Angiopoietin-2 Regulates Gene Expression in TIE2-Expressing Monocytes and Augments Their Inherent Proangiogenic Functions

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Abstract

TIE2-expressing monocytes/macrophages (TEMs) are a highly proangiogenic subset of myeloid cells in tumors. Here, we show that circulating human TEMs are already preprogrammed in the circulation to be more angiogenic and express higher levels of such proangiogenic genes as matrix metalloproteinase-9 (MMP-9), VEGFA, COX-2, and HIF1A than TIE2+ monocytes. Additionally, angiopoietin-2 (ANG-2) markedly enhanced the proangiogenic activity of TEMs and increased their expression of two proangiogenic enzymes: thymidine phosphorylase (TP) and cathepsin B (CTSB). Three "alternatively activated" (or M2-like) macrophage markers were also upregulated by ANG-2 in TEMs: interleukin-10 (IL-10), mannose receptor (MRCl), and CCL17. To investigate the effects of ANG-2 on the phenotype and function of TEMs in tumors, we used a double-transgenic (DT) mouse model in which ANG-2 was specifically overexpressed by endothelial cells. Syngeneic tumors grown in these ANG-2 DT mice were more vascularized and contained greater numbers of TEMs than those in wild-type (WT) mice. In both tumor types, expression of MMP-9 and MRCl was mainly restricted to tumor TEMs rather than TIE2+ macrophages. Furthermore, tumor TEMs expressed higher levels of MRCl, TP, and CTSB in ANG-2 DT tumors than WT tumors. Taken together, our data show that although circulating TEMs are innately proangiogenic, exposure to tumor-derived ANG-2 stimulates these cells to exhibit a broader, tumor-promoting phenotype. As such, the ANG-2-TEM axis may represent a new target for antiangiogenic cancer therapies. Cancer Res; 70(13); 5270-80. ©2010 AACR.

Introduction

TIE2-expressing monocytes/macrophages (TEMs) are a subpopulation of circulating and tumor-infiltrating myeloid cells with profound proangiogenic activity, found in both humans and mice (1–4). TEM ablation studies in mice have shown that this subpopulation plays a greater role in regulating tumor angiogenesis than TIE2+ tumor-associated macrophages (TAM; refs. 1, 5). Similarly, when circulating TEMs are coinjected with Matrigel in mice, microvessel density (MVD) is higher than that seen with TIE2+ monocytes, suggesting that they possess an inherent ability to stimulate angiogenesis (1, 4). Various phenotypic differences have emerged recently between TEMs and TIE2+ TAMs in murine tumors, with TEMs exhibiting various markers of an alternatively activated (i.e., M2-like) phenotype (5).

Angiopoietins are a family of molecules known to bind to, and activate, the TIE2 receptor on endothelial cells (EC; refs. 6–9). Angiopoietins play an essential role in regulating angiogenesis and vascular homeostasis. Angiopoietin-1 (ANG-1) maintains the integrity of the endothelium, whereas angiopoietin-2 (ANG-2) was thought until recently to destabilize the vasculature (10). However, it now seems that the exact influence of ANG-2 on endothelium is highly dependent on the local cytokine milieu. Together with other cytokines such as vascular endothelial growth factor (VEGF), ANG-2 stimulates angiogenic responses, but without such cofactors, it elicits vessel regression (7, 11, 12). During inflammation, ANG-2 also sensitizes the endothelium to tumor necrosis factor α (TNFα), and together, they regulate expression of adhesion molecules and leukocyte adherence (13).
In human tumors, the ANG-1/ANG-2 balance is often skewed in favor of ANG-2 and vascular remodeling. ANG-2 overexpression has been shown in several tumor types (14–19), where it is produced by the endothelium and occasionally by tumor cells (14, 20). ANG-2 has a complex and sometimes contradictory role during tumor progression. For example, ANG-2 overexpression by tumor xenografts leads to advanced proliferation, increased angiogenesis, and enhanced invasiveness (11, 14–16, 21–23), but it delays tumor growth and disrupts angiogenesis in other tumor types (24, 25). Syngeneic tumors grown in Ang-2 knockout mice show slower proliferation during the initial stages of tumor progression, decreased vessel diameter, and increased pericyte vessel coverage (26).

