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p40phox Expression Regulates Neutrophil Recruitment and Function during the Resolution Phase of Intestinal Inflammation

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NADPH oxidase is a multisubunit complex that assembles during phagocytosis to generate reactive oxygen species. Several components of this complex have been implicated in chronic granulomatous disease and Crohn’s disease, highlighting the importance of reactive oxygen species in regulating host immune response. In this study, we use genetically deficient mice to elucidate how p40phox, one subunit of the NADPH oxidase complex, functions during intestinal inflammation. We show that p40phox deficiency enhances inflammation in both dextran sulfate sodium-induced and innate immune-mediated murine colitis models. This inflammation is characterized by severe colonic tissue injury, increased proinflammatory cytokines, and increased neutrophil recruitment. We demonstrate that neutrophils are essential during the recovery phase of intestinal inflammation and that p40phox expression is necessary for this restitution. Lastly, using an integrative bioinformatic approach, we show that p40phox deficiency leads to upregulation of chemokine receptor 1 and downregulation of enzymes involved in glycan modifications, including fucosyltransferases and sialyltransferases, during inflammation. We propose that p40phox deficiency enhances intestinal inflammation through the dysregulation of these two pathways in neutrophils. The Journal of Immunology, 2012, 189: 3631–3640.

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Abbreviations used in this article: CD, Crohn’s disease; CGD, chronic granulomatous disease; C5, threshold cycle; DAL, disease activity index; DKO, double knockout; DSS, dextran sulfate sodium; IBD, inflammatory bowel disease; iNOS, inducible NO synthase; FNM, polymorphonuclear neutrophil; ROS, reactive oxygen species; WT, wild-type; XCGD, X-linked chronic granulomatosus disease.

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mation, particularly during the recovery phase. Additionally, p40phox−/−-deficient mice are more susceptible to an innate immune model of colitis, which is dependent on anti-CD40 pathway engagement. We demonstrate that neutrophils are essential during the recovery phase of intestinal inflammation and that p40phox expression is necessary for the neutrophil-mediated restitution response. Based on these observations, we developed a bioinformatic approach that integrates analyses of clinical gene expression signatures in CGD patient neutrophils and temporal gene expression profiles during murine DSS colitis (18, 19). Using this method, we were able to identify novel mechanisms and regulators that promote intestinal inflammation in the context of NADPH oxidase deficiency. By applying this analysis to our functional animal model, we propose that p40phox is essential for the resolution of inflammation through downregulation of Ccr1 and upregulation of enzymes involved in glycan modifications in neutrophils.

Materials and Methods

Animals

Mice were maintained in specific-pathogen-free facilities at Massachusetts General Hospital (Boston, MA). All animal studies were conducted under protocols approved by the Subcommittee on Research Animal Care at Massachusetts General Hospital. p40phox−/− mice were provided by Phillip T. Hawkins (Babraham Institute, Cambridge, U.K.). Generation of this knock out line has been previously described, and these mice have been backcrossed to the C57BL/6 background (20). Rag1−/− mice were purchased from The Jackson Laboratory (Bar Harbor, ME). All mice were maintained on food and water ad libitum. Mice were used between 7 and 9 wk and strains were age- and gender-matched for each experiment.

DSS colitis

Mice were fed 3% (w/v) DSS (MP Biomedicals; m.w., 36,000–50,000) dissolved in sterile, distilled drinking water ad libitum. Mice were treated with 3% DSS for 7 d, followed by 5 d regular drinking water. Animals were monitored daily for weight loss, survival, and disease activity. Disease activity index (DAI) was scored as previously described, based on the average of three parameters: stool consistency (0, 2, 4), fecal blood (0, 2, 4), and percentage weight loss (0–4) (21, 22). Animals that did not survive the full experimental course were not included in body weight and DAI analyses. Colon tissue was harvested at indicated time points for histology, RNA, and flow cytometry analyses.

Anti-CD40 colitis

Acute, innate-mediated colitis was induced as previously described (23). Briefly, Rag1−/− and p40phox−/− × Rag1−/− double knockout (DKO) mice were injected i.p. with 200 µg FGK4.5 anti-CD40 mAb (BioXCell, West Lebanon, NH). Age- and sex-matched control mice were treated with a rat IgG2a isotype control, 2A3 (BioXCell). Animals were monitored daily for weight loss and disease activity for 7 d. DAI was scored based on the sum of parameters previously detailed, including hunching (0, 1), wasting (0, 1), stool consistency (0–3), proximal colon thickness (0–3), medial colon thickness (0–3), and distal colon thickness (0–3) (24). Colon was harvested for histology 7 d after induction of colitis.

Histology

Colon tissue was fixed in 10% buffered formalin and embedded in paraffin. Five-micrometer sections were cut and stained with H&E. Longitudinal sections were scored in a blinded fashion using methods previously established in each colitis model, with slight modification (23, 25). Colon tissues from DSS colitis experiments were scored by the following parameters: severity of inflammation (0–3), depth of injury/inflammation (0–3), and crypt damage (0–4). DSS histological scores were multiplied by a factor representing the percentage of tissue involvement: ×1 (0–25%), ×2 (26–50%), ×3 (51–75%), and ×4 (76–100%). Thus the maximum colitis score in the DSS model is 40 (25).

Colon tissues from anti-CD40 colitis experiments were prepared in the same manner and scored by the following parameters: epithelial hyperplasia (0–3), goblet cell depletion (0–3), lamina propria infiltrate (0–3), and epithelial cell damage (0–3). Proximal, medial, and distal portions of the colon were individually scored in this model, and the colitis score is the sum of all three sections (maximum, 36).

