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CXCR2 intrinsically drives the maturation and function of neutrophils in mice

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20 Abstract

21 Neutrophils play a major role in the protection from infections but also in inflammation related to 22 tumor microenvironment. However, cell-extrinsic and -intrinsic cues driving their function at steady 23 state is still fragmentary. Using Cxcr2 knock-out mice, we have evaluated the function of the 24 chemokine receptor Cxcr2 in neutrophil physiology. We show here that Cxcr2 deficiency decreases the percentage of mature neutrophils in the spleen, but not in the bone marrow (BM). There is also an 25 increase of aged CD62L^{lo} CXCR4^{hi} neutrophils in the spleen of KO animals. Spleen Cxcr2^{-/-} 26 27 neutrophils display a reduced phagocytic ability, whereas BM neutrophils show an enhanced phagocytic ability compared to WT neutrophils. Spleen Cxcr2^{-/-} neutrophils show reduced reactive 28 oxygen species production, F-actin and α -tubulin levels. Moreover, spleen Cxcr2^{-/-} neutrophils 29 30 display an altered signaling with reduced phosphorylation of ERK1/2 and p38 MAPK, impaired 31 PI3K-AKT, NF- κ B, TGF β and IFN γ pathways. Altogether, these results suggest that Cxcr2 is 32 essential for neutrophil physiology.

34

35 Introduction

36 One of the first line of defense against pathogens such as bacteria, fungi, or parasites involves 37 neutrophils, which are key mediator of innate immunity and inflammation. Neutrophils use different 38 ways to clear the infection, including bacterial uptake (phagocytosis), phagolysosomal degradation of 39 bacteria with a cocktail of antimicrobial factors and reactive oxygen species (ROS) (oxidative burst) 40 or release of granules to neutralize extracellular pathogens (degranulation) (1). In addition, when 41 intruders are too large or have escaped the other microbial killing processes, neutrophils can extrude 42 a physical barrier to pathogen dissemination, called a neutrophil extracellular trap (NET), containing 43 DNA, histones and granule proteases (2). 44 Neutrophils are the most abundant circulating leukocytes, representing 50% to 70% of all circulating 45 leukocytes in humans and about 10 to 25% in mice (3). Neutrophils are relatively short lived cells 46 (4), even if recent studies have questioned this aspect and it is now believed that human and murine 47 neutrophils could have a half-life of 5 days or 18h, respectively (5). 48 Neutrophils arise from granulocyte–monocyte progenitors (GMPs), mostly within the bone marrow 49 (BM) during hematopoiesis in response to several cytokines, principally granulocyte colony– 50 stimulating factor (G-CSF) (6), but also from extramedullary tissues such as spleen (7-9). The first 51 progenitor that is 'neutrophil committed' is the neutrophil promyelocyte (10), which then maturates 52 through granulocyte-committed precursors comprising myeloblasts, promeylocytes and myelocytes, 53 to a post-mitotic or transition pool of metamyelocytes, band cells and segmented neutrophils (11). 54 Mature post-mitotic neutrophils are released from the BM into the peripheral blood, extravasate from 55 circulation into the tissues under the coordinate regulation of various adhesion molecules and 56 chemokines (12). They are involved not only in the control of inflammation following infections or 57 injuries but have also pro or anti-tumoral actions as tumor associated neutrophils (TANs) (13-15). In 58 inflammatory sites, neutrophils fight the injury or infection and undergo apoptosis and are

59 phagocyted by macrophages, once inflammation has been resolved (16). Senescent neutrophils can 60 also home back to the BM in a Cxcr4-dependent mechanism (17). The terminal differentiation of 61 neutrophils in the BM, before release into the bloodstream, is still a subject of debate, as some steps 62 of maturation could occur in other organs such as the spleen (9) and in the same line, neutrophil 63 progenitors have been found in the spleen (18). Maturation markers of neutrophils are also currently 64 discussed, but classically Ly6G, Cd101, Cxcr4 and Cxcr2 are used in mice (8, 12). 65 Cxcr2 appears as one of the key chemokine receptor expressed by neutrophils both in mice and 66 humans (19, 20). Cxcr2 binds the chemokines Cxcl1, 2, 3, 5, 6, 7 and 8 in human, which all have pro-67 angiogenic properties and are located in a short cluster of chromosome 4 (21-23). Cxcr2 ligand action 68 is conditioned by its interaction with proteoglycans (24) and Cxcr2 signals through multiple 69 pathways including PI3K and Src (25). In addition, recent work has highlighted the role of Cxcr2 in 70 tumorigenesis, in particular through tumor-associated neutrophils (14, 23, 26, 27), but also in the 71 effects microbiota on pituitary function (28). Cxcr2 knockout mice have been generated and are 72 characterized by a splenomegaly due to an increase of metamyelocytes, mature neutrophils and B 73 lymphocytes (29). These mice also display a defect in neutrophil recruitment after infection (30). 74 So far, the mechanism of Cxcr2 action in neutrophils remains poorly understood. In this study, we 75 have investigated the role of Cxcr2 in mouse neutrophils in the spleen and the BM, taking advantage of Cxcr2^{-/-} mice. Our data show that Cxcr2 impairment in neutrophils affects differently spleen and 76 77 BM neutrophils in terms of maturation, phagocytosis and ROS production. Moreover, we analyzed at 78 the transcriptomic level the pathways that were altered by Cxcr2 deletion in neutrophils. Altogether, 79 these results suggest that proper Cxcr2 expression and function is required for maturation and 80 effector functions of peripheral neutrophils. 81

