Transient SNAIL1 Expression Is Necessary for Metastatic Competence in Breast Cancer

Hung D. Tran1, Krishna Luitel1, Michael Kim1, Kun Zhang1,2, Gregory D. Longmore1,2,3,4, and David D. Tran1,4

Abstract

SNAIL1 has been suggested to regulate breast cancer metastasis based on analyses of human breast tumor transcriptomes and experiments using cancer cell lines and xenografts. However, in vivo genetic experimental support for a role for SNAIL1 in breast cancer metastasis that develops in an immunocompetent tumor microenvironment has not been determined. To address this question, we created a genetic SNAIL1 model by coupling an endogenous SNAIL1 reporter with an inducible SNAIL1 transgene. Using multiple genetic models of breast cancer, we demonstrated that endogenous SNAIL1 expression was restricted to primary tumors that ultimately disseminate. SNAIL1 gene deletion either during the premalignant phase or after primary tumors have reached a palpable size blunted metastasis, indicating that late metastasis was the main driver of metastasis and that this was dependent on SNAIL1. Importantly, SNAIL1 expression during breast cancer metastasis was transient and forced transient, but not continuous. SNAIL1 expression in breast tumors was sufficient to increase metastasis. Cancer Res; 74(21): 1–11. ©2014 AACR.

Introduction

The transcription repressor SNAIL1 has been shown to be one of the earliest epithelial–mesenchymal transition (EMT) regulators during development (1), critical for cancer EMT (1), and its expression in primary human breast tumors strongly associated with metastasis (2–4). Despite these observations, the role of SNAIL1-initiated EMT during tumor metastasis remains contentious (5, 6). In humans, metastatic cells have been isolated from the periphery and in most instances they appear epithelial, not mesenchymal (7, 8). These results have been used to argue against a significant role for EMT in tumor metastasis. However, most available isolation methods are biased toward epithelial cells as they often target epithelial markers (e.g., EpCAM) to capture circulating tumor cells (CTC). In addition, metastatic cells isolated from the periphery may not reflect their cellular status in primary tumors where the initiation of invasion leading to metastasis occurs. In fact, cancer EMT is thought to be a transient process (9, 10). In recent studies, transient, not continuous, TGFβ stimulation can result in reversible induction of SNAIL1 and EMT (4, 7). Similarly, in human breast cancer, SNAIL1 expression in primary tumors correlates with overt metastasis, whereas its expression in bone marrow disseminated tumor cells (BM DTC) does not (4).

To date, most SNAIL1 animal models have utilized cancer cell lines induced to express SNAIL1 before being injected intravenously, resulting in more lung metastases (11, 12). While these suggest that SNAIL1 contributes to extravasation, colonization, or reactivation of growth of DTCs, they do not address whether SNAIL1 is required in primary tumors to initiate invasion and intravasation. Other approaches employed tumor xenografts that overexpress SNAIL1, leading to increased metastasis (4, 7). However, xenograft models do not account for the critical interaction between a tumor and its microenvironment and immune system. Without genetic evidence, what have remained unclear are whether (i) SNAIL1 expression in primary tumors that develop de novo in immunocompetent hosts is necessary and sufficient to promote tumor cell invasion and metastasis and (ii) SNAIL1 downregulation in metastatic tumor cells after initial invasion is required for DTCs to form overt metastases.

Here, we describe the generation of a mouse model harboring an endogenous SNAIL1 reporter coupled with a tetracycline (tet)-inducible SNAIL1 transgene. By crossing these mice and previously characterized floxed SNAIL1 mice (13) with multiple genetic breast cancer mouse models, we demonstrate that conditional deletion of the SNAIL1 gene in primary breast tumors resulted in a significant reduction in both DTCs and lung metastases, indicating that breast cancer metastasis is
highly dependent on SNAIL1. In addition, SNAIL1 expression during breast cancer metastasis was transient. Forced, continuous overexpression of SNAIL1 starting in primary tumors led to a decrease in lung metastasis despite an increase in DTC number. In contrast, transient overexpression of SNAIL1 increased both DTC number and lung metastasis.

Materials and Methods

**Generation of SNAIL1-CBR mice**

B6/129/SvJ hybrid XY ES cells were electroporated with the targeting construct, and 200 G418-resistant clones screened by PCR to obtain four recombinants. Two recombinants were transiently transfected with CRE, and 100 ganciclovir-insensitive clones screened by PCR to obtain five CRE-excised recombinants. Two recombinants were laser-injected into eight cell-staged blastomeres, producing 100% F1 XY mice (14), which were crossed with wild-type females to produce the SNAIL1-CBR line.

