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# EGF as a New Therapeutic Target for Medulloblastoma Metastasis

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# Abstract

Medulloblastoma (MB) is a malignant pediatric brain tumor known for its aggressive metastatic potential. Despite the well-documented migration of MB cells to other parts of the brain and spinal column, MB chemotaxis is poorly understood. Herein, we examined the *in vitro* migratory and cellular responses of MB-derived cells to external signaling of Epidermal Growth Factor (EGF), hepatocyte growth factor (HGF), platelet-derived growth factor (PDGF-BB), and the stromal cell-derived factors 1-alpha (SDF-1). Experiments utilized transwell assays and immunocytochemistry to identify receptor activation in MB migration, and used a microfluidic platform to examine directionality, trajectory, and gradient-dependence of motile cells. Data illustrates that MB-derived cells respond strongly to EGF in a dosage and gradient-dependent manner with increased EGF-R activation, and show that high EGF gradient fields cause an increased number of cells to migrate longer directed distances. Our results provide evidence that EGF and its receptor play an important role than previously documented in MB chemotactic migration than previously documented and should be considered for developing migration-target therapies against MB metastasis.

# Keywords

Pediatric cancer; chemotaxis; microfluidics; gradients

# INTRODUCTION

Medulloblastoma (MB) is a family of highly-invasive tumors most commonly diagnosed in the pediatric central nervous system <sup>(7, 28, 38, 41, 50)</sup>. While clinical treatments have more

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CONFLICTS OF INTEREST:

Jennifer Rico-Varela, declares that she has not conflicts of interest. Tanya Singh, declares that she has not conflicts of interest.

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than doubled the overall 5-year survival rate to upwards of 60% (16, 28, 44, 52), additional therapies are needed to target the aggressive MB migration that is uncharacteristic of other brain tumors, but is a hallmark of MB recurrence, metastasis, and radioresistivity (13, 21, 24, 28, 41, 55, 61, 70). The migration of cancer cells within the CNS is decidedly complex, affected by cellular interactions with heterogeneous extracellular matrix (ECM) as well as mixed cellular responses to concentration fields of biomolecules (1, 14, 19, 60, 65). However, the mechanisms behind the migration of MBderived cells along CNS gradients of biomolecular concentration, or chemotaxis, remain understudied and incompletely understood (14, 28). Particular complexities arise in MB. because chemoattractant fields that rouse cells away from primary tumors can be secreted by healthy or transformed distant and neighboring cells (1, 3, 9, 34, 58, 76). Further, clinical studies have illustrated that the spread of MB cells occurs predominantly to the spinal column via a combination of two-dimensional (2D) and three-dimensional (3D) movements (6, 51, 67, 77, 83). Such spreading results from tumor cells that drop into the cerebrospinal fluid and tend to seed in parts of the spine (53, 74, 77, 79, 84). As a result, the movement of MB cells on the surface of the spinal column can be examined on 2D substrata to plausibly physiologically approximate the metastatic behavior of these pediatric brain tumors.

Traditional cell migration studies have looked to transwell <sup>(27, 48, 81)</sup> and wound healing assays (36, 54, 78) to report numbers of cells that become motile in response to external signaling from growth factors, such as Epidermal Growth Factor (EGF) and Platelet-Derived Growth Factor (PDGF)<sup>(4)</sup>. However, chemotaxis is becoming more-commonly examined via the physical microenvironment of the cell, where dynamic concentration fields facilitate ligand-receptor bindings which initiate signal transduction cascades <sup>(1, 8, 59)</sup>. Here, precise manipulation of the cell microenvironment has been facilitated by the wide-adaptation of benchtop microfluidic devices <sup>(26, 27, 29)</sup>, which enable multifaceted evaluation of cell migratory behaviors in lieu of cell numbers alone. A large number of laboratories have demonstrated concentration- and concentration gradient-dependent behavior of noncancerous cells, such as fibroblasts (33), retinal progenitor cells (69) and keratinocytes (64), as well as tumors found in breast <sup>(57)</sup>, colon <sup>(17)</sup> and CNS cancers <sup>(2)</sup>. Our own laboratory has illustrated that select populations of cells derived from CNS tumors can respond acutely via migration to ultra-low concentration gradients of select chemoattractants <sup>(2, 14, 33)</sup>, while others have shown greater chemotactic response with specific dosage <sup>(3, 49, 56)</sup>. Microfluidic analysis is, thus, well positioned to meaningfully aid in the development of migrationtargeted therapies for MB via insight of migratory parameters relevant to metastasis, such as cell distance traveled, motility, gradient-sensitivity, ECM interaction and numerous others.

