

2009). The deregulation of the expression of miRNAs has been shown to contribute to cancer development through various kinds of mechanisms, including deletions, amplifications, or mutations involving miRNA loci, epigenetic silencing, the dysregulation of transcription factors that target specific miRNAs, or the inhibition of processing (Kim et al. 2009).

The expression of microRNA-145 (miR-145), for example, is reported to be low in self-renewing human embryonic stem cells (hESCs) but highly upregulated during differentiation (Xu et al. 2009). Increased miR-145 expression inhibits hESC self-renewal, represses expression of pluripotency genes, and induces lineage-restricted differentiation. On the other hand, miR-145 is reported to be downregulated and to act as a tumor suppressor in various tumors (Chiyomaru et al. 2010). In the same chromosomal region of miR-145, miR-143 is found and reported to act as a tumor suppressor function in the lung metastasis of osteosarcoma (Osaki et al. 2011).

miRNA is also reported to regulate the differentiation of MSC. The role of miRNA in the osteogenic differentiation of MSCs has been indicated by several studies. MiR-125b, 206, and 26a acted as negative regulators of osteoblast differentiation of bone marrow-derived MSCs through negative regulation of ERBB2, Connexin 43, and SMAD1, respectively (reviewed in Guo et al. 2011). MiR-133 and -135 functionally inhibited the differentiation of osteoprogenitors by attenuating RUNX2 and SMAD5 pathways that synergistically contribute to bone formation. On the other hand, miR-196a, -210, and -2861 were shown to enhance osteogenic differentiation, possibly through its target genes *HOXC8*, *ACVR1b*, and *HDAC5*, respectively. Five miRNAs (miR-130b, -152, -28, -26b, and -193b) were found to be differentially expressed during chondrogenic differentiation of MSCs through microarray analysis, and four of them were confirmed by real-time polymerase chain reaction analysis. Furthermore, in the multipotent MSC line C2C12, miR-1, miR-206, and miR-133 exhibited opposing roles in modulating skeletal muscle proliferation and differentiation (reviewed in Guo et al. 2011). These miRNAs might regulate the phenotype of CSCs of sarcoma.

As for the regulation of the CSCs in sarcoma, several studies have emerged. High-throughput microRNA (miRNA) expression analysis revealed that the expression of miR-140 was associated with chemosensitivity in osteosarcoma tumor xenografts (Song et al. 2009). Tumor cells ectopically transfected with miR-140 were more resistant to MTX and 5-fluorouracil (5-FU). Overexpression of miR-140 inhibited cell proliferation in both osteosarcoma U-2 OS (wt-p53) and colon cancer HCT 116 (wt-p53) cell lines. Furthermore, the expression of endogenous miR-140 was significantly elevated in CD133⁺/CD44⁺ colon CSCs that exhibit a slow proliferation rate and strong chemoresistance. However, the effect of miR-140 on CSC of osteosarcoma has not been clarified.

Riggi et al. found that the EWS-FLI-1 fusion gene induces expression of stem cell genes *Oct-4*, *SOX2*, and *Nanog* in human pediatric MSCs (hpMSCs). hpMSCs expressing EWS-FLI-1 generate a cell subpopulation displaying ESFT CSC features *in vitro*. Their further analysis demonstrated that induction of the ESFT CSC phenotype is the result of the combined effect of EWS-FLI-1 on its target gene expression and repression of miR-145 promoter activity. Subsequently, EWS-FLI-1 and miR-145 proved to function in a mutually repressive feedback loop and identify their common target gene, *SOX2*, in addition to miR-145 itself, as key players in ESFT cell differentiation and tumorigenicity (Riggi et al. 2010).