We recently reported that ANG-2 modulates the secretion of certain inflammatory cytokines by human monocytes in vivo (3, 4). However, information about the role of ANG-2 in regulating the tumor-promoting functions of TEMs is lacking. We therefore examined the influence of ANG-2 on expression of various tumor-promoting genes by human circulating TEMs in vitro and murine tumor-infiltrating TEMs in vivo.

Materials and Methods

Monocyte isolation and culture

Monocytes were isolated as previously described (3, 27). Pacific blue–conjugated anti-CD14 (1:20 per 10^6 cells; clone M5E2; BD Biosciences) and allophycocyanin (APC)–conjugated anti-TIE2 (1:10 per 10^6 cells; clone 83715; R&D Systems) antibodies were used to identify TEMs. Monocytes were sorted into cold Iscove's modified Dulbecco's medium (IMDM; BioWhittaker) containing 2% fetal bovine serum (FBS) and 2 mmol/L l-glutamine (Sigma-Aldrich) using a FACSAria II flow cytometer (BD Biosciences). Typically, 2 × 10^6 cells were collected from each sort with a purity of ≥90%. When required, 10^6 cells were seeded onto plastic with IMDM–2% FBS and then placed into a humified 37°C incubator with 5% CO_2.

Quantitative real-time PCR

Total RNA was extracted from monocytes using RNeasy kit (Qiagen). RNA from 10^6 cells was isolated immediately following fluorescence-activated cell sorting (FACS). For experiments involving ANG-1/ANG-2 treatment, sorted populations were cultured overnight, washed the next day, and then exposed to 300 ng/mL of recombinant angiopoietins (R&D Systems) for 6 hours. RNA (250–500 ng) was reverse transcribed using Precision RT kit (PrimerDesign). cDNA was amplified with Taqman master mix (Applied Biosystems) or Precision Mastermix (PrimerDesign) containing SYBR Green. PCR cycling conditions were as described using ABI 7900HT Sequence Detection System (Applied Biosystems; ref. 27). Samples were run on the same plate as the housekeeping gene [tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein (YWHAZ1) for SYBR Green probes, and β2-microglobulin for Taqman probes] in triplicate. Experiments were performed four to six times. Differences in gene expression were determined by the quantitative comparative C_t (threshold value) method.

Soluble protein analysis

Conditioned medium was collected from sorted monocyte subsets after 24 hours in culture. VEGF, interleukin (IL)-6, and IL-10 were quantified by cytometric bead array using a FACSArray bioanalyzer (BD Biosciences). Epidermal growth factor (EGF) levels were measured by ELISA (PreproTech). Matrix metalloproteinase-9 (MMP-9) activity was assessed by zymography in which proteins were separated in 10% SDS-polyacrylamide gels containing 0.1% gelatin. Following incubation in developing buffer, the gels were washed in distilled water and then stained with SimplyBlue SafeStain (Invitrogen). Quantification of band intensity was performed by using Imagej software (NIH, Bethesda, MD). Human ANG-2 (hANG-2) blood serum levels in mice were detected by ELISA (R&D Systems) after 1:2 dilution. All other soluble factors were analyzed with Bio-Plex Cytokine Assays (Bio-Rad).