Real-time quantitative PCR

Proximal, medial, and distal colon tissues were harvested at the end of each course of colitis and stored in RNAlater (Ambion, Austin, TX) per the manufacturer’s protocol prior to RNA isolation. RNA was extracted from homogenized tissues using the RNeasy kit (Qiagen, Valencia, CA) according to the manufacturer’s protocol. All RNA samples were reverse-transcribed using the iScript cDNA synthesis kit (Bio-Rad Laboratories, Hercules, CA). Using the iQ SYBR Green Supermix (Bio-Rad) for quantitative PCR, mRNA levels were determined using the iCycler with an iQ5 multi-color real-time PCR detection system (Bio-Rad). The reaction conditions consisted of 37 cycles of PCR with an annealing temperature of 59°C. The following primers were used: Ccr1 forward, 5′-AAGACGGCTGAG-CACTGGA-3′; reverse, 5′-CAGATGTAAGGCTGTCAGA-3′; Tnfα forward, 5′-GACCTGAACAGCGAAAGAG-3′; reverse, 5′-TGTTGAGTGT-GTTGAGTGAG-3′; IFN-γ forward, 5′-ATGAAAGCTTACACACT-CATC-3′; reverse, 5′-CCTACTTTTCGCCAGTGTCTC-3′; IL-1β forward, 5′-GCCCATCTCTGTAGTCACT-3′; reverse, 5′-AGGCAAGAGATTTCGGT-GTCG-3′; IL-6 forward, 5′-GTAGCTATGTTGACTAGGAGA-3′; reverse, 5′-AGATGATGGACTTGCGAGA-3′; IL-17A forward, 5′-CTTCACTCCTTGCGAAA-3′; reverse, 5′-CTTTCTTCGTCCTAGCAC-3′; inducible NO synthase (iNOS) forward, 5′-CGTGTAGTTGAGACGAGAAC-3′; reverse, 5′-CATGCAAATCTTCTCCTGAC-3′; Ccl5 forward, 5′-ACGTCAGAGATTTCCTAC-3′; reverse, 5′-GATATATTCTGTGAGA-3′; Ccl2 forward, 5′-AGATGTCGACCTGAG-3′; reverse, 5′-TCCCAAACCTTCCTCATTG-3′; St3gal4 forward, 5′-GGCTCTCAACAAAGAGCGAC-3′; reverse, 5′-GATGGCAGAATGAGACCA-3′; St6gal1 forward, 5′-CTGCCCAAGGAACATCAG-3′; reverse, 5′-AGCGGTCTTTGCTGAGAC-3′; Fut4 forward, 5′-GCCATCTGCTGTTGAAGTA-3′; reverse, 5′-TGGGTTGACCTGAAAAGAG-3′; Fut4 forward, 5′-CTCTTCTGCAGTGAGAAC-3′; reverse, 5′-GAATGGCTGGCCATAGTCT-3′; HexA forward, 5′-GGGCATGACTCTGTGATC-3′; reverse, 5′-ACCTCTTTCACATTGTCG-3′. The threshold cycle (Ct) for each sample was determined for each gene and was normalized to the Ct value of the endogenous housekeeping gene GAPDH. Data were calculated using the 2−ΔΔCt method (26, 27).

Bacterial translocation

Spleen and mesenteric lymph nodes from DSS-treated mice were weighed and homogenized in 500 µl sterile PBS. Homogenates were plated on tryptic soy broth agar plates and incubated overnight at 37°C before quantification. Data are shown as CFUs per gram of tissue.

Lamina propria isolation

Colon lamina propria cells were isolated as previously described (28). Briefly, colonos were harvested at indicated time points and inverted onto polystyrene tubing (Beckman-Coulter, Brea, CA). Lactose was added in calcium- and magnesium-free PBS, colonos were incubated with DTT (Sigma-Aldrich, St. Louis, MO), followed by 30 mM EDTA, all at room temperature. The remaining tissue was further digested using type IV collagenase (108 U/ml; Sigma-Aldrich) for 90 min. The filtered cells from the digested tissue were then layered on a 45/72% Percoll (GE Healthcare, Waukesha, WI) gradient and harvested at the interface after centrifugation (650 × g, 15 min) (28).

Flow cytometry

Colon lamina propria cells (2 × 107) were washed in PBS supplemented with 3% FBS. Cells were first incubated with 2.4G2 mouse Fc block in PBS supplemented with 3% FBS (BD Pharmingen, San Diego, CA) for 20 min at 4°C. Cells were then washed and stained with fluorescent-conjugated Abs for 20 min at 4°C. The following Abs were purchased from BD Pharmingen and used for our analysis: Ly-6G-FITC, F4/80-PE, and CD11b-allophycocyanin. The anti-Ccr1 Ab and isotype control were purchased from R&D Systems and used per the manufacturer’s recommendations. Fluorescently labeled lamina propria cells were acquired on a FACSCalibur flow cytometer (BD Biosciences, San Jose, CA) and analyzed using FlowJo analysis software (Tree Star, Ashland, OR).

Neutrophil cytospin

Total lamina propria cells were isolated from mice treated with DSS as described above, and Ly-6G−CD11b−F4/80− cells were FACS sorted. Cells (1 × 107) were spun down onto a slide using a Cytospin 3 (Thermo Shandon, Waltham, MA) and subjected to Wright’s staining.
Neutrophil depletion

Where indicated, mice were treated with anti-Ly-6G mAb (clone 1A8, BioXCell) 24 h prior to DSS or anti-CD40 administration (4 mg/kg body weight i.p.). Age- and sex-matched littermates were injected with PBS. For neutrophil depletion in the DSS model, 24 h postdepletion, mice were administered 3% DSS for 7 d, followed by regular drinking water for 5 d. Mice received the same dose of anti-Ly-6G every 3 d during the course of the experiment. For neutrophil depletion in the anti-CD40 model, 24 h postdepletion, mice were administered anti-CD40 as described above. Mice received the same dose of anti-Ly-6G on day 3 of the 7-d course. Neutrophil depletion efficiency was determined by FACS staining in blood, spleen, bone marrow, and lamina propria.

Bioinformatic analysis

To identify NADPH oxidase-regulated genes underlying pathogenesis in the DSS colitis model, two publicly available datasets were analyzed. The first dataset provides temporal, whole-genome expression profiling during DSS colitis treatment in mice (18). Colon tissue from 12- to 14-wk-old DSS-treated C57BL/6J mice was collected at 0, 2, 4, and 6 d. The second dataset provides global gene expression patterns in polymorphonuclear neutrophils (PMNs) from X-linked chronic granulomatous disease (XCGD) patients and healthy control individuals (19, 29). PMNs were profiled at 0, 90, 180, and 360 min after stimulation with IgG and C3bi-coated latex beads to activate phagocytosis. Both datasets were normalized separately using a GC robust multi-array average routine in MATLAB. Probes were filtered with low absolute expression values, low entropy, and variance less than the 10th percentile. DSS colitis data were analyzed for differential expression using a two-tailed, two-sample t test between pairs of data collected from consecutive time points (Supplemental Fig. 1A). Significant genes (L = 1283) were identified with expression change >2-fold and an adjusted p value of <0.05. We followed a similar strategy for the PMN data and performed a differential-of-differential analysis to identify 124 genes that were significantly differentially expressed in healthy PMNs relative to XCGD PMNs (Supplemental Fig. 1B).

