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

Shinya Ohashi1,5,8, Mitsuteru Natsuizaka1,5, Seiji Naganuma1,5,9, Shingo Kagawa1,5, Sotai Kimura9, Hiroshi Itoh9, Ross A. Kalman1,5, Momo Nakagawa1,5, Douglas S. Darling10, Devraj Basu2,7, Phyllis A. Gimotty4,5, Andres J. Klein-Szanto6, J. Alan Diehl3,5, Meenhard Herlyn7, and Hiroshi Nakagawa1,5

Institute, Philadelphia, Pennsylvania; 8Division of Gastroenterology and Medical Sciences, University of Fukui, Eiheiji, Fukui, Japan; and10Department of Pathological Sciences, School of Medicine, Faculty of Medicine, University of Fukui, Eiheiji, Fukui, Japan.

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); 1–12. ©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 [CBAF1/RBP-jk, 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 also 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, p53Del17/18, 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 (CaCl2), 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 DNAML1 (10) and tetra-cycline-inducible lentiviruses (Open Biosystems) expressing shRNA directed against ZEB1 (clones V2THS_116663 and V2THS_116659), ZEB2 (clones V2THS_95420 and V3THS_373827), or a nonsilencing control sequence (clone RH54743) 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 DNAML1) 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 Plus 2.0; Affymetrix) 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;
*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 basaloid type, reminiscent of EMT. *ZEB1* was not detected in the normal adult esophageal epithelia. 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.

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 DNAML1, a genetic pan-Notch inhibitor (Supplementary Fig. S6A). We used EPC2-T because it maintains epithelial characteristics unlike T-TeRAS and HCE7 cells. DNAML1 prevented ICN, an active form of NOTCH1, from activating a CSL reporter and Notch target genes in EPC2-T cells (Supplementary Fig. S6B and S6C). DNAML1 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). 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.
Supplementary Fig. S6). 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 comprised 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−/− murine 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
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-
b (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-
b (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 upregula-
tion of ZEBs and enhancement of malignant potentials impli-
cated 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 Master-
mind-like as a coactivator (2). However, knockdown of
NOTCH3 also induced ZEBs and EMT (Fig. 6), implying Notch
signaling more specifi
cally in restriction of the EMT-compe-
tent 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

**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); **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.
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 NE21 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 downregulation of the miR-200 family (Fig. 2B and Supplementary Figs. S4 and S5). Therefore, ZEBs and the miR-200 family may influence Notch signaling in a cell-type or context-dependent manner.

Finally, this study revealed NOTCH3 as a critical determinant in epithelial versus mesenchymal specification. ICN3 was upregulated in most ESCC cells. Thus, NOTCH3 may maintain commitment of ESCC cells toward squamous cell differentiation with its potential downstream effectors such as KLF4 and ID1. In turn, acquisition of mesenchymal traits as observed in HCE7 cells may require inactivation of NOTCH3. Our data imply NOTCH3 in regulation 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.

Acknowledgments

The authors thank Dr. Warren S. Pear (Penn) for reagents and discussion, and Rachel Hammond, Drs. Don Baldwin and John Tobias (Penn Microarray Facility Bioinformatics Group), Dr. Charles H. Fletcher (Flow Cytometry & Cell Sorting Facility), Dr. Gary P. Swain and Daniela Budo (Morphology Core), and Drs. Gary D. Wu and Sue Keilbaugh (Molecular Biology/Gene Expression Core) for assistance in data collection and analysis. They are also appreciative of discussions with the laboratory of Dr. Anil K. Rustgi and his editorial help.

Grant Support

This study was supported, in part, by NIH grants R01DK077005 (M. Natsuizaka, S. Ohashi, H. Nakagawa), P01-CA-098101 (Mechanisms of Esophageal Carcinogenesis to H. Nakagawa, S. Ohashi, M. Natsuizaka, S. Kagawa, A.J. Klein-Szanto, M. Herlyn, J.A. Diebl), R01DE01923 and P30ES014441 (D.S. Darling), P30-DK050306 (R.A. Kalman and M. Nakagawa), University of Pennsylvania Bioepithelial Cancer Research Center.
University Research Foundation Award (H. Nakagawa), University of Pennsylvania, Abramson Cancer Center Pilot Project Grant (to H. Nakagawa), Japan Society for the Promotion of Science Grant-in-Aid for Young Scientists B-21790382 (S. Nagamura), American Gastroenterological Association Foundation Student Research Fellowship Award (M. Nakagawa), and the NIH/NIDDK Center for Molecular Studies in Digestive and Liver Diseases (P30-DK050306) and its core facilities (Molecular Pathology and Imaging, Cell Culture, Molecular Biology/Gene Expression).

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received March 14, 2011; revised August 25, 2011; accepted August 30, 2011; published OnlineFirst September 2, 2011.

References

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

Shinya Ohashi, Mitsuteru Natsuizaka, Seiji Naganuma, et al.

Cancer Res  Published OnlineFirst September 2, 2011.