Dynamic Interactions between Cancer Cells and the Embryonic Microenvironment Regulate Cell Invasion and Reveal EphB6 as a Metastasis Suppressor

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Abstract

Metastatic dissemination drives the high mortality associated with melanoma. However, difficulties in visualizing in vivo cell dynamics during metastatic invasion have limited our understanding of these cell behaviors. Recent evidence has revealed that melanoma cells exploit portions of their ancestral embryonic neural crest emigration program to facilitate invasion. What remains to be determined is how embryonic microenvironmental signals influence invasive melanoma cell behavior, and whether these signals are relevant to human disease. To address these questions, we interrogated the role of the neural crest microenvironment in dictating the spatiotemporal pattern of melanoma cell invasion in the chick embryo using 2-photon time-lapse microscopy. Results reveal that both permissive and inhibitory neural crest microenvironmental signals regulate the timing and direction of melanoma invasion to coincide with the neural crest migration pattern. These cues include bidirectional signaling mediated through the ephrin family of receptor tyrosine kinases. We demonstrate that EphB6 reexpression forces metastatic melanoma cells to deviate from the canonical migration pattern observed in the chick embryo transplant model. Furthermore, EphB6-expressing melanoma cells display significantly reduced metastatic potential in a chorioallantoic membrane (CAM) metastasis assay. These data on melanoma invasion in the embryonic neural crest and CAM microenvironments identify EphB6 as a metastasis suppressor in melanoma, likely acting at the stage of intravasation.

Implications: This article links cellular metastasis to behaviors observed in the ancestrally related embryonic neural crest and demonstrates the powerful influence of the embryonic microenvironment in regulating cell migratory behavior.

Introduction

The vast majority of all cancer-related deaths can be ascribed to metastasis. With tumor cell–microenvironment interactions at the forefront of metastatic disease progression, insufficient attention has been given to the role of the microenvironment in regulating cell migratory behaviors. This is primarily due to the inherent challenges associated with studying migratory behaviors throughout the metastatic cascade in vivo (1–3).

The embryonic neural crest offers a unique model system in which to study cell–microenvironment interactions in vivo. The neural crest is a highly invasive, multipotent cell population that displays a regulated spatiotemporal migratory pattern in the vertebrate embryo (4). Neural crest cells emigrate from the dorsal neural tube in a rostral-to-caudal manner all along the vertebrate axis, including from rhombomere segments (r1–r7) of the hindbrain. During emigration, the neural crest follows stereotypical migratory pathways that are thought to be sculpted by both intrinsic and extrinsic guidance cues found within the neural tube and surrounding microenvironment (5, 6). Importantly, several tumor types, including melanoma and neuroblastoma, originate from neural crest–derived cells. This has led to the hypothesis that neural crest–related malignancies may be intrinsically predisposed to increased metastatic potential due to the inherent invasive abilities of the neural crest (7–9).

Our laboratory has developed a model system using the chick embryo to help overcome the significant roadblocks to studying the cellular and molecular dynamics of melanoma metastasis in vivo (10). This model system takes advantage of the accessibility of the embryonic microenvironment to in vivo imaging and molecular intervention, allowing us to directly investigate how melanoma cells respond to microenvironmental signals. We and others have shown that
metastatic melanoma cells transplanted into the chick neural crest embryonic microenvironment migrate along stereotypic neural crest migratory pathways (7, 10–12). However, the mechanisms guiding their migration are not known. To address this, we recently performed a molecular analysis comparing transplanted melanoma cells and the neural crest, which revealed that metastatic melanoma cells revive portions of the embryonic neural crest emigration program (7). Thus, metastatic melanoma cells appear to hijack inherent neural crest–related developmental signaling pathways to enhance their metastatic potential. However, what remains unclear is how the embryonic microenvironment dictates melanoma cell migratory behavior. Specifically, what are the embryonic signals that guide melanoma migration, and can perturbation of those signals significantly alter migratory behavior? Here, we asked to what extent the chick embryonic neural crest microenvironment regulates the timing and migratory behavior of melanoma cells. We also asked to what extent we could alter the migratory phenotype by perturbing cell–microenvironment interactions. We compared the invasion patterns of melanoma cells transplanted into the chick hindbrain at various developmental stages and axial positions. Single melanoma cell dynamics were observed in vivo using 2-photon microscopy. To perturb cell–microenvironment interactions, we examined how changes in Eph expression in transplanted melanoma cells affected cell invasion patterns. Finally, to address the relevance of our studies to human disease, we assayed the tumorigenicity and metastatic potential of melanoma cells transplanted onto the highly vascularized chick chorionallantoic membrane (CAM). Our results highlight the importance of tumor cell–microenvironment interactions in promoting, inhibiting, and guiding tumor cell movements and elucidate the antitumorigenic properties of EphB6 in vivo.

