RNA Trafficking by Acute Myelogenous Leukemia Exosomes

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Abstract
Extrinsic signaling cues in the microenvironment of acute myelogenous leukemia (AML) contribute to disease progression and therapy resistance. Yet, it remains unknown how the bone marrow niche in which AML arises is subverted to support leukemic persistence at the expense of homeostatic function. Exosomes are cell membrane–derived vesicles carrying protein and RNA cargoes that have emerged as mediators of cell–cell communication. In this study, we examined the role of exosomes in developing the AML niche of the bone marrow microenvironment, investigating their biogenesis with a focus on RNA trafficking. We found that both primary AML and AML cell lines released exosome-sized vesicles that entered bystander cells. These exosomes were enriched for several coding and noncoding RNAs relevant to AML pathogenesis. Furthermore, their uptake by bone marrow stromal cells altered their secretion of growth factors. Proof-of-concept studies provided additional evidence for the canonical functions of the transferred RNA. Taken together, our findings revealed that AML exosome trafficking alters the proliferative, angiogenic, and migratory responses of cocultured stromal and hematopoietic progenitor cell lines, helping explain how the microenvironmental niche becomes reprogrammed during invasion of the bone marrow by AML. Cancer Res 73(2); 918–29. ©2012 AACR.

Introduction
Although the majority of patients with acute myelogenous leukemia (AML) achieve remission, nearly half will die from disease relapse. The contribution of microenvironmental cues to the survival, spread, and relapse of AML in the marrow are increasingly recognized as crucial in the process of leukemic evolution (1, 2). The bone marrow is structurally and functionally specialized to sustain lifelong hematopoietic and immune function; its infiltration by leukemia is associated with the acquisition of unique properties that make the bone marrow a sanctuary for persistent disease (3, 4). Even as differences emerge that distinguish the leukemic microenvironment from the homeostatic hematopoietic stem cell (HSC) niche, the mechanisms whereby malignant cells reprogram the niche remain to be clarified (4–6). Instances of extrinsic resistance are illustrated in the treatment of high-risk AML associated with internal tandem duplication (ITD) mutations in FMS-like tyrosine kinase 3 (FLT3), in which specific inhibitors eliminate circulating blasts without eradicating leukemic cells in the bone marrow (7). Conversely, FLT3-ITDpos AML cells are sensitized to the tyrosine kinase inhibitor sorafenib by inhibition of chemokine receptor-4 (CXCR4)-SDF-1α niche signaling with bone marrow stromal cells (2). Although integrin-α5, chemokine- and cytokine-mediated adhesive and paracrine interactions all contribute to drug resistance, none of these fully address how marrow invasion by leukemia cells results in niche remodeling (6).

Conventional intercellular signaling relies on direct cell–cell contact or the action of secreted molecules, but more recent studies indicate an additional, evolutionarily conserved mechanism whereby cells communicate via the exchange of extracellular vesicles carrying protein and RNA cargo (8, 9). As a unique consequence of cell–cell vesicle trafficking, the cytoplasmic delivery of mRNA, miRNA, or protein can circumvent transcriptional controls. Vesicle trafficking of receptors between cells, for example, may transcend niche signaling that is based on conventional restrictions of cell-specific ligand or receptor expression and modulate growth factor signaling cascades. Vesicles ranging in size from 30 to 100 nm (exosomes) to 100 to 1,000 nm (broadly termed microvesicles) have been detected in the urine and plasma of patients with diverse malignancies (10). However, detailed studies of vesicle biology in AML have not been reported (11, 12).

The results presented here show the release of exosome-sized vesicles by AML cells and illustrate how vesicle trafficking alters gene expression, protein secretion, and behavior of...
bystander cells. We show that vesicles contain diverse RNA species, including mRNAs and miRNAs relevant to AML biology and with broad biomarker potential. In aggregate, our work indicates that trafficking of AML exosomes elicits broad functional changes in bystander cells.