**Antibodies and reagents**

The following antibodies were used: rabbit anti-SNAIL1 (Cell Signaling Technology); mouse anti-E-cadherin (BD Biosciences); mouse anti-vimentin (Cell Signaling Technology); mouse anti-pan-keratin (Cell Signaling Technology); mouse anti-NeuNT (Fisher Scientific); mouse anti-CD45 (Cell Signaling Technology); mouse anti-FLAG (Sigma); and mouse anti-actin (Sigma). All secondary antibodies were from Jackson ImmunoResearch. The following reagents were used: neutral buffer Kit (Invitrogen); DAPI (Sigma); donkey serum and Fab fragment for blocking for immuno fluorescence staining in DTCs (Jackson ImmunoResearch). The following reagents were used: neutral buffered formalin (Fisher Scientific); hematoxylin (Sigma); eosin (Fisher Scientific); carmine alum buffer (StemCell Technologies); RBC lysis buffer (Sigma); HistoMouse Broad Spectrum Kit (Invitrogen); DAPI (Sigma); donkey serum and Fab fragment for blocking for immuno fluorescence staining in DTCs (Jackson ImmunoResearch); Feket solution (Fisher Scientific); Indian ink (Fisher Scientific); doxycycline (Sigma); carbon tetrachloride (CCL4, Sigma); and o-luciferin (Sigma).

**Histologic analyses**

Breast whole mount was performed with carmine alum as previously described (15). Picrosirius stain of liver sections was performed as previously described (16). Immunohistochemistry (IHC) was performed per the manufacturer’s instructions (Invitrogen). For immunofluorescence of DTCs, total lung cells were obtained by dissociating a section of lung without visible metastases with collagenase and bone marrow cells isolated from both femurs and tibias and depleted of red blood cells, then adhered to poly-L-lysine–treated slides, fixed, permeabilized, and stained with indicated antibodies per standard protocol.

**Lung metastasis analysis by Indian ink stain**

Lungs were removed and inflated with 2 mL of 15% Indian ink by intratracheal injection. Ink-injected lungs were washed with Feket solution and then bleached overnight with fresh Feket solution (17). The numbers of surface lung metastases were quantitated using a magnifying glass.

**BM DTC enrichment and Her2Neu FACS analyses**

BM DTCs were enriched from total erythrocyte-depleted bone marrow cells by CD45+ selection using CD45 MicroBeads (Miltenyi Biotec) and an antiMACS Separator as per the manufacturer’s instructions. Both CD45+ and unlabeled CD45 fractions were collected, fixed with 0.01% formaldehyde, permeabilized with 0.1% Triton X-100, stained anti-Her2Neu monoclonal antibody and fluorescently labeled secondary antibody, and analyzed using a standard FACS protocol.

**Spatiotemporal analyses of SNAIL1 and EMT phenotypes**

For primary tumors, individual tumors were obtained from independent mice and sections stained for SNAIL1, E-cadherin, and vimentin by IHC and the percentage of tumors that had detectable SNAIL1 expression determined. For bone marrow and lung DTCs, spreads of pooled whole bone marrow cells or pooled dissociated whole lung cells from the same mice were coimmunostained for Her2Neu and SNAIL1, E-cadherin, or vimentin. The percentage of cells that was positive for SNAIL1 in 150 Her2Neu-positive DTCs was determined. For lung metastases, lung sections from the same mice were stained for SNAIL1, E-cadherin, and vimentin by IHC and the percentage of metastases that were positive for SNAIL1 in 150 individual metastatic foci determined.

**Statistical analysis**

Mean values were compared using a Student unpaired, two-tailed t test.

**Results**

**Creation and characterization of a coupled endogenous SNAIL1 reporter and inducible SNAIL1 mouse (SNAIL1-CBR)**

To determine the spatiotemporal expression and role for SNAIL1 during cancer metastasis in vivo, we created a multi-functional SNAIL1 mouse model: SNAIL1-CBR mouse (Fig. 1A and Supplementary Fig. S1A and S1B). To generate a SNAIL1 reporter that would allow for in vivo, real-time detection of endogenous SNAIL1 expression, we introduced a cDNA encoding a clic beetle red luciferase (CBR) in frame with the third exon of the endogenous SNAIL1 locus. In addition, we inserted a tet-inducible SNAIL1 transgene (TRE-SNAIL1–3FLAG) 3’ to the SNAIL1-CBR gene so as to be able to inducibly overexpress SNAIL1 in vivo in a tissue-specific manner. Both fusion constructs SNAIL1-CBR and SNAIL1–3Flag retain the function of SNAIL1 as an EMT-inducing factor as measured by their ability to downregulate E-cadherin, upregulate vimentin, and induce classical morphologic changes of EMT (Supplementary Fig. S1C and S1D; refs. 18, 19).