In this work, we examine MB migratory behavior in response to external signaling from 4 of the most extensively studied chemoattractants of CNS tumors using benchtop assays and microfluidics: Epidermal Growth Factor (EGF), Platelet-derived Growth Factor (PDGF), Hepatocyte Growth Factor (HGF), and Stromal Derived Growth Factor (SDF-1 or CXCL12). Our results illustrate that MB-derived cells exhibit gradient-dependent behavior in EGF fields, which are able to guide MB along longer migration distances with superior directionality and increased receptor activation. These results distinguish EGF as a principal

molecule with meaningful potential impact as an anti-migratory therapeutic to MB metastasis.

# MATERIALS AND METHODS

#### Cell culture

In vitro cell culture was maintained using Daoy cell line (ATCC, Cat. No.HTB-186) <sup>(14, 60)</sup>, Eagle's Minimal Essential Medium (EMEM) (VWR, Cat. No.12001-582) supplemented with 10% fetal bovine serum (VWR, Cat. No.45000-734), 2% L-glutamine (VWR, Cat. No. 45000-676) and 1% Penicilin-Streptomycin (VWR, Cat. No.45000-650). Intact monolayers were maintained and harvested cells were seeded onto sterile polystyrene tissue culture flasks (VWR, Cat. No.BD353136). MB cells were incubated at 37 °C with 5% CO<sub>2</sub> with cell medium changed every 2 days. Cell migration experiments were initiated with cells that were inserted into microchannel after MB cells reached 80% confluence.

#### **Cell Migration Assay**

The Boyden chamber assay <sup>(2, 14)</sup> was used to measure the number of MB cells that migrated towards different concentrations of external growth factors. This widely-used assay consists of two compartments filled with EMEM medium and separated by an 8 micronporous membrane (VWR, Cat. No.62406-198), as shown in Figure 1.A. MB cells were seeded in the upper compartment and were allowed to migrate through the porous membrane into the lower compartment for 6 hours at 37 °C in a 5% CO<sub>2</sub> incubator. Approximately  $1 \times 10^6$  cells/mL were seeded in 300µl of EMEM complete medium (EMEM with FBS) in each upper chamber, while 700µl of serum-free medium (EMEM only) was pipetted into each lower chamber. Lower chambers also contained concentrations of 1, 10, 100, and 1000 ng/mL of EGF (Life Technologies Corporation, Cat. No.E3476); HGF (R&D Systems, Cat. No.2207-HG/CF); PDGF-BB (R&D Systems, Cat. No.220-BB-010); and finally SDF-1 (PreporTech, Cat. No.250-20A). All growth factor solutions were diluted in EMEM serumfree medium using serial dilution. After 6 hours of incubation, the membrane was fixed and stained with fixative solutions (VWR, Cat. No. B4132-11A), which stained the cell cytoplasm and nuclei. The number of cells that migrated to the underside of each membrane was determined by using the convectional checkerboard analysis (2, 14, 82).

#### Immunostainning of Receptors

MB cells were plated at a concentration of  $1 \times 10^3$  cells/mL in EMEM complete, on borosilicate glass well plates (Lab-Tek, Cat. No.155383). The cells were incubated for 2 hours at 37°C in 5% CO<sub>2</sub> to facilitate attachment. Adhered cells were exposed to ligands at concentrations that resulted in the largest numbers of motile cells in the transwell assay results. At 37°C, each cell plate was exposed to 5 minutes of: 100ng/mL EGF (Life Technologies, Cat. No.PGH0311), 100ng/mL CXCL12 (Life Technologies, Cat. No.PHC1364), 10ng/mL HGF (Life Technologies, Cat. No.PHG0324), and 100ng/mL PDGF-BB (Life Technologies, Cat. No.PHG0044). The supernatant was then aspirated and each well was rinsed 3 times with 0.5 mL phosphate buffered saline solution (PBS), (Sigma-Aldrich, Cat. No.HT501128) for 10 minutes, and rinsed twice with PBS. The samples were

permeabilized using a 1% solution of Triton-X (Sigma-Aldrich, Cat. No.X100) and 0.1%BSA in PBS solution for 10 minutes, then blocked for 60 minutes with 1% BSA in PBS blocking solution and rinsed twice with the same blocking solution.

Samples were then exposed to the primary antibody for each receptor studied for 2 hours at 22°C: 5µg/mL anti-EGFR (Life Technologies, Cat. No.700308), 5µg/mL anti-CXCR4 (Life Technologies, Cat. No.35-8800), 2µg/mL anti-c-Met (Millipore, Cat. No.072242), and 3µg/mL anti-PDGFR (Life Technologies, Cat. No.701142). Each well was rinsed 3 times with 1% BSA blocking solution. A fluorescent secondary anti-rabbit IgG (Millipore, Cat. No.AP132F) was used for EGFR, c-Met, and PDGFR samples, and a fluorescent anti-mouse secondary antibody (Millipore, Cat. No.MAB1976) was used for CXCR4 samples. All samples were exposed to the secondary antibody at a concentration of 5µg/mL for 30 minutes at 22°C, and then rinsed twice with blocking solution. Nuclear staining (Life Technologies, Cat. No.R37605) was performed for 20 minutes at 22°C, after which the samples were rinsed twice with PBS and covered in glycerol (Life Technologies, Cat. No. 15514-011) for preservation. In addition, the expression of EGFR was measured at different time points of 0, 14, 22, 36, and 42 hours. The immunocytochemistry assay was performed as described above using goat-anti mouse IgG secondary antibody (Life Technologies, Cat. No. A-11005) for EGFR.

