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Dominik Rückerl,1 Stephen J. Jenkins,1 Nouf N. Laqtom,1,2 Iain J. Gallagher,3 Tara E. Sutherland,1 Sheelagh Duncan,1 Amy H. Buck,1 and Judith E. Allen1

1Institute of Immunology and Infection Research, Centre for Immunity, Infection and Evolution, School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom; 2Department of Biology, King Abdulaziz University, Jeddah, Saudi Arabia; and 3Medical Research Council Centre for Regenerative Medicine, University of Edinburgh, Edinburgh, United Kingdom

Macrophage (MΦ) activation must be tightly controlled to preclude overzealous responses that cause self-damage. MicroRNAs promote classical MΦ activation by blocking antiinflammatory signals and transcription factors but also can prevent excessive TLR signaling. In contrast, the microRNA profile associated with alternatively activated MΦ and their role in regulating wound healing or antihelminthic responses has not been described. By using an in vivo model of alternative activation in which adult Brugia malayi nematodes are implanted surgically in the peritoneal cavity of mice, we identified differential expression of miR-125b-5p, miR-146a-5p, miR-199b-5p, and miR-378-3p in helminth-induced MΦ. In vitro experiments demonstrated that miR-378-3p was specifically induced by IL-4 and revealed the IL-4–receptor/PI3K/Akt-signaling pathway as a target. Chemical inhibition of this pathway showed that intact Akt signaling is an important enhancement factor for alternative activation in vitro and in vivo and is essential for IL-4–driven MΦ proliferation in vivo. Thus, identification of miR-378-3p as an IL-4Rα–induced microRNA led to the discovery that Akt regulates the newly discovered mechanism of IL-4–driven macrophage proliferation. Together, the data suggest that negative regulation of Akt signaling via microRNAs might play a central role in limiting MΦ expansion and alternative activation during type 2 inflammatory settings. (Blood. 2012;120(11):2307-2316)

Introduction

Macrophages (MΦ) are involved centrally in recognizing and containing pathogens. Subsequently, they ensure the efficient induction and upkeep of a protective adaptive immune response. MΦ also help to limit the ensuing immune reaction as well as clear apoptotic cells and other debris. The adaption of MΦ to these diverse roles is reflected in the multitude of activation phenotypes that have been described. Classical (or M1) and IL-4Rα–driven alternative (or M2) activation represent the 2 most divergent phenotypes, with the former thought to be proinflammatory and important for the clearance of microbial pathogens, whereas the latter are predominantly found during helminth infections and are associated with wound healing and immunosuppression. In either case, MΦ activation must be closely controlled because excessive activation can lead to tissue destruction or fibrosis, respectively. Control is achieved by external signals, including cytokines (e.g., IL-10, IL-27) and hormones (e.g., glucocorticoids) but also by MΦ–intrinsic mechanisms. For example, classically activated MΦ become unresponsive to secondary stimulation with lipopolysaccharide (LPS) as the result, at least in part, of the induction of negative feedback loops blocking or limiting activating signaling cascades. The possibility that microRNAs may mediate such feedback mechanisms has recently attracted considerable interest.

MicroRNAs (miRNA) are short (18-24 nt), noncoding RNAs that influence the translation of specific genes by binding to the 3′-untranslated region (3′UTR) of the target messenger RNAs (mRNAs). The interaction between a miRNA and mRNA generally results in destabilization of the mRNA and repression of translation. In MΦ, miRNAs have so far been mainly studied during classical activation, where several miRNAs have been found to be differentially regulated (reviewed in O’Neill et al13). miR-125b-5p initially is down-regulated by LPS/TNF-induced Akt signaling to allow efficient TNF production14,15 but is induced during later stages, where it acts to limit further TNF production. Similarly miR-146a-5p is up-regulated upon stimulation with LPS and targets the MAPK-signaling pathway of TLRs, specifically IRAK1 and TRAF6. Thus, these miRNAs are part of feedback loops that prevent excessive MΦ activation and limit potentially harmful proinflammatory responses. Another M1-associated miRNA, miR-155, can suppress M2 activation by targeting the IL-13 receptor, suggesting that miRNAs also are involved in shaping the M1/M2 balance. Furthermore, miRNAs have been shown to control cellular proliferation, which has potential relevance to M2 MΦ activation because of the recent discovery that MΦ expansion can occur by IL-4–driven local proliferation rather than recruitment from the blood.