Differentially expressed genes identified in the DSS colitis dataset were clustered into three groups: early responders, middle-to-late responders, and late responders (Supplemental Fig. 2). Each of these groups was then separately analyzed for gene set overlap using the canonical pathway gene sets from mSigDB (30). The differentially expressed genes in the PMN dataset were similarly clustered into two groups: genes that were induced or genes that were suppressed in the absence of ROS (Supplemental Fig. 3). This was followed by a gene set overlap analysis (see Fig. 6C).

To identify NADPH oxidase-dependent genes that were important during DSS-induced colitis, the intersection of the two lists of differentially expressed genes from both DSS and PMN datasets was determined and yielded a set of 10 genes (see Fig. 6C).

Enrichment score

Enrichment scores were calculated as previously described (31).

Isolation of lamina propria neutrophils

Lamina propria cells were isolated from wild-type (WT) and p40phox−/− mice as described above. Ly-6G+ cells were isolated via MACS positive selection cell separation kits (Miltenyi Biotec, Auburn, CA). Isolated lamina propria cells were isolated from wild-type (WT) and p40 phox−/− mice as described above. Ly-6G+ cells were isolated via MACS positive selection cell separation kits (Miltenyi Biotec, Auburn, CA). Isolated lamina propria neutrophils were washed twice with ice-cold PBS and cell pellets were stored at −80°C until RNA was extracted using the RNasy kit (Qiagen) according to the manufacturer’s protocol. Quantitative RT-PCR was performed as described above.

In vivo CCR1 antagonist treatment

One hour prior to DSS treatment, WT C57BL/6 mice were injected i.p. with 10 mg/kg body weight of the CCR1 antagonist J113863 (Tocris Bioscience, Bristol, U.K.) dissolved in PBS, as described with other CCR1 antagonists (32). Mice were injected once daily thereafter. Asays from treated mice were conducted as described above.

Statistical analysis

Unless otherwise stated, a Student t test was used to assess the significance of observed differences. A p value <0.05 was considered significant. A logarithm test was used to assess significance in survival curve comparisons. A two-sided Wilcoxon rank sum test was used to assess significance for DAI scores. The test rejected the null hypothesis at the 5% significance level (p = 0.0095). All error bars represent SD.

Results

p40phox−/− mice develop severe colitis during the recovery phase of DSS-induced colitis

We first assessed the role of p40phox in intestinal inflammation through the use of an epithelial injury model, consisting of 3% DSS treatment for 7 d followed by 5 d recovery. p40phox−/−-deficient mice lost significantly more weight than did their WT littermates by day 6 during DSS colitis and were unable to recover from this weight loss (Fig. 1A). Additionally, p40phox−/−-deficient mice exhibited a higher mortality rate throughout the course of DSS treatment (Fig. 1B). p40phox−/−-deficient mice had significantly more severe disease activity based on a composite index (Fig. 1C) and more severe colonic inflammation on day 12 as shown by a significant decrease in colon length (Fig. 1D) and increase in histology score (Fig. 1E). H&E staining of colon sections revealed inflammation in p40phox−/−−/− mice characterized by epithelial ulceration and leukocyte infiltration (Fig. 1F). Consistent with the inflammation observed in p40phox−/−−/− mice, local TNF-α, IPN-γ, IL-1β, IL-6, iNOS, and IL-17A levels were significantly higher in p40phox−/−−/− mice than in WT mice on day 12 (Fig. 1G, 1H). Notably, similar levels of the anti-inflammatory cytokine IL-10 were observed in DSS-treated WT and p40phox−/−−/− colon after 12 d (data not shown). To determine whether NADPH oxidase deficiency affects epithelial permeability during intestinal inflammation, we assessed bacterial translocation to the spleen and mesenteric lymph nodes during DSS colitis. p40phox−/−−/− mice had significantly greater numbers of CFUs per gram of tissue in both spleen and mesenteric lymph node, suggesting an inability to effectively clear microbes (Fig. 1I). p40phox−/−−/− mice show no spontaneous defect in intestinal permeability, as no bacteria were detected in the peripheral organs without DSS treatment, similar to WT mice (data not shown). Collectively, the data demonstrate that p40phox is necessary for the resolution of DSS-induced inflammation and that p40phox deficiency enhances proinflammatory cytokine production during intestinal inflammation.

p40phox−/− × Rag1−/− mice develop severe colitis during the recovery phase of DSS-induced colitis

To determine the contribution of the innate immune compartment in this phenotype, we next assessed whether p40phox deficiency also promotes intestinal inflammation in a Rag1-deficient mouse model, which lacks an adaptive immune system. For these experiments, p40phox−/− × Rag1−/− DKO mice were treated with DSS as described above, and the resulting phenotypes were compared with Rag1−/− lymphocyte-deficient mice. As shown in Fig. 2A, DKO mice lost more weight during DSS treatment than did their Rag1−/− counterparts, most notably during the recovery phase (Fig. 2A). Additionally, when compared with the weight loss observed in p40phox−/−−/− mice treated with DSS (Fig. 1A), DKO mice lost a comparable percentage at day 12 (p40phox−/−−/−, 20 ± 2.1%; DKO, 22.1 ± 1.2%). Histological and clinical examination demonstrated greater inflammation during DSS in DKO mice than in their Rag1−/− littermates (Fig. 2B–D). The histological score for the DKO group, although significantly greater than the Rag1−/− control cohort, was lower than that seen previously in the lymphocyte-sufficient mice (Fig. 1E), suggesting a potential, albeit secondary, role for lymphocytes in colitis progression. These data indicate that p40phox deficiency renders mice more susceptible to intestinal inflammation, even in the absence of B and T lymphocytes.

p40phox−/− mice are more susceptible to anti-CD40–induced colitis

To define the contribution of p40phox in innate immunity, we next used an anti-CD40 model of colitis. Injection of CD40 mAb into T
Bacterial translocation to MLNs and spleen was determined on day 12 after DSS administration. The number of CFUs per gram of tissue is shown (determined by a two-sided Wilcoxon rank sum test; the test rejected the null hypothesis at the 5% significance level). Consistency, and stool blood content were assessed daily to determine DAI. The median DAI scores for days 6 and 12 are shown. Significance was determined using a Student’s t test. For all panels, data were generated from four independent experiments.