#### Bridged µLane and Experimental Set up

Our microfluidic device, the  $\mu$ Lane, was utilized to image the real-time migratory responses of individual MB cells within microenvironments of defined EGF and SDF-1 gradient profiles. The bridged  $\mu$ Lane system operates via a combination of uniaxial bulk convection and diffusion to achieve controlled chemical concentration gradients over time, as described previously <sup>(2, 32, 33)</sup>. This mass transfer mechanism termed as convective-diffusion has been widely-studied by several groups for bioengineering applications, to determine the transport of differently sized solutes and proteins through the walls of capillaries <sup>(11, 12, 20)</sup> and arteries <sup>(25, 30, 39, 66, 80)</sup>, skeletal muscle fibers <sup>(31, 35, 45)</sup>, and intervertebral discs <sup>(18, 62, 63)</sup>. The two-dimensional mass transport of ligands within the microsystem was modeled via finite-element-analysis (FEM) in Matlab 7.7 (MathWorks, Natick, MA) and verified experimentally as described previously by our group <sup>(32, 33)</sup>.

The framework of the  $\mu$ Lane system consists of two layers of Polydimethylsiloxame (PDMS) (Fisher Scientific, Cat. No.NC9644388) bonded to a glass slide using ozone gas. The first layer of PDMS consists of a closed microchannel of 100 $\mu$ m-width and 1.3cm-length with a volume of 0.1 $\mu$ L, which connects two fluidic reservoirs of 9 $\mu$ L each, called the source (SRR) and the sink (SKR) reservoir. The second layer of PDMS consists of two chambers of 170 $\mu$ L each, called the source (SRC) and the sink (SKC) chamber, connected by an open, hemispherical bridge channel to maintain the hydrostatic equilibrium of the system <sup>(32, 33, 69)</sup>. Both chambers are vertically and fluidically connected with both reservoirs (Figure 3).

The  $\mu$ Lane system works by using the larger volumes of the SRC, SKC and bridge channel on the second layer of PDMS to generate concentration gradients within the smaller volumes of the SRR, SKR and microchannel on the first layer <sup>(14, 32, 33, 69)</sup>. After inserting cells

along the microchannel length, the cell culture media is used to fill the SRR, SKR, SRC, SKC, and the bridge channel. The ligand solutions (EGF or SDF-1) are then manually inserted drop-wise into the SRC until the solution makes contact with the cell culture media solution within the bridge channel and SKC to initiate the molecular transport within the system. The small differences in the density of the reagents and in the liquid levels in the SRR and SKR generate hydrostatic pressure differences that initiate an ultra-low bulk flow within the microchannel in the first layer (32, 33, 69). This minuscule bulk flow was measured to be 0.37  $\mu$ m/sec using fluorescent beads, as described previously <sup>(32)</sup>. Such a low bulk flow facilitates the transport of ligand solutions from the SRR to the SKR, to accelerate the time required to attain a steady-state gradient profile of ligand solutions along the 13-mm length of the microchannel. In the absence of this bulk flow, the transport of our reagent via diffusion alone would require over 470 hours to reach a steady-state distribution within the length of the  $\mu$ Lane instead of the 18 hours measured, as reported by our group (14, 32). We note that because the time required for the overall system to reach steady-state is much larger than the time needed for steady-state concentration gradients to be generated within the  $\mu$ Lane system alone. Thus, the operation of the system is 'best' described as 'quasisteady-state' (5, 10, 40, 68, 71, 73). However, because this work focuses exclusively on smaller time scales of the microchannel only, the term steady-state would be used for simplicity. Mathematical models of reagent transport within our  $\mu$ Lane system were performed via MatLab to determine the steady-state concentration distribution as seen in Figure 4.A. The initial EGF or SDF-1 concentration within the SKC, SKR, microchannel and SRR was set to 0-ng/mL, as per absence of ligand. The initial ligand concentration within the SRC was set to 100-ng/mL to reflect the sample concentration used during experiments. These boundary conditions were solved using Equation (1), as shown below  $^{(32)}$ ,

$$\frac{\partial C}{\partial t} + \underline{u} \cdot \underline{\nabla} C = D \nabla^2 C \quad (1)$$

Where *C* (ng/mL) is ligand concentration, *t* (hours) is time, *u* ( $\mu$ m/sec) is fluid velocity, and *D* (cm<sup>2</sup>/s) is diffusion coefficient, or diffusivity, of the reagent molecule. Experimental validation was also performed using fluorescently labeled Dextran (~ MW 10KDa), to confirm steady-state is reached in our system after 18 hours, and is maintained for several days <sup>(14, 32)</sup>.