However, the miRNA-profile associated with alternative activation of MΦ has yet to be described. We therefore aimed to identify miRNAs differentially expressed in an in vivo model of alternative activation and dissect their functional roles. Microarray analysis of MΦ elicited by exposure to the nematode Brugia malayi identified miR-378-3p as one of the most robustly regulated...
miRNAs in this Th2 infection context, and experiments in vitro demonstrated that miR-378-3p was induced upon stimulation with IL-4. In silico analysis and miRNA manipulation studies identified potential miR-378-3p targets in the PI3K/Akt-signaling cascade, downstream of the IL-4 receptor. The finding that Akt is a target of miR-378-3p led us to test the consequences of Akt inhibition, revealing this signaling pathway as a critical component of IL-4–driven MΦ proliferation and alternative activation in vivo. Thus, it is likely that miRNAs are a general mechanism for limiting MΦ activation in both alternative and classical activation settings.

Methods

Mice and infection

Wild-type (WT; BALB/c or C57BL/6) and IL-4 receptorα–deficient (IL-4Rα−/−) mice on a BALB/c background were bred in house. Mice were 6-10 weeks of age at the start of each experiment, and all work was performed in accordance with the United Kingdom Animals (Scientific Procedures) Act of 1986. Adult B malayi parasites were isolated from the peritoneal cavity of infected jirds purchased from TRS Laboratories or eBioscience (both purchased from BioLegend or eBioscience) reaching purities of >80% pure LPS (100 ng/mL; Peprotech), LPS (100 ng/mL; Sigma-Aldrich), and recombinant IFNγ (rIFNγ; 20 ng/mL; Peprotech) or medium alone were added and incubated for various periods of time as indicated in the “Results.” For triciribine (1,5-dihydro-5-methyl-1-oxo-2H-furo[2,3-b]pyridine) or scrambled miRNA control, 5 μg of rIL-4 complexed to 25 μg of lipid (Exiqon), and hybridization and washing were carried out by following the manufacturer’s instructions. Results were analyzed using Bio-Rad’s Gene被捕放mits Luminator (BMG Labtech) following the manufacturer’s instructions. Relative luminescence was measured with the Dual-Luciferase Reporter Assay System (Promega) on a LumiStar luminometer (BMG Labtech) following the manufacturer’s instructions. Relative luminescence values were used for statistical analysis. Differences between groups were assessed by a Student t test (WT vs IL-4Rα−/− and WT vs Thio). The regulated miRNAs in each comparison were then selected on the basis of those with 2 or more significantly regulated probes and a log2 median intensity on the array greater than the 50th percentile. Our second analysis strategy used the limma suite in bioconductor. A linear model was fitted to each probe across all 4 groups and regulated miRNAs extracted by contrast. Similarly to our analysis of medians, we selected miRNAs as regulated if 2 or more probes for the miRNA had significant uncorrected P values and the median was greater than the 50th percentile. Lists from each analysis were then examined and overlapping miRNAs chosen for follow-up analysis. Microarray data have been deposited to NCBI’s Gene Expression Omnibus and are accessible through GEO Series accession no. GSE35047 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35047).

Dual-luciferase reporter assay

Whole 3′UTRs of target genes (ie, Akt1, Grb2) were cloned into the psiCHECK-2 vector (Promega) immediately downstream of the Renilla luciferase gene. Mutations in the 3′UTR of Akt1 or Grb2 were generated with the QuikChange Lightning Multi Site-Directed Mutagenesis Kit (Stratagene), resulting in altered binding sites for miR-378-3p (AGUC-CAG → AGUGGAG). NIH-3T3 fibroblasts were cotransfected with 200 ng of the psiCHECK-2 constructs and 2.5 pmol of synthetic miR-378-3p precursor (hsa-miR-378 premiR; Applied Biosystems) or scrambled miRNA control (premiR neg. control no. 1; Applied Biosystems) using Lipofectamine 2000 (Invitrogen). At 48 hours after transfection, relative luminescence was measured with the Dual-Luciferase Reporter Assay System (Promega) on a LumiStar luminometer (BMG Labtech) following the manufacturer’s instructions. Results were analyzed using Bio-Rad’s Gene被捕放mits Luminator (BMG Labtech) following the manufacturer’s instructions. Relative luminescence values were used for statistical analysis. Differences between groups were assessed by a Student t test (WT vs IL-4Rα−/− and WT vs Thio). The regulated miRNAs in each comparison were then selected on the basis of those with 2 or more significantly regulated probes and a log2 median intensity on the array greater than the 50th percentile. Lists from each analysis were then examined and overlapping miRNAs chosen for follow-up analysis. Microarray data have been deposited to NCBI’s Gene Expression Omnibus and are accessible through GEO Series accession no. GSE35047 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35047).