and B lymphocyte-deficient Rag1−/− mice induces acute gastrointestinal inflammation and wasting disease within 2 d and is largely driven by local IL-23 production (23). The histological hallmarks of this colitis model include leukocyte infiltration into the lamina propria, goblet cell depletion, and marked epithelial hyperplasia (23). During the first 4 d following CD40 mAb treatment, p40phox−/− × Rag1−/− DKO mice lost weight with similar kinetics as did their Rag1−/− control littermates. However, DKO mice were unable to recover similarly to their anti-CD40–treated Rag1−/− littermates on days 5–7 (p < 0.01, Fig. 3A). As previously reported, Rag1−/− mice injected with isotype control Ab did not show weight loss (23). In addition to the inability to recover from anti-CD40–induced colitis, DKO mice had significantly greater DAI values as assessed by wasting, stool consistency, and colonic thickness (p < 0.001, Fig. 3B). Similar to the enhanced inflammation of p40phox−/− mice to DSS, DKO mice had a significantly higher histology score in comparison with Rag1−/− mice (Fig. 3C). Colonic tissues displayed greater inflammation in DKO mice, characterized by polymorphonuclear cell infiltration (Fig. 3D). Taken together, these data demonstrate that p40phox expression is a key component in preserving intestinal homeostasis in an innate immunity model of colitis.

Neutrophil recruitment in the colon is augmented in p40phox−/− mice during DSS colitis

Given the exacerbated response of p40phox−/− deficient animals to murine models of colitis, we next assessed the cellular composition of the colonic lamina propria in WT and p40phox−/− mice after DSS colitis. Flow cytometric analysis revealed a population of Ly-6G+CD11b+F4/80− cells in p40phox−/− deficient colon whose frequency was significantly greater than their WT counterparts (representative histograms shown in Fig. 4A; WT, 5.4 ± 3%; p40phox−/−, 39.9 ± 5%). Based on cell surface molecule expression, Ly-6G+CD11b+F4/80− cells would be defined as neutrophils; however, to definitively categorize this population, the morphology of FACS-sorted Ly-6G+CD11b+F4/80− cells was examined on day 12 after DSS colitis in p40phox−/− mice. Wright’s staining revealed that the sorted Ly-6G+CD11b+F4/80− cells possessed multilobulated nuclei, the hallmark characteristic defining neutrophil morphology (Fig. 4B). Total neutrophil numbers were increased in p40phox−/− lamina propria at day 6 (Fig. 4C; WT, 0.3 × 105 ± 0.1 × 105; p40phox−/−, 4.9 × 105 ± 1 × 105) and day 12 (Fig. 4D; WT, 1.2 × 105 ± 0.5 × 105; p40phox−/−, 10.9 × 105 ± 2 × 105). Thus, our data demonstrate enhanced neutrophil recruitment to the colon in p40phox−/− mice following DSS treatment.

p40phox−/− sufficient neutrophils play a protective role in intestinal inflammation

Given the increased susceptibility to DSS during the recovery phase and the enhanced neutrophil infiltration in p40phox−/− mice, we next addressed the role of neutrophils in intestinal inflammation in the context of p40phox deficiency. Neutrophils are responsible for initiating early responses in inflammation by aiding in pathogen-
FIGURE 2. *p40<sup>lox<sup>−/−</sup> × Rag1<sup>−/−</sup> mice show increased susceptibility to DSS colitis. (A) Age- and weight-matched mice were given 3% DSS in drinking water ad libitum for 7 d, followed by 5 d regular drinking water. Changes in body weight were monitored daily (n = 10/group; *p < 0.01). (B) Animal weight, stool consistency, and stool blood content were assessed daily to determine DAI. The median DAI scores for days 6 and 12 are shown. Significance was determined by a two-sided Wilcoxon rank sum test; the test rejected the null hypothesis at the 5% significance level (n = 10/group; *p = 0.0095). (C) Colonic tissues were blindly scored for inflammation on day 12. Grading parameters include severity of inflammation, depth of injury, and crypt damage (n = 10/group: Rag1<sup>−/−</sup> average, 6.5 ± 2.4; DKO average, 12.3 ± 2.6; p = 0.005). (D) Representative colon sections stained by H&E (top panel, original magnification ×10; bottom panel, original magnification ×20). Unless otherwise noted, significance was determined using a Student t test. For all panels, data were generated from two independent experiments.

killing ROS generation, epithelial imprinting, and immune cell recruitment (33, 34). During the resolution phase of inflammation, however, neutrophils promote wound healing via heterotypic cell interactions with the epithelium, inducing the expression of enzymes that facilitate the production of anti-inflammatory lipid mediators and mucins (35–38).

To complement our genetic model involving NADPH oxidase-deficient neutrophils and to determine whether neutrophils contribute to intestinal homeostasis, we next depleted neutrophils during DSS inflammation using a Ly-6G–specific depletion Ab (39). We monitored body weight and survival during DSS administration (7 d), followed by a water recovery period (5 d) (Fig. 5). Interestingly, WT mice that had been depleted of neutrophils prior to DSS treatment lost significantly more weight than did their neutrophil-intact counterparts and had a 100% mortality rate by day 10 (Fig. 5A, 5C), indicating a protective role for neutrophils during DSS colitis. In contrast, *p40<sup>lox<sup>−/−</sup> mice exhibited no significant difference in body weight loss with or without neutrophils (Fig. 5B, 5D), demonstrating that the protective role of neutrophils is dependent on *p40<sup>lox<sup> expression. We next assessed the role of neutrophils in the anti-CD40 model and found that 100% of the neutrophil-depleted mice did not survive past day 4, indicating that neutrophils are also necessary for recovery in this colitis model (Fig. 5E–H). Taken together, these observations indicate that neutrophils are critical for resolution of intestinal inflammation and that *p40<sup>lox<sup> expression is necessary for this process.