Others. Li et al. demonstrated that diallyltrisulfide (DATS), a volatile organosulfur compound derived from garlic, could confer drug resistance of osteosarcoma by downregulation of P-glycoprotein. Their previous report had showed CD133⁺ SaOS2 cells over expressed MDR1 (P-gp) in comparison with CD133⁻ SaOS2 cells. The ratio of CD133⁺ cells in flow cytometric analysis showed no significant difference (around 5.0%) under 0, 0.001, 0.01, 0.1, and 1 ppc of MTX without DATS. However, the ratio decreased (5.4, 3.2, 2.7, 1.4, and 0.92%, respectively) with the same concentration range of MTX in combination with 10 μ M DATS (Li et al. 2009).

Niche. The concept of “niche” defined as a specialized microenvironment that can promote the emergence of tumor stem cells and provide all the required factors for their development has recently emerged in the literature. Whereas the role of the niche in maintaining stem cells has been shown in several systems, the sarcoma CSC niche has not been identified. However, if sarcoma CSCs arise from MSCs or NCSCs, it is presumable that they might reside within the proposed niche. Several studies suggest that MSCs reside in a perivascular niche in almost all adult tissues, where they are in close contact with blood vessels (Shi and Gronthos 2003, da Silva Meirelles et al. 2008). The location of MSCs within perivascular niches is proposed to support the migration of MSCs in response to injury or disease (Kuhn and Tuan 2010). Similarly, location within a perivascular niche may support the metastasis of sarcomas.

There are some implications that niche plays a certain role in sarcoma CSCs (Siclari and Qin 2010). First, the differences in behavior of sarcoma CSCs grown *in vitro* compared to *in vivo* have been observed. For example, whereas the CSCs are characterized by being quiescent *in vivo*, they are more proliferative than the non-CSCs *in vitro* (Gibbs et al. 2005, Iwasaki et al. 2009). Secondly, especially with relation to bone sarcomas, the bone tissue is a hypoxic environment (Heddeleston et al. 2010, Siclari and Qin 2010). Activation of the hypoxia signaling pathway activates many pathways important for stem cell and CSC maintenance, such as brain CSC, which includes HIF-1 α and HIF-2 α (Heddeleston et al. 2010). In osteosarcoma,

studies have revealed that the expression of hypoxia-relevant genes occurs mainly in necrotic areas, which suggests that there is an *in vivo* relationship between HIF-1 α and apoptosis (Ishenko et al. 2008). In the cases of chondrosarcoma, HIF-1 α protein might be a useful prognostic marker due to its important role in tumor angiogenesis and cellular proliferation (Kubo et al. 2008). In Ewing sarcoma, Aryee et al. found that the EWS-FLI1 protein was upregulated in a HIF-1 α -dependent manner and that HIF-1 α induced EWS-FLI1 accumulation in a time-dependent dynamic study (Aryee et al. 2010). Thirdly, there are some reports on morphological implications. David et al. presented "bone niche" in chondrosarcoma. Pathological findings of chondrosarcoma include infiltration of chondrosarcoma cells into the bone tissue (permeation) and chondrosarcoma development associated with bone resorption foci. They assume that chondrosarcoma growth is strongly linked to bone tissue (David et al. 2011). Indeed, permeation of bony trabeculae is considered an absolute sign of chondrosarcoma and is useful in differentiating Grade 1 chondrosarcoma (malignant) from enchondroma (benign).

These findings support the concept of a niche; however, there is no evidence identifying the role of a niche in sarcoma CSC biology, which had been anticipated.

Immunotherapy

Many clinical trials of CTL-based immunotherapy using peptide vaccination have demonstrated the potency of this new therapeutic modality for various cancers that are resistant to standard chemotherapy (Tsukahara et al. 2004). However, it remains unknown whether CTL-based immunotherapy can kill CSC. Kano et al. found that the SP cells showed the expression of the human leukocyte antigen (HLA) Class I molecules on the cell surface. The CTL clone Tc4C-6, induced by mixed lymphocyte tumor cell culture using autologous peripheral blood mononuclear cells and freshly isolated SP cells, showed specific cytotoxicity against the SP cells. Moreover, the cytotoxicity against SP cells was blocked by the anti-HLA Class I antibody W6/32. These results indicate that CTL-recognizing CSCs certainly exist in the tumor microenvironment and circulating peripheral blood and that SP cells can be killed by CTL. Therefore, CTL-based immunotherapy could be one of the options for targeting sarcoma CSCs.