Affymetrix messenger RNA array and data analysis

To determine genes potentially regulated by miR-378-3p, NIH-3T3 cells were reverse-transfected with a miR-378-3p mimic or inhibitor (25nM) and compared with control-transfected RNA-induced silencing complex (RISC)–free siRNA cells. A total of 300 ng of total RNA was converted to cdNA with the GeneChip WT cDNA Synthesis and Amplification Kit (Affymetrix) and hybridized to Affymetrix GeneChip Mouse Gene 1.0 ST Array according to the manufacturer’s instructions. For the bioinformatic analysis, Partek Genomics Suite Version 6.5 software (Partek Inc) was used to assess the GeneChip quality control and perform gene expression analysis using Affymetrix metafiles. Data from 9 chips met the quality control requirements; thereby, all were included.

The RNA method was used to normalize and summarize the intensity levels of all 28 853 probes. On the basis of the (log 2 value) of negative control probes of each chip, the background fluorescence was calculated in StatPlus statistical tool pack software (AnalytSoft) and then used to statistically eliminate the microarray’s background noise generating a list of 12 665 probes. We used Partek software to compute the fold change and statistical significance (false discovery rate–adjusted P value) using 1-way ANOVA test. Microarray data have been deposited to NCBI’s Gene Expression Omnibus and are accessible through GEO Series accession no. GSE34873 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE34873).

In vivo IL-4 complex treatment

MΦ proliferation in vivo was stimulated by intraperitoneal injection of 5 μg of rIL-4 complexed to 25 μg of anti-IL-4 antibody (IL-4c; clone: 11B11; molar ratio 2:1). Where indicated, mice were pretreated intraperitoneally with triciribine (1 mg/kg) 1 hour before injection of IL-4c. At 21 hours after IL-4c injection, mice received 100 μL of BrdU (10 mg/mL; Sigma-Aldrich) subcutaneously, and PECs were harvested 3 hours later.
MΦ transfection experiments

RAW264.7 cells were stained with 5μM of Vybrant CFDA SE cell tracer (Invitrogen) followed by reverse transfection with a miR-378-3p mimic or inhibitor (25nM) as described previously and analyzed for cellular expansion after 24 hours and 48 hours. At 4 hours before the end of the incubation, 100 μL of alamarBlue was added to the culture. Cell proliferation was analyzed by measuring alamarBlue conversion in a Fluostar (BMG Labtech) fluorescence plate reader and Vybrant CFDA SE dilution by FACS analysis. Data were pooled from 3 experiments and are presented as percent of control to account for inter-experimental changes in staining intensity.

Statistical analysis

Statistical analysis was performed with JMP statistical analysis software (JMP 8.0.1; SAS Institute Inc). Differences between groups were determined by ANOVA followed by a Tukey-Kramer HSD multiple comparison test. In some cases, data were log-transformed to achieve normal distribution as determined by optical examination of residuals, or where this was not possible, a Kruskal-Wallis test was used. Differences were considered statistically significant for P<.05.

Results

To identify miRNAs differentially regulated in alternatively activated MΦ in vivo, we performed a miRNA array screen on peritoneal MΦ isolated from mice surgically implanted with the parasitic nematode B. malayi. As described previously, B. malayi implant results in a very strongly Th2-biased immune response and induces the accumulation of alternatively activated MΦ at the site of implantation. For comparison, we used IL-4Rα-deficient (IL-4Rα−/−) animals whose MΦ fail to express alternative activation markers in this model. Additional WT mice underwent sham surgery and were injected with Thio 3 days before necropsy to generate inflammatory MΦ not associated with helminth infection. A 2-way comparison of WT nematode-elicited MΦ (NeMΦ) with Thio-elicited MΦ (Thio-MΦ) or IL-4Rα−/− NeMΦ allowed us to identify infection-dependent and IL-4Rα-independent miRNAs, respectively. At 3 weeks after implantation, MΦ were isolated from the peritoneal cavity by adherence to cell-culture plates and total RNA extracted. The expression levels of 648 unique human and mouse miRNAs in their mature form were determined by use of the Exiqon miRCurry 8.1 array platform. Bioinformatic analysis (see “miRNA microarray” for details) revealed differential expression of 19 miRNAs in WT NeMΦ compared with either Thio-MΦ or IL-4Rα−/− NeMΦ (supplemental Table 2).

We then chose to validate expression levels of the 10 most differentially regulated miRNAs (ie, greatest fold change) identified in the array. A proportion of the originally isolated RNA was subjected to quantitative RT-PCR (qRT-PCR), with further analysis in 2 subsequent experiments using FACS-sorted MΦ (>90% F4/80"CD11b") of the macrophage population (Table 1 and Figure 1A). miR-125b-5p, miR-199b-5p, and miR-378-3p were found to be significantly up-regulated in vivo, whereas miR-146a-5p showed a tendency toward an IL-4Rα-dependent downmodulation (Figure 1A). This tendency in miR-146a-5p expression was statistically significant (P=.0022) when all 3 experiments were combined. To confirm the activation state of the isolated MΦ, expression of the alternative activation marker chitinase 3-like 3 (Chi3l3/Ym1) was measured and, as expected, found to be exclusively up-regulated in WT NeMΦ but not in IL-4Rα−/− MΦ (Figure 1B).