NADPH oxidase activity regulates expression of chemokine receptor 1 and enzymes involved in glycan modifications

We next developed an integrative bioinformatic approach to identify novel NADPH oxidase-dependent genes and pathways important during intestinal inflammation, particularly in the neutrophil compartment (Fig. 6, Supplemental Fig. 1). We first assessed time course gene expression patterns from whole murine colon tissue collected from C57BL/6 WT mice treated with DSS (18). After normalization and analysis of the microarray data, we identified 1283 differentially expressed genes (Supplemental Fig. 2). Most of the early responding genes (days 0–2) were suppressed by day 2 and were largely enriched for sonic hedgehog and Wnt signaling pathways (Fig. 6A, Supplemental Fig. 2). The group of middle- to late-responding genes (days 2–6) were enriched for the glycosphingolipid biosynthesis pathway (Fig. 6A, Supplemental Fig. 2). Eight of 26 genes in the glycosphingolipid biosynthesis pathway (Fig. 6A, Supplemental Fig. 2) were early- and late-responding genes (days 0–2) and 2–6) were suppressed by day 2 and were largely enriched for sonic hedgehog and Wnt signaling pathways (Fig. 6A, Supplemental Fig. 2). The group of middle- to late-responding genes (days 2–6) were enriched for the glycosphingolipid biosynthesis pathway (Fig. 6A, Supplemental Fig. 2). Eight of 26 genes in the glycosphingolipid biosynthesis pathway (Fig. 6A, Supplemental Fig. 2) were significantly differentially downregulated during this acute DSS phase (Supplemental Fig. 2). Finally, the late-responding genes showed significant enrichment for the cytokine–cytokine receptor interactome (Fig. 6A, Supplemental Fig. 2). Notably, these genes included chemoketic receptors and ligands such as Ccr1, Ccl2, and Ccr2. Thus, the analysis of temporal gene expression profiles
FIGURE 4. Enhanced neutrophil recruitment during DSS colitis in p40\textsuperscript{phox\lendash\lendash} mice. (A) Colonic lamina propria cells were isolated after recovery from DSS (day 12) and stained for flow cytometry analysis. The percentages of Ly-6G\textsuperscript{+} cells in WT and p40\textsuperscript{phox\lendash\lendash} lamina propria are shown in the top histograms; CD11b and F4/80 expression of the Ly-6G\textsuperscript{+} populations are shown in the lower dot plots (n = 10/group; representative data shown). (B) Cell morphology was assessed in FACS-sorted Ly-6G\textsuperscript{+} CD11b\textsuperscript{+}F4/80\textsuperscript{+} cells from p40\textsuperscript{phox\lendash\lendash} mice (day 12) using Wright’s staining after cytopsin. Original magnification ×40. (C) The total numbers of Ly-6G\textsuperscript{+}CD11b\textsuperscript{+}F4/80\textsuperscript{+} neutrophils were calculated during acute and recovery phases of DSS colitis. The average of 10 mice per group is displayed (*p < 0.001). Significance was determined using a Student t test. For all panels, data were generated from three independent experiments.

FIGURE 5. Ly-6G\textsuperscript{+} neutrophils are necessary for recovery from DSS and anti-CD40 colitis. For DSS colitis, age- and weight-matched mice were pretreated with either PBS or Ly-6G neutrophil depletion Abs prior to DSS administration. Changes in body weight (A, B) and animal survival (C, D) were monitored daily (n = 8/group). Significance was determined using a Student t test for body weight (*p < 0.01) and a log-rank test for survival [p < 0.001 for (C); p = 0.399 for (D)]. For anti-CD40 colitis, age- and weight-matched mice were pretreated with either PBS or Ly-6G neutrophil depletion Abs prior to anti-CD40 administration. Changes in body weight (E, F) and animal survival (G, H) were monitored daily (n = 5/group). Significance was determined using a Student t test for body weight (*p < 0.01) and a log-rank test for survival [p = 0.0002 for (G); p = 0.0043 for (H)]. For all panels, data were generated from two independent experiments.
compare with Fig. 4A). However, WT mice that received the CCR1 antagonist experienced significantly greater weight loss, more severe inflammation, and increased bacterial translocation compared with nontreated animals (Fig. 7F–H). Taken together, these data suggest that Ccr1 expression and subsequent neutrophil recruitment are required for DSS recovery, a process that is dysregulated in the absence of NADPH oxidase.

The glycosphingolipid biosynthesis pathway was highlighted in our analysis of both DSS and XCGD datasets, suggesting that this pathway may be important in neutrophils during inflammation. Within this pathway, the overlap specifically highlighted HexB and St3gal6, enzymes that are involved in the synthesis and termination of carbohydrate chains and that modify glycolipids and glycoproteins. We confirmed in our DSS model that St3gal6 is downregulated during acute colitis; however, as inflammation resolved during the recovery period, St3gal6 transcript levels increased and were significantly higher in WT mice compared with p40<sup>phox</sup><sup>−/−</sup> mice (Figs. 6C, 8A) (18). St3gal6 is a transferase involved in the biosynthesis of carbohydrates, particularly through sialylation, and has been implicated in diseases characterized by aberrant mucus production (41–43). In addition to St3gal6 and two fucosyltransferases (Fut4 and Fut9) that are downregulated during acute colitis and are also involved in glycan modifications. We investigated the expression of these genes during DSS treatment and observed that each gene was expressed at significantly lower levels in p40<sup>phox</sup><sup>−/−</sup> mice during colitis and, unlike WT mice, expression of these transferases remained low after the recovery phase at day 12.
that neutrophils are the relevant cell type driving this phenotype. Therefore, we next investigated the expression levels of the target genes in colon harvested from neutrophil-depleted WT mice after DSS. Expression of all six glycan-modifying proteins was significantly diminished in neutrophil-depleted WT mice compared with WT mice during DSS colitis. In contrast, Bao et al. (15) reported less colonic tissue damage and reduced myeloperoxidase levels after 7 d 2.5% DSS in g91\(^2\)−/−-deficient mice compared with WT mice. Although these studies have reported that susceptibility to DSS colitis is not affected by p47\(^2\)-deficiency and is lessened in the absence of g91\(^2\)-phox, we hasten to note that the recovery phase of inflammation was not investigated in these studies (15–17).