Materials and Methods

Cell lines and cell culture
AML cell lines (HEL, HL-60, Molm-14, and U937) were provided by Dr. Jeffrey (Oregon Health & Science University) Tyner and cultured in RPMI (Invitrogen) with 10% vesicle-free FBS. Vesicle-free FBS was produced by centrifugation of FBS (Gemini Bio-Products) at 100,000 × g for 2.5 hours. Patient samples (with >90% leukemic blasts) were obtained under Oregon Health & Science University-Institutional Review Board (OHSU-IRB; Portland, OR)—approved protocol from treatment-naïve patients. Primary cells were cultured in EGM-2 media (Lonza) OP9 cells, from Dr. William H. Fleming (Oregon Health & Science University), were cultured in α-minimum essential media (Invitrogen) with 20% FBS and 60 μmol/L 2-mercaptoethanol. Igf-1r knockout (R-/-) mouse embryonic fibroblasts and R-/- cells expressing human insulin-like growth factor (IGF)-IR cDNA (termed R’-/-), provided by Drs. Briony Forbes and Douglas Tee, respectively, were cultured in Dulbecco’s Modified Eagle’s Medium (Invitrogen) with 10% FBS (13). Cryopreserved human CD34+–enriched bone marrow cells (Stem Cell Technologies) were cultured in serum-free expansion media with the StemSpan CC110 cytokine cocktail for 5 to 7 days. All cultures contained 50 μg/mL Pen/Strep (Invitrogen). Cell lines were obtained from reliable sources without additional authentication beyond what is shown in the content of the experiments described.

Vesicle preparation and staining
Vesicles were isolated from cell lines and primary AML cells after 48 to 72 hours culture via centrifugation at 300 × g for 10 minutes. The supernatant was sequentially centrifuged at 2,000 × g for 20 minutes, at 10,000 × g for 20 minutes, and at 100,000 × g for 2 hours. The resulting pellet was washed with PBS and then centrifuged at 100,000 × g for 2 hours. For sucrose gradient density purification, the pellet from the first 100,000 × g spin was resuspended in 200 μL PBS by shaking for 4 hours at 4°C. The suspension was transferred to a sucrose step gradient (8%/15%/30%/45%/60%) and centrifuged at 150,000 × g for 90 minutes. The 30%/45% interface was harvested, diluted 10-fold with PBS, and the ultracentrifugation was repeated. The pellet was resuspended in 200 μL of PBS (methods adapted from ref. 8). For PKH26 (Sigma) staining, exosomes were isolated with the following changes: following the first 100,000 × g centrifugation, the pellet was resuspended in 1 mL PKH26 membrane dye-diluent C (Sigma) by shaking for 30 minutes at 4°C, along with a control aliquot containing diluent only.

Vesicle transfer assays
Transwell experiments were carried out in 6-well plates using 0.4-μm pore size inserts (Corning). Target cells were seeded at 2 × 10⁶ cells per well. A total of 1 to 2 × 10⁶ cells were added into the transwell insert and cocultured for 48 hours. Media collected from vesicle preparations after the 10,000 × g spin was termed vesicle-rich media (VRM). Two milliliters VRM were cocultured with 2 × 10⁶ target cells per well in 6-well plate. Target cells were incubated with the vesicle pellets resuspended in RPMI or PBS for 48 hours in 2 mL of media, then washed twice. For real-time PCR (RT-PCR), RNA was extracted using either the RNeasy (Qiagen) or miRNeasy kit (Qiagen). Transwell cocultures with CD34+ cells were not conducted because of culture media incompatibility and the limited availability of cells.