<table>
<thead>
<tr>
<th>miRNA-ID</th>
<th>Array</th>
<th>qRT-PCR</th>
<th>miRNA-Id</th>
<th>Array</th>
<th>qRT-PCR</th>
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<td>4.90</td>
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<tr>
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<td>–</td>
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<tr>
<td>miR-150-5p</td>
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<td>–</td>
<td>–1.97</td>
<td>–2.15</td>
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<td>4.59</td>
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<tr>
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<tr>
<td>miR-222-3p</td>
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<tr>
<td>miR-342-3p</td>
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<td>–1.81</td>
<td>–</td>
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<tr>
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<td>2.28</td>
<td>2.14</td>
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</tr>
<tr>
<td>miR-689</td>
<td>–</td>
<td>–</td>
<td>–2.56</td>
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– indicates not significant.

It was possible that the changes we observed were the result of secondary (IL-4Rα-dependent) events occurring in vivo and not because of direct MΦ activation via IL-4/13. Thus, we tested the expression of miR125b-5p, miR-146a-5p, miR-199b-5p, and miR-378-3p in Thio-MΦ stimulated in vitro with rIL-4 and LPS and rIFNγ (Figure 1C). qRT-PCR revealed significant up-regulation of miR-125b-5p and miR-378-3p after treatment with IL-4 but not after LPS/IFNγ-stimulation, confirming the association of these miRNAs with the alternative activation phenotype. In contrast, miR-199b-5p was not altered by IL-4 or LPS/IFNγ treatment, indicating that the observed up-regulation in vivo is not because of direct effects of IL-4–signaling on MΦ. miR-146a-5p has previously been found to be highly up-regulated in classically activated MΦ and was consequently specifically induced by LPS/IFNγ stimulation, but no change in expression could be detected by IL-4 stimulation in vitro at this time point (Figure 1C). Successful and specific induction of alternative activation under these conditions was confirmed by Chi3l3-expression (Figure 1D).

miR-125b expression in MΦ has previously been demonstrated to be modulated by factors other than IL-4,15,16 We selected miR-378-3p for further investigation into its potential to regulate alternative activation of MΦ because it appeared to be the most specific for IL-4Rα-mediated signals. Furthermore, miR-378-3p was of particular interest because it is encoded in an intronic region of the peroxisome proliferative–activated receptor, gamma, coactivator 1 β gene (Ppara/lb),26 which has previously been shown to be associated with the alternative activation phenotype.27 To evaluate whether up-regulation of miR-378-3p was a prerequisite for alternative MΦ activation or a consequence thereof, we performed in vitro time-course experiments of IL-4 stimulation (Figure 2) in which Thio-MΦ were incubated with murine rIL-4 for 1, 4, 16, 28, and 45 hours. Cells were subsequently analyzed for miRNA and mRNA expression with qRT-PCR. Significantly increased levels of Chi3l3 expression were detectable as early as 4 hours after treatment of MΦ with IL-4 and continued to increase until the end of the experiment. In contrast, miR-378-3p was not significantly up-regulated until 16 hours after the addition of IL-4 but remained elevated thereafter. Notably, classical activation of MΦ via the use of LPS/IFNγ did not result in the up-regulation of Chi3l3 or miR-378-3p at any time point but potentially induced expression of inducible nitric oxide synthase 2 (Nos2) and miR-146a-5p as described previously,17,28 Interestingly, in line with our in vivo data (Figure 1A), miR-146a-5p was...
significantly reduced after IL-4 stimulation at very late time points (45 hours) but not at 24 hours. This finding might explain why we were unable to detect a direct effect of IL-4 on miR-146a-5p expression in the previous in vitro experiments measured at 16 hours after treatment (Figure 1C).

To examine cellular genes that respond to changes in miR-378-3p expression, we used a murine fibroblast cell line that expresses miR-378-3p and supports miRNA overexpression and inhibition analysis, as described. NIH-3T3 fibroblasts were transfected with either miR-378-3p-mimics or inhibitors and resulting changes in gene expression analyzed with an Affymetrix-mRNA array. We were able to identify 491 significantly differentially expressed genes (false discovery rate; \( P < .05 \)) with more than 1.4-fold change in either of the 2 conditions compared with a negative-control. Pathway enrichment analysis of these differentially expressed genes by DAVID Bioinformatics Resources for gene annotation and KEGG pathway analysis (http://david.abcc.ncifcrf.gov/tools.jsp) revealed the Jak-STAT signaling pathway as significantly over-represented (EASE-score \( P < .05 \)).