In vitro EC activation assays

Medium was conditioned by TIE2–monocytes or TEMs for 24 hours and then incubated with 20 μmol/L MMP-9 Inhibitor I (Calbiochem), which inhibits MMP-1, MMP-9, and MMP-13, or 0.4% DMSO (vehicle control) for 1 hour at 37°C. The water-soluble thymidine phosphorylase (TP) inhibitor AEAC (6-[2-aminoethyl]amino-5-chlorouracil; 25 μmol/L; a gift from Dr. Edward Schwartz, Albert Einstein College of Medicine, Bronx, NY; refs. 28, 29) was incubated with sorted monocyte populations 1 hour before exposure to 300 ng/mL ANG-2, and then medium was collected after 24 hours. For the tubule formation assay, serum-starved human umbilical vein ECs (HUVEC; 8,000 cells/96-well) were resuspended in conditioned medium and seeded onto growth factor–reduced Matrigel (BD Biosciences). After 6 hours, tubule formation was measured using ImageJ software. For the spheroid/spouting assay, HUVEC spheroids (400 cells) were generated as described previously (30) and incubated for 24 hours with conditioned media. Images of sputing spheroids were taken with an Axiovert 100M microscope and Plan-NEOFLUAR 10×/0.30 objective lens. Capillary sputing length was quantified using AxiosVision Rel 4.4 digital imaging software (Zeiss). Every sput from 10 spheroids per group was measured, and the mean cumulative sput length was calculated. Both sets of in vitro assays were performed three times.

Immunoprecipitation and immunoblot analysis

Serum-starved HUVECs (2 × 10^6) or human monocytes (2 × 10^6) were treated with 300 ng/mL ANG-2. Cells were lysed in 50 mmol/L Tris and 100 mmol/L NaCl with 1% Triton X-100 containing protease and phosphatase inhibitors. After spinning at 14,000 rpm for 10 minutes, supernatant was collected. Protein lysates (40 μg) were precleared with protein A/G beads (Santa Cruz Biotechnology) and then incubated with 5 μg anti-TIE2 (clone 83711; R&D Systems) overnight at 4°C. Protein A/G beads were added for 2 hours at 4°C. IgG–protein A/G complexes were collected by centrifugation,
washed, and boiled in loading buffer before loading into 8% SDS-polyacrylamide gels. Separated proteins were transferred to nitrocellulose, blocked with 5% milk in TBS–Tween 20, and probed with anti–phospho-TIE2 (0.5 μg/mL; Y992; R&D Systems) overnight at 4°C. Membranes were washed and incubated with biotin-conjugated anti-rabbit antibodies (1:5,000; R&D Systems) for 1 hour at room temperature, followed by streptavidin–horseradish peroxidase (HRP; 1:200; R&D Systems) for 1 hour at room temperature. Bands were visualized by enhanced chemiluminescence (Amersham). Membranes were then stripped and reprobed with anti-TIE2 (1:250; clone 83711; R&D Systems) followed by HRP-conjugated goat anti-mouse antibodies (1:5,000; Dako). Similar experiments were repeated three times using three different blood donors.

For detection of TP, adherent human monocytes were treated with 300 ng/mL ANG-2, washed in cold PBS, and lysed. Proteins were separated on 10% SDS-polyacrylamide gels and transferred onto nitrocellulose. The remainder of the procedure was carried out as above using anti-TP antibodies (1:1,000; clone P-GE44C) purchased from Abcam followed by anti-mouse secondary.

**Murine tumor model**

TIE1-tTA–driven hAng-2 double-transgenic (DT) mice were generated as previously described (Supplementary Fig. S4A; refs. 31, 32). Mice were depleted of doxycycline were inoculated s.c. and allowed to propagate for 4 weeks (Supplementary Fig. S4A; refs. 31, 32). Mice were depleted of doxycycline 2 weeks before implantation of tumor cells (Supplementary Fig. S4B). Syngeneic Lewis lung carcinoma (LLC) cells (2 × 10⁶) were inoculated s.c. and allowed to propagate for 2 weeks. Caliper measurements were taken every 3 days, and tumor volume was calculated with the following formula: length × width²/2. Each group consisted of at least five mice and experiments were repeated four times. Animals were cared for in accordance with German Legislation on the Care and Use of Laboratory Animals.