Fluorescence microscopy
Cells were exposed to 25 μL of PKH26-stained, sucrose-purified exosomes or PKH26-stained diluent C for 2 hours, followed by wash and fixation in 4% paraformaldehyde (Sigma) before treatment with Fluoromount G (Southern Biotech). Fluorescence microscopy was conducted with an Olympus IX71 microscope and DeltaVision SoftWoRx, using a ×60 1.4NA oil lens. Z-stacks were acquired every 0.2 μm for the complete depth of the cells. A reference bright-field image was captured from the center of each Z-stack. Particle quantification was conducted using ImarisCell (Bitplane, Inc.). For live-cell imaging, cells were plated on poly-L-lysine (Sigma)-coated chamber wells, treated with 5 μg/mL Hoechst 33342 and 2.5 μmol/L N-Rh-PE (Avanti Polar Lipids) for 1.5 hours followed by wash and resuspension in RPMI media with 9% horse serum (Invitrogen) and 9% FBS (Gemini Bioproducts). Images were acquired every 2.5 minutes for 2 hours, at 37°C and 5% CO₂. For colocalization studies, cells were treated with 3 μmol/L N-Rh-PE for 1 hour, fixed for 15 minutes, permeabilized with NET (NaCl + EDTA + Tris) buffer, cytospin and blocked with 2% FBS for 30 minutes at 4°C. Fixation precluded N-Rh-PE polarization seen during live cell imaging. Permeabilized cells were stained with anti-human CD63 hybridoma supernatant and anti-human Tsg101 antibodies (Abcam). AlexaFluor488 anti-mouse immunoglobulin G (IgG) and AlexaFluor647 anti-rabbit IgG (Invitrogen) were used as the secondary antibodies. Cells were stained with 4,6-diamidino-2-phenylindole (DAPI; Invitrogen).

Transmission electron microscopy
Exosome preparations (10 μL) were deposited onto UV-activated carbon formvar 400-mesh copper grids (Ted Pella 01822-F) for 3 minutes, rinsed and stained in filtered 1.33% uranyl acetate, and then air-dried. Samples were imaged at 100 kV on a Philips CM120 transmission electron microscope. The size distribution of exosomes was determined by averaging the maximum and minimum diameters of at least 100 vesicles imaged at ×37,000 magnification.

Dynamic light scatter
Light-scattering experiments were conducted in a DynaPro molecular sizing instrument (Protein Solutions). A sample in PBS buffer was loaded into a quartz cuvette and analyzed with a 488 nm laser. Fifty spectra were collected at 25°C to estimate diffusion coefficient and relative polydispersity. Data
were analyzed with Dynamics software V.5.25.44 (Protein Solutions) and vesicle size was measured as the mean hydrodynamic radius.

RNA analysis and qRT-PCR
RNA was extracted using miRNeasy (Qiagen) or RNeasy (Qiagen) kits and quantified using a Nanodrop 2000c (Thermo). RNA integrity was measured using the Agilent Bioanalyzer Pico Chip or small RNA Chip (Agilent). For RT-PCR, RNAs were converted into cDNA using the SuperScript III First Strand Synthesis Kit (Invitrogen) with oligo-dT priming followed by PCR. See Supplementary Table S1 for primer sequences. For quantitative PCR (qPCR), human IGF-IR primers/probe (forward primer: AACTTTCTCCCTCATCGGCCG; reverse primer: GTGTGTCCGCACGCTGTCT; probe: FAM-CGCTGATTCTCTGTTGGAGAG), mouse VEGF, mouse c-fox, human GAPDH, and mouse GAPDH (Applied Biosystems) were used. Relative quantification was calculated using ΔΔCT algorithm with glyceraldehyde-3-phosphate dehydrogenase (GAPDH) as the endogenous control. For miRNA quantitation, TaqMan Assay Kits (Applied Biosystems) were used for reverse transcription and qRT-PCR. For PCR array analysis, reverse transcription was conducted using the RT2 First Strand (Qia- gen) Kit. PCR arrays (SA Biosciences) were run according to manufacturer’s instructions.