To determine whether SNAIL1-CBR expression was properly regulated in cells, we determined protein and mRNA expression of SNAIL1 and SNAIL1-CBR in the targeted ES cells induced to differentiate by removing the leukemia-inhibitory factor (LIF) from culturing media. Consistent with previous reports (20, 21), expression of both wild-type SNAIL1 and SNAIL1-CBR was detected 3 days after LIF withdrawal (Fig. 1C). This indicated that the introduction of CBR did not alter the transcriptional regulation of the SNAIL1 locus. To determine the inducibility of the TRE-SNAIL1–3FLAG transgene in cells, we introduced into targeted ES cells a tet-on DNA

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transactivator (rtTA). In the resultant cells, SNAIL1–3Flag protein and mRNA were detected only in the presence of doxycycline (Fig. 1D).

SNAIL1-CBR heterozygous mice were fertile and phenotypically indistinguishable from wild-type mice. A survey of organs from these mice revealed low bioluminescence signals in mammary glands and most internal organs (Supplementary Fig. S1E and S1F), possibly due to physiologic expression of SNAIL1 in activated resident fibroblasts (13). To demonstrate the utility and reliability of the SNAIL1-CBR reporter in vivo, we measured tissue-specific bioluminescence intensity during both physiologic and pathologic EMT processes known to be SNAIL1 dependent. Placental development is a robust EMT process and SNAIL1 has been implicated in trophoblast differentiation and uterine invasion (22, 23). At 7.5 days after coitus (dpc), when trophoblast EMT is high (24), uterine SNAIL1-CBR signal was 5-fold higher compared with the basal signal (Fig. 1E). We cannot exclude the possible contribution of increased SNAIL1-CBR signal from embryonic gastrulation, another contemporaneous SNAIL1-dependent EMT event (25), to the uterine signal. Pathologically, SNAIL1 has been implicated in CCl4-induced liver fibrosis (26). SNAIL1-CBR mice treated with intraperitoneal CCl4 developed liver fibrosis, as evidenced by the increased collagen deposition (Fig. 1G) and hepatic SNAIL1-CBR signal concurrently increased approximately 5-fold compared with the vehicle control (Fig. 1F). These control experiments indicated that SNAIL1-CBR expression is properly regulated, readily detectable during in vivo EMT, and thus a reliable reporter of endogenous SNAIL1 expression in vivo.

The SNAIL family of transcription factors (SNAIL1 and SNAIL2) has been suggested to play a role in mammary development (27, 28). Therefore, to determine the functionality of the TRE-SNAIL1–3Flag transgene in vivo, we crossed...
SNAIL1-CBR mice with mice carrying the mouse mammary tumor virus promoter driving expression of rtTA (MMTV-rtTA or MTA; ref. 29). TRE-SNAIL1–3FLAG transgene expression was detected in mammary tissue only in the presence of both MTA and doxycycline (Fig. 11) and resulted in increased ductal branching compared with control SNAIL1-CBR mice lacking MTA (Fig. 1H). This result indicated that the TRE-SNAIL1–3FLAG transgene was expressed and functional in vivo.

SNAIL1 expression in primary breast tumors strongly correlates with metastasis

As SNAIL1 expression in primary human breast tumors correlates with higher rates of metastasis (4), we asked whether a similar association also holds true in mouse breast cancer models. To do so, we first crossed SNAIL1-CBR mice with the MMTV-NeuNT breast cancer model (MMTV-neuNT; SNAIL1-CBR mice), which produces breast tumors similar to ER-negative, Her2Neu-positive human breast tumors (30, 31), and determined SNAIL1 expression within emerging breast tumors through SNAIL1-CBR bioluminescence and correlated the signal intensity with the development of lung metastasis (Fig. 2A–C). A remarkably strong positive correlation between SNAIL1-CBR expression in primary tumors and incidence of lung metastasis was observed. No mouse with primary breast tumors that all exhibited SNAIL1-CBR intensity of \( \leq 3 \times 10^6 \) photons/cm\(^2\) (mean of 2.5 \( \times 10^6 \)) had detectable lung metastases.

**Figure 2.** SNAIL1 expression in primary breast tumors strongly correlates with increased metastasis and an invasive phenotype in MMTV-neuNT mice.