For our experiments, the  $\mu$ Lane system was coated with 10- $\mu$ g/mL of laminin (Becton, Dickinson and Company, Cat. No.354232) <sup>(14, 60)</sup>, and allowed to gel for one hour at room temperature (25°C) under sterile conditions. Unbound laminin was aspirated and cells were manually seeded into the microchannel using a 1-mL syringe (VWR, Cat. No.BD309659). A cell solution (1×10<sup>6</sup> cells/mL) was injected into the SRR and SKR. Cells were allowed to adhere and visibly spread prior to the initiation of the experiment as illustrated in Figure 3.D. Finally the bridge channel was loaded with EMEM complete medium to connect the SRC and SKC, initiating the system. In this work, EGF (100-ng/mL) or SDF-1 (100-ng/mL) was individually loaded drop-wise into the SRC and allowed to reach steady state in the microchannel for 18 hours at 37°C <sup>(32)</sup>, prior to imaging of MB cell migration within this precise biochemical environment; therefore, all data is collected within steady-state

concentration gradient fields for 24 hours. Our group has previously showed that MB cells migrate and proliferate *in-vitro* until 72 hours in the  $\mu$ Lane system <sup>(14)</sup>.

#### Statistics

One-way ANOVA and Post Hoc Test (Tukey) were used to analyze the data using IBM SPSS Statistics Program (IBM Corp., Released 2011, version 20.0. Armonk, NY). A oneway ANOVA test at a 95% confidence interval was performed for statistical significance across growth factors. The Post Hoc Test (Tukey) was performed to determine the disparity among different groups. Only p-values <0.05 were considered statistically significant. Unpaired student's t-test at a 95% confidence interval was implemented to determine significance of relative receptor expression using IBM SPSS Statistics Program (IBM Corp., Released 2011, version 20.0. Armonk, NY).

#### **Imaging and Processing**

Transmitted light microscopy images were obtained using an inverted microscope (Nikon TE2000) and a cooled CCD camera (CoolSNAP EZ CCD Camera, Photometrics, Tucson, AZ) with a 20X objective magnification (Nikon Plant 20X, Morrell Instrument Company Inc., Melville, NY). Fluorescent imaging was performed using Leica CLSM confocal microscope and a Zeiss LSM 710 confocal microscope, both at 63x magnification with oil immersion objective. Image J was utilized to track cells and process images (Chemotaxis and Migration Tool plugin (ImageJ 1.46r) <sup>(14, 15)</sup>. Fluorescence intensity was measured using an average over the entire cell area via ImageJ. Transmitted light image data was analyzed using Nikon software (Nikon Instrument Element 2.30 with 6D module, Morrell Instrument Company Inc., Melville, NY) and ImageJ (NIH) Software. Bright field images of the microchannel were automatically captured every hour for 24 hours at every 1000 microns in the y-direction of the µLane, followed by cell tracking ( $n_{cells}$ ~180 cells) and analysis. Lastly, the cell tracking software was used to develop Wind-Rose plots <sup>(33, 69)</sup> of cell trajectories in response to EGF and SDF-1 gradient fields, over 24 hours.

# RESULTS

This work examined the migratory and cellular responses of MB-derived cells in response to external signaling from EGF, HGF, PDGF-BB, and SDF-1.

#### **Motility Studies**

The first set of experiments measured the average numbers of MB-derived cells that migrated toward different concentrations of EGF, HGF, PDGF-BB, and SDF-1 through transmembrane assays, as illustrated in Figure 1 and Table 1. As seen, numbers of motile cells were statistically different in response to signaling from different concentrations of EGF and HGF when compared to controls (i.e. no ligand). Further, a mid-level concentration of 100-ng/mL of EGF was observed to attract the largest numbers of motile cells overall (Fig. 1.B.2). By contrast, the number of MB cells that migrated in response to external signaling from concentrations of SDF-1 did not exhibit statistical difference from controls or each other (Fig. 1.B.4). Similarly, the number of motile MB in response to

signaling from different concentrations of PDGF-BB did not display statistical differences from controls (Fig. 1.B.3).

#### **Relative Receptor Expression**

The basal expression levels of the respective receptors were then compared against their activation levels upon ligand stimulation. Confocal images in Figure 2 illustrate differences in cellular distribution of activated receptors, as well as differences in fluorescent intensity after ligand stimulation. As seen, basal receptor expression appears to be uniformly distributed throughout the cell cytosol, with lowest intensities measured for EGF-R. Upon ligand activation, receptor expression is increased, but remains largely distributed throughout the cytosol. However, EGF-R expression is also observed to be acutely concentrated along the outer cell membrane. Analysis of fluorescence intensity then represented relative receptor expression levels upon ligand-stimulation. MB stimulated with EGF exhibited the highest increase in receptor expression for EGF-R, with a 3.5-fold increase in intensity over basal EGF-R expression measured in unstimulated controls (Fig. 2.A). By contrast, the expression of CXCR4, the receptor for SDF-1, was approximately 2fold higher than its basal intensity levels in cells unstimulated with ligand (Fig. 2.B), while no statistical difference was measured between the activation levels of c-Met, the receptor for HGF (Fig. 2.C), and control cells, as well as between PDGFR-BB (Fig 2.D) in ligandstimulated cells compared to controls. MB cells stimulated with EGF for different time points of 0, 14, 22, 36, and 42 hours displayed no relevant significant difference in receptor expression for EGF-R across time points, and were all higher than the unstimulated control (See supplementary Figure 1).