Flow-cytometry analysis
For IGF-IR detection, target R- murine embryonic fibroblasts (MEF) were trypsinized after coculture, washed, and resuspended in staining buffer (1% bovine serum albumin in PBS, w/v). Cells were stained with mouse anti-human IGF-IR-PE antibody (BioLegend) or CXCR4-APC antibody (eBioscience) × 30 minutes at 4°C, washed twice, propidium iodide (PI) was added and cells analyzed with a FACSCalibur (BD Biosciences). Data were analyzed using FlowJo software (Tree Star).

Transwell migration and cell proliferation
Ba/F3 cells were cultured for 48 hours in the presence or absence of VRM by plating 5 × 10^5 cells in 2 mL Ba/F3 media with 4 mL of either vesicle-rich or base media. Ba/F3 cells were washed and plated on 8-μm transwell inserts in plates containing either media alone or SDF-1α gradient. After 2 hours, transwells were removed, migrated cells were washed and counted using a Guava PCA cytometer (Millipore). For proliferation assays, 5 × 10^5 R- MEFs were cocultured with 1 × 10^6 HL-60 cells in 0.4-μm transwells for 48 hours, after which R- MEFs were counted. IGF-IR inhibitor picropodophyllin (PPP; CalBiochem) was added at 100 nmol/L before coculture.

Western blotting
Protein lysates were generated using RIPA buffer with protease inhibitors (Thermo Scientific) and protein concentrations quantified by BCA Protein Assay (Pierce). Lysates were loaded on 4% to 15% SDS-PAGE gels (Bio-Rad) for transfer and Ponceau S stain. IGF-IR was detected using rabbit anti-human IGF-IRβ (Cell Signaling Technology) and anti-rabbit IgG-HRP (Thermo Scientific). Actin was detected using mouse anti-human pan-actin (Millipore) and anti-mouse IgG-HRP (Jackson ImmunoResearch Laboratories). Chemiluminescence was detected by the Supersignal West Pico Chemiluminescent substrate (Pierce).

Results

AML cells release exosomes
To systematically examine AML vesicle release, we used several AML cell lines and patient cells. Primary AML samples phenotyped by flow-cytometry showed more than 90% of cells expressing leukemia-associated antigens (data not shown). Vesicles were isolated from culture media using differential centrifugation and sucrose gradient purification (Fig. 1A and B). Transmission electron microscopy (TEM) revealed that both HL-60 and primary AML cells released vesicles primarily between 30 and 100 nm in diameter (Fig. 1C), the size range of exosomes (9). To exclude detection method- or purification-protocol bias, we conducted dynamic light scattering (DLS) measurements comparing HL-60 vesicle preparations purified by sucrose gradient versus differential centrifugation (capturing larger vesicles; Fig. 1D). Results mirrored the TEM size and distribution profile without significant method specific bias. To show direct exosome release from AML cells, we imaged primary AML cells labeled with N-Rh-PE, a marker dye routed from the endocytic compartment to the multivesicular body (MVB) and released within exosomes (14). Representative time-lapse images from stained primary AML blasts show the polarized aggregation of dye-labeled MVB’s at the plasma membrane before release of the exosome content, representative of 53% of cells in 3 primary AML samples (Fig. 1E; ref. 15). The canonical N-Rh-PE trafficking and vesicle budding provide further evidence that primary AML cells release exosomes. When we conducted immunofluorescent imaging for exosomal markers Tsg101 and CD63 (16, 17), the N-Rh-PE-stained compartment in primary AML cells colocalized with CD63 in more than 90%, with Tsg101 in 70%, and with both proteins in 29% of cells (Fig. 1F). Together, these experiments provide strong complementary evidence that AML cell lines and primary AML cells give rise to exosomes. Hereafter, we use the term "exosomes" specifically and "vesicles" generically.