Conclusions and Perspectives

A great deal of effort has been made in the research on not only the origin of sarcomas but also cancer stem cells of sarcomas. Considering the characteristics of sarcoma CSCs, such as their self-renewal, resistance to

systemic therapy, and high migratory ability, sarcoma CSCs seem to have a lot of similarities with normal tissue stem cells, such as MSCs and NCSCs. However, the relationship between tissue stem cells and cancer stem cells remains unclear. This might be because of the problems categorized below.

The first problem is on the ambiguity of the definitions of cancer stem cells and mesenchymal stem cells. These precise definitions remain to be developed. Clarke et al. reported in 2006 that the consensus definition of a cancer stem cell that was developed for the American Association for Cancer Research (AACR) Workshop was “a cell within a tumor that possesses the capacity to self-renew and to cause the heterogeneous lineages of cancer cells that comprise the tumor.” In addition, cancer stem cells could “only be defined experimentally by their ability to recapitulate the generation of a continuously growing tumor” (Clarke et al. 2006). On the other hand, MSC is also defined only by its pluripotent “ability” as described above. The next step would be the identification of the common and different features between the cells that meet the “concept” of these cells. In agreement with the theory that tumorigenesis could be seen as aberrant organogenesis (Reya et al. 2001), mutated MSCs have all that they need to source and maintain sarcoma (Honoki 2010) as recently exemplified by the effects of HMGA2 alteration in mesenchymal stem-like cells (Henriksen et al. 2010). However, it is of interest that mutated MSC or NCSC possesses malignant phenotypes, such as chemoresistance and metastasis.

The second problem is that any reliable markers for the sarcoma CSC have not been specified. Although sarcoma stem cells have been isolated and identified by various methods, no one has been able to completely eliminate non-CSCs. The final achievement in detecting CSC markers would be identifying the makers specific to sarcoma CSCs; however, only one or two markers seem too simple to represent sarcoma CSCs, which possess the multiple phenotype described above. Thus, further markers adding to current ones should be discussed to purify sarcoma CSCs more exclusively. The ideal goal would be to apply these CSC markers to practical pathological use to help make decisions regarding treatment strategies, including the current molecular therapeutics of CSCs.

For the achievement of this purpose, more evidence on clinical biology is also needed. The essence of identifying CSCs in sarcoma lies in their clinical implications. Therefore, the third problem is that there is no evidence of the correlation between sarcoma CSCs and clinical behaviors. A major goal in order to discover the best therapies against tumor progression and to address the question of CSC hypothesis would require analyzing patient samples at different stages of disease and, in particular, a follow-up of CSC numbers during and after treatment. Little evidence is available that deals exclusively with sarcoma biopsy specimens; moreover, there is still no

study in which the specimens of post-chemotherapy and metastasis have been analyzed. This is an important aspect remaining to be addressed to confirm the clinical significance of this research.

Despite the inconsistency in the definition and the CSC markers, new approaches have to be developed to overcome the most lethal characteristics, such as chemoresistance and metastasis. The final problem deals with targeting and killing these cells. Several suggestions and trials demonstrated in this chapter are summarized below.