**Immunohistochemistry and immunofluorescence confocal microscopy**

Detection of blood vessels and pericytes, assessment of MVD, and pericycle coverage were as described previously (33) using rat anti-mouse CD31 (BD Biosciences) and anti–α-smooth muscle actin (αSMA; Sigma). CD45, Gr-1, CD3, and B220 antibodies were purchased from BD Biosciences. Images were taken with a Nikon 80i microscope, and staining was analyzed with Soft Imaging Analysis System software at ×10 magnification. ApopTag In Situ Apoptosis Detection kit (Chemicon) was used as before (33). Assessment of hypoxic tumor regions was conducted as described previously (27) using Hypoxyprobe (HPI).

Detection of F4/80⁺TIE2⁻ TAMs and TEMs was performed using FITC-conjugated anti-F4/80 (1:25, clone CI:A3-1; AbD Serotec) and phycoerythrin-conjugated antimurine TIE2 (1:50; eBioscience). Anti–MMP-9 (1:500; a gift from Dr. Zena Werb, University of California, San Francisco, San Francisco, CA), anti–cathepsin B (CTSB; 15 μg/mL; R&D Systems), anti-TP (1:500; Abcam), and anti-MRC1 (1:25; R&D Systems) antibodies were detected by Alexa Fluor or 647–conjugated anti-goat or anti-rabbit secondary antibodies (1:500; Invitrogen). The anti–hANG-2 antibody (clone 180102) was from R&D Systems and used at 1:500. TP and ANG-2 antibodies were preabsorbed with secondary antibodies before incubation with tissue. Tumor vasculature was identified using APC-conjugated anti-CD31 (1:50; eBioscience). Nuclei were highlighted using 30 nmol/L 4’,6-diamidino-2-phenylinde (DAPI; Invitrogen) for 2 minutes. Images were captured using a Zeiss LSM 510 laser scanning confocal microscope. Further details about microscopy can be found in the Supplementary Data.

**Statistical analysis**

Student’s two-tailed t test (paired or unpaired as appropriate) or one-way ANOVA was used to determine P values using GraphPad Prism software. A P value of <0.05 was considered statistically significant. All data shown are mean ± SE.

**Results**

**Human TEMs are more proangiogenic than TIE2− monocytes in vitro**

Human TEMs and TIE2− monocytes were isolated from peripheral blood by FACS (Supplementary Fig. S1A), and increased TIE2 expression in TEMs was confirmed using quantitative real-time PCR (qPCR; Supplementary Fig. S1B). Interestingly, flow cytometry revealed that, unlike ECs, TIE1 expression on both monocyte subpopulations was negligible (Supplementary Fig. S2).

In the EC spheroid/sprouting assay, we found that TEMs induced significantly more sprouts than TIE2− monocytes (Fig. 1A). In the tubule formation assay, TEM-conditioned medium also significantly increased EC tubule length (Fig. 1B) and tubule area (47.9 ± 3.7 versus 32.5 ± 2.8 μm²; P = 0.02; data not shown) when compared with TIE2− monocyte-conditioned medium. Furthermore, addition of an MMP inhibitor significantly reduced the formation of tubules by TEMs (33.8 ± 3.6% reduction for length, 23.4 ± 4.1% reduction for area) but not TIE2− monocytes (data not shown).

We then used qPCR to examine mRNA expression levels of various tumor-promoting and M2 (i.e., alternatively activated macrophage)–associated genes, including proangiogenic factors (MMP-9, VEGF, EGF, FGFR, COX-2, CTSB, WNT5A, and TP/EGF1), immunomodulatory cytokines (TNFα, IL-1β, IL-6, IL-8, and IL-10), cell adhesion molecule (ICAM-1), and cell surface receptors (mannose receptor (MRCl), CXCR4, TLR-2, and TLR-4). TEMs expressed significantly higher levels of MMP-9 (Fig. 1C). Densitometric analysis of gelatin zymography showed a significant difference between the amount of pro–MMP-9 released by the cells (Fig. 1C), with TEMs producing more pro–MMP-9 than TIE2− monocytes (421.3 ± 42.1 versus 570.8 ± 57.1 relative units; P = 0.047; data not shown). MMP-2 activity was not detected.