Materials and Methods

Cell culture

Cells were kindly provided by Dr. Mary Hendrix, Children’s Memorial Research Center (Chicago, IL). Cells were maintained in RPMI supplemented with 10% FBS. For drop culture conditions, cells were resuspended in RPMI plus 10% FBS at a concentration of 4e6 cells per mL. A 20 μL drop was hung from the lid of a 35-mm culture dish and incubated for 40 hours under standard culture conditions.

EphB6 cloning, lentiviral infection, and Western blotting

The vector containing wild-type human EphB6 was kindly provided by Dr. Andrew Freywald, University of Saskatchewan (Saskatoon, SK, Canada). From this vector, EphB6 was PCR amplified and inserted into the Nhel and BamH1 sites of the lentiviral vector pCDH-CMV-MCS-EF1-RFP (System Biosciences) using the following PCR amplification primers: forward, 5′-AGTCGCTAGCATG-GTGTGAGCCCTATGGGTGC-3′; reverse, 5′-GACTG-GATCCTCAGACCTCCACTGAGCCCT-3′. Lentiviral particles were prepared using the ViraPower Lentiviral Packaging mix. Lipofectamine 2000, and the 293FT cell line according to the manufacturer’s directions (Invitrogen). Supernatant was collected at 48 and 72 hours posttransfection and was concentrated using PEG precipitation. Briefly, the supernatant was collected, spun at 3,000 rpm for 5 minutes, and then filtered using a 0.45-μm filter. For the precipitation, 3 mL of filter-sterilized 40% PEG-8000 in PBS and 180 μL FBS was added to each 9 mL of supernatant. The virus was allowed to precipitate for at least 72 hours before pelleting at 1,500 × g for 10 minutes. The supernatant was removed and the tube was spun down again at 1,500 × g for 1 minute to remove residual PEG solution. The viral pellet was resuspended in culture media by gently pipetting up and down, before being stored at −80°C before use. Supernatant was concentrated 1:500 to 1:1,000, resulting in viral titers as high as 108 titerable units (TU)/mL. For infection, C8161 cells were seeded into 24-well plates at 1 × 10⁵ cells per well and allowed to adhere overnight. The next day, the cells were infected at various multiplicity of infection (MOI) in culture media in the presence of 6 μg/mL polybrene (Sigma-Aldrich) overnight, before undergoing a media change. The cells were then expanded before transplant experiments. EphB6 protein expression was verified by Western blotting. Equal amounts of cellular protein were subjected to SDS-PAGE and Western blot analysis using an antibody specific for EphB6 (EphB6 monoclonal antibody M03, clone 5D8, Abnova H00002051-M03).

Chick embryo transplants

Fertile white leghorn chick eggs were acquired from Centurion Poultry. Eggs were incubated at 38°C for approximately 39 hours until the 9-somite stage of development. Eggs were windowed and embryos were visualized following the injection of a solution of 10% India ink in Howard Ringer’s solution below the blastodisc. Embryos were staged according to the criteria of Hamburger and Hamilton (Hamburger and Hamilton, 1951), denoted as stage 10 (HH10), for example. Transplantation of the embryos was performed as previously described (10). Briefly, C8161 hanging drop cultures were cut with a finely pulled glass needle to approximately 50 μm³ (corresponding roughly to 300 cells). Tumor cell transplants were grafted into the lumen of the chick embryo neural tube through a slit along the dorsal midline. Eggs were sealed with cellophane tape and incubated for 24 hours.