#### Migratory response to controlled concentration and gradient fields

The migratory behavior of MB was next examined using our microfluidic system, called the  $\mu$ Lane and shown in Figure 3, for real-time cell imaging and analysis. The transport of EGF and SDF-1 along the  $\mu$ Lane was modeled computationally, and verified experimentally as previously reported by our group <sup>(32)</sup>. The system produced a range of concentration gradients along the microchannel length at steady-state, as shown in Figure 4.A (14, 33). Concentration gradients of this study are defined as the average difference in growth factor concentration (ng/mL) along the microchannel length (mm). Five orders of concentration gradient, G<sub>1</sub>-G<sub>5</sub>, were delineated along the microchannel as illustrated in Figure 4.A:  $10^{+1} < G_1 < 10^0 \text{ ng/(mL.mm)}, 10^0 < G_2 < 10^{-1} \text{ ng/(mL.mm)}, 10^{-1} < G_3 < 10^{-2} \text{ ng/(mL.mm)},$  $10^{-2} < G_4 < 10^{-3}$  ng/(mL.mm), and  $10^{-3} < G_5 < 0$ . The lowest gradient, G<sub>5</sub>, was located near the source reservoir (growth factors only) and occupied approximately 1-mm-length of the microchannel, while the highest gradient, G<sub>1</sub>, was located near the sink reservoir and occupied an approximate, 3-mm-length of microchannel. Concentration gradients, G<sub>2</sub>, G<sub>3</sub>, and G<sub>4</sub>, occupied the remaining 9-mm-length of microchannel (distance in between the source and the sink reservoirs) with approximately 4 mm, 3 mm and 2 mm segments, respectively. Note, the core distributions of EGF and SDF-1 along the microchannel are very similar to one another given their respective molecular weights of 6.045 KDa and 7.9 KDa, and hence only one representative gradient distribution is shown. Further, cells were evenly distributed along all segments of the channel prior to the start of experiments.

The migration of MB-derived cells in response to the different concentration gradient fields of EGF and SDF-1 were described using three parameters: (1) Fraction of motile cells, **f**, defined as the number of cells that migrated more than two cell diameters in the $\mu$ Lane, normalized by the total number of cells within the channel; (2) cell directionality, **D**, defined as the percentage of cells whose net center of mass was preferably towards the positive, x-displacement or along the gradient direction; and (3) Average cell path length, **PL**, defined as the total distance traveled by cells.

First, the average percentage of motile cells along the entire microchannel was similar for both growth factors. Table 2 shows that 72.82% of MB became motile in response to EGF signaling, while an average 67.3% of MB became motile in response to SDF-1 concentration fields. Values of motile fraction varied with gradient fields,  $\mathbf{f}^{G1}$ - $\mathbf{f}^{G5}$ , for both EGF and SDF-1, as shown in Table 3. As seen, the highest fraction of MB cells became motile when exposed to higher concentration gradient fields of EGF, G<sub>1</sub> (f1=28.3%) and G<sub>2</sub> (f2=18.6%), followed by decreasing percentages of motile cells within lower gradient fields of EGF, G<sub>3</sub> (f3=11.9%), G<sub>4</sub> (f4=10.3%) and G<sub>5</sub> (f5=3.7%). Similarly decreasing fractions of cells were seen to migrate in response to concentration gradient fields of SDF-1, with highest fractions at G<sub>1</sub> (f1=18.2%) and G<sub>2</sub> (f2=20%), followed by significant decreases in the fraction of motile cells at concentration gradient fields G<sub>3</sub> (f3=13.8%), G<sub>4</sub> (f4=8.7%) and G<sub>5</sub> (f5=6.5%). As shown in Figure 4.B, the fraction of nonmotile cells was 27.2% and 32.8%, when exposed to similar concentration gradients of EGF and SDF-1, respectively. Statistical significance was observed between concentration gradient fields of EGF while no statistical significant difference was found across the gradient fields of SDF-1.

