Gata6 regulates aspartoacylase expression in resident peritoneal macrophages and controls their survival

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Gata6 regulates aspartoacylase expression in resident peritoneal macrophages and controls their survival

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The transcription factor Gata6 regulates proliferation and differentiation of epithelial and endocrine cells and cancers. Among hematopoietic cells, Gata6 is expressed selectively in resident peritoneal macrophages. We thus examined whether the loss of Gata6 in the macrophage compartment affected peritoneal macrophages, using Lyz2-Cre x Gata6flox/flox mice to tackle this issue. In Lyz2-Cre x Gata6flox/flox mice, the resident peritoneal macrophage compartment, but not macrophages in other organs, was contracted, with only a third the normal number of macrophages remaining. Heightened rates of death explained the marked decrease in peritoneal macrophage observed. The metabolism of the remaining macrophages was skewed to favor oxidative phosphorylation and alternative activation markers were spontaneously and selectively induced in Gata6-deficient macrophages. Gene expression profiling revealed perturbed metabolic regulators, including aspartoacylase (Aspa), which facilitates generation of acetyl CoA. Mutant mice lacking functional Aspa phenocopied the higher propensity to death and led to a contraction of resident peritoneal macrophages. Thus, Gata6 regulates differentiation, metabolism, and survival of resident peritoneal macrophages.

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to proliferate during an inflammatory challenge was compromised (Rosas et al., 2014) and identification of retinoic acid as a signal that induces Gata6 in peritoneal macrophages (Okabe and Medzhitov, 2014). However, neither study explained what cellular events caused contraction of the macrophage pool within the peritoneum under resting conditions. Here, we show that apoptosis is induced in peritoneal macrophages in the absence of Gata6, at least in part because Gata6 expression either directly or indirectly supported expression of aspartoacylase (Aspa) that deacetylates N-acetyl aspartate. Mice bearing mutations in Aspa likewise displayed reduced macrophage counts concomitant with increased death. However, only the more global Gata6 deficiency, but not single deficiency in Aspa, resulted in a selective and seemingly cell autonomous polarization of peritoneal macrophages toward an alternatively activated phenotype. Collectively, these data delineate a role for Gata6 in regulating macrophage survival and activation state.

RESULTS AND DISCUSSION

The transcription factor Gata6 was expressed only in F4/80\(^{hi}\) peritoneal macrophages, corresponding with ICAM-2\(^{+}\) peritoneal macrophages (Gautier et al., 2012), within the entire hematopoietic system (Fig. 1, A and B). Thus, we crossed mice expressing the Cre recombinase downstream of the Lyz2 promoter, active in myeloid cells including macrophages (Clausen et al., 1999), with mice bearing floxed Gata6 alleles (Sodhi et al., 2006), generating mice specifically lacking Gata6 in macrophages (Gata6\(^{flox/flox}\)) to be compared with controls bearing the floxed alleles in the absence of Cre recombinase (Gata6\(^{flox/flox}\), Fig. 1 C). Total cell numbers from the peritoneum were reduced by 25 \(\pm\) 13%. Moreover, the frequency of F4/80\(^{hi}\) ICAM-2\(^{-}\) was selectively reduced in Gata6\(^{flox/flox}\) mice, to 54 \(\pm\) 16% of control mice. Together, these changes led to a marked reduction in Gata6\(^{flox/flox}\) peritoneal macrophages compared with control mice (Fig. 1 D). A second, minor CD115\(^{+}\) F4/80\(^{lo}\) ICAM-2\(^{-}\) macrophage population residing in the peritoneum (Gautier et al., 2013), which did not express Gata6 (Fig. 1 B), was unaffected in Gata6\(^{flox/flox}\) mice (Fig. 1 E). Macrophage frequency in other organs was unchanged (Fig. 1 E). Increased activated caspase 3 and Annexin V in Gata6\(^{flox/flox}\) macrophages revealed augmented apoptosis (Fig. 1 F). Consistent with previous work (Jenkins et al., 2013), infection with the parasite Heligmosomoides polygyrus led to a greater than fivefold increase in peritoneal macrophages in control mice, as the ICAM-2\(^{+}\) resident macrophage population associated with Gata6 expression was induced to proliferate during infection (Fig. 1 G). Percentage of cycling macrophages was not significantly affected in Gata6\(^{flox/flox}\) macrophages compared with controls before or after infection (Fig. 1 G). However, Gata6\(^{flox/flox}\) macrophage numbers scarcely elevated above baseline numbers observed in uninfected control mice (Fig. 1 G) because of markedly elevated apoptosis (Fig. 1 G). Thus, F4/80\(^{hi}\) ICAM-2\(^{-}\) resident peritoneal macrophage survival was selectively impaired in resting and parasite-challenged Gata6\(^{flox/flox}\) mice.