Static imaging

Individual embryos were removed from eggs with paper rings, rinsed with Ringer’s solution, and placed dorsal side up within a thin ring of high-vacuum grease (Dow Corning) on 22 × 75 mm² microslides. Embryos were imaged using a Zeiss 710 multi-photon upright microscope. 2-photon z-stacks of dual labeled C8161 Gap43-CFP::H12B-YFP were acquired at a wavelength of 850 nm. RFP-labeled EphB6+ C8161 cells were imaged with an excitation of 561 nm. Images using a W Plan-Apochromat 20×/1.0 DIC objective (Zeiss).
EphB6 Is a Metastasis Suppressor in Melanoma

Photoconversion

C8161 cells were dual labeled with H2B:mCherry and H2B:PSCFP2 (photo-switchable cyan fluorescent protein) by lentiviral infection. Cells were transplanted into the chick embryo neural tube as described above. A Teflon membrane window was installed in the egg as previously described (13). H2B:PSCFP2-labeled cells were photoconverted within 1 hour following transplantation. Photoconversion was performed on a Zeiss 710 multiphoton upright microscope using 2-photon excitation at 780 nm and a W Plan-Apochromat 20×/1.0 DIC objective (Zeiss).

Time-lapse imaging

The time-lapse imaging platform, including sample preparation, is detailed in a previously published protocol (13). Briefly, Teflon windows were placed over the developing chick embryo and sealed with beeswax. The egg was maintained in an environmental box placed around a Zeiss 710 multiphoton upright microscope stage and heated to 38°C. The chamber was humidified with a sponge placed in a dish of water. Nonevaporating immersion liquid (Immersol W, Carl Zeiss) was used to bridge the W Plan-Apochromat 20×/1.0 DIC objective (Zeiss) with the Teflon membrane. Simultaneous 2-photon excitation of the dual-labeled C8161 Gap43:CFP::H2B::YFP cells was achieved at a wavelength of 850 nm. Z-stacks with a 10-μm z-slice were acquired every 7 minutes for 18 hours.

CAM metastasis assay

Fertil white leghorn chick eggs were incubated for 7 hours, following which an artificial air sac was created in the egg by removing 4-mL albumin from the egg with an 18-gauge needle. The puncture hole was sealed with cellophane tape and the egg was further incubated for 7 days. At the time of transplantation, a small section (2 × 2 mm²) of the surface periderm of the CAM was removed with filter paper (Whatman) in a manner that did not compromise the integrity of the basal layer. Disruption of the periderm is required for tumor cells to gain access to the underlying mesoderm (14). Following periderm removal, eggs were allowed to recover for 2 hours before placing cells on the CAM. For transplantation, cells were suspended at a concentration of 1e5 cells/μL. A total of 1e6 cells (10 μL) was placed on the CAM. The egg was resealed with cellophane tape and incubated for 48 hours. Following this incubation, the egg was bisected along the longitudinal axis, and the CAM from the lower half of the egg was placed in a 15-mL conical tube and flash frozen in liquid nitrogen. The frozen tissue was then ground with a chilled mortar and pestle in the presence of liquid nitrogen. gDNA was extracted from the ground tissue using the Wizard Genomic DNA Puri- fication kit (Promega) according to the manufacturer’s protocol. Resulting DNA was quantified using a Nanodrop spectrophotometer.

Quantitative PCR

Human DNA was detected and quantified using Alu (YB8 subfamily) element-based PCR (15). Quantitative PCR (qPCR) was performed on an ABI7500 (Applied Biosystems Inc.) in optical 96-well reaction plates using the following 3-stage cycling protocol: 50°C for 2 minutes, 95°C for 10 minutes and 40 cycles of 95°C for 15 seconds and 68°C for 1 minute. The following Alu-specific primers and probe were used: forward, 5'-GTC-AGGAGATCGAGACCATCTCC-3'; reverse, 5'-AGT-GGCGCAATCTCGGC-3' and the following probe: 5'-6-FAM-AGCTACTCGGAGGCTGAGGCAGGATA-MRA-3' as previously reported (16). Each 50 μL qPCR reaction included 2 μg genomic DNA, 25 μL 2X Gene Expression Master Mix (Applied Biosystems Inc.), 25 pmol forward primer, 25 pmol reverse primer, and 12.5 pmol probe. Resulting cycle threshold values (Ct) were compared with a serial dilution of human gDNA from C8161 cells, from which quantitative DNA amounts were extrapolated.