In this study, we show that the absence of p40\(^2\)-phox in Rag1\(^−/−\) mice enhances susceptibility to anti-CD40–induced colitis, suggesting that ROS in the innate compartment is essential during intestinal inflammation. However, in p40\(^2\)-phox \(\times\) Rag1\(^−/−\) DKO mice, DSS-induced inflammation was less severe than in p40\(^2\)-phox−/− mice, implying a contribution from lymphocytes. Given that NADPH oxidase activity has recently been shown to play a role in T cell differentiation and activation, p40\(^2\)-phox-deficient mice may have altered T cell responses in addition to the neutrophil phenotype. p47\(^2\)-phox deficiency has been associated with impaired T regulatory cell induction (44, 45) and increased IL-23 and Th17 response (44, 45). Indeed, we observed 50% fewer peripheral T regulatory cells in p40\(^2\)-phox−/− mice than in WT mice (data not shown). Although our data highlight an important role for p40\(^2\)-phox in neutrophils, we recognize that NADPH oxidase activity may affect other components of the inflammatory response.

We demonstrate that neutrophil infiltration in p40\(^2\)-phox−/− mice is coincident with greater inflammation during DSS challenge. However, despite greater numbers of recruited lamina propria neutrophils in p40\(^2\)-phox−/− mice during DSS colitis, the ROS-deficient phagocytes are unable to control infiltrating bacteria, as demonstrated by greater bacterial translocation to peripheral lymph nodes. This inability to efficiently kill microbes during DSS colitis may contribute to the exacerbated inflammation described in this NADPH oxidase-deficient model. During inflammation, ROS produced by neutrophils are thought to not only assist in antibacterial clearance but also to damage surrounding tissue (33, 34). However, mice deficient in the neutrophil chemokine Cxcl1 fail to recruit neutrophils during DSS colitis and show more severe symptoms, highlighting a role for neutrophils in restoring mucosal barrier integrity (46). To address whether neutrophils are necessary for recovery from DSS- and/or anti-CD40–induced colitis, as well as to establish whether p40\(^2\)-phox−/− neutrophils are pathogenic, we performed in vivo neutrophil depletion experiments. Depletion of WT neutrophils increased disease severity and induced 100% mortality by day 10 during DSS colitis and by day 4
during anti-CD40 colitis, suggesting that neutrophils are important in the resolution of intestinal inflammation. Neutrophil depletion in p40<sup>phox</sup>−/− mice treated with DSS, however, induced no significant differences in weight loss and inflammation compared with their p40<sup>phox</sup>−/− neutrophil-replete counterparts, suggesting that an inflammatory threshold had already been met in the absence of ROS. Previous reports using the RP-3 mAb suggested that neutrophil depletion in WT rats suppresses DSS colitis; however, this Ab targeted the Gr1 Ag, which consists of both Ly-6G and Ly-6C molecules and therefore depleted not only neutrophils but also a subset of macrophages. Thus, we propose that the observed differences may be due to the depletion of several immune populations in previous studies and/or the kinetics of Ab administration (47). Our experimental design, in which a Ly-6G neutrophil-specific depletion Ab was repeatedly injected throughout the DSS course, differs from one-time depletion studies in which new neutrophils may be generated and recruited to assist in the resolution of inflammation at later stages of DSS. Using another anti-Gr1 Ab (RB6-8C5), Qualls et al. (48) demonstrated protection from DSS at early time points, which was lost by day 7 of treatment. Thus we extend these reports by describing a role for neutrophils during the resolution phase of intestinal inflammation.

To identify disease-relevant pathways mediated by p40<sup>phox</sup>, we developed an integrative approach by combining functional studies of genetically deficient mice and murine models of IBD with cell-specific data extracted from clinical microarray studies of CGD. Bioinformatic analysis of the XCGD human PMN dataset revealed a signature in NF-κB signaling, suggesting that NADPH oxidase deficiency induces hyperactivity of this pathway. Data obtained from our murine model confirmed that proinflammatory cytokine expression was indeed higher in p40<sup>phox</sup>−/− mice than in WT mice during DSS colitis, correlating with the degree of inflammation in the colon. Thus, our model mimics human disease and demonstrates a role for p40<sup>phox</sup> in the regulation of proinflammatory mediators.

We identified a subset of genes whose expression is affected both by impaired NADPH oxidase activity in XCGD neutrophils and by inflammation in mouse colon. Given our in vivo data implicating aberrant neutrophil recruitment, the neutrophil cell-specific analysis was key to unraveling the underlying mechanisms of increased colitis severity in p40<sup>phox</sup>-deficient mice. Validating the findings from our computational analysis, we confirmed that during early DSS colitis, induction of the neutrophil chemokine receptor Ccr1 was significantly higher in p40<sup>phox</sup>−/− colon compared with WT. Analysis of isolated lamina propria cells confirmed that in the context of NADPH oxidase deficiency, Ccr1 expression on neutrophils is significantly higher, despite equal levels of Ccl3 and Ccl5 chemotactants present in the colon. As Ccr1 plays a key role in neutrophil infiltration (32, 40), its upregulation in p40<sup>phox</sup>−/− neutrophils likely accounts for the observed enhanced neutrophil recruitment in p40<sup>phox</sup>−/− colon during DSS. However, despite their greater recruitment, p40<sup>phox</sup>−/− neutrophils are unable to resolve intestinal inflammation. By using a Ccr1 antagonist in WT mice, we were able to block neutrophil recruitment to the colon during DSS colitis. Interestingly, we observed greater disease susceptibility in this setting, in agreement with a key role for neutrophils during healing. These data, as predicted by bioinformatic analyses, show not only that Ccr1 is regulated by p40<sup>phox</sup> but, moreover, that neutrophils are necessary during the restitution phase of DSS.