After flow cytometric cell sorting and gene expression analysis using whole mouse genome arrays, we found that notably elevated mRNA transcripts in Gata6\(^{flox/flox}\) macrophages were those associated with alternative activation (Gordon and Martinez, 2010) of macrophages, including mRNA transcripts encoding CD163, Lyve-1, Arg1, Clec10a (CD301), Chi3L3, and CD206 (mannose receptor, Mr1; Fig. 2 A and Table S1), as well as mRNA for MARCO, which is associated with innate macrophage activation (Mukhopadhyay et al., 2014). Increased cell surface levels of corresponding proteins were accordingly observed (Fig. 2 B). Functional evidence in support of alternative activation included a significant increase in peritoneal eosinophils (Fig. 2 B) associated with type 2 immune responses (Gause et al., 2013), along with expanded resident B1a lymphocytes, whereas T cell counts were unchanged (Fig. 2 C). Infiltrating monocytes and neutrophils were not found, ruling out generalized local inflammation. Gata6\(^{flox/flox}\) macrophages metabolism was oriented to oxidative phosphorylation, another feature of alternative activation (Vats et al., 2006; Pearce and Pearce, 2013), as observed by increased oxygen consumption rates (OCR; Fig. 2 D). Profiling of metabolic intermediates from sorted control and Gata6\(^{flox/flox}\) macrophages, respectively, revealed greater ADP (34 \(\pm\) 3 vs. 58 \(\pm\) 12 pmol/10\(^6\) cells), citrate or isocitrate (CIT/ICIT; 76 \(\pm\) 12 vs. 129 \(\pm\) 46 pm/10\(^6\) cells), NAD\(^+\) (1.1 \(\pm\) 0.4 vs. 2.1 \(\pm\) 0.5 pmol/10\(^6\) cells), and malate (MAL; 120 \(\pm\) 28 vs. 167 \(\pm\) 23 pmol/10\(^6\) cells) levels in Gata6\(^{flox/flox}\) macrophages, with reduced amounts of FAD (6.9 \(\pm\) 0.4 vs. 5.5 \(\pm\) 0.5 pmol/10\(^6\) cells), consistent with a more active citric acid cycle (Fig. 2 E).

Deletion of Gata6 correlated with decreased F4/80 expression (Fig. 1 D, events below blue line in Gata6\(^{flox/flox}\) gate), but a minority of macrophages, i.e., 19.9 \(\pm\) 10.2% of remaining ICAM-2\(^{-}\) macrophages, retained the originally high levels of F4/80 (Fig. 1 D) and only these cells immunostained with Gata6 mAb (Fig. 2 F). Among flow-sorted Gata6\(^{flox/flox}\) macrophages with higher F4/80, only 26 \(\pm\) 7% of nuclei had deleted Gata6, whereas 99 \(\pm\) 0.4% had deleted Gata6 among Gata6\(^{flox/flox}\) macrophages with reduced expression of F4/80. Thus, the persistence of some resident macrophages that remained Gata6\(^{+}\), clearly demarcated by the same high expression of surface F4/80 as in WT mice, allowed us to address whether alternative activation was confined to macrophages that lost Gata6. Indeed, resident peritoneal macrophages with efficient deletion of Gata6 (F4/80 reduced) expressed higher level of CD206, CD301, and Lyve-1 compared with F4/80\(^{hi}\) macrophages or macrophages from control mice (Fig. 2 F). However, the population of macrophages that did not delete Gata6 (F4/80\(^{hi}\)) were those that induced Marco (Fig. 2 F). Macrophages in the splenic red pulp, lung (Fig. 2 G), or brain (not depicted) did not increase alternative activation markers in Gata6\(^{flox/flox}\) mice. These data, therefore, indicate that deletion of Gata6 renders peritoneal macrophages prone to alternative activation. They may be more sensitive to external stimuli that promote alternative activation or there may be a derepression of an alternative activation program in a cell autonomous manner.
Figure 1. Gata6 deficiency decreases peritoneal macrophage density and induces apoptosis. (A) Expression of mRNA for the GATA family of transcription factors within the resting hematopoietic system profiled by the Immunological Genome Project. Arrowhead points to peritoneal macrophage. (B) Signal intensity of gene expression for Gata6 from array data comparing resident macrophages from multiple organs. Dotted line, cutoff representing positive expression after data normalization. (C) Immunoblot for Gata6 on sorted macrophages, in which all ICAM-2+ macrophages were collected from each genotype. (D) Gata6+ macrophages quantified after cell counts and gating during flow cytometric analysis on cells expressing F4/80, ICAM-2, and CD115. Blue line in gate delineates loss of F4/80 surface intensity in most Gata6ΔMac macrophages. (E) Macrophage counts in various organs are plotted. (F) Percent macrophages expressing active caspase 3 or Annexin V. (G) Peritoneal macrophages quantified in mice infected with *H. polygyrus*. Enumeration of these macrophages plotted in control Gata6floxflox mice (black) or Gata6ΔMac mice (red); baselines for each strain shown as dotted line in same color. Percent macrophages positive for active caspase 3 after *H. polygyrus* infection are plotted, and S phase was analyzed in unchallenged and infected mice. Data are derived from 2–8 experiments, with 2–5 replicates per group, performed for each part of the figure. Means ± SEM are shown. *, P < 0.05; **, P < 0.001 relative to controls using two-tailed Student's t tests. Statistical significance in S phase analysis is not depicted, but all S phase analyses are statistically significant (one-way ANOVA) comparing unchallenged control mice to infected mice, P < 0.05, but differences between genotypes in the same condition are not significant.
were indeed down-regulated in Gata6-deficient macrophages (Fig. 3 A). Others in the same modules not originally identified to be specific for peritoneal macrophages were notably up-regulated, including Arg1, which encodes arginase-1, an enzyme associated with canonical alternative activation (Fig. 3 A). Thus, we examined the expression of genes involved in metabolism and lipid synthesis. Whereas many metabolic genes were up-regulated, Aspa mRNA encoding a key enzyme at an early step in the pathway leading to acetyl CoA synthesis, asparto-acylase, was among the most down-regulated genes (Fig. 3 B).