Data analysis and statistics, image processing

Three-dimensional images acquired from 2-photon static and time-lapse imaging were analyzed with Imaris software (Bitplane Scientific Software). Analysis included spots detection cell tracking, tracks translation, displacement vector analysis, and movie creation and editing. For the cylindrical coordinate conversion, Cartesian coordinates from Imaris were converted to cylindrical coordinates using standard mathematical methods. Densitometric scatterplots were created in MatLab. Histograms and curve-fitting analyses were created and performed using OriginPro software. Curve fitting was based on a Gaussian peak function, where Xc is the center of the peak and W equals 2 times the SD of the Gaussian distribution (~0.849 the width of the peak at half height). Statistical analysis was performed using Microsoft Excel and the Data Analysis Tools pack. For migratory distance comparisons, a single-factor ANOVA was used to calculate the P value. For the CAM metastasis assay, a 2-sample equal variance t test with 2-tailed distribution was used. Statistically significant P values are <0.05. Figure processing was performed with Adobe Photoshop CS3.

Results

Melanoma cells transplanted into the chick embryonic neural crest microenvironment sense and respond to micro-environmental cues by following host cranial neural crest cell migratory pathways (7, 10). However, it remained unclear whether there was a temporal and/or spatial restriction to melanoma migration that corresponded to the developmental pattern of the host cranial neural crest.

To examine this question, we transplanted human C8161 melanoma cells into different rhombomere segments at peak and off-peak times of cranial neural crest cell migration (Fig. 1). Cranial neural crest cells begin to migrate from r1 at Hamburger and Hamilton stage 8 + (HH18 +) and migration typically ceases (from r7) by HH111 + (17). We observed maximal invasion of C8161 cells when transplanted into r4 at HH10. Under these conditions, C8161 cells invaded the permissive area adjacent to r4, travelling as a discrete multicellular stream while respecting inhibitory cues present in
and adjacent to r3 and r5 that are thought to help sculpt the neural crest migration pathway (Fig. 1B). To analyze migratory behaviors, positions of invasive cells from 9 different transplants were quantified using a cylindrical coordinate system (Fig. 1A and B). The embryonic dorsal midline and the r4–r5 rhombomere boundary were used as fiducial landmarks (Fig. 1A and B). The cell invasion pattern revealed a tight cluster of endpoint cell positions located along the r4 stream approximately 25 μm rostral to the r4–r5 boundary, demonstrating reproducible, guided directional migration (Fig. 1B). Following 24 hours, the average migratory distance was 200 μm, with some cells migrating nearly 600 μm (Fig. 1C).

Importantly, guided directional migration was observed for other embryonic and neural crest–related cell types, including neuroblastoma, but not for the invasive breast cancer cell line MDA-MB-231 (Supplementary Fig. S1). This suggests that embryonic neural crest signals are nonpermissive to cells lacking the appropriate signaling mechanism.

Cranial neural crest streams are sculpted by both permissive and inhibitory signals present within the microenvironment, with inhibitory neural crest cell–free zones located adjacent to neural crest migratory streams (5, 18). As such, we investigated the extent to which inhibitory cues associated with r3 and r5 also regulate melanoma cell migration. For this, we transplanted C8161 cells into r3 and r5 and quantified their migratory behaviors. Cells transplanted into either r3 or r5 displayed a significant reduction in migration compared with cells transplanted into r4 (Fig. 1B and C). C8161 cells transplanted into r3 showed an average migratory distance of 104 μm, representing a 50% reduction in migration compared with cells transplanted into r4 (Fig. 1C). Cells transplanted into r5 displayed even greater inhibition, with an average migratory distance of only 66 μm. Those cells showing a propensity to migrate appeared as multicellular streams oriented rostrally or caudally toward adjacent neural crest migratory streams. This suggests that the microenvironments...
within and adjacent to r3 and r5 induce potent antimigratory responses.

Cranial neural crest cells at the r4 axial level cease to emerge from the dorsal neural tube at approximately HH11+ (17). We asked whether age-related changes in the neural crest microenvironment would affect tumor cell behaviors in later staged transplants. To test this, we transplanted C8161 cells into r4 at HH12 (Fig. 1B). We found that melanoma cells transplanted into r4 at later developmental stages spread radially from the transplant site, without respecting the neural crest cell–free zones (Fig. 1B). Furthermore, cells migrated independent of one another and did not appear to form discrete multicellular streams like those observed in cells transplanted at HH10 (Fig. 1B). Interestingly, with an average migratory distance of 172 μm, these cells also migrated less (based on total displacement) than cells transplanted at stage HH10 (Fig. 1C). From this, we conclude that guidance factors present in the embryonic microenvironment at HH10 do not appear to guide migration at later developmental stages.