1) Inhibition of the self-renewal pathway: The major focus has been on developmental signaling pathways, including Hedgehog, Notch, and Wnt, and novel agents inhibiting these pathways that have been used to target CSCs in multiple diseases. Clinical trials using inhibitors of the Hedgehog pathway (GDC-0449, PF-04449913, BMS-833923, IPI-926, and TAK-441), Notch pathway (RO4929097, BMS-906024, and MK0752), Wnt pathway (PRI-724 and telomerase [GRN163L]) have begun to emerge, but their efficacy against CSC function remains to be determined (Rasheed et al. 2011). Since little has been tried on sarcomas, novel trials against sarcomas would be expected. 2) Inhibition of the other molecular pathways: Although not reached to clinical trials, MEK inhibitor has been proposed for osteosarcoma CSC treatment. The evidences on the activation of MAPK pathways have emerged also in the other cancers. Then, multiple pathways including self-renewal or the other molecular pathways might be associated with the CSC phenotypes. Therefore, the most influential pathways should be discussed in each type of sarcomas. However, we have no idea how many pathways are enough to be inhibited for regulation of CSC phenotypes. Further analysis above single molecular pathways would be required. 3) Antibody drugs: Targeting antibodies specific to CSCs would be the ideal approach for the elimination of CSCs. However, a commonly used marker in CSC studies, CD133 (also known as prominin) for example, has been implied as a normal stem cell marker. Thus, targeting CD133 has the potential for significant side effects. This makes it difficult to target on the reported markers of CSCs, so that the novel markers that specify only cancer cells would be required. 4) microRNA: The use of a natural miRNA to suppress the CSC phenotypes is also a promising possibility as a new therapeutic strategy for the treatment of CSCs. miRNA also possesses the potential for use as a biomarker. The development of biomarker strategies that quantify CSCs in a serial fashion may provide novel endpoints to monitor CSC-based clinical trials. 5) Immunotherapy: The CTL-based immunotherapy targeting on SP cells has been recently proposed. Further analysis including in vivo assay or the strategy targeting on the other CSC markers would raise expectations for sarcoma treatments. 6) Others: The other alternatives include oncolytic viruses that seem to be well suited to eliminate CSCs because the viruses are

cytotoxic and not subject to the drug efflux, such as ABC transporters and defective apoptotic signaling (Cripe et al. 2009). Virotherapy could also be used to sensitize tumor cells to radiation and as tools for immunotherapy (Thorne et al. 2010). Furthermore, the stem cell niche should be analyzed and targeted because of the implications of their essential role in deciding the stem cell fate and resistance to therapeutic drugs.

CSC studies on sarcoma are in their infancy compared to studies of carcinomas and hematopoietic malignancy. In this regard, we hope for the increasing preclinical and clinical trials of targeting on sarcoma CSCs. Researchers would have to continue their efforts to provide better prognosis for many sarcoma patients all over the world.

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Competitive Interactions of Cancer Cells and Normal Cells via Secretory MicroRNAs^{*[5]}

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Background: Homeostatic cell competitive system between cancerous cells and non-cancerous cells is considered as the reason for tumor initiation.

Results: Exosomal tumor-suppressive microRNAs secreted by non-cancerous cells inhibit the proliferation of cancerous cells.

Conclusion: Exosomal tumor-suppressive microRNAs act as an inhibitory signal for cancer cells in a cell-competitive process.

Significance: This provides a novel insight into a tumor initiation mechanism.

Normal epithelial cells regulate the secretion of autocrine and paracrine factors that prevent aberrant growth of neighboring cells, leading to healthy development and normal metabolism. One reason for tumor initiation is considered to be a failure of this homeostatic cell competitive system. Here we identify tumor-suppressive microRNAs (miRNAs) secreted by normal cells as anti-proliferative signal entities. Culture supernatant of normal epithelial prostate PNT-2 cells attenuated proliferation of PC-3M-luc cells, prostate cancer cells. Global analysis of miRNA expression signature revealed that a variety of tumor-suppressive miRNAs are released from PNT-2 cells. Of these miRNAs, secretory miR-143 could induce growth inhibition exclusively in cancer cells *in vitro* and *in vivo*. These results suggest that secretory tumor-suppressive miRNAs can act as a death signal in a cell competitive process. This study provides a novel insight into a tumor initiation mechanism.