A, representative image of SNAIL1-CBR bioluminescence in MMTV-NeuNT mice with SNAIL1-CBR-positive or -negative tumors. B, representative images of superficial lung metastases as seen grossly (top, black arrow) and after Indian ink stain as white lesions on a black background (bottom, white arrow). C, a histogram of incidence of lung metastasis in mice with SNAIL1-CBR-positive or -negative primary tumors. D, representative images of BM DTCs as detected by Her2Neu immunofluorescence in mice with SNAIL1-CBR-positive or -negative primary breast tumors. E, a histogram of number of BM DTCs per 10\(^6\) bone marrow cells in mice with SNAIL1-CBR-positive or -negative primary breast tumors. F, representative images of SNAIL1-CBR-positive and -negative primary breast tumors. G, a histogram of distribution of invasive carcinomas and adenomas by gross appearance of SNAIL1-CBR-positive and -negative tumors. H, representative images of hematoxylin and eosin (H&E)-stained primary tumor sections, revealing a typical protrusion into surrounding stroma in a Snail1-CBR-positive tumor (black arrow) compared with the smooth contour in a Snail1-CBR-negative tumor. I and J, representative images of SNAIL1 and E-cadherin IHC of sections from SNAIL1-CBR-positive (I) and -negative (J) primary tumors, revealing SNAIL1-positive cells (red arrowheads) in an invasive front of SNAIL1-CBR-positive tumor where E-cadherin expression was decreased. Mus, muscle.
metastasis, whereas in mice with at least 1 primary breast tumor that exhibited an intensity of $\geq 10^7$ photons/cm² (mean of 1.75 $\times$ 10⁶), 100% developed lung metastasis (Figs. 2C and Supplementary Fig. S2A). In all subsequent experiments, we defined primary breast tumors exhibiting $<3 \times 10^7$ photons/cm² as SNAIL1-CBR-negative and $>10^7$ photons/cm² as SNAIL1-CBR-positive (Supplementary Fig. S2A).

In human breast cancer, SNAIL1 expression in primary tumors predicts for distant metastasis; however, its expression in BM DTCs does not (4), suggesting that SNAIL1 may be important in primary tumors to initiate invasion and migration of cancer cells that ultimately give rise to DTCs, as opposed to playing a role in the outgrowth of DTCs to form overt metastases. If so, then SNAIL1 expression in primary tumors might be associated with higher numbers of DTCs. We chose to focus on DTCs instead of blood-borne CTCs because DTCs are considered to have completed the metastatic cascade (i.e., local invasion, intravasation, extravasation, and survival in secondary organs). In addition, it is unclear what fraction of CTCs eventually gives rise to DTCs as the majority fail to complete the metastatic process (32). To test this possibility, we collected total dissociated lung cells and total erythrocyte-depleted bone marrow cells, then quantified the number of DTCs through Her2Neu IF using a mouse monoclonal antibody specific for human and rat, but not mouse, Her2Neu (33). In mice with SNAIL1-CBR-positive primary tumors, there was a 10-fold greater number of BM DTCs compared with SNAIL1-CBR-negative primary tumor-bearing mice (Fig. 2D and E). A similar strong positive correlation was also observed between the number of lung DTCs and SNAIL1 expression in primary tumors (Supplementary Fig. S2B). In addition, the numbers of bone marrow and lung DTCs correlated well with each other (Supplementary Fig. S2C). As the bone marrow afforded greater reliability of enriching for DTCs and there is less chance of contamination with tumor cells from metastatic foci than in the lung, we focused on BM DTCs for the remainder of the experiments. We could not exclude the possibility that some DTCs could have lost Her2Neu expression; however, the contribution of Her2Neu-negative DTCs, if any, to the total number of DTCs would be expected to be similar in animals with either SNAIL1-CBR-positive or -negative primary tumors because the ratio of Her2Neu-positive and -negative cells in primary tumors was similar between SNAIL1-CBR-positive and -negative primary tumors (Supplementary Fig. S2D).

In summary, these results indicated that SNAIL1-CBR (i.e., SNAIL1) expression in primary mouse breast tumors was a strong predictor for the production of DTCs and subsequent overt lung metastases.

Next, we asked whether SNAIL1-CBR-positive primary tumors were associated with a more invasive phenotype that is associated with increased metastatic disease, Grossly, SNAIL1-CBR-positive primary tumors [confirmed by real-time (RT)-PCR; Supplementary Fig. S3A] were irregular in shape with multiple protrusions penetrating into and tightly attached to underlying fascia and muscles, whereas SNAIL1-CBR-negative tumors were round and loosely adhered to the fascia (Fig. 2F and G). Microscopically, SNAIL1-CBR-positive tumors exhibited multiple invasive projections, in which numerous cells expressed SNAIL1 and lacked E-cadherin expression [Fig. 2H (left, black arrows) and 2I (red arrowheads) and Supplementary Fig. S3B, left]. In contrast, a smooth contour distinguished SNAIL1-CBR-negative tumors from surrounding extracellular matrix and in these tumor cells, E-cadherin expression was present [Fig. 2H (right) and 2J and Supplementary Fig. S3B, right]. Thus, expression of SNAIL1 in primary breast tumors is associated with an aggressive carcinomatous phenotype, characterized by local invasion, whereas primary tumors not expressing SNAIL1 were adenoma like.