Our integrated bioinformatic analysis further identified NADPH oxidase activity as a novel regulator of the enzymes involved in the modification of glycan structures during intestinal inflammation. Six genes identified through our integrative genomics approach (St3gal6, St3gal4, St6gal1, Fut4, Fut9, and HexA) were significantly impaired in p40<sup>phox</sup>−/− mice during acute and recovery phases of DSS colitis. Moreover, by assessing these genes in neutrophil-depleted WT mice, we were able to demonstrate that p40<sup>phox</sup>-intact neutrophils are required for their expression during DSS inflammation. Sialyltransferases and fucosyltransferases such as St3gal4, St6gal1, Fut4, and Fut9 are key regulators of leukocyte trafficking through selectin ligand modification. For example, St3gal4 promotes neutrophil adhesion (49, 50), whereas St6gal1 deficiency has been reported to induce neutrophilic inflammation (51). Thus, decreased expression of sialyltransferases and fucosyltransferases in the absence of p40<sup>phox</sup> may contribute to aberrant neutrophil trafficking. Furthermore, alterations in mucosal thickness and mucin structure have been reported in IBD and other mucosal disorders due to aberrant glycosylation (41–43, 52–57). St3gal6, St3gal4, Fut4, and Fut9 have been implicated in intestinal mucin modification, and their impaired expression in p40<sup>phox</sup>−/− mice may compromise the protective mucosal barrier integrity, resulting in enhanced inflammation (37, 58). Moreover, Fut4 contributes to epithelial wound repair during airway inflammation (59, 60), suggesting that its decreased expression in p40<sup>phox</sup> deficiency may contribute to impaired resolution of inflammation. Taken together, our observations indicate that p40<sup>phox</sup> deficiency leads to alterations in the expression of enzymes modifying glycan structures, which may induce aberrant intestinal neutrophil recruitment and impaired wound healing.

By combining functional studies in genetically engineered murine models with computational analysis, we have demonstrated that p40<sup>phox</sup> deficiency induces an aberrant neutrophil inflammation in response to intestinal injury, likely due to alterations in the mechanisms controlling leukocyte recruitment and wound healing.

Acknowledgments

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Disclosures

The authors have no financial conflicts of interest.

References

Figure Legends for Supplemental Data

Supplemental Figure 1. Differential expression analysis of temporal microarray data.

Supplemental Figure 2. Clustering and gene set overlap analysis of differentially expressed genes in DSS colitis model. (A) Early responding genes (days 0-2). (B) Mid-to-late responding genes (days 2-6). (C) Late responding genes (days 4-6).

Supplemental Figure 3. Clustering and gene set overlap analysis of differentially expressed genes in XCGD PMNs stimulated for phagocytosis.
Identify significantly differentially expressed genes using two-tailed two-sample $t$ test between pairs of data collected from consecutive time points.

Normalize microarray data collected from colon-extracted RNA on Day 0, 2, 4 and 6, using GCRMA; filter probes with low absolute expression values, low entropy, and variance less than 10th percentile.

Fold-change cutoff: 2-fold; $p$ value cutoff: < 0.05

Identified 1283 genes that are significantly differentially regulated in DSS colitis colon tissue.

Identify genes regulated in DSS colitis model

Identify genes regulated in DSS colitis model

Identify ROS-dependent genes regulated in neutrophils

Treated with 3% DSS

Treated with Water

C57BL/6J 12-14 wk

Healthy Subject Cohort

XCGD Patient Cohort

Polymorphonuclear neutrophils

PMNs stimulated for phagocytosis

Unstimulated PMNs

C57BL/6J

Healthy Subject

Cohort

XCGD Patient

Cohort

PMNs

Polymorphonuclear neutrophils

Identify significantly differentially expressed genes using two-tailed two-sample $t$ test between pairs of data collected from consecutive time points.

Normalize microarray data collected from in vitro-stimulated or resting PMNs at 0, 90, 180, and 360 minutes, using GCRMA; filter probes with low absolute expression values, low entropy, and variance less than 10th percentile.

Fold-change cutoff: 2-fold; $p$ value cutoff: < 0.05

Differential-of-differential analysis: Identify genes that are significantly differentially expressed in healthy PMNs relative to XCGD PMNs using two-tailed two-sample $t$ test between pairs of normalized fold change data.

Identified 124 genes that are significantly differentially regulated in healthy (stimulated) PMNs compared to XCGD (stimulated) PMNs.

Map orthologs in mice.
### Early Responding Genes (Temporal Profile Cluster 1)

**Gene Set Name** | **Gene Set # (K)** | **Description** | **# Genes in Overlap (k)** | **p value**
--- | --- | --- | --- | ---
KEGG: REdoxKINASE SIGNALING PATHWAY | 19 | Hepatitis signaling pathway | 7 | 9.15 e-4
KEGG: WNT SIGNALING PATHWAY | 11 | Wnt signaling pathway | 13 | 1.2 e-3
KEGG: Glycerolipid biosynthesis | 22 | Glycerophospholipid biosynthesis – lacto and neolacto series | 3 | 1.39 e-3
SA: PI3K-AKT-SIGNALING | 37 | Genes involved in AKT phosphorylation targets in the cytosol | 2 | 2.84 e-5
REACTOME: FAS SIGNALING | 6 | Bcl-2-associated death agonist, Fas induces apoptosis on ligand binding | 4 | 2.53 e-3
BIOCARTA: COMP_PATHWAY | 19 | Genes involved in complement and coagulation cascade | 6 | 5.33 e-5
CHEMOKINES | 26 | Genes involved in chemokine-like ligand receptors | 10 | 7.09 e-3

### Mid-to-Late Responding Genes (Temporal Profile Cluster 2)

**Gene Set Name** | **Gene Set # (K)** | **Description** | **# Genes in Overlap (k)** | **p value**
--- | --- | --- | --- | ---
KEGG: Glycerolipid biosynthesis | 22 | Glycerophospholipid biosynthesis – lacto and neolacto series | 4 | 2.2 e-4
KEGG: NEURONAL RELEASE CYCLE | 14 | Genes involved in dopamine neurotransmitter release | 2 | 2.2 e-4
KEGG: GLUCOCORTICOID NONRECEPTOR SIGNALING | 29 | Genes involved in adrenocorticotropin hormone release cycle | 3 | 1.11 e-3
KEGG: NEURONAL RELEASE CYCLE | 14 | Genes involved in serotonin neurotransmitter release cycle | 4 | 1.47 e-5
KEGG: ATRACHTED-TOXICITY OF NEUROTRANSMITTERS | 17 | Genes involved in acetylcholine neurotransmitter release cycle | 5 | 2.55 e-5
KEGG: CIRCadian RHYTHM: MAMMALS | 18 | Calcium cycle – circadian rhythm | 3 | 6.56 e-4
KEGG: Glycerolipid biosynthesis | 22 | Glycerophospholipid biosynthesis – lacto and neolacto series | 3 | 3.76 e-4
KEGG: PHOSPHATIDYLCHOLINE BIOSYNTHESIS | 14 | Genes involved in acetylcholine neurotransmitter release cycle | 10 | 1.16 e-3
KEGG: PHOSPHATIDYLCHOLINE BIOSYNTHESIS | 14 | Genes involved in acetylcholine neurotransmitter release cycle | 6 | 3.92 e-2
KEGG: PHOSPHATIDYLCHOLINE BIOSYNTHESIS | 14 | Genes involved in acetylcholine neurotransmitter release cycle | 2 | 4.65 e-3