Exosomes traffic mRNA between AML and stromal cells
Vesicles transfer protein and RNA between cells (18), leading us to investigate the trafficking of AML exosomes to bystander cells. To determine exosome entry, GFP-expressing murine OP9 bone marrow stromal cells were exposed to PKH26-stained exosomes from HL-60 cells (19). Fluorescence microscopy images revealed rapid and significant uptake of PKH26-stained exosomes as early as 15 minutes and increasing until 2 hours after initial exposure (Fig. 2A–F), at which time their number per cell reached a plateau (data not shown). To ascertain the transfer of specific RNA transcripts via AML exosomes, we cultured leukemia cells across a 0.4-μm transwell membrane from OP9 cells. After 48 hours of coculture, OP9 cells were harvested, RNA was
extracted and reverse-transcribed. RT-PCR with species-specific primers confirmed the presence of leukemia-derived (human) CXCR-4 transcripts in murine OP9 cells after coculture with HL-60 or primary AML cells (Fig. 2G). These experiments show that AML exosomes transfer leukemia-derived mRNA to murine bone marrow stromal cells.

AML exosomes contain RNA with broad regulatory potential

Given the diagnostic and prognostic relevance of molecular abnormalities in AML, we decided to focus on the analysis of exosomal RNA. We initially quantified total exosome RNA among 4 leukemia cell lines, 5 different primary AML samples, and primary CD34⁺ bone marrow cells. Total vesicle RNA content varied considerably among cell lines and primary AML cells after standardized culture for 48 hours (Fig. 3A). Comparing the spectrum of vesicle and cellular RNA using a bioanalyzer, we found a similar size distribution, with pronounced ribosomal and small RNA peaks (Fig. 3B). This pattern was observed in RNA obtained from cell lines and several AML samples (Fig. 3C). Because we were interested in transfer of mRNA with potential to alter the recipient cell phenotype, we used a PCR array to screen for a set of 59 transcription factors. Many transcripts seemed either decreased or enriched relative to cellular background (adjusted for GAPDH, β-2-microglobulin and HPRT1 controls; Fig. 3D). We selected a subset of 9 transcripts for further validation based on their involvement in hematopoiesis and/or leukemogenesis; that is, GATA1, FOXP3, SHIP1, ID1, E2F1, CEBP-α and -β, Myc, and MEF2C (20). Judged by RT-PCR, all were present in vesicle RNA from cell lines and most in primary samples, with some patient–patient variability (Fig. 3E). Our data on exosome RNA spectrum and abundance suggested strong potential for a role in AML biology.

Exosomes carry RNA transcripts with prognostic relevance in AML

Given evidence of transcript enrichment and the equilibrium of vesicles between tissue compartment and bloodstream shown by others, we evaluated exosomes for AML-relevant transcripts as potential biomarkers (21–23), specifically, nucleophosmin 1 (NPM1), FLT3, CXCR4, MMP9, and...
IGF-IR (21, 24, 25). RT-PCR analysis revealed the presence of all 5 candidate transcripts in exosomes from patient AML blasts, primary CD34\(^+\) bone marrow cells, and leukemia cell lines (Fig. 4A and B and Table 1). Indeed, exosome RNA reproduced the FLT3 allelic diversity (\textit{wt} vs. \textit{ITD} transcripts), including multiple unique ITDs present in the bulk cell population from which they were derived (Fig. 4A and B; ref. 26). Similarly, we were able to detect transcripts bearing mutations in exon 12 of NPM1 (confirmed by sequencing and capillary gel electrophoresis) in matched exosomal and cellular RNA (Fig. 4A). We next determined relative IGF-IR transcript levels in RNA from AML patient cells and vesicles.
Figure 3. AML exosomes contain unique RNA profiles. A, quantification of AML or control vesicle RNA. BM: CD34\(^+\) bone marrow progenitors. Data represent at least 3 individual experiments. B and C, bioanalyzer electropherograms of RNA from cells and vesicles of AML cell lines and primary samples. D, transcription factor array comparison of exosomal RNA from Molm-14 cells, expressed as fold change in vesicles versus cells. E, RT-PCR for select transcription factors in RNA from primary AML cells and vesicles from 4 patients. Data represent at least 3 individual experiments.
When normalized to GAPDH, IGF-IR mRNA levels differed substantially between primary AML samples (28). Yet, expression in both cellular and exosomal RNA was generally 2- to 5-fold higher in AML samples than in CD34⁺ progenitors (Fig. 4C). A direct comparison of IGF-IR mRNA levels confirmed exosome enrichment over matched cellular RNA, by up to 1,000-fold in 2 of the samples tested (Fig. 4D). This relative enrichment of IGF-IR mRNA (normalized to GAPDH) seemed to be specific for leukemia-derived vesicles, as primary CD34⁺ bone marrow vesicles exhibited IGF-IR mRNA levels proportional to those found in cells (Fig. 4D).