Next, the average directionality of motile MB was determined by examining individual cell trajectories. The term directionality was previously introduced by our group as the ratio of the number of cells whose centroids migrated more than 80 µm to the total number of cells in the microchannel <sup>(33)</sup>. The paths of MB cells in the presence of EGF and SDF-1 concentration gradient fields were optically tracked within the  $\mu$ Lane system to generate the representative Wind-Rose plots shown in Figure 5.A. Note that although cell trajectories are each positioned at a common origin for comparison, cell paths were measured along all microchannel segments, exposed to all gradient fields G1-G5. Representative trajectories illustrate that cells migrated preferentially towards lower concentration gradients of EGF (i.e., towards the right). By contrast, SDF-1 fields resulted in MB migration that was both towards and away from lower SDF gradients without preference. The directionality of motile cells along the entire microchannel was higher for cells stimulated with EGF (61.6%) than SDF-1 (44.2%), shown in Table 2. As seen, cell directionality within specific gradient fields, DG1-DG5, decreased with decreasing gradient for both EGF and SDF-1, shown in Table 3. EGF DG1 indicates that 28.3% of motile cells migrated directionally when exposed to G<sub>1</sub> of EGF (i.e. within the first 3mm of channel length), while SDF D<sup>G1</sup> denotes that only 18.4% displayed directional migration for the same gradient field of SDF-1. The highest fraction of MB cells directionality was reported at higher concentration gradient fields of EGF, D<sup>G1</sup> (28.3%) and D<sup>G2</sup> (15%), followed by decreasing percentages for directionality within lower gradient fields of EGF, D<sup>G3</sup> (7%), D<sup>G4</sup> (8.6%), and D<sup>G5</sup> (2.7%). Similarly decreasing fractions of directionality were reported in response to concentration gradient

fields of SDF-1, with highest fractions at  $D^{G1}$  (18.4%) and  $D^{G2}$  (10.5%), followed by decreasing fractions of directionality at  $D^{G3}$  (9.8%),  $D^{G4}$  (2.2%), and  $D^{G5}$  (3.3%).

In addition, Wind-Rose plots display the average maximum cell path length, **PL**, of motile cells tracked along the entire microchannel. Using this data, 32% of motile MB migrated distances greater than 200 microns (or 20 cell-diameters) when exposed to EGF gradient fields, as seen in Figure 5.B. By contrast, 97.3% of cells exposed to SDF-1 gradients migrated distances less than 200 microns. MB within our  $\mu$ Lane system in the absence of growth factors or concentration gradients (i.e. controls) displayed migration distances between 50 and 200 microns <sup>(14)</sup>. As shown, increasing percentages of cells were seen to migrate in response to higher gradient fields of EGF. A larger percentage of motile MB were observed in response to G<sub>1</sub> fields of EGF at every distance, while only cells exposed to G<sub>1</sub> migrated the longest distances greater than 300 microns. In comparison, MB exposed to lower gradient fields of SDF-1 (G<sub>3</sub>-G<sub>5</sub>) exhibited the longest migration. Notably, zero cells were observed to migrate less than 100 microns when exposed to any EGF gradient field G<sub>1</sub>-G<sub>5</sub>, while zero cells were seen to migrate greater than 300 microns when exposed to any SDF-1 gradient fields G<sub>1</sub>-G<sub>5</sub>.

# DISCUSSION

The chemotactic migration of MB-derived cells has been surprisingly understudied despite its well-known metastatic potential and aggressive invasion into the brain and spinal cord <sup>(14, 43)</sup>. Our study is among the first to examine and compare the migratory responses of MB to dosage-dependent signaling from EGF, HGF, PDGF-BB, and SDF-1, the most widely-acknowledged chemoattractants of CNS tumor cells <sup>(37)</sup>. The first set of experiments utilized conventional transwell assays to illustrate that MB migration was most concentration-dependent to EGF signaling. As shown in Figure 1, MB exhibited dosagedependent migration in response to signaling from EGF and HGF, but seemingly dosageindependent responses to PDGF and SDF-1 signaling. Further, EGF simulated the migration of approximately twice the number of MB cells than did PDGF, HGF, or SDF-1. Results from immunocytochemistry support the strength of MB chemotactic response to EGF signaling, as activation of its receptor, EGF-R, was two times larger than activation of other respective receptors. While strong MB chemotactic response to EGF signaling is consistent with previous findings from our group and others (14, 42), it is most significant here because it is signaling from SDF-1, rather than EGF, that has been reported as the strongest MB chemoattractant <sup>(56)</sup>. Inhibitor AMD310, which cleaves CXCR4, has been reported to decrease MB tumor growth in mouse xenografts, chemotaxis and proliferation (56). However, in vivo use of EGF-R inhibitors such as Tarceva and Gefitinib have reported no changes in motility of cells derived from glioma <sup>(47)</sup>, and non-small-cell lung cancer <sup>(23)</sup>, and thus, were minimally used on MB. We contend that MB chemotactic response may not have been measured most meaningfully in the past, which has stymied development of antimigratory therapies for MB metastasis. For this reason, we used microfluidic systems to more precisely study MB migratory responses using parameters relevant to metastasis.