**SNAIL1 expression in primary breast tumors precedes detection of DTCs, but SNAIL1 is not expressed by DTCs and lung metastases.**

If SNAIL1 expression in primary tumors drives EMT and thereby invasion and intravasation, then SNAIL1 expression in primary tumors might be predicted to precede the detection of DTCs. To test this hypothesis, we made use of the tet-inducible activated rat Her2Neu mouse breast cancer model (MMTV-rtTA; TetO-neuNT or MTA; TAN) because of its predictable and reproducible tumor penetrance and latency (34), two key characteristics necessary for a temporal analysis (Fig. 3A).

SNAIL1 mRNA expression in primary tumors and the number of BM DTCs were determined in mice after 5 to 8 weeks of doxycycline treatment, a time well before evident lung metastases. BM DTCs were scored by Her2Neu IF. Low-level SNAIL1 mRNA was present after 5 weeks of doxycycline treatment, a time when primary tumors were barely palpable (Fig. 3B). This increased 3- to 5-fold by 6–8 weeks of doxycycline treatment (Fig. 3B). BM DTCs were barely detectable after 6 weeks of doxycycline treatment but rose sharply beginning at weeks 7 and 8 (Fig. 3C). It was unlikely that the initial upsurge in both primary tumor SNAIL1 mRNA levels and BM DTCs was due to growth of primary tumors, as there was no significant difference in these parameters between weeks 7 and 8 despite a simultaneous 3-fold growth in total primary tumor burden (Fig. 3D). Thus, SNAIL1 expression in primary tumors preceded the detection of BM DTCs.

In another approach testing this hypothesis, we crossed the SNAIL1-CBR mouse with the MMTV-PyMT breast cancer model, which, like the MTA;TAN model, also has a predictable and uniform, albeit more accelerated, course of tumor development (30, 35). Again, a similar temporal relationship between SNAIL1 expression in primary tumors and generation of DTCs was observed in MMTV-PyMT; SNAIL1-CBR mice: SNAIL1-CBR reporter and SNAIL1 mRNA expression followed first palpable tumors (Supplementary Fig. S4A–S4C) and preceded the increase in BM DTCs (Supplementary Fig. S4D).

In sum, these two experiments indicated that SNAIL1 expression within primary tumors immediately preceded the detection of DTCs.

To determine whether SNAIL1 contributed to later stages of metastasis when DTCs reactivated growth to form overt metastases, we measured SNAIL1 mRNA expression in sets of primary tumors, BM DTCs, and isolated lung metastases from the same mice. MTA/TAN mice were treated with doxycycline for 12 weeks (from 6 to 18 weeks of age) when nearly all had...
developed lung metastasis (Fig. 3A), then tissues harvested. BM DTCs were enriched >100-fold by depleting CD45^+ hematologic BM cells (not shown). Relative to primary tumors, SNAIL1 mRNA level was >4- and >3-fold less in BM DTCs and lung metastases, respectively (Fig. 3E). This decrease was also apparent at the protein level as assessed by SNAIL1 IHC and IF (Table 1). Of 25 primary tumors, 13 (52%) exhibited detectable SNAIL1 expression at invasive fronts where there was decreased E-cadherin and increased vimentin. In contrast, SNAIL1 expression was rarely found in Her2Neu-positive BM DTCs (4%) and lung DTCs (not shown), and lung metastases (5%).

Historically, the majority of lung metastases appeared more epithelial than mesenchymal (Fig. 3F). Similar results were observed in MMTV-PyMT; SNAIL1-CBR mice (Supplementary Table S1 and Supplementary Fig. S4E).

Taken together, these results indicated that SNAIL1 expression was restricted to primary tumors and associated with a mesenchymal phenotype, whereas overt lung metastases were more epithelial appearing, suggesting a reversal of EMT, possibly through the mesenchymal–epithelial transition or MET, in metastases. However, the possibility that some lung metastases were formed through SNAIL1-independent events cannot be excluded.