Competitive interactions among cells are the basis of many homeostatic processes in biology. In *Drosophila*, normal epithelial cells compete with transformed ones for individual survival, which is a process called cell competition (1, 2). If a given group of cells was exposed to some stress, it would be separated into subpopulations of cells with different levels of damage. In noncompetitive conditions, cells with severe damage die in a

short time, whereas moderately damaged cells survive to the next generation, indicative of the transduction of a negative phenotype. On the other hand, in competitive conditions even slightly damaged cells are eliminated from the cell group because healthy cells, the “winners,” convey death signals to damaged cells, the “losers,” and the losers reciprocally confer growth signals to the winners. This feed-forward regulation enables the cell population to eradicate abnormal cells and maintain the same number of normal cells in a limited niche.

Oncogenesis is characterized by genetic and metabolic changes reprogramming living cells to undergo uncontrolled proliferation (3). This suggests that the abnormal cells that are originally destined for elimination can survive and expand against the cell competitive regulation, leading to the formation of a tumor mass. Consistently with this concept, Bondar and Medzhitov (4) showed that the cell competition process involves p53, a tumor-suppressive gene, between the hematopoietic stem cells and progenitor cells, suggesting that gene modifications of p53 could disturb the homeostatic mechanism and give rise to tumor initiation. It is conceivable that p53 target genes could be associated with intercellular communication between winners and losers; however, this literature has not answered the question of whether this regulatory system is mediated by contact-dependent or contact-independent manner. More than 10 years ago a pioneer study suggested that non-cancerous cells co-cultured with cancer cells inhibit the growth of cancer cells *in vitro* (5). This result indicated that humoral factors could be involved in cell competition as intercellular communicators (6).

As recently as a few years ago it was believed that RNAs could not behave as extracellular signal molecules because of their vulnerability to the attack of ribonucleases largely existing in body fluid. Evidence is presently increasing to show that miRNAs⁴ contained in exosomes are released from mammalian

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⁴ The abbreviations used are: miRNA, microRNA; CM, conditioned medium; luc, luciferase; MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; QRT-PCR, quantitative real time PCR.

Secretory miR-143 as an Anti-cancer Signal

cells and act as a signal transducer (7). It is important that many different tumor-suppressive miRNAs, such as miR-16 and miR-143, are down-regulated in cancer cells, resulting in tumorigenesis, tumor progression, and metastasis (8–11). Taken together, these findings suggest that secretory miRNAs may have favorable aspects for anti-proliferative signals mediating cell competition.

In this report we show that miR-143 expression in normal prostate cells, PNT-2 cells, is higher than that in prostate cancer cells, PC-3M-luc cells, and that miR-143 released from non-cancerous cells transfers growth-inhibitory signals to cancerous cells *in vitro* and *in vivo*. These results suggest that secretory tumor-suppressive miRNAs might be a death signal from winners to losers in the context of cell competition. Secretory miRNAs can be conducive to the maintenance of normal growth and development.

EXPERIMENTAL PROCEDURES

Reagents—Mouse monoclonal anti-KRAS (F234) (sc-30) was purchased from Santa Cruz. Rabbit polyclonal anti-ERK5 (#3372) was purchased from Cell Signaling. Mouse monoclonal anti-actin, clone C4 (MAB1501), was obtained from Millipore. Mouse monoclonal anti-human-CD63 antibody (556019) was purchased from BD Pharmingen. Peroxidase-labeled anti-mouse and anti-rabbit antibodies were included in the Amersham Biosciences ECL PLUS Western blotting Reagents Pack (RPN2124) (GE Healthcare). Synthetic *Caenorhabditis elegans* miRNA cel-miR-39 was synthesized by Qiagen (Valencia, CA). Synthetic hsa-miR-143 (pre-miR-143), the negative control 1 (NC1), has-miR-143 inhibitor molecule (anti-miR-143), and the negative control inhibitor molecule (anti-NC) were purchased from Ambion (Austin, TX). GW4869 was purchased from Calbiochem. Geneticin was purchased from Invitrogen.