Using the  $\mu$ Lane system, we were able to image real-time cell behavior in response to a wide range of concentrations and gradients of EGF and SDF-1, and distinguish directed-migration

of chemotaxis. MB migratory behavior was observed to be concentration gradient-dependent for both EGF and SDF-1 signaling, as the fraction of motile cells decreased with decreasing concentration gradient in both cases. However, motile MB traveled longer distances within the  $\mu$ Lane in response to EGF signaling, with an average PL of 264.5 ± 67.8  $\mu$ m, compared to an average PL of  $125.5 \pm 48.6 \,\mu\text{m}$  when responding to signaling from SDF-1. Further, cell trajectories illustrated an MB directional bias towards decreasing EGF gradients not present with SDF-1 signaling, with 18.3% of cells migrating towards decreasing EGF gradients compared to 15.3% of MB in response to decreasing SDF-1 gradients. Importantly, this behavior was observed along the entire  $\mu$ Lane length, for cells exposed to all concentration gradient fields, G<sub>1-5</sub>. Here, the cell directionality compared to other methods provides insight into whether MB cells stimulated with ligand solutions (EGF or SDF-1) followed a directional migration along gradient fields. Other methods to measure cell migration include the persistence length and average velocity to determine the chemotactic sensitivity of stable gradients in 3D (22, 46, 72, 75). While the persistence length provides the ratio of the net distance traveled to the total distance, it would not report the number of cells that migrate along ligand concentration gradients, which is highly significant to studies developing migration-targeted therapies for tumors of the CNS.

This consistent MB behavior illustrates that EGF signaling from high concentration gradients initiates the most motile MB, and further enables cells to travel the longest distances. MB cells were seen to migrate towards increasing ligand concentration, which also corresponds to decreasing EGF gradient fields in our system. This response is significant because it reflects MB sensitivity to high concentration gradients (G<sub>1</sub>-G<sub>2</sub>), which were generated via much greater nonlinear changes in ligand concentration as compared to low gradient fields (G<sub>3</sub>-G<sub>5</sub>). Previous work from our group has illustrated keen abilities of MB to migrate in larger numbers in response to increasing EGF concentration via pERK signaling <sup>(14)</sup>. In that work, MB cells were seen to travel out of a cell reservoir when exposed to increasing gradients and concentration. In the current study, we now demonstrate that MB can become less motile when exposed to signaling from increasing concentration but diminishing EGF gradient fields.

Data from the current study highlights the high fraction of motile MB in response to high concentration gradients of EGF. These results have high clinical interpretation, as they point to high gradient fields and low concentration fields as optimal for MB migration. This is an *in-vivo* scenario where paracrine signaling from neighboring cells initiate the most MB migration, such that cell displacement diminishes as cells approach the signaling source, where gradients are low and concentration is high. In addition, our findings may aid clinical development of anti-migratory therapeutics with the potential to inhibit MB metastasis along the spinal column via EGF signaling.

### CONCLUSION

In summary, our results illustrate that MB migration is both concentration and concentration gradient-dependent in response to EGF signaling. Further, our findings illustrate that high gradient fields of EGF result in the largest number of motile cells, which travel long

distances, and in a highly directional manner towards decreasing EGF gradients. These findings point to EGF as a viable molecule for migration-targeted therapies for MB.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Figure 1. Migration of MB-derived cells to different concentrations of selective chemotactic ligands

(A1) Schematic of transwell assay with motile cells attached to the underside of the porous membrane. (A2) Stained nuclei and cytoplasm of motile MB-derived cells toward different concentrations of (B1) EGF, (B2) HGF, (B3) PDGF, and (B4) SDF-1. The control groups indicate number of cells that migrated towards serum-free medium. An asterisk (\*) indicates statistically significant data with p-values <0.05 against control group.



#### Figure 2. Receptor activation within motile MB-derived cells

Immunocytochemistry of basal receptor expression of MB cells without ligand stimulation to (A1) EGF, (B1) SDF-1, (C1) HGF, and (D1) PDGF-BB. Receptor activation poststimulation with (A2) EGF, (B2) SDF-1, (C2) HGF, and (D2) PDGF-BB. The expression level of receptor following ligand stimulation of (A3) EGFR, (B3) CXCR4, (C3) c-Met, and (D3) PDGFR-BB normalized to basal control levels. Scale bars are 100µm. An asterisk (\*) indicates statistically significant data with p-values <0.05.

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#### Figure 3. The *µ*Lane system and MB migratory responses

(A) Schematic of the bridged  $\mu$ Lane system, showing cells inserted within the sink (SKR) and source (SRR) reservoir, and adhered along the microchannel. Chemotactic agents (e.g. EGF, SDF-1) are loaded into the source chamber (SRC), and transported to SKR to reach steady-state concentration distribution. (B) Top view image of the first layer PDMS bonded onto a glass slide. Two 9-nL reservoirs are connected by a microchannel of 13mm in length and 100 $\mu$ m in diameter. (C) Top view image of second layer PDMS bonded to the first layer. The source (SRC) and sink (SKC) chambers are connected by a bridge channel. (D)

Raw data image of motile MB cells within  $\mu$ Lane system at (D1) source reservoir, (D2) mid channel, and (D3) sink reservoir.