The ability to migrate is cell-autonomous

These results suggest that the embryonic neural crest microenvironment regulates melanoma migratory behaviors when transplantation is correlated with the developmental timing of cranial neural crest migration. We next asked whether the proximity of a melanoma cell to the microenvironment (neural tube lumen) influences melanoma cell invasion. To test this, we used an in vivo selective cell labeling technique in which H2B-PSCFP2 (photoswitchable cyan fluorescent protein)-labeled C8161 cell clusters were transplanted into the embryo (r4, HH10). Using 2-photon microscopy, we photoconverted a small number of cells located either within the core or at the periphery of the transplant (Fig. 2A and B; Supplementary Video S1). Following 24 hours, photoconverted cells were scored as migratory or nonmigratory.

Figure 2. Migratory ability is cell-autonomous. A, cartoon depicting the 2-photon in ovo photoconversion of H2B:PSCFP2-labeled C8161 melanoma cells. Following transplantation into the chick embryo (r4, HH10), subpopulations of tumor cells in either the core or the perimeter of the graft were photoconverted with a 2-photon microscope using a wavelength of 780 nm. B, representative micrographs showing the photoconversion of tumor cells at t = 0 hour in either the core or the periphery of the graft. XY and XZ views are provided. C, representative micrographs showing the locations of migratory photoconverted tumor cells at t = 24 hours. The white circles outline the initial transplant graft location and show the nonmigrating cells remaining in the neural tube. D, pie charts depicting the percentage of photoconverted migratory versus nonmigratory cells. Cells were scored as migrating or nonmigrating based on their location within or without this circle. E, in vitro time-lapse analysis of a C8161 melanoma cell cluster placed on a basement membrane matrix. Cells were labeled based on position (red = periphery, green = core). Migratory tracks are shown at 5 hours. F, rose plot comparing cell directionality in vitro with directionality observed in the embryo. In the embryo, 90 degrees represents the anterior–posterior embryo axis. Cell positions were calculated for all migrating cells from 9 different transplants (r4, HH10, >1,000 cells). Angles between cell trajectory and the horizontal r4 migratory stream were then determined. The size of each bar depicts the number of binned cells for a given angle. The colored segments depict the distance migrated by cells within the bin.
found that migratory cells derived from either the periphery or core were similarly likely to be located in the leading population of migratory cells as those that started at the periphery (Fig. 2C and D). This contrasted with melanoma cell clusters placed on a basement membrane matrix in culture. In vitro, cells spread radially and without direction from the microenvironment, with the cells originating at the outer rim of the cluster remaining on the migratory front (Fig. 2E and F). Thus, the ability to sense and respond to migratory and directional cues within the embryonic neural crest microenvironment appears to be cell autonomous.

The embryonic neural crest microenvironment dictates migratory behaviors
We next verified by in ovo 2-photon time-lapse microscopy that migratory cells unpredictably arose from anywhere within the transplant cluster, with no observed bias for any given region (Fig. 3A; Supplementary Video S2). Yet it remained unclear whether cells migrated independently or in association with neighboring cells. Thus, for each of the 10 most invasive cells identified in the transplant, we analyzed directional migration for the highly invasive cell’s 6 closest neighbors (Fig. 3B–D, Supplementary Video S3). This 3D analysis revealed that displacement vectors for neighboring cells rarely pointed in the same direction as the most invasive cell (Fig. 3C). We calculated the average deviation between the displacement vector of the invasive cell and those of its neighbors to be 32 degrees, indicating that neighboring cells do not tend to follow the direction of the highly migratory cells (Fig. 3D). We conclude that highly invasive tumor cells migrate independently of neighboring cells and do not adopt a follow-the-leader pattern of migration.

We then investigated whether the location of a cell within the cluster at the time of transplantation could predict the timing and trajectory of its invasion pattern (Fig. 4A and B; Supplementary Video S4). We pseudocolored invasive melanoma cells at endpoint times based on whether the cell had migrated to the left or to the right of the embryo anterior–posterior axis along the dorsal midline. We then rewound the time-lapse to reveal the cell’s initial position (Fig. 4A and B). We observed that cells that had migrated to the right side of the embryo originated from the right half of the transplant cluster and vice versa, mimicking the host embryonic neural crest dispersion pattern. This suggested that transplanted melanoma cells were sorted by microenvironmental signals at the dorsal midline.