More specifically, in conjunction with the online prediction software TargetScan (TargetScanMouse; Release 5.1:April 2009; http://www.targetscan.org) several potential target-genes within the
Figure 3. miR-378-3p targets the IL-4R/Pi3K/Akt-signaling pathway. (A) Schematic depiction of the IL-4R–signaling cascade highlighting putative targets for miR-378-3p. Yellow indicates predicted by TargetScan (yellow) and differentially expressed in pre- and anti-miR-378-3p–transfected fibroblasts. (B) Analysis of rIL-4–elicited STAT-6 phosphorylation by intracellular FACS staining. Histogram of STAT-6 (pY641) expression in Thio-MΦ preincubated with rIL-4 (orange line) or medium (red line) for 24 hours before restimulation with rIL-4 (open histograms) or medium (filled gray histograms) for 5 minutes. Timeline of pSTAT-6 (pY641) expression in rIL-4 (orange squares) or medium (red circles) pretreated, rIL-4–stimulated (colored symbols) or unstimulated (gray symbols) cells. Data show median fluorescence intensity of 6 individual animals ± SEM. For unstimulated controls, cells were pooled from several animals. Asterisks indicate statistical differences between rIL-4–preincubated and freshly stimulated MΦ. ***P < .001; **P < .01. (C) Luciferase-assay using the 3’UTR of wild-type Akt-1 (Akt-1) or constructs with mutated seed-region binding sites for both predicted miR-378-3p binding sites (mut) or without insert (empty). Data indicate cotransfection with a miR-378-3p mimic (black bars) or a scrambled control (open bars). Data are pooled from 5 separate experiments and depicted as relative luminescence compared with no-RNA controls (gray bars). Bars not connected by the same letters are statistically significantly different. (D) Representative Western blot analysis of RAW264.7 cells 12 hours after transfection with a mimic (pre-378) or inhibitor (anti-378) of miR-378-3p or appropriate negative controls (pre- and anti-neg). Samples were separated on 4%-12% Bis-Tris gels and stained for Akt-1 and j-actin at the same time. (E) Densitometric analysis of the samples analyzed in panel D. Data are representative of 4 separate experiments. Columns not connected by the same letters are statistically significantly different.

IL-4Rα/Pi3K/Akt–signaling cascade could be identified. Figure 3A illustrates the components of the IL-4Rα pathway that were predicted by TargetScan (yellow) and differentially expressed in transfected fibroblasts (red). In particular Akt-1 was identified in both analyses. This finding suggested the possibility that IL-4 induction of miR-378-3p results in a negative feedback on the IL-4 signaling pathway. Because receptor “tolerance” has not previously been described for this pathway, we tested whether IL-4 does induce a negative feedback-mechanism by measuring STAT-6–phosphorylation in Thio-MΦ after secondary IL-4 stimulation. As outlined in Figure 3B, MΦ that had previously been exposed to IL-4 showed reduced and delayed STAT-6 phosphorylation in response to secondary IL-4 stimulation.

To obtain direct evidence that miR-378-3p targets the Pi3K/Akt1-pathway, we generated Luciferase-constructs containing the 3’UTR of thymoma viral proto-oncogene 1 (Akt1) or a mutated version thereof where 2 nucleotides within both seed-region-binding sites for miR-378-3p were altered (supplemental Figure 1A). As shown in Figure 3C, cotransfecting NIH-3T3 fibroblasts with a mimic of miR-378-3p significantly inhibited Luciferase expression compared with cells transfected with the Luciferase construct alone or cotransfected with a negative control RNA. Importantly, these effects were lost when both miR-378-3p–binding sites within the Akt1-3’UTR were mutated. Furthermore, transfection of RAW264.7 cells led to a marked decrease in Akt-1 protein levels as assessed by Western blot analysis (P < .01 in every comparison; Figure 3D-E).

Similar results were obtained for growth factor receptor–bound protein 2 (Grib2; P < .05; supplemental Figure 1B-D). Interestingly, the use of a miR-378-3p inhibitor increased protein expression of Akt-1 in some experiments, but this was not significant when the data of several experiments were combined (Figure 3D-E).

The identification of Akt as a target of miR-378-3p led us to assess the potential influence of Akt-inhibition on MΦ alternative activation by using a specific Akt inhibitor, triciribine (Figure 4). Preincubation of Thio-MΦ with triciribine severely disrupted their ability to fully alternatively activate in a dose-dependent manner as shown for the expression of Chi3l3, resistin-like α (Retnla/Relm-α) and arginase 1 (Arg1; Figure 4). Of note, Akt inhibition differentially affected the expression of these markers with complete abrogation of IL-4–driven Retnla but only partial inhibition of Chi3l3 and Arg1 induction. In contrast, other marker genes of alternative MΦ activation (eg, Cd36, Pparg, Pparc1b) were not negatively influenced by the inhibition of Akt. Thus, limiting Akt-signaling does not completely block IL-4–mediated alternative activation but changes the associated gene expression profile, perhaps to generate cells better suited to chronic type-2 inflammatory settings.

