esophageal cells (Supplementary Fig. S6). However, we observed additional changes in transformed cells.

First and foremost, Notch inhibition resulted in upregulation of ZEBs and enhancement of malignant potentials implicated by EMT, invasion, anchorage-independent growth, and tumor formation (Figs. 3–5, Supplementary Figs. S7 and S8). One may argue this as an off-target effect of DNMAML1. Transcription factors other than CSL may recruit Mastermind-like as a coactivator (2). However, knockdown of NOTCH3 also induced ZEBs and EMT (Fig. 6), implying Notch signaling more specifically in restriction of the EMT-competent cells. Although TGF-β and Notch signaling may cooperate to promote EMT during development and cancer progression (20), TGF-β robustly induced EMT in the presence of DNMAML1, suggesting that canonical Notch signaling may be dispensable. In addition, TGF-β suppressed CK13 and IVL (Supplementary Fig. S10). Therefore, concurrent Notch

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Figure 6. Notch3 knockdown promotes EMT with upregulation of ZEBs and impairs squamous differentiation mechanisms in human esophageal cells. EPC2-hTERT derivatives expressing 2 independent shRNA sequences directed against NOTCH3 (Notch3-A and Notch3-B) or a nonsilence control sequence (Scramble) were analyzed to validate the microarray data. A, real-time RT-PCR determined mRNA for indicated genes with β-actin as an internal control. CDH1, E-cadherin; CDH2, N-cadherin; *, P < 0.01 versus Scramble (n = 3–6). B, phase-contrast images were taken to score spindle-shaped cells (arrows) as represented in the histogram. *, P < 0.01 versus Scramble (n = 6). Scale bar, 50 μm. Representative data (Notch3-A) are shown with comparable results using Notch3-A and Notch3-B.
NOTCH3 Restricts ZEB1-Positive EMT-Competent Cells to Expand

Figure 7. Model. Notch signaling regulates squamous differentiation in the normal esophageal epithelium. Notch signaling also contributes to keratin pearl formation in well-differentiated tumor nests. ZEB1 is expressed at the invasive fronts where tumor cells do not undergo squamous differentiation. In early lesions such as carcinoma in situ, ZEBs may be induced in response to oncogene activation (e.g., EGFR) to negate oncogene-induced senescence as a cellular fail-safe mechanism (23). In advanced ESCCs, NOTCH3 may be downregulated, resulting in dedifferentiated status where microenvironmental cues (e.g., TGF-β) and hypoxia (b) may promote EMT in concert with ZEBs, leading to invasive growth and tumor cell dissemination. In this study, either DNMAML1 or shRNA directed against NOTCH3 (N3) was used to suppress canonical Notch-mediated squamous differentiation to facilitate ZEB-mediated EMT.

inhibition and TGF-β stimulation may drive cancer cell fate toward a migratory mesenchymal cell lineage while suppressing squamous differentiation (Fig. 7).

Second, our data extend the current view of Notch as a tumor suppressor in skin SCCs. DNMAML1 promotes SCC in the mouse skin (8) and transforms epidermal keratinocytes in concert with oncogenic Ras. Moreover, DNMAML1 may enhance epidermal keratinocyte stem cell populations (5). Increased colony formation efficiency in soft agar and tumorigenesis by DNMAML1 (Fig. 3) may be indicative of potential cancer stem cells where ZEBs and the miR-200 family may have a critical role. Such a possibility is currently under investigation. Interestingly, the growing list of validated targets for the miR-200 family includes Notch signaling components such as Jag1, Maml2, and Maml3 (26). In fact, MAML2 and MAML3 were found upregulated with reciprocal downregulation of the miR-200 family in the presence of DNMAML1 (Supplementary Figs. S6 and S9). Although Notch signaling may contribute to ZEB1 induction in pancreatic cancer cells (47), it is unlikely that MAML2 and MAML3 have a role in ZEB1 induction in our system, as DNMAML1 interferes with all MAML family members (48). Consistent with such a notion, Notch was not activated in HCE7 cells showing upregulation of ZEBs and the miR-200 family (Fig. 6A and Supplementary Fig. S16). Moreover, NOTCH3 inhibition implicated many genes encoding essential cytokines, growth factors, and enzymes such as interleukin 6, fibroblast growth factor 2, and PTGS2 (i.e., COX-2; Supplementary Table S4). Interestingly, NOTCH3 activity contributes to non–small-cell lung cancer stem cells (49) and promotes tissue site–specific transformation of glial precursor cells (50). Therefore, it is imperative to understand the biological roles and regulation of NOTCH3 in the context of the tumor microenvironment as well as the molecular basis of NOTCH3-mediated regulation of ZEBs and the miR-200 family in cancer stem cells.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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