EphB6 reexpression in melanoma cells alters migratory behavior
What embryonic neural crest microenvironmental factors are responsible for directing melanoma cell migratory behaviors? As Eph/ephrin signaling is known to direct embryonic neural crest migration (19–21), we sought to identify novel migratory phenotypes resulting from altered Eph expression. To accomplish this, we reexpressed EphB6, a kinase-defective Eph receptor, in C8161 melanoma cells. EphB6 protein expression was confirmed by Western blotting (Supplemental Fig. S2). We previously demonstrated that EphB6 gene expression was silenced in C8161 cells but present in both primary melanocytes and poorly invasive C816-1 melanoma cells (7). Furthermore, EphB6 has been shown to dimerize with, and modulate the activities of, several other Eph receptors. These include EphB1, EphB2, EphB4, and EphA2, all of which are highly expressed in C8161 cells (7, 22–24). As such, we hypothesized that EphB6 reexpression would have significant effects on the interaction between transplanted C8161 cells and the chick microenvironment. To test this, we transplanted EphB6+ C8161 cells into the embryo (r4, HH110) and quantified the resulting cell invasion pattern (Fig. 5). EphB6+ C8161 cells initially exited the neural tube at the proper location rostral to the r4–r5 boundary. However, after encountering the microenvironment adjacent to r4, EphB6+ cells altered their
trajectories away from the area adjacent to r4 and toward the area adjacent r5 (Fig. 5A–F). This resulted in a caudal shift in the mean position of migrating cells (~75 μm) along the rostral–caudal axis (Fig. 5F and G). Importantly, the EphB6+ cells maintained the discrete multicellular streaming behavior observed in transplanted parental C8161 cells, suggesting that cell–cell interactions among the melanoma cells was not altered. Also, the overall distance that EphB6+ C8161 cells invaded into the embryonic neural crest microenvironment was unaffected (Fig. 5H).

EphB6 is a metastasis suppressor in melanoma

Following this observation, we investigated whether the altered cell directionality observed in the embryo reflects a change in tumorigenicity or metastatic potential (Fig. 6). Parental C8161 cells or EphB6+ C8161 cells were placed onto the highly vascularized CAM of an E10 chick embryo and incubated for 48 hours. We observed that EphB6+ C8161 cells maintained their ability to form tumors on the CAM in a similar manner to that observed with parental C8161 cells (Fig. 6A). The isogenic but poorly aggressive melanoma cell line C81-61 did not form tumors when placed on the CAM but rather remained as a monolayer of dispersed cells (Fig. 6A).

To test whether EphB6 reexpression directly affects metastasis, we examined the ability of tumor cells to invade into the host vasculature. To assay invasation, the bottom half of the CAM was removed 48 hours posttransplantation and assayed for the presence of human DNA. Because of physical and temporal constraints, tumor cells must intravasate into the blood or lymph circulation to populate the bottom half of the CAM within 48 hours (25, 26). PCR amplification of a human-specific Alu repeat sequence allowed us to quantify the presence of metastatic human cells (15, 27). We evaluated 16 replicates from both parental C8161 cells and EphB6+ C8161 cells. We observed that 50% of the parental C8161 samples showed high metastatic ability, with maximal rates observed at more than 900 pg human DNA per 2 μg chick DNA (Fig. 6C). Parental C8161 cells showed an average of 225 pg human DNA per sample over 48 hours (corresponding roughly to 45 cells per sample, based on 1 cell = 5 pg DNA, Fig. 6C). In contrast, EphB6+ C8161 cells displayed a marked reduction in metastatic ability (17 pg per sample or 3.4 cells). These results support the hypothesis that EphB6 acts as a metastasis suppressor in melanoma cells and suggest invasation as the step likely blocked by EphB6.

Discussion

In the present study, we sought to use an embryonic model system to examine the role of the microenvironment in promoting and directing metastatic invasion in vivo. Using a dynamic in vivo imaging platform to assess single-cell behaviors, we discovered 3 main results. First, embryonic neural crest microenvironmental signals regulate the timing, trajectory, and order of metastatic melanoma dissemination...
human melanoma cell dynamics at the single-cell level within the embryonic neural crest and vascularized CAM microenvironments.