We recently demonstrated that proliferation of the local MΦ population is an integral part of Th2-mediated inflammation with no requirement for blood monocyte recruitment. The expansion in cell numbers after surgical implantation of B malayi nematodes occurs as an early burst of rapid cellular proliferation, which then
subsides (supplemental Figure 4 in Jenkins et al20). Of note, RNA isolated from these MΦ revealed a delayed increase in miR-378-3p expression that peaked when MΦ proliferation subsided and Akt1 gene expression declined (Figure 5). Critically, injection of active IL-4 alone can drive this proliferative program in vivo. Because both miRNAs and the PI3K/Akt pathway inherently are associated with cellular growth and proliferation, we speculated that IL-4–
driven MΦ proliferation is mediated via Akt signaling, with miR-378-3p and possibly other miRNAs acting as negative regulators.

We thus chose to test the role of Akt-signaling during IL-4–
mediated MΦ proliferation. For this, mice received a single dose of
triciribine or vehicle control intraperitoneally 1 hour before the injection of IL-4 complexed with anti–IL-4 antibody (IL-4c), which allows sustained delivery of active cytokine.20 After 21 hours, mice were injected with BrdU to label cells in the S-phase, and 3 hours later peritoneal exudate cells were analyzed for expression of proliferation and alternative activation markers by FACS. Pretreatment with triciribine completely abrogated IL-4c–induced Mφ proliferation as measured by the incorporation of BrdU or expression of Ki67 (Figure 6A). Simultaneously, protein levels of the alternative activation marker Relm-α were only partially reduced and YM-1 expression did not seem affected at all. These data indicate that similar to the effects observed in vitro, IL-4–induced Akt-signaling is responsible for only specific features of alternative Mφ activation but is essential for IL-4–driven proliferation.

Furthermore, to establish a role for miR-378-3p in the regulation of Mφ proliferation, we transfected RAW264.7 cells with a miR-378-3p mimic or inhibitor and analyzed the resulting changes in cellular expansion. Conversion of alamarBlue and loss of Vybrant CFDA SE staining were used to monitor cell expansion and cell division, respectively. During a 24-hour period, cells transfected with the miR-378-3p mimic displayed a significantly reduced increase in the conversion of alamarBlue (Figure 6B) and loss of Vybrant CFDA SE staining (Figure 6C), demonstrating that miR378-3p negatively regulated cell proliferation. Transfection with the miR-378-3p inhibitor had no effect on cellular expansion, indicating that only enhanced miR-378-3p expression as found after IL-4 stimulation regulates proliferation. What is more, gene-expression analyses of RAW264.7 cells transfected with miR-378-3p showed significant reduction in expression of Akt-1 and Grb2, as well as the putative target Pik3cb (Figure 3A) and the proliferation marker Mki67 (Figure 6D). Taken together, these results are consistent with a negative regulation of Mφ proliferation by miR-378-3p through modulation of the PI3K/Akt-signaling pathway.

IL-4 impacts the activation state of many cell types, and the PI3K/Akt pathway regulates cellular expansion in various biologic settings. Thus, to determine whether induction of miR-378-3p and therefore potential regulation of PI3K/Akt signaling was a general characteristic of either Mφ proliferation or IL-4 signaling in other cell types, we analyzed miR-378-3p expression in Mφ during IL-4–independent, M-CSF–driven proliferation and in B and T cells after IL-4c stimulation in vivo. As expected, treatment of Thio-Mφ with rM-CSF in vitro stimulated Mφ proliferation as confirmed by increased gene expression of Mki67 (Figure 7A). However, at no point after stimulation could the induction of miR-378-3p or its parent gene (Pparg1b) be detected.