In addition to MMP-9, TEMs expressed higher levels of VEGFA mRNA and released higher levels of VEGFA and TNFα protein than TIE2− monocytes (Fig. 1C). TEMs expressed higher levels of COX-2, MRCl, and WNT5A.
mRNA (Fig. 1C) but significantly lower levels of EGF mRNA
(−1.7 ± 0.1 fold difference; P = 0.007; data not shown) and
protein (13.2 ± 3.2 versus 4.6 ± 1.2 pg/mL; P = 0.035; data not
shown) than TIE2− monocytes. Expression of CTSB, CXCR4,
TP, ICAM-1, IL-1β, IL-6, IL-8, IL-10, TLR2, TLR4, or TNFα mRNA
was not significantly different between the two populations.
FGF2 mRNA was not detected in either subset.

**Agonistic effects of ANG-2 on human TEMs in vitro**

To investigate the possible effect of ANG-2 on the pheno-
type and function of TEMs, we first exposed freshly isolated
human monocytes and HUVECs to ANG-2 and examined
phosphorylation of TIE2. Activation typically occurred within
10 minutes of ANG-2 stimulation in both cell types, as vari-
ation between monocyte donors was minimal (Fig. 2A). Den-
sitometry revealed a 50% increase in phosphorylation at
10 minutes for monocytes.

Although expression of VEGF and MMP-9 mRNA was
not further increased by ANG-2 in TEMs (Fig. 2B), it sig-
nificantly upregulated expression of two other proangiogen-
ic enzymes, CTSB and TP (Fig. 2B and C), an effect
not seen in TIE2− cells. Increased TP protein levels were
confirmed by Western blot following exposure to ANG-2
(Fig. 2C).

The ability of ANG-2 to further enhance the inherent
proangiogenic functions of TEMs was then assessed. ANG-2
treatment of TIE2− monocytes failed to augment their rela-
tively low capacity to induce EC sprouts or tubule formation
(data not shown), whereas ANG-2 significantly increased the
ability of TEMs to activate ECs in both assays (Fig. 2D). This
stimulatory effect (64% increase for cumulative sprout length, 39% increase for tubule length, and 91% increase for tubule area) is greater than that reported previously for VEGF and FGF2 (34). Exposure of TEMs to a specific TP inhibitor had no effect on cell viability (data not shown) but significantly reduced their ability to activate ECs in response to ANG-2 (Fig. 2D).

In addition to CTSB and TP, ANG-2 also significantly up-regulated the expression of the two M2-associated genes, IL-10 and MRC1, by TEMs (Fig. 3A and B, left). IL-10 protein levels were significantly higher in TEM-conditioned medium following ANG-2 treatment (Fig. 3A, right), and flow cytometry showed an increase in MRC1 expression on TEMs following ANG-2 treatment (Fig. 3B, right). Both the percentage of TEMs expressing MRC1 [control (11.0 ± 5.3%) versus ANG-2 (17.1 ± 5.4%)] and the median fluorescence intensity [MFI: control (1.399 ± 58.1 arbitrary units) versus ANG-2 (1.918 ± 220.6 arbitrary units)] were significantly higher in the ANG-2–treated group (P = 0.0012 and 0.045, respectively). TEM expression of IL-6 mRNA was significantly reduced following ANG-2 stimulation; however, the amount of IL-6 secreted was not significantly different following ANG-2 treatment of TEMs (Fig. 3C). CCL17 mRNA was also significantly increased in TEMs by ANG-2 (2.7 ± 0.9 fold increase; P = 0.013; data not shown). All the other mRNA species screened by qPCR (EGF, COX-2, WNT5A, TNFa, IL-1β, IL-6, IL-8, ICAM-1, CXCR4, TLR-2, and TLR-4) were not altered by ANG-2 in either population (data not shown). Of note, only TEMs, not TIE2− monocytes, responded to ANG-2, indicating that the TIE2 receptor is required for its effects on TEMs.