**Transfer of IGF-IR mRNA modulates cellular responses in Igf-Ir-deficient cells**

To show proof-of-principle for the specific functional consequences of AML exosome trafficking to bystander cells, we set up contact-independent cocultures of HL-60 or Molm-14 donor cells and (murine) OP9 target cells. Under all 3 experimental modalities (transwell coculture, vesicle-rich media exposure, and purified vesicle exposure), human-specific IGF-IR transcripts were detected in OP9 recipient cells (Fig. 5A). To determine if AML vesicle-derived IGF-IR contributes to target cell signaling after transfer, we cocultured leukemia cells across a transwell from Igf-Ir knockout mouse embryonic fibroblasts (R⁻ MEF; refs. 13, 29). In flow-cytometry analysis, R⁻ MEFs cocultured with HL-60, Molm-14, or U937 cells expressed human IGF-IR, although at a level less than that of R⁺ cells stably transfected with human IGF-IR cDNA (termed R⁺; Fig. 5B). Protein lysates from AML cells and vesicles revealed broad differences in banding profile, reflecting the disparity between vesicle and cellular protein content that includes conventional controls, such as actin and GAPDH, or tubulin (data not shown). Even when loading 3-fold the amount of vesicle than cell protein lysate (reflected in the Ponceau S stain), significantly less actin was detected in vesicles. IGF-IR protein, as well, was present only at very low levels in AML exosomes by Western blot analysis, although it was readily detected in both WT HL-60 cells and HL-60 overexpressing IGF-IR (Fig. 5C; Supplementary Fig. S1A and S1B; ref. 30). Allowing for small amounts of IGF-IR protein in vesicles, these results nonetheless suggest that transferred human IGF-IR mRNA may be successfully translated and
trafficked to the cell surface of R−/C0 MEFs after coculture with AML cells. This observation is corroborated at the functional level by measuring rates of IGF-I–stimulated proliferation in R−/C0 MEFs (13). In experiments using transwell cocultures of HL-60 with R−/C0 MEFs, we observed increased proliferation in cocultured R−/C0 MEFs compared with R−/C0 MEFs alone (Fig. 5D). This proliferative response was specifically abrogated in response to the IGF-IR–specific inhibitor PPP, which similarly decreased proliferation in R−/C0 MEFs, indicating that the altered proliferation kinetics resulted from the transfer of IGF-IR mRNA. In addition to its mitogenic activity, IGF-IR signaling has been shown to upregulate VEGF expression (31, 32). When we assessed the effect of coculture on VEGF expression in target cells, we found that R−/C0 MEF cells exhibited increased VEGF transcript levels by qRT-PCR following coculture with HL-60 cells (Fig. 5E). As another canonical IGF signaling response, we observed upregulation of the early response gene c-fos under these conditions, although this did not reach statistical significance (Fig. 5F; ref. 33). Our experiments show that exosomal transfer of IGF-IR can modulate proliferative signaling in bystander cells and promote expression of VEGF. Exosomal induction of transcripts promoting angiogenesis in bystander cells is further corroborated in the exposure of OP9 cells to Molm-14 coculture (Supplementary Fig. S2A–S2C) and Molm-14 vesicles (Supplementary Fig. S3A and S3B). We observed substantial changes in growth factor secretion into OP9 culture supernatant using commercial (murine) arrays. Despite apparent differences in secretion resulting from the presence of soluble factors under coculture conditions versus concentrated vesicle exposure, several relevant proteins whose secretion was upregulated after coculture (angiopeptin 1, endothelin 1, CXCL4, and FGF-2) were also elevated following treatment with purified vesicles. VEGF was consistently elevated after both treatments, whereas secreted osteopontin (OPN) and SDF-1 were decreased after vesicle treatment despite an increase following coculture. To validate these results (and discrepancies), we investigated several of these targets at the mRNA level with qRT-PCR, and found that while SDF-1 and VEGF mRNA tracked with secreted protein levels, OPN transcription had increased after vesicle exposure without changes in its secretion. These results illustrate that physiologic vesicle transfer occurs in the context of other secreted effectors, which act in concert to influence surrounding cells.