Cell Culture—PNT-2 cells, immortalized normal adult prostatic epithelial cell line, were purchased from the DS Pharma Biomedical Co., Ltd. (Osaka, Japan). HEK293 cells, a human embryonic kidney cell line (CRL-1573), were obtained from American Type Culture Collection (Manassas, VA). HEK293 cells were cultured in Dulbecco's modified Eagle's medium containing 10% heat-inactivated fetal bovine serum (FBS) and an antibiotic-antimycotic (Invitrogen) at 37 °C in 5% CO₂. PNT-2 and the prostate cancer cell line, PC-3M-luc cells, continuously expressing firefly luciferase (Xenogen, Alameda, CA), were cultured in RPMI containing 10% heat-inactivated FBS and an antibiotic-antimycotic at 37 °C in 5% CO₂.

Preparation of Conditioned Medium and Exosomes—Before the collection of culture medium, cells were washed 3 times with Advanced RPMI containing an antibiotic-antimycotic and 2 mM L-glutamine (medium A), and the medium was switched to fresh medium A. After incubation for 3 days, medium A was collected and centrifuged at 2000 × *g* for 10 min at room temperature. To thoroughly remove cellular debris, the supernatant was centrifuged again at 12,000 × *g* for 30 min at room temperature or filtered through a 0.22-μm filter (Millipore). The conditioned medium (CM) was then used for miRNA extraction and functional assays as well as exosome isolation.

For exosome preparation the CM was ultracentrifuged at 110,000 × *g* for 70 min at 4 °C. The pellets were washed with 11

ml of PBS, and after ultracentrifugation they were resuspended in PBS. The exosome fraction was measured for its protein content using the Micro BCA Protein Assay kit (Thermo Scientific, Wilmington, DE).

Isolation of MicroRNAs—Isolation of extracellular and cellular miRNAs was performed using the miRNeasy Mini Kit (Qiagen). Two hundred microliters of conditioned medium or cell lysate was diluted with 1 ml of Qiazol Solution. After 5 min of incubation, 10 μl of 0.1 nM cel-miR-39 was added to each aliquot followed by vortexing for 30 s. Subsequent extraction and filter cartridge work were carried out according to the manufacturer's protocol.

Quantitative Real Time PCR (QRT-PCR)—The method for QRT-PCR has been previously described (7). PCR was carried out in 96-well plates using the 7300 Real Time PCR System (Applied Biosystems). All reactions were done in triplicate. All TaqMan MicroRNA Assays were purchased from Applied Biosystems. Cel-miR-39 and RNU6 were used as an invariant control for the CM and cells, respectively.

Immunoblot Analysis—SDS-PAGE gels, SuperSep Ace 5–20% (194–15021) (Wako), were calibrated with Precision Plus Protein Standards (161–0375) (Bio-Rad), and anti-KRAS (1:100), anti-ERK5 (1:1000), anti-CD63 (1:200), and anti-actin (1:1000) were used as primary antibodies. The dilution ratio of each antibody is indicated in parentheses. Two secondary antibodies (peroxidase-labeled anti-mouse and anti-rabbit antibodies) were used at a dilution of 1:10,000. Bound antibodies were visualized by chemiluminescence using the ECL PLUS Western blotting detection System (RPN2132) (GE Healthcare), and luminescent images were analyzed by a Luminomager (LAS-3000; Fuji Film, Inc.). Only gels for CD63 (BD Biosciences) detection were run under non-reducing conditions.