**SNAIL1 is required for breast cancer metastasis.**

To determine whether SNAIL1 was necessary for breast cancer metastasis, we made use of a previously characterized floxed SNAIL1 mouse (13). Although SNAIL1 expression in primary tumors of MMTV-PyMT mice was first detected when primary tumors reached approximately 0.5 cm in diameter...
between these two possibilities, we determined the status of CRE-mediated SNAIL1 deletion due to the mosaic MMTV promoter could have arisen from metastatic cells that had escaped CRE-mediated gene rearrangement in primary tumors (Supplementary Fig. S4B and S4C). It is possible that earlier low level or transient SNAIL1 expression occurs and, if so, this could be important to promote invasion in humans and mouse models, early dissemination from premalignant lesions such as ductal carcinoma in situ (DCIS) has been described (33, 36–38). Whether metastatic cells derived from early dissemination possess the same potential to develop overt metastases as those from later dissemination remains unclear.

Therefore, to test the requirement for SNAIL1 in breast cancer metastasis, we decided to delete the SNAIL1 gene either early (MMTV-Cre) or late (TetO-Cre) during PyMT-induced breast cancer development (Fig. 4A).

The MMTV-Cre transgene expresses CRE in the mammary epithelia concurrently with oncogenic MMTV-PyMT expression. We confirmed CRE expression from MMTV-Cre in the breast epithelium using ROSA26-LSL-tdTomato mice (39). In 8-week-old mice, tdTomato was present in most, but not all, cells in the mammary ductal epithelia, consistent with known mosaicism of the MMTV promoter, but not in surrounding stromal cells (not shown) (29). For late deletion of SNAIL1, we treated SNAIL1fl/fl; MMTV-PyMT; TRE-Cre; MTA with doxycycline when the size of primary tumors had reached 0.5 cm in diameter and SNAIL1-CBR bioluminescence not detected (Fig. 4B). Upon detection of palpable primary tumors increases metastasis (Supplementary Fig. S5C). This result indicated that the few lung metastases present in early KO mice likely arose due to incomplete deletion of the floxed SNAIL1 gene in primary tumor cells.

In summary, both early and late SNAIL1 deletion in the MMTV-PyMT metastatic breast cancer model indicated that SNAIL1 was required for breast cancer metastasis.

### Transient, but not continuous, SNAIL1 overexpression in primary breast tumors increases metastasis

The presence of SNAIL1 expression in primary tumors yet absence in DTCs and lung metastases suggested that SNAIL1 expression during metastasis could be transient, or alternatively, needs to be turned off for effective metastasis to occur. To test this hypothesis, we overexpressed SNAIL1 either transiently or continuously in MMTV-neuNT mice, as this model has modest metastatic potential (~25%) and asked whether these manipulations affected the extent of metastasis (Fig. 5A).

We generated MMTV-neuNT; SNAIL1-CBR; MTA and control MMTV-neuNT; SNAIL1-CBR mice (unresponsive to doxycycline). Upon detection of palpable primary breast tumors (~0.5 cm in diameter and SNAIL1-CBR bioluminescence not detected), mice were fed 1 mg/mL doxycycline-containing water, either continuously (12 weeks; Continuous SNAIL1) or transiently (4 weeks followed by 8 weeks of doxycycline-free water; Transient SNAIL1), then the number of BM DTCs and incidence of lung metastasis determined for all groups (Fig. 5A). The selection of 4-week doxycycline treatment as the transient treatment window was based on the time course from initial SNAIL1 expression in primary breast tumors to initial appearance of lung metastases in MTA/TAN mice (Fig. 3A).

Tumor latency was similar between Transient and Continuous SNAIL1 and control mice with means of 23 and 24 weeks, respectively. Primary tumor burden was not higher in SNAIL1-overexpressing mice compared with controls. Continuous SNAIL1 overexpression in breast tumor cells increased the number of BM DTCs 3-fold over that in controls (Fig. 5C). Surprisingly, however, the percentage of mice that developed metastasis, we decided to delete the SNAIL1 gene either early (MMTV-Cre) or late (TetO-Cre) during PyMT-induced breast cancer development (Fig. 4A).

The MMTV-Cre transgene expresses CRE in the mammary epithelia concurrently with oncogenic MMTV-PyMT expression. We confirmed CRE expression from MMTV-Cre in the breast epithelium using ROSA26-LSL-tdTomato mice (39). In 8-week-old mice, tdTomato was present in most, but not all, cells in the mammary ductal epithelia, consistent with known mosaicism of the MMTV promoter, but not in surrounding stromal cells (not shown) (29). For late deletion of SNAIL1, we treated SNAIL1fl/fl; MMTV-PyMT; TRE-Cre; MTA with doxycycline when the size of primary tumors had reached 0.5 cm in diameter and SNAIL1-CBR bioluminescence not detected (Fig. 4B). Upon detection of palpable primary tumors increases metastasis (Supplementary Fig. S5C). This result indicated that the few lung metastases present in early KO mice likely arose due to incomplete deletion of the floxed SNAIL1 gene in primary tumor cells.