### miRNA enriched in AML exosomes regulates the biologic function of neighboring cells

Our initial bioanalyzer data suggested the enrichment of miRNA in exosomes (Fig. 3B and C; ref. 34). The RNA size range between 0 and 150 nts was therefore further evaluated using the small RNA bioanalyzer chip. Results confirmed abundant representation of small RNAs (defined as 0–150 nts) and miRNAs (40–80 nts; Fig. 6A). Remarkably, when comparing the calculated concentrations, we found 2-fold enrichment of small RNAs and 5- to 13-fold greater gains among miRNAs in vesicles versus parental cells across several cell lines.

### Table 1. Transcripts detected in AML exosomes

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<th>Sample ID</th>
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Abbreviations: LA, leukapheresis cells; ND, not done; NL, normal bone marrow cells; PB, peripheral blood cells; +, detected; –, not detected.
2- to near 40-fold enrichment compared with cells among this set of miRNA (Fig. 6C). When we conducted a qRT-PCR array study to profile 234 human miRNAs, our screen detected miRNAs in both Molm-14 cellular and exosomal RNA (Fig. 6D). Many miRNA were enriched in vesicles, indicated by data point skewing toward the y-axis, with approximately 83% of miRNAs detected in both cells and vesicles. Among miRNA represented by the array, 40 were excluded from exosomes, whereas 1 miRNA (miR-146a) was present at a detectable level only in exosomes.

One functional consequence of leukemic invasion of the niche is the displacement of hematopoietic stem and progenitor cells from the bone marrow microenvironment through altered migration and retention (4). The CXCR4/SDF-1α signaling axis plays a crucial role in this, and CXCR4 itself was recently shown to be a target of miR-150 (4, 35). We therefore examined the effect of Molm-14 exosomes (enriched in miRNA-150) on migration of Ba/F3 cells, a conditionally SDF-1α-responsive murine B-precursor cell line (36). Remarkably, Ba/F3 cells cultured for 48 hours in the presence of Molm-14-derived, vesicle-rich media and placed on 8-μm Transwell grids showed significantly decreased migration toward SDF-1α (Fig. 6E; ref. 2). Moreover, vesicle exposure specifically reduced the surface expression of CXCR4, the cognate SDF-1α receptor, by 50% as judged by median fluorescence intensity (Fig. 6F).

Taken together, our results reveal that AML vesicles alter transcriptional responses, protein secretion, and migration in bystander cells.

Discussion

A specialized AML stromal niche is thought to account, in part, for the evasion of cells from therapy-induced apoptosis and is implicated in relapse (1–3). Conceptually, niche conversion requires the successive displacement and suppression of hematopoietic function and establishment of conditions conducive to leukemic spread. The mechanisms underlying this process, however, remain to be clarified (1, 4). On the basis of the established potential for exosomes to mediate cell-to-cell communication (8, 18, 37), and increasing evidence of their relevance in cancer (17, 28, 38), we investigated a role for exosomes in modulating signaling between cells in the AML microenvironment.