Plasmids—The primary-miR-143 expression vector was purchased from TaKaRa BIO. For luciferase-based reporter gene assays, pLucNeo was constructed by inserting a firefly luciferase gene derived from the pGL3-control (Promega) into the pEYFP-1 vector (Clontech) at BglII and AflIII sites. The sensor vector for miR-143 was constructed by introducing tandem binding sites with perfect complementarity to miR-143 separated by a four-nucleotide spacer into the NotI site of psiCHECK2 (Promega). The sequences of the binding site are as follows: 5'-AAACCTAGAGCGGCCGCGAGCTACAGTCTTCATCTCAAAGAATTCTTGAGCTACAGTGCTTCATCTCAGCGGCCGCTGGCCGCAA-3' (sense) and 5'-TTGCGGCCAGCGGCCGCTGAGATGAAGCACTGTAGCTCAAGAATTCTTTGAGATGAAGCACTGTAGCTCGCGCCGCTCTAGGTTT-3' (antisense). The "seed" sequence of miR-143 is indicated by bold italics. In a mutated miR-143 sensor vector, the seed sequence, TCATCTC, was displaced with GACGAGA. All the plasmids were verified by DNA sequencing.

Transient Transfection Assays—Transfections of 10 nM miR-143 mimic and 3 nM anti-miR-143 were accomplished with the DharmaFECT Transfection Reagent (Thermo Scientific) according to the manufacturer's protocol. The total amounts of miRNAs for each transfection were equally adjusted by the addition of NC1 and anti-NC, respectively.

Establishment of Stable Cell Lines—Stable HEK293 cell lines that express miR-143 were generated by selection with 300 $\mu\text{g}/\text{ml}$ Geneticin. HEK293 cells were transfected with 0.5 μg of the pri-miR-143 expression vector at 90% confluency in 24-well dishes using a Lipofectamine LTX reagent in accordance with the manufacturer's instructions. Twelve hours after the transfection, the cells were re-plated in a 10-cm dish followed by a 3-week selection with the antibiotic. Ten surviving single colonies were picked up from each transfectant and then cultured for another 2 weeks. The cells expressing the largest amount of miR-143 among transfectants were used as miR-143 stably expressing cells.

Luciferase Reporter Assay—HEK293 cells were cultured at a density of 1×10^4 cells/well in 96-well tissue culture plates overnight, and miRNA transfections or the addition of CM was performed. The cells were harvested, and renilla luciferase activity was measured and normalized by firefly luciferase activity (10). All assays were performed in triplicate and repeated at least three times, and the most representative results are shown.

Cell Growth Assay—PC-3M-luc cells were seeded at a density of 2×10^3 cells/well in a 96-well plate. The following day the cells were transfected with mature miRNAs or incubated with a CM. Twenty-four hours later the culture medium of the transfected cells was switched to medium A, whereas the conditioned medium was not changed. After a 3-day culture, cells were harvested for the measurement of firefly luciferase activity. To know the cellular proliferation by the tetrazolium-based colorimetric MTT assay, 20 μl CM of TetraColor ONE (SEIKAGAKU Corp., Tokyo, Japan) was added to each well after 72 h of culture. After 2–4 h of incubation at 37 °C, the optical density was measured at a wavelength of 450 nm using a microplate reader.

PKH67-labeled Exosome Transfer—Purified exosomes derived from PNT-2 CM were labeled with a PKH67 green fluorescent labeling kit (Sigma). Exosomes were incubated with 2 μM PKH67 for 5 min, washed 4 times using a 100-kDa filter (Microcon YM-100, Millipore) to remove excess dye, and incubated with PC-3M-luc cells at 37 °C.

Co-culture Experiment—In co-culture experiments, 2×10^5 cells/well of PNT-2 cells were plated in 6-well plates. To stain the PNT-2 cells with BODIPY-TR-ceramide (Invitrogen), 5 μM BODIPY-TR-ceramide in a non-serum culture medium was added and incubated with the cells at 37 °C. After 30 min the cells were rinsed several times with a non-serum culture medium and incubated in a fresh medium at 37 °C for an additional 30 min. After the staining of PNT-2 cells by BODIPY-TR-ceramide, labeling of PC-3M-luc cells with PKH67 was performed in accordance with the manufacturer's instructions. After that, labeled PC-3M-luc cells were added and co-cultured with PNT-2 cells for 12 h at 37 °C.