Figure 2. ANG-2 induces phosphorylation of TIE2 and enhances the proangiogenic ability of human TEMs in vitro. A, human monocytes and HUVECs were exposed to 300 ng/mL of recombinant ANG-2, TIE2 was then immunoprecipitated from cell lysates, and phosphorylation was analyzed by immunoblotting. B, qPCR analysis of VEGF, MMP-9, and CTSB mRNA. C, upregulation of TP expression by ANG-2 as assessed by qPCR and immunoblotting. D, HUVEC sprouting assay (left) and tubule formation (right) after incubation with conditioned medium from untreated or ANG-2–treated TEMs. Where indicated, cells were preincubated with 25 μmol/L TP inhibitor (AEAC) before exposure to ANG-2. *, P < 0.05; **, P < 0.01, compared with TIE2− monocytes. †, P < 0.05; ‡, P < 0.01, compared with untreated TEMs. §, P < 0.05, compared with untreated TEMs + TP inhibitor; ¶, P < 0.05, compared with ANG-2–treated TEMs. Data from at least four replicate assays shown. Sprouting assay data are representative of three independent experiments.
Differential effects of ANG-1 on human TEMs in vitro

Unlike ANG-2, ANG-1 had no effect on TP, MRC1, IL-10, or CTSB mRNA levels in TEMs but significantly downregulated CCL17 mRNA and upregulated EGF mRNA levels (Supplementary Fig. S3). Like ANG-2, only TEMs responded to ANG-1, indicating that the TIE2 receptor is required for its effects on TEMs.

Effects of ANG-2 overexpression on the growth and vasculature of LLC tumors in vivo

We used a DT mouse model in which the vasculature specifically overexpresses hANG-2—termed ANG-2 DT (Supplementary Fig. S4A; ref. 32). LLCs were grown s.c. in these mice, and upregulation of hANG-2 in plasma was confirmed using ELISA (Supplementary Fig. S4C). The EC-specific upregulation of hANG-2 was validated by the immunofluorescent labeling of CD31, TIE2, and hANG-2 in LLCs (Supplementary Fig. S4D). Approximately 60% to 70% of CD31+ blood vessels expressed hANG-2 in ANG-2 DT tumors, with negligible expression seen in LLC grown in wild-type (WT) mice.

Although tumor volumes were not significantly different between WT and ANG-2 DT mice (Supplementary Fig. S5A), excised tumors from the latter group were more hemorrhagic than those grown in WT mice (Supplementary Fig. S5B) and contained significantly higher numbers of CD31+ microvessels (Fig. 4A). The vessels in ANG-2 DT tumors exhibited an immature phenotype (i.e., little or no pericyte coverage) and displayed increased levels of EC apoptosis (Fig. 4A). This accords well with the finding that ANG-2 DT tumors were more hypoxic than WT tumors (Fig. 4A).

Overexpression of ANG-2 increases TEM infiltration into tumors

As we previously showed that ANG-2 is a potent chemoattractant for human TEMs in vitro (3, 4), we investigated whether TEM infiltration into tumors was altered by hANG-2 overexpression. Immunohistochemistry showed that CD45+ leukocyte tumor infiltration (assessed as a proportion of total tumor area) was significantly increased in ANG-2 DT compared with WT tumors, with the majority of these cells being F4/80+ macrophages (Supplementary Fig. S5C). Similarly, immunofluorescent analysis replicated this increase in F4/80+ macrophages but also found a greater increase in the proportion of F4/80+TIE2+ cells (TEMs) than F4/80+TIE2− TAMs in ANG-2 DT tumors, suggesting selective recruitment of TEMs (Fig. 4B). These data were confirmed by flow cytometry analysis of enzymatically dispersed tumors (data not shown). The frequency of other leukocytes was unaffected, including Gr-1+ cells, CD3+ T cells, and B220+ B cells (data not shown). No differences in any leukocyte subsets were seen between normal tissues (i.e., brain, heart, and spleen) of WT and ANG-2 DT mice (data not shown).