Figure 4. Concentration distribution along  $\mu$ Lane and number of motile cells (A) Concentration profile of EGF and SDF-1 along 13-mm microchannel length of  $\mu$ Lane system. Concentration gradients are identified by five orders of magnitude in the microchannel:  $10^{+1}$ <G<sub>1</sub>< $10^{0}$  ng/(mL.mm),  $10^{0}$ <G<sub>2</sub>< $10^{-1}$  ng/(mL.mm),  $10^{-1}$ <G<sub>3</sub>< $10^{-2}$  ng/(mL.mm),  $10^{-2}$ <G<sub>4</sub>< $10^{-3}$  ng/(mL.mm), and  $10^{-3}$ <G<sub>5</sub><0 ng/(mL.mm). (B) Fraction of MB-derived cells observed to respond via migration to the different concentration gradient fields (G<sub>1</sub> through G<sub>5</sub>) of EGF and SDF-1.



#### Figure 5. Motility of MB-derived cells in the $\mu$ Lane system

(A) Representative trajectories of cells that migrated in response to 100ng/mL of EGF and 100 ng/mL of SDF-1 stimulation. Three cell paths are shown in dashed for EGF and three in solid for SDF-1, 24 hours post steady-state. Note that concentration gradients decrease from left to right within the  $\mu$ Lane. (B) Maximum accumulated distance of motile cells stimulated by concentration profiles generated by using 100ng/mL of EGF and 100 ng/mL of SDF-1, respectively, in the SRR of the  $\mu$ Lane.

#### Table 1

# Transwell Results<sup>1</sup>.

Growth Factors	0 ng/mL [Mean ± SD cells]	1 ng/mL [Mean ± SD cells]	10 ng/mL [Mean ± SD cells]	100 ng/mL [Mean ± SD cells]	1000 ng/mL [Mean ± SD cells]
EGF	$102 \pm 5$	*	$156\pm5$	$212 \pm 7$	$174 \pm 5$
SDF-1	$60 \pm 2$	$67 \pm 6$	$69\pm14$	$72\pm5$	$74 \pm 4$
HGF	$99\pm5$	$126 \pm 10$	160 ±13	$122 \pm 7$	*
PDGF-BB	$82\pm5$	83 ± 5	$93\pm 8$	$100 \pm 5$	*

<sup>I</sup>Average numbers of MB-derived cells that migrated in transwell assays towards different concentrations of examined growth factors. Values were experimentally measured and are shown with mean and standard deviation.

\* denotes growth factor concentrations not measured in the current study.

## Table 2

Summary of migration parameters for EGF and SDF-1.<sup>2</sup>

Migration Parameters	EGF	SDF-1
Fraction of motile cells (f) [%]	72.8%	67.3%
Cell Directionality (D) [%]	61.6%	44.2%
Average Maximum Cell Path Length (PL) in µm [Mean ± SD]	$264.5\pm67.9\mu m$	$125.5\pm48.6\mu m$

<sup>2</sup>Migratory parameters of MB-derived cells along the  $\mu$ Lane system in response to concentration gradients generated by 100ng/mL of EGF and 100 ng/mL of SDF-1, respectively. Values were experimentally measured and shown as percentages, means and standard deviations. (n<sub>cells</sub> ~ 180 cells for each ligand).

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# Table 3

Summary of migration parameters in response to gradient fields of EGF and SDF-1.<sup>3</sup>

		EGF	Gradient F	ields			SDF-1	Gradient F	ields	
Migration Parameters	$G_1$	$\mathbf{G}_2$	G <sub>3</sub>	$G_4$	$G_5$	$\mathbf{G}_1$	$\mathbf{G}_2$	G <sub>3</sub>	$G_{G4}$	G5
Fraction of motile cells (f) [%]	28.3	18.6	11.9	10.3	3.7	18.2	20	13.8	8.7	6.5
Cell Directionality (D) [%]	28.3	15	7	8.6	2.7	18.4	10.5	9.8	2.2	3.3
Average Cell Path Length (PL) in $\mu m$ [Mean $\pm$ SD]	$281 \pm 21$	$267 \pm 40$	$226 \pm 23$	$284\pm28$	$389 \pm 20$	$154 \pm 34$	$114 \pm 39$	$124 \pm 42$	$94 \pm 18$	$127 \pm 37$

Figure 1, Rico, CMB

 $^3$ Migratory parameters of MB-derived cells in response to gradient fields, G1-G5, generated by of 100ng/mL of EGF or SDF-1 along the  $\mu$ Lane system, respectively. Fraction (f) and directionality (D) of motile cells shown as percentages of total cell numbers. Average maximum cell path lengths (PL) shown with mean and standard deviation. (ncells ~ 180 cells for each ligand).