Classes of cell membrane–derived vesicles produced by different cell types can be distinguished on the basis of size, density, and characteristic marker proteins (39). Our studies provide compelling evidence that AML cells produce primarily exosome-sized vesicles, capable of rapid entry and cargo transfer to bystander cells. Given the importance of molecular abnormalities in AML risk stratification, we decided to examine exosomal RNA content, and observed a broad spectrum, including small RNA. Profiling the RNA content of these vesicles revealed the presence of transcripts relevant to AML (Fig. 6B). We conducted qRT-PCR assays to quantify specific miRNAs in Molm-14 cells and vesicles, including Let-7a, miR-9, miR-99b, miR-150, miR-155, miR-191, and miR-223. Using the noncoding small nuclear U6 RNA for normalization, we observed significant incorporation in vesicles, ranging from
Reinforcing the regulatory potential of AML exosome RNA in target cells, we found several transcription factor transcripts important to hematopoiesis and a range of AML-relevant miRNA (20).

To show the functional significance of exosome trafficking, we focused on the consequences of transfer on IGF-IR signaling in stromal cells and CXCR4 signaling in progenitor cells. Not only is IGF-IR mRNA enriched in AML exosomes, but we found that its transfer led to the induction of downstream gene expression and changes in cell proliferation that were abrogated by specific inhibition of IGF-IR kinase function. miRNA-150 was previously reported to suppress erythropoiesis and...
target CXCR4 transcripts for degradation (33). Although both miR-150 and CXCR4 mRNA are present in AML exosomes, miR-150 is highly enriched therein, and exosome transfer to Ba/F3 progenitor cells was associated with a loss of CXCR4 surface expression and consequent decrease in cell migration toward SDF-1α. Several caveats remain: we did not titrate vesicle doses and it is possible that some of these effects will reveal exosome dose–response kinetics. At the same time, our data caution against the direct extrapolation of vesicle effects to biologic response, as both the cell coculture and VRM treatment provide further physiologic modulation via soluble factors, illustrated in Supplementary Figs. S2 and S3. This is to be expected, as the exosome transfer of a receptor, for example, would be expected to result in differential signaling events in the presence of media containing the cognate ligand. The diverse exosome cargo highlights the inherent challenge in assigning a specific functional outcome to the transfer of an individual exosomal protein or RNA transcript in the context of many others. The presence of prognostically relevant mRNA in AML-derived exosomes implies their potential development as a minimally invasive AML biomarker platform. Here, it will be important to see the extent to which specific AML exosome content will track with diagnostic parameters and change during the course of treatment.

Taken together, our results show that exosome trafficking by AML cells can alter the function of bystander cells. Our observations show the complexity of cell–cell communication and emphasize the potential impact of exosome trafficking on AML physiology. Coding and noncoding RNAs are key determinants of the cellular phenotype, and in vitro RNA transfer can produce experimental phenotype conversion (37, 41). The transfer of transcription factor and miRNA from AML to bystander cells presents a compelling paradigm for cell–cell communication in the leukemic niche.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Conception and design: J. Huan, C.T. Roberts Jr, P. Kurre
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Acknowledgments
The authors thank experimental contributions by Dr. Thomas Russell. The authors also thank Drs. Jeffrey Tyner (Oregon Health & Science University), Bruno Forbes (University of Adelaide), and Douglas Yee (University of Minnesota) for generous provision of cell lines.

Grant Support
This study was supported by the Friends of Doernbecher and Hyundai Hope on Wheels Foundations.

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Received May 31, 2012; revised October 12, 2012; accepted November 5, 2012; published OnlineFirst November 13, 2012.

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RNA Trafficking by Acute Myelogenous Leukemia Exosomes


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doi:10.1158/0008-5472.CAN-12-2184

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