In summary, both early and late SNAIL1 deletion in the MMTV-PyMT metastatic breast cancer model indicated that SNAIL1 was required for breast cancer metastasis.

<table>
<thead>
<tr>
<th>Tumor site</th>
<th>Total number of tumors, DTCs, and lung metastases examined from four animals</th>
<th>Number of SNAIL1-positive tumors, DTCs, and lung metastases</th>
<th>Percent SNAIL1 positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary tumors</td>
<td>25</td>
<td>13</td>
<td>52</td>
</tr>
<tr>
<td>BM DTCs</td>
<td>150</td>
<td>6</td>
<td>4</td>
</tr>
<tr>
<td>Lung metastases</td>
<td>150</td>
<td>7</td>
<td>4.7</td>
</tr>
</tbody>
</table>

NOTE: Three 10-μm sections each of primary tumors and lungs with metastases and BM DTC spreads from four animals were subjected to IHC for SNAIL1 (primary tumors and lungs) or coimmunofluorescence for Her2Neu and SNAIL1 (BM DTCs) and the SNAIL1-positive percentage in each tissue type determined. Related to Fig. 3E and F.
lung metastasis was reduced 3-fold (8.7% vs. 25% in controls; Fig. 5B). When SNAIL1 was transiently overexpressed, the number of BM DTCs also increased but now was 15-fold higher than in controls (Fig. 5C; 5-fold higher than in Continuous SNAIL1). More than 60% of Transient SNAIL1 mice developed lung metastasis compared with only 25% of controls and 8.7% of Continuous SNAIL1 mice (Fig. 5B).

The number of primary tumors expressing SNAIL1 and exhibiting a mesenchymal phenotype (i.e., low E-cadherin and high vimentin), at the time of analysis, in Transient SNAIL1 mice was comparable with controls and 4-fold lower than that in Continuous SNAIL1 mice (Fig. 5B).

The number of primary tumors expressing SNAIL1 and exhibiting a mesenchymal phenotype (i.e., low E-cadherin and high vimentin), at the time of analysis, in Transient SNAIL1 mice was comparable with controls and 4-fold lower than that in Continuous SNAIL1 mice (Fig. 5B). SNAIL1 and in contrast to primary tumors in Continuous SNAIL1 mice, most lung metastases in mice of all groups exhibited an epithelial-like phenotype (i.e., low SNAIL1, high E-cadherin, and low vimentin; Table 2; and Supplementary Fig. S6).

Taken together, these results indicated that SNAIL1 was necessary and sufficient to induce DTCs and overt lung metastases. Transient SNAIL1 overexpression increased both the number of BM DTCs and the incidence of lung metastasis, whereas continuous SNAIL1 overexpression decreased the incidence of lung metastasis. This suggested the possibility that SNAIL1 expression needs to be downregulated after tumor cells exit the primary tumor for overt lung metastases to form.
Discussion

Using a novel SNAIL1-CBR reporter mouse model and a previously characterized conditional SNAIL1 KO mouse (13) crossed to several genetic models of breast cancer, we have demonstrated that SNAIL1 plays a critical role in breast cancer metastasis in vivo. Specifically, SNAIL1 expression (i) is restricted to metastatic primary breast tumors, particularly at invasive fronts; (ii) immediately precedes detection of DTCs; and (iii) is required and sufficient for efficient breast cancer metastasis.

Multiple EMT factors are often present simultaneously in the same tumors (4, 12). Recent studies suggest a spatiotemporal hierarchy among these factors in developmental and cancer EMT with SNAIL1 considered one of the earliest master regulators of EMT initiation (4, 40). This was validated in the genetic models detailed herein. SNAIL1 expression was detected in primary tumors but only rarely in DTCs and lung metastases. The spatiotemporal expression of SNAIL1 appears to be important for effective metastasis as continuous SNAIL1 overexpression decreased while transient overexpression greatly increased the incidence of lung metastasis. This could be due to the growth inhibitory properties of SNAIL1 and EMT factors in general and is consistent with recent reports on inhibitory effects of prolonged SNAIL1 expression on the renewal capacity of tumor-initiating cells (41) and on spatiotemporal regulation of other EMT factors such as Twist1 and Prrx1 (1, 4, 9, 10, 12). We cannot exclude the possibility that some lung metastases, especially those exhibiting detectable SNAIL1 expression, could have developed from a SNAIL1-independent mechanism. However, the contribution of such a pathway to metastasis is likely to be insignificant as lung metastasis was severely impeded when SNAIL1 was deleted or overexpressed continuously.