TEM phenotype is affected by ANG-2 overexpression in vivo

A significantly greater number of MMP-9−expressing TEMs but not TIE2− TAMs were present in ANG-2 DT than WT tumors (Fig. 5A). This could be explained by the fact that virtually all TEMs—and <10% F4/80+TIE2− TAMs—expressed MMP-9 in both tumor types, and this difference in MMP-9 expression between these two macrophage populations was significant (Fig. 5A). In agreement with our in vitro studies, ANG-2 overexpression had no effect on the level of MMP-9 expression/TEM as assessed by the MFI per cell (Fig. 5A).

The frequency of MRC1+ TEMs was also greater in ANG-2 DT tumors than WT, with MRC1 expression being largely confined to TEMs and absent in F4/80+TIE2− TAMs (Fig. 5B). Figure 6 shows that the majority of both TEMs and TIE2− TAMs expressed CTSB and TP, but both were more abundant in ANG-2 DT tumors (due to increased numbers of TEMs and TIE2− TAMs in ANG-2 DT tumors).
Moreover, the expression of MRC1 (Fig. 5B), CTSB (Fig. 6A), and TP (Fig. 6B) per TEM was significantly increased in ANG-2 DT tumors.

Discussion

Myeloid cells are essential for blood vessel formation, maintenance, and function in tumors (35), and TEMs are one of the most proangiogenic subsets of these cells (1, 4, 5). It has previously been suggested that circulating human or mouse TEMs may be innately proangiogenic, as mice inoculated with tumor cells and TEMs form more vascularized tumors than those injected with tumor cells alone (1, 4). In the present study, we confirm that circulating human TEMs are indeed more proangiogenic than TIE2− monocytes and express higher levels of such potent proangiogenic factors as MMP-9, VEGF, COX-2, and WNT5A.

Interestingly, we also found that MMP-9 was widely expressed by the vast majority (>90%) of TEMs in tumors. Use of an MMP-9 inhibitor in vitro suggests that this enzyme plays an important role in mediating the innate, proangiogenic function of circulating TEMs. However, it should be noted that this inhibitor also reduces MMP-1 and MMP-13 activities, so the relative contribution of these three enzymes awaits further study.

We reported previously that ANG-2 is a chemoattractant for human TEMs in vitro, an effect mediated by TIE2 (3, 4). Our data here show that ANG-2 overexpression by the tumor vasculature results in greater infiltration of murine TEMs into tumors. This observation could be due to the direct chemotactic effect of ANG-2 on TEMs and/or the increased number of blood vessels present in ANG-2 DT tumors, allowing TEMs and other leukocytes greater access into tumors. At first glance, the latter possibility seems to be supported...
by our finding that the frequency of all CD45+ leukocytes was increased in ANG-2 DT tumors. However, the majority of CD45+ cells were F4/80+ TAMs and TEMs, whereas the number of Gr-1+ granulocytes, T cells, and B cells was not increased in ANG-2 DT tumors. The enhanced recruitment of TEMs may also be due to the increased level of tumor hypoxia seen in ANG-2 DT tumors, as hypoxia-induced CXCL12 attracts increased numbers of TEMs into tumors (36).

Here, we confirm that ANG-2 stimulates TIE2 receptor phosphorylation in human TEMs and upregulates their expression of several tumor-promoting factors. This result may seem unexpected given that some *in vitro* studies report...
that ANG-2 simply inhibits or dampens TIE2 signaling in response to ANG-1 in ECs (7). However, as mentioned previously, tumors often produce higher levels of ANG-2 than ANG-1 (10, 14–20), so the antagonistic role of ANG-2 on ANG-1 signaling is likely minimal in such tissues. Moreover, agonistic effects of ANG-2 on ECs and its ability to phosphorylate TIE2—even in the absence of ANG-1—have been reported (37, 38). TIE1 receptors on ECs can also modulate the effect of angiopoietins on TIE2 (39–41), although the agonistic effects of ANG-2 do not involve TIE1 (39, 41). As TIE1 is absent on TEMs, the agonistic effects of ANG-2 reported here also seem to be independent of TIE1.