### Late Responding Genes (Temporal Profile Cluster 3)

**Gene Set Name** | **Gene Set # (K)** | **Description** | **# Genes in Overlap (k)** | **p value**
--- | --- | --- | --- | ---
REACTOME: Chemokine receptors binding | 15 | Genes involved in chemokine receptors binding | 18 | 5.32 e-5
BIOCARTA: LAR_PATHWAY | 17 | Cells and molecules involved in local resolving inflammatory response | 8 | 4.6 e-3
BIOCARTA: CLASSIC_PATHWAY | 14 | Classical complement pathway | 7 | 1.14 e-5
BIOCARTA: GRANULOCYTES_PATHWAY | 14 | Adhesion and dispersion of granulocytes | 7 | 1.14 e-5
KEGG: CYTOKINE CYTOKINE RECEPTOR KIT | 27 | Cytokine-cytokine receptor interaction | 36 | 2.43 e-5
BIOCARTA: MONOCYTE_PATHWAY | 14 | Monocyte and its surface molecules | 6 | 2.07 e-4
KEGG: COMPLEMENT AND COAGULATION CASCADES | 9 | Complement and coagulation cascade | 10 | 2.87 e-7
BIOCARTA: Peptide ligand binding receptors | 17 | Genes involved in peptide ligand binding receptors | 36 | 5.21 e-1
KEGG: Chemokine signaling pathway | 14 | Chemokine signaling pathway | 27 | 1.01 e-1
BIOCARTA: COMP_PATHWAY | 13 | Complement pathway | 7 | 1.25 e-3
### Genes / Gene sets activated in the absence of ROS

<table>
<thead>
<tr>
<th>Gene Set Name (# Genes (K))</th>
<th>Description</th>
<th># Genes in Overlap (k)</th>
<th>k/K</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>REACTOME_NF_KB_IS_ACTIVATED_AND_SIGNALS_SURVIVAL [10]</td>
<td>Genes involved in NF-kB is activated and signals survival</td>
<td>2</td>
<td></td>
<td>8.84e-4</td>
</tr>
<tr>
<td>REACTOME_P75NTR_RECRUITS_SIGNALLING_COMPLEXES [10]</td>
<td>Genes involved in p75NTR recruits signalling complexes</td>
<td>2</td>
<td></td>
<td>8.84e-4</td>
</tr>
<tr>
<td>REACTOME_P75NTR_SIGNALS_VIA_NFKB [13]</td>
<td>Genes involved in p75NTR signals via NF-kB</td>
<td>2</td>
<td></td>
<td>1.52e-3</td>
</tr>
<tr>
<td>REACTOME_SIGNALLING_BY_NGF [215]</td>
<td>Genes involved in Signalling by NGF</td>
<td>5</td>
<td></td>
<td>2.61e-3</td>
</tr>
<tr>
<td>BIOCARNA_NFKB_PATHWAY [23]</td>
<td>NF-kB Signaling Pathway</td>
<td>2</td>
<td></td>
<td>4.79e-3</td>
</tr>
<tr>
<td>REACTOME_P75NTR_RECEPTOR_MEDIATED_SIG_SIGNALLING [82]</td>
<td>Genes involved in p75 NTR receptor-mediated signalling</td>
<td>3</td>
<td></td>
<td>5.95e-3</td>
</tr>
<tr>
<td>KEGG_MAPK_SIGNALLING_PATHWAY [267]</td>
<td>MAPK signalling pathway</td>
<td>5</td>
<td></td>
<td>6.59e-3</td>
</tr>
<tr>
<td>KEGG_APOPTOSIS [88]</td>
<td>Apoptosis</td>
<td>3</td>
<td></td>
<td>7.23e-3</td>
</tr>
<tr>
<td>BIOCARNA_IL1R_PATHWAY [33]</td>
<td>Signal transduction through IL1R</td>
<td>2</td>
<td></td>
<td>9.72e-3</td>
</tr>
<tr>
<td>REACTOME_PI3K_AKT_SIGNALLING [37]</td>
<td>Genes involved in PI3K/AKT signalling</td>
<td>2</td>
<td></td>
<td>1.21e-2</td>
</tr>
</tbody>
</table>

### Genes underlying the enrichment signature

- IRAK1
- SQSTM1
- RASGRF1
- NR4A1
- CDKN1A
- IL1R1
- GADD45B
- DDIT3
- CASP7

### Genes / Gene sets suppressed in the absence of ROS

<table>
<thead>
<tr>
<th>Gene Set Name (# Genes (K))</th>
<th>Description</th>
<th># Genes in Overlap (k)</th>
<th>k/K</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>KEGG_OTHER_GLYCAN_DEGRADATION [16]</td>
<td>Other glycan degradation</td>
<td>3</td>
<td></td>
<td>7.57e-4</td>
</tr>
<tr>
<td>SA_PROGRAMMED_CELL_DEATH [12]</td>
<td>Programmed cell death, or apoptosis, eliminates damaged or unneeded cells.</td>
<td>2</td>
<td></td>
<td>8.15e-3</td>
</tr>
<tr>
<td>KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_AR_METABOLISM [44]</td>
<td>Amino sugar and nucleotide sugar metabolism</td>
<td>2</td>
<td></td>
<td>1.42e-2</td>
</tr>
<tr>
<td>BIOCARNA_MCM_PATHWAY [18]</td>
<td>CDK Regulation of DNA Replication</td>
<td>3</td>
<td></td>
<td>1.42e-2</td>
</tr>
<tr>
<td>BIOCARNA_PS3HYPOXIA_PATHWAY [23]</td>
<td>Hypoxia and p53 in the Cardiovascular system</td>
<td>2</td>
<td></td>
<td>2.88e-2</td>
</tr>
</tbody>
</table>

### Genes underlying the enrichment signature

- HEXA
- HEXB
- NEU1
- MCM2
- MCM6
- BAX
- BCL2L11
- GNPDA1
- GU1
- TXNRD1
- IGFBP3