Table 2. Spatiotemporal expression of SNAIL1 in MMTV-neuNT mice

<table>
<thead>
<tr>
<th>Duration of exogenous SNAIL1 expression in primary tumors</th>
<th>Tumor site</th>
<th>Number of tumors and lung metastases examined from five mice (#)</th>
<th>Number of SNAIL1-positive tumors and lung metastases</th>
<th>Percent SNAIL1 positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control (Endogenous SNAIL1)</td>
<td>Primary tumors</td>
<td>25</td>
<td>4</td>
<td>16</td>
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<tr>
<td></td>
<td>Lung metastases</td>
<td>50</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>Continuous SNAIL1 (#)</td>
<td>Primary tumors</td>
<td>15</td>
<td>12</td>
<td>80</td>
</tr>
<tr>
<td></td>
<td>Lung metastases</td>
<td>24</td>
<td>4</td>
<td>17</td>
</tr>
<tr>
<td>Transient SNAIL1</td>
<td>Primary tumors</td>
<td>25</td>
<td>5</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td>Lung metastases</td>
<td>50</td>
<td>1</td>
<td>2</td>
</tr>
</tbody>
</table>

NOTE: Three 10-μm sections each of primary tumors and lungs with metastases from five control, two continuous SNAIL1 (#: only 2 in 23 mice had lung metastasis), and five transient SNAIL1 mice were subjected to IHC for SNAIL1, E-cadherin, and vimentin and the SNAIL1-positive percentage in each tissue type determined. Related to Fig. 5 and Supplementary Fig. S6.
What maintains metastatic cells in EMT after SNAIL1 downregulation remains incompletely understood. Other EMT factors could cooperate with SNAIL1 to maintain EMT in DTCs until they reactivate growth to form overt metastases. In human breast cancer patients, expression of Twist1 in BM DTCs has been shown to correlate with subsequent development of overt metastases (4). In these metastatic breast cancer models, the EMT state appears to persist, at least partially, in DTCs as evidenced by absence of E-cadherin expression in these cells while only a few exhibited vimentin expression. Whether other EMT factors, such as Twist1, replace SNAIL1 in DTCs in these models remains to be determined.

Although we have not conclusively established that SNAIL1 downregulation in metastatic cells is mechanistically linked to subsequent MET, the current results suggest that primary site of function of SNAIL1 is at invasive fronts of primary tumors and not at metastatic sites and therefore therapeutic targeting of SNAIL1 is unlikely to exert significant effects on DTCs and may have clinical benefit in inhibiting cancer EMT initiation and invasion in the first place. However, a note of caution to such an approach is warranted given the possibility that low SNAIL1 expression in DTCs may be required, perhaps in cooperation with Twist1, to promote EMT and dormancy, and that inhibiting SNAIL1 in preexistent DTCs may inadvertently induce them to exit EMT to undergo MET, resulting in increased metastatic disease, as has been suggested by other recent studies with other EMT factors (9, 10).

Metastasis has been proposed to occur early in breast tumorigenesis. In several human breast cancer series, up to 19% of patients with DCIS had detectable CTCs. Yet, the risk of developing overt metastases was <1% among these patients (36, 37), suggesting that the vast majority of detected CTCs in these patients are highly inefficient at colonizing secondary organs and being reactivated to form metastases. In both NeuNT and PyMT-induced breast cancer mouse models, dissemination of cancer cells was also observed in the premalignant phase (33). Our results in MMTV-PyMT mice suggest that late dissemination contributes the greatest to overall metastasis and is highly dependent on SNAIL1. Although these results do not address whether early dissemination requires SNAIL1 function, early dissemination does not appear to be the main driver of metastasis, perhaps due to the need for early DTCs to acquire additional genetic and/or epigenetic changes and stimuli that promote efficient migration, colonization, and reactivation of growth. In fact, Husemann and colleagues demonstrated that early DTCs from premalignant lesions required further stimulation from growth factors and a supportive BM environment to form apparent metastases (33).

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

References


Authors’ Contributions

Conception and design: H.D. Tran, G.D. Longmore, D.D. Tran
Development of methodology: H.D. Tran, K. Zhang, G.D. Tran
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): H.D. Tran, K. Luitel, M. Kim, K. Zhang, G.D. Longmore, D.D. Tran
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): H.D. Tran, M. Kim, K. Zhang, G.D. Longmore, D.D. Tran
Writing, review, and/or revision of the manuscript: H.D. Tran, G.D. Longmore, D.D. Tran
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): H.D. Tran, M. Kim, K. Zhang, G.D. Longmore, D.D. Tran
Study supervision: H.D. Tran, G.D. Longmore, D.D. Tran

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