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- 83

84 Materials and methods

85 Animal Models and housing

All animal experiments conformed to our animal protocols that were reviewed and approved by the
Institutional Animal Care and Use Committee. *Cxcr2^{-/-}* mice (29) were obtained from the Jackson
Laboratory. *Cxcr2^{-/-}* mice were backcrossed in FVB genetic background for more than 12 generations.
Control (WT) mice were also in a FVB background. All mice were housed in a SOPF (Specific and
Opportunistic Pathogen Free) animal facility.

91 **Isolation of cells**

92 Cells from the BM were isolated by centrifugation from the femurs and tibias of the animals, whereas 93 spleens were mashed on 100 µm nylon cell strainer. After centrifugation, red blood cells were 94 eliminated by treatment with ACK buffer (0.155 mM NH4Cl, 1 mM KHCO3, 0.1 mM EDTA) and 95 filtered on a 40 µm nylon cell strainer. After ACK treatment, cells were filtered on a 40 µm nylon cell 96 strainer. For neutrophil isolation, a first enrichment with EasySep[™] Mouse CD11b Positive Selection 97 kit (StemCell technologies, Grenoble, France) was performed followed by cell sorting of CD45+ 98 CD11b+ Ly6G+ F4/80- cells on an ARIA IIu FACS sorter (Becton Dickinson, Le Pont-de-Claix, 99 France).

100 Flow cytometry

Flow cytometry experiments were performed with the following conjugated antibodies from Biolegend (London, United Kingdom): anti-mouse CD11b (clone M1/70), CD45 (clone 30-F11), Cxcr2 (clone SA044G4), Ly6G (clone 1A8), CD62L (clone MEL-14) or BD Biosciences (BD Biosciences, Le Pont-de-Claix, France): Cxcr4 (clone 2B11), or Ebiosciences (Fisher Scientific, Illkirch, France): CD101 (clone Moushi101), Fixable viability dye (65-0866). Flow analysis was performed on live singlets with a LSR II Fortessa flow cytometer (Becton Dickinson, Le Pont-de-Claix, France). Data were analyzed using FlowJo (Tree Star).

109 Intracellular flow cytometry

110 Cells were first stained with antibodies directed against extracellular markers (CD45, CD11b, Ly6G) 111 and then permeabilized with Cytofix/Cytoperm and Permwash buffer (BD Biosciences). Intracellular 112 staining of F-actin was performed with Phalloidin, Fluorescein Isothiocyanate Labeled (Sigma-113 Aldrich, ref P5282), whereas α -tubulin was labeled with α -Tubulin antibody (clone 11H10, Cell 114 Signaling, ref 2125) followed by secondary an anti-rabbit IgG antibody coupled to Alexa Fluor 555 115 (ThermoFisher, ref A27039). Phospho-p42/44 MAPK ERK1/2 (Thr 202/ Tyr 204) (Cell signaling, ref 116 4370) followed by secondary an anti-rabbit IgG antibody coupled to Alexa Fluor 555 (ThermoFisher, 117 ref A27039) was used to detect Phospho-p42/44 MAPK ERK1/2. p-p38 MAPK (Thr 180/ Tyr 182) 118 coupled to PE (cell Signaling 6908), was used to detect phospho-p38 MAPK. 119 Annexin V staining and measure of mortality 120 To determine the proportion of apoptotic and dead cells, fresh neutrophils were stained with Annexin-121 FITC and propidium iodide (PI) according to manufacturer instruction (Invitrogen, ref V13242). 122 Phagocytosis assay

CD45+ CD11b+ Ly6G+ neutrophils were incubated for various times at 37°C with with E. coli Red
Phrodo bioparticles (ThermoFisher, Illkirch, France) at a concentration of 15 μg/ml and analyzed in
a kinetic manner by flow cytometry with a LSR II Fortessa flow cytometer (Becton Dickinson, Le
Pont-de-Claix, France). Data were analyzed using FlowJo (Tree Star). When opsonized particles were
used, they were opsonized for 1h at 37