Our work approaches discerning just how susceptible tumor cells are to microenvironmental migration cues and whether an understanding of those cues might help predict metastatic behaviors. The early embryonic hindbrain uses a complex set of signaling mechanisms to control and guide the invasion of the neural crest (5). These same signals appear to be sufficient to regulate melanoma invasion in both time and space, including directional and nonpermissive cues. Melanoma cells transplanted at a developmental stage after neural crest cells have emigrated from the hindbrain, or into odd-numbered rhombomere hindbrain segments (that typically support fewer migrating neural crest cells) fail to replicate the behaviors of cells transplanted into r4 at stage HH10 (Fig. 1). These observations demonstrate that confined microenvironments can directly regulate tumor cell

Figure 5. Reexpression of EphB6 in C8161 melanoma cells results in aberrant directional migration without affecting migratory ability. A, cartoon depicting the transplant of EphB6⁺ C8161 melanoma cells into r4 at HH10. B, representative micrograph showing migratory behaviors of transplanted EphB6⁺ C8161 cells. The neural tube boundary is outlined in yellow and the position of the otic vesicle (ov) is shown by the dotted yellow line. Individual rhombomeres are also labeled. C, densitometric scatterplot of the cell invasion pattern of the positions of the 30 most invasive cells from 10 transplant experiments. The y-axis represents the embryo midline. The x-axis represents lateral migration and is given in degrees (cylindrical coordinates). The r4–r5 boundary is depicted by the red line. D and E, cartoons depicting the invasion patterns of parental C8161 cells (from Fig. 1) and EphB6⁺ C8161 cells. F, an overlay of the cell invasion pattern from parental C8161 cells (green) and EphB6⁺ C8161 cells (red), highlighting the caudal shift in cell positions at t = 24 hours. G, Gaussian fit to a histogram comparing cell positions of parental C8161 cells and EphB6⁺ C8161 cells along the rostral-caudal axis at t = 24 hours. H, Gaussian fit to a histogram comparing total distance migrated (total displacement) between parental C8161 cells and EphB6⁺ C8161 cells. Xc is the center of the peak and represents the average X-value. W equals 2 times the SD of the Gaussian distribution or approximately 0.849 the width of the peak at half height. *, P < 0.05.

Figure 6. Reexpression of EphB6 in C8161 melanoma cells causes a significant loss of metastatic potential but does not affect tumorigenicity in a CAM metastasis assay. A, images of a native chick embryo CAM and representative tumors from parental C8161 cells (green) and EphB6⁺ C8161 cells (red) grown on the CAM. 1x10⁶ cells in suspension (10 µl) were dropped onto the CAM at day E10. Tumor formation occurred over 48 hours. Nonmetastatic C8161-61 cells did not form tumors. The black meter bar represents 1 cm and the white meter bars represent 2.5 mm. B, cartoon depicting the CAM metastasis assay. Tumor cells are placed onto the upper CAM through a window in the egg shell. The egg is resealed for 48 hours. The lower CAM is removed and genomic DNA is harvested from the tissue. Metastatic human cells are detected by qPCR using primers that amplify a human-specific Alu element. C, scatterplot showing detected amounts of human DNA per 2 µg chick CAM DNA. Each X represents one biologic replicate. A t test was used to calculate statistical significance.
migratory behaviors such as migratory capacity and directionality and suggest that an understanding of these signals may provide insight into the metastatic abilities of tumor cells.

The establishment of nonpermissive tissue boundaries is critical for maintaining discrete neural crest migratory routes. What are these cues and can we use them to obstruct the metastatic process? The neural crest provides a superb model system in which to study cell–microenvironment exchanges during cell invasion.

One key question was whether the microenvironment dictated which cells would migrate, as the majority of transplanted tumor cells remain in the neural tube 24 hours posttransplantation. If the microenvironment was responsible for inducing the migratory phenotype, we would expect to observe a reduction in migratory efficiency in cells at the core of the transplant that are insulated from direct contact with the embryo. Likewise, if all cells responded to the microenvironment equally, we would expect cells at the perimeter to migrate farther simply because they could more rapidly delaminate from the tumor graft (as was observed in vitro). However, we were able to show that migratory cells originated from the core of the transplant at nearly the same rate as cells located on the periphery and that these core cells could be found at the leading front of invasion (Fig. 2). This suggests that heterogeneities among the transplanted cells enabled some cells to recognize the proper migratory cues present in the microenvironment, independent of cell position.

Dynamic in vivo 2-photon time-lapse microscopy provided further insights into how the embryonic microenvironment regulates tumor cell migration. First, we observed that transplanted cells are compliant to signals establishing a dorsal midline boundary (Fig. 4). This same midline segregation is observed during neural crest migration and is thought to be induced by direct cell guidance mechanisms, including Slit-Robo signaling (28). We postulate that a similar guidance mechanism segregates migrating tumor cells. Also, cells do not maintain strict neighbor relationships but act independently in responding to microenvironmental signaling cues (Fig. 3). We conclude that the ability to migrate is cell-autonomous, whereas specific migratory behaviors are dictated by the microenvironment.