Microarray Analysis—To detect the miRNAs in exosomes and cells derived from PNT-2 and PC-3M-luc cells, 100 ng of total RNA was labeled and hybridized using a human microRNA microarray kit (Agilent Technologies) according to the manufacturer's protocol (Protocol for Use with Agilent MicroRNA Microarrays Version 1.5). Hybridization signals were detected using a DNA microarray scanner (Agilent Tech-

nologies), and the scanned images were analyzed using Agilent Feature Extraction software.

Evaluation of Tumor-suppressive miRNA Delivery to Subcutaneously Implanted Prostate Cancer Cell Line in Mice—Animal experiments in this study were performed in compliance with the guidelines of the Institute for Laboratory Animal Research, National Cancer Center Research Institute. Seven-week-old male Balb/c athymic nude mice (CLEA Japan, Shizuoka, Japan) were anesthetized by exposure to 3% isoflurane for injections and *in vivo* imaging. Four days ahead of the first CM injection, the anesthetized animals were subcutaneously injected with 5×10^5 PC-3M-luc cells suspended in 100 μl of sterile Dulbecco's phosphate-buffered saline into each dorsal region. Five hundred μl of CM derived from miR-143-overexpressing HEK293 cells and control cells were daily injected into each tumor from day 0 to 6. For *in vivo* imaging, the mice were administered D-luciferin (150 mg/kg, Promega) by intraperitoneal injection. Ten minutes later, photons from animal whole bodies were counted using the IVIS imaging system (Xenogen) according to the manufacturer's instructions. Data were analyzed using LIVINGIMAGE 2.50 software (Xenogen).

RESULTS

Suppression of Prostate Cancer Cell Proliferation by Conditioned Medium Isolated from Non-cancerous Prostatic Cell—Cell competition is a homeostatic mechanism for the accommodation of an appropriate number of cells in a limited niche or stroma (1). Based on this idea it is possible that the cell competition between normal and abnormal cells frequently occurs in a precancerous state. Of note is that non-cancerous cells suppress cancer cell development by contact-independent interaction (12). For instance, endothelial cells provide the major extracellular heparan sulfate proteoglycan as anti-proliferative signals (12); however, the molecular mechanism by which the other types of cells in a tumor environment associate with cancer cells is not fully understood.

To analyze the mechanism, we treated a hormone-insensitive prostatic carcinoma cell line, PC-3M-luc cells, with a CM from the non-cancerous prostate cell line PNT-2 cells. After a 3-day incubation, the PNT-2 CM inhibited the growth of the PC-3M-luc cells up to $\sim 10\%$ compared with the cell growth treated by fresh culture medium (Fig. 1A; compare lanes 1 and 3). In contrast, the growth of PC-3M-luc cells incubated in the CM of PC-3M-luc cells themselves showed no inhibitory effect (Fig. 1A; compare lanes 1 and 2). To determine that the performed treatments did not affect the luciferase activity, we also used the colorimetric MTT assay to measure the cell growth of PC-3M-luc cells. As shown in supplemental Fig. 1A, not only luciferase assay but also MTT assay show the inhibition of PC-3M-luc cell proliferation by the addition of PNT-2 cells derived CM, indicating that our treatment did not affect the luciferase activity. These results indicate that the non-cancerous cells may secrete some molecules that can suppress cancer cell proliferation.

In a recent report we showed that miRNAs contained in exosomes are secreted and that their secretion is tightly regulated by neutral sphingomyelinase 2, which is known to hydrolyze sphingomyelins to generate ceramides and trigger the budding