As mentioned, alternative activation has been linked to changes in cellular metabolic orientation (Vats et al., 2006; Pearce and Pearce, 2013). Furthermore, mRNA transcripts that distinguish peritoneal macrophages from other macrophages were especially those associated with lipid synthesis and signaling (Gautier et al., 2012). Several such transcripts were among those that were confined to modules of genes predicted by the Ontogenet algorithm to be regulated in peritoneal macrophages by Gata6 (Gautier et al., 2012). Most mRNA transcripts that were peritoneal macrophage-specific within these modules were indeed down-regulated in Gata6-deficient macrophages (Fig. 3 A). Others in the same modules not originally identified to be specific for peritoneal macrophages were notably up-regulated, including Arg1, which encodes arginase-1, an enzyme associated with canonical alternative activation (Fig. 3 A). Thus, we examined the expression of genes involved in metabolism and lipid synthesis. Whereas many metabolic genes were up-regulated, Aspa mRNA encoding a key enzyme at an early step in the pathway leading to acetyl CoA synthesis, asparto-acylase, was among the most down-regulated genes (Fig. 3 B).
of macrophages that corresponded to those that deleted Gata6 (Fig. 3 D). To test whether loss of Aspa might be relevant to the loss of viable macrophages in the peritoneum, we quantified peritoneal macrophages in Nur7 mutant mice that bear a non-sense mutation in the Aspa (Traka et al., 2008). These mutants showed a 37% reduction in resident peritoneal macrophages (Fig. 3 E), along with enhanced apoptosis indicated by increased active caspase 3 (Fig. 3 E), although the extent of the loss in overall macrophage numbers was not as large as observed in Gata6ΔMac macrophages. As the mutant mice lack aspartoacylase wherever it is expressed, we cannot be sure that the increased death of peritoneal macrophages is due to inherent lack of aspartoacylase expression. However, it is interesting to note that Aspa mutant mice trended to reduced red pulp macrophages (P = 0.06), whereas macrophages in lung and brain,
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MATERIALS AND METHODS

Mouse strains. Gata6flox/flox mice on a mixed 129S1/SvEvJ and CD-1 background were bred with Ly2-Cre+ on a C57BL/6 background to yield C57BL/6 × (129S1 × Gata6flox/flox) interlitter control mice. Nur7 mice bearing mutant Aspa alleles were on a C57BL/6J background and compared with C57BL/6J mice. All experimental procedures were approved by the Animal Studies Committee at Washington University in St. Louis.

Gene expression analysis. RNA was amplified and hybridized on the Affymetrix Mouse Gene 1.0 ST array by the ImmGen Project consortium with double-sorted cell populations sorted directly into TRIzol (Life Technology). Blots were then incubated with fluorescent secondary Abs and immunoblots were incubated with primary Abs against Gata6 (D61E4; Cell Signaling Technology) or aspartoacylase (GeneTex) and β-actin (Cell Signaling Technology). Blots were then incubated with fluorescent secondary Abs and proteins were detected using the fluorescence-based Odyssey Infrared Imaging System (LI-COR Biosciences).

Metabolomics. FACS-sorted macrophages (10^6 cells) were pelleted and rapidly washed (<10 s) with a mass spectrometry–compatible buffer (150 mM ammonium acetate solution) to prevent the presence of sodium and phosphate in the residue and limit interference with LC-MS analyses. After a second step of centrifugation, dry pellets were immediately frozen in liquid nitrogen to quench metabolism according to the University of Michigan Molecular Phenotyping Core facility’s instructions. Samples were shipped on dry ice to the Molecular Phenotyping Core facility where metabolites were extracted by exposing the cells to a chilled mixture of 80% methanol, 10% water, and 10% water. Glycolytic and citric acid metabolites were then analyzed by the Molecular Phenotyping Core facility using LC-MS.

Statistical analysis. The statistical significance of differences in mean values was analyzed with the unpaired t test or ANOVA for multiple comparisons. P values < 0.05 were considered statistically significant. Errors shown in bar graphs and mentioned in text refer to standard deviations.

Supplemental material. Table S1 summarizes up-regulated mRNA transcripts in Gata6flox/flox macrophages compared to Gata6flox/flox macrophages. Table S2 summarizes down-regulated mRNA transcripts in Gata6flox/flox macrophages compared to Gata6flox/flox macrophages. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20140570/D1.

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