We show that exposure to ANG-2 enhances the angiogenic potential of human TEMs in vitro by augmenting expression of two proangiogenic genes: TP and CTSB. TP catalyzes the breakdown of thymidine that forms a proangiogenic sugar,
2-deoxy-D-ribose (42). Previously, we and others reported that human TAMs express TP and that this correlates positively with tumor angiogenesis (43, 44). CTSB expression in human cancers has also been implicated in tumor progression and poor prognosis (reviewed in ref. 45). Recently, TAMs have been shown to be the major source of CTSB in various tumor models, and the proteolytic activity of this enzyme is critical for tumor growth, angiogenesis, and invasion (46, 47). Consistent with our in vitro results using human TEMs, murine TEMs in ANG-2 ΔT tumors exhibited greater expression of TP and CTSB than in WT tumors. ANG-2 upregulation of both TEM infiltration into tumors and their expression of such proangiogenic enzymes could explain the increased number of microvessels in ANG-2 ΔT compared with WT tumors. However, the tumor-promoting effect of these activated TEMs may have been countered by the direct deleterious effect of ANG-2 overexpression on the maturity and viability of ECs in ANG-2 ΔT mice, resulting in similar growth between tumor types.

We previously showed that human TEMs respond to ANG-2 by decreasing their expression of TNFα and IL-12 (3). We report here that ANG-2 further stimulates their high basal level of MRC1 in vitro. Although care needs to be taken when comparing the responses to ANG-2 of human blood TEMs in vitro with those of murine tumor TEMs in vivo, it is interesting to note that MRC1 expression by murine TEMs was higher in ANG-2 ΔT than WT tumors. We also found that ANG-2 upregulated the expression of the potent immunosuppressive factor IL-10 and the regulatory T-cell (Treg) chemokine CCL17. Interestingly, high levels of IL-10, CCL17, and MRC1 coupled with low levels of TNFα, IL-12, and IL-6 expression are indicative of an alternative ("M2") activation status in macrophages, a phenotype commonly associated with TAMs (48, 49). Furthermore, Pucci and colleagues (5) recently reported that murine tumor TEMs express a pronounced M2 phenotype. Our data indicate that ANG-2 in tumors may drive this M2-like polarization of TEMs. By contrast, ANG-1 induced a completely different gene expression profile from that seen with ANG-2, suggesting that TEMs can be skewed away from an M2-like phenotype in tissues where ANG-1 is more abundant.

In our study, high levels of ANG-2 expressed by the tumor vasculature seem to act in an autocrine manner, causing vascular disruption, as shown by increased EC apoptosis and consequent tumor hypoxia. Such antivascular effects of high-dose ANG-2 may override the enhanced, proangiogenic activity of ANG-2–stimulated TEMs. However, such effects of ANG-2 may be dose dependent and it is possible that lower levels of ANG-2 in tumors might have less pronounced antivascular effects so that ANG-2–stimulated TEMs would then induce further tumor angiogenesis and progression. On the other hand, the genetic knockout of Ang-2 in tumor models increases vascular maturation and pericyte coverage, resulting in an “angiostatic” phenotype, possibly from the enhanced availability of TIE2 to bind ANG-1 in the absence of ANG-2 (26). Our data (Supplementary Fig. S3) also suggest that, in the absence of ANG-2, ANG-1 stimulation of TEMs would not induce a proangiogenic or tumor-promoting phenotype. It will be interesting to investigate the effects of depleting ANG-2 in tumors on these two cell types using new-generation anti–ANG-2 inhibitors (50). Such studies are now warranted to see whether the ANG-2/TEM axis is a suitable target for anticancer therapy, as drugs that selectively target the ANG-2–TIE2 interaction may impair the biological activity of both angiogenic ECs and proangiogenic TEMs in the tumor microenvironment. However, it also remains to be seen whether other tumor-derived signals also contribute to shaping the proangiogenic activity and the insidious functions of TEMs in tumors.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Angiopoietin-2 Regulates Gene Expression in TIE2-Expressing Monocytes and Augments Their Inherent Proangiogenic Functions

Seth B. Coffelt, Andrea O. Tal, Alexander Scholz, et al.

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