Similarly, enhanced expression of miR-378-3p and Pparg1b after IL-4c injection in vivo was found in peritoneal Mφ (F4/80+CD11b+) but not in B cells (CD19+FcγR), CD4+ (CD4+CD11b−), or CD8+ lymphocytes (CD8+CD11b−) isolated...
2 independent experiments, except for the CD8
Bars depict mean and SEM of 10 individual animals per group pooled from
types, the mechanisms controlling these effects are governed by
although IL-4 signaling has widespread effects on various cell
miR-378-3p in other cells stimulated with IL-4c shows that
dependent or independent. Furthermore, the lack of induction of
in M-CSF–stimulated macrophages indicates that miR-378-3p is
confirmed in our data by increased expression of cyclin A2
(Ccna2
previously, miR-378-3p is encoded in an intronic region of
form of miR-378-3p is delayed with respect to its parent gene and
targets of IL-4–induced gene transcription. However, the mature
expression, which would suggest that
pressed by 4 hours after IL-4 stimulation, which would suggest that
activation.
other factors and/or that IL-4 is not sufficient. Interestingly
another miRNA, miR-223-3p, has recently been described to be
associated with the alternative activation phenotype.
Indeed, miR-223-3p was significantly enhanced in WT NeMΦ vs IL-
4Rα−/− NeMΦ in our array but was not among the most highly
differentially expressed microRNAs in this in vivo setting and thus
differently in this study.
Both miR-125b-5p and miR-146a-5p have already been associated
with classical MΦ activation. miR-125b-5p expression is
initially reduced after LPS stimulation, allowing efficient production
of its target, the proinflammatory cytokine TNF-α, but
miR-125b-5p is then up-regulated during LPS-tolerance to prevent
further/excessive TNF production. Thus, miR-125b-5p up-
regulation in alternatively activated MΦ may represent a failsafe
switch preventing concomitant production of proinflammatory
mediators like TNF-α. miR-146a-5p, on the other hand, is normally
induced after classical activation of monocytes and is presumed to
act in a feedback loop, blocking further TLR and cytokine
signaling. Downmodulation of this miRNA in IL-4–stimulated
MΦ could enhance TLR signaling and thus seems counterintuitive.
However, reduced levels of miR-146a-5p did not occur until very
late after IL-4 stimulation (Figure 3), and long-term preincubation
of MΦ with IL-4 has previously been shown to potentiate
production of proinflammatory cytokines after secondary stimula-
tion with LPS. Thus, whereas up-regulation of miR-125b-5p
might help prevent concomitant production of inflammatory mediators like TNF-α, miR-146a-5p–downmodulation may simultaneously sensitize
MΦ for potential bacterial pathogens and allow MΦ to quickly adapt their activation phenotype to newly arising challenges. Further experiments are needed to determine the exact role of these
2 miRNAs in shaping MΦ activation.

Figure 7. Induction of miR-378-3p is specific to IL-4–mediated signaling in MΦ.

(A) Thio-elicited, adherence-purified MΦ were incubated with rIL-4 (black squares),
m-CSF (gray circles), or with medium alone (open squares) for the indicated time
and analyzed for miRNA and mRNA expression. Statistics indicate differences
between M-CSF–treated samples and rL-4 controls. ***P < .001. Each data point
represents mean and SEM of 6 individual animals. Results from a single experiment
shown. (B) CD11b+/F4/80+ (MΦ), CD19+/F4/80− (B cells), CD4+/CD11b−
lymphocytes (CD4+) and CD8+ CD11b− lymphocytes (CD8+) were FACS-sorted from IL-4c
injected (filled bars) or PBS-injected control animals (open bars) and subjected to
qRT-PCR. Data are depicted as fold change above PBS controls. Statistics indicate
differences between IL-4c–treated samples and PBS-controls. ***P < .001; *P < .05.
Bars depict mean and SEM of 10 individual animals per group pooled from
2 independent experiments, except for the CD8+ data, which is from 1 representative
experiment. The second experiment is not shown because Ccna2 in the PBS
controls was not detectable resulting in a fold change of infinity for the IL-4c treatment.

from the same animal (Figure 7B). Of note, IL-4c has previously
been shown to also induce proliferation of CD8+ lymphocytes, as
confirmed in our data by increased expression of cyclin A2 (Ccn2).
The failure to induce miR-378-3p in these cells as well as
in M-CSF–stimulated macrophages indicates that miR-378-3p is
not a general feature of cellular proliferation, whether IL-4
dependent or independent. Furthermore, the lack of induction of
miR-378-3p in other cells stimulated with IL-4c shows that
although IL-4 signaling has widespread effects on various cell
types, the mechanisms controlling these effects are governed by
different regulatory mechanisms. Induction of miR-378-3p there-
fore appears to be a very specific feature of alternative MΦ
activation.

Discussion

MΦ isolated from mice infected with the human filarial parasite
B malayi become alternatively activated because of exposure to
Th2 cells. In this in vivo setting, we have identified changes in
MΦ expression of miR-125b-5p, miR-199b-5p, miR-378-3p, and
miR-146a-5p associated with IL-4Rα–driven alternative activation.
In vitro confirmation revealed that miR-125b-5p, miR-378-3p,
and miR-146a-5p were directly regulated by IL-4, whereas
miR-199b-5p was not, suggesting miR-199b-5p is induced in vivo
by other factors and/or that IL-4 is not sufficient. Interestingly
another miRNA, miR-223-3p, has recently been described to be
associated with the alternative activation phenotype.
Indeed, miR-223-3p was significantly enhanced in WT NeMΦ vs IL-
4Rα−/− NeMΦ in our array but was not among the most highly
differentially expressed microRNAs in this in vivo setting and thus
not pursued in this study.

Both miR-125b-5p and miR-146a-5p have already been associated
with classical MΦ activation. miR-125b-5p expression is
initially reduced after LPS stimulation, allowing efficient production
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MΦ for potential bacterial pathogens and allow MΦ to quickly adapt their activation phenotype to newly arising challenges. Further experiments are needed to determine the exact role of these
2 miRNAs in shaping MΦ activation.

Here we focus on the new finding that up-regulation of
miR-378-3p is part of the alternative MΦ activation program. This
finding is consistent with a report that miR-378-3p is up-regulated
in a model of allergic airway inflammation. Although the authors
did not perform cell-type specific analyses, the inflammatory
response in these models is characterized by the accumulation of
MΦ exhibiting an alternative activation phenotype. As noted
previously, miR-378-3p is encoded in an intronic region of
Ppargc1b, a protein associated with alternative activation.
Thus, coexpression of miR-378-3p may have evolved to complement
the role of the protein-encoding gene. Ppargc1b is expressed by 4 hours after IL-4 stimulation, which would suggest that
Ppargc1b and the primary transcript of miR-378-3p are primary
targets of IL-4–induced gene transcription. However, the mature
form of miR-378-3p is delayed with respect to its parent gene and
other alternative activation markers and thus secondary factors may be needed to regulate its processing.

We identified several miR-378-3p targets within the IL-4R–signaling cascade and more specifically within the PI3K/Akt-signaling pathway. Previous work by MacKinnon et al showed that signaling via PI3K is important for full alternative activation of MΦ.\(^{38}\) and we have extended these findings by using the Akt–specific inhibitor triciribine, confirming Akt as an important downstream target of PI3K during IL-4–induced alternative activation. Interestingly Varin et al showed that pretreatment of MΦ with IL-4 prevented subsequent Akt signaling induced by *Neisseria meningitidis*, suggesting the induction of a feedback inhibitory mechanism by IL-4.\(^{39}\) Importantly these effects were not observed until approximately 12 hours after IL-4 stimulation, a time point that roughly coincides with the induction of miR-378-3p in our experiments. In addition miR-378-3p has been predicted to target the progesterone-receptor,\(^{40}\) and progesterone has been shown to be an important enhancement factor for alternative activation in wound healing.\(^{41}\) Taken together, these findings strongly suggest a role for miR-378-3p as feedback inhibitor of alternative activation.

In this context PI3K/Akt signaling has been shown to enhance antiinflammatory cytokine production during classical MΦ activation and simultaneously reduce production of proinflammatory cytokines.\(^{42}\) Thus, induction of miR-378-3p and limitation of Akt-signaling in alternatively activated MΦ could, similar to our findings with miR-146a-3p, indicate a sensitization for potential concomitant bacterial infections.

PI3K/Akt is a central signaling pathway important for cellular growth and survival, triggered by various growth factors and insulin but also by cytokines and TLR stimulation.\(^{43}\) Although tissue MΦ typically have been regarded as nondividing, recent data show that resident MΦ numbers can be maintained by proliferation.\(^{20,44,45}\) We further demonstrated that tissue MΦ can undergo rapid and extensive proliferation in vivo in response to IL-4 as a mechanism of Th2–driven inflammation that can replace monocyte proliferation. This study has generated the novel and important finding that miR-378-3p is an IL-4–dependent miRNA up-regulated in MΦ both in vitro and in vivo, which targets the Akt-signaling pathway. Importantly, this finding has led to the independent observation that the local MΦ proliferation that occurs during Th2 mediated inflammation relies on Akt. This has important therapeutic implications as PI3K/Akt inhibitors are already being developed to target proliferation during cancer\(^{50,51}\) and thus might have off target effects on MΦ. In addition, efforts to target this pathway may generate important therapeutics to control MΦ proliferation, which is believed to exacerbate diseases such as glomerulonephritis and atherosclerosis.\(^{52,53}\)

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**Authorship**

Contribution: D.R. designed and performed research, analyzed and interpreted data, and wrote the manuscript; S.J.J. performed research, analyzed and interpreted data, and contributed vital new analytical tools; N.L. performed research, analyzed and interpreted data; I.G. analyzed and interpreted data; T.E.S. contributed vital new tools; S.D. performed research; and A.H.B. and J.E.A. contributed to data interpretation, manuscript preparation, and project supervision.

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Correspondence: Judith E. Allen, The University of Edinburgh, Institute of Immunology and Infection Research, Ashworth Laboratories, West Mains Rd, EH9 3JT Edinburgh, United Kingdom; e-mail: j.allen@ed.ac.uk.

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