Several guidance mechanisms are used by the embryo to sculpt discrete neural crest migratory streams and direct cells to precise destinations (13). Among these mechanisms, Eph/ephrin signaling has been well described in guiding neural crest migration in both the hindbrain and the trunk (19–21, 29). In the hindbrain, distinct combinations of Ephs and ephrins are thought to help establish boundaries that sculpt neural crest streams en route to their respective branchial arches.

Aberant Eph/ephrin signaling has also been reported to mediate cancer metastasis (30). In the current study, we show that EphB6 reexpression altered tumor cell invasion directionality and significantly reduced metastatic potential (Fig. 6). EphB6 has been identified as reduced or absent in several metastatic solid tumor types, including breast cancer, lung cancer, and melanoma (31–33). As Eph/ephrin signaling is commonly associated with cell–cell repulsion, it is tempting to speculate that the ephrin signature expressed by the host neural crest or the underlying mesenchymal cells induces an inhibitory response in EphB6þ C8161 cells. This would act to divert the melanoma cells away from the r4 migratory route. This is supported by work from Matsuoka and colleagues which demonstrates that EphB6 is repelled by high concentrations of the ligand ephrin-B2, which is thought to be expressed by migrating cranial neural crest cells (21, 34). However, it has also been suggested that varying concentrations of EphB6 may induce a switch from repulsion to attraction (34). Indeed, ephrin-B1 has been shown to be expressed by non–neural crest cells lining neural crest migratory boundaries in the chick hindbrain, including areas around the otic vesicle (21). Thus, it is possible that typically repulsive ephrin-B1 signals have become attractive to EphB6þ C8161 cells.

Importantly, the reduction in metastatic potential observed in EphB6þ cells did not likely result from a migratory phenotype, as EphB6þ C8161 cells traveled a similar distance as parental cells in our transplant model (Fig. 5). As such, we hypothesize that EphB6 may function to perturb the process of intravasation, as our CAM assay uniquely assesses intravasation potential by specifically identifying and quantifying tumor cells that were able to intravasate into the CAM vasculature (Figs. 6 and Fig. 7, model). Specifically, we postulate that EphB6 may function to regulate the tumor cell–endothelial cell interaction, possibly receiving a repulsive signal following engagement with ephrins expressed on endothelial cells. Endothelial cells have been reported to express multiple Ephs and ephrins, including ephrin-B2, which has been shown to have a repulsive effect on EphB6 (34, 35). Eph/ephrin signaling has also recently been reported to play a role in the transendothelial migration of some immune cells (35, 36). Thus, we hypothesize that the endothelium becomes an impenetrable barrier to cells expressing a specific Eph/ephrin signature that includes EphB6, whereas the absence of EphB6 may facilitate passage across the endothelium (Fig. 7, model).

In summary, the focus of this study was to understand how metastatic tumor cells respond to and interact with their microenvironment at the level of a single cell. We show that the embryonic neural crest microenvironment exerts a powerful, controlling influence on the migratory behaviors of an aggressive metastatic melanoma (C8161). This regulation is enacted both temporally and spatially by the embryo and was most evident by the induction of a spatially controlled symmetric exit pattern of melanoma cells from the neural tube. These data highlight the idea that successful invasion (and metastasis) of tumor cells requires that a cell be able to interpret complex microenvironmental cues encountered along the route of invasion and either be guided or adapt to overcome those cues that are meant to disrupt or block migration. As an example, we show that EphB6 acts specifically as a...
metastasis suppressor. Because EphB6⁺ cells maintain their invasiveness and tumorigenicity, we postulate that metastasis suppression occurs as EphB6 disrupts intravasation by forcing the tumor cell to recognize a nonpermissive endothelial boundary. These findings were made possible by studying melanoma metastasis within the accessible embryonic neural crest microenvironment.

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

Authors’ Contributions
Conception and design: C.M. Bailey, P.M. Kulesa
Development of methodology: C.M. Bailey, P.M. Kulesa
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): C.M. Bailey, P.M. Kulesa
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): C.M. Bailey, P.M. Kulesa
Writing, review, and/or revision of the manuscript: C.M. Bailey, P.M. Kulesa

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): P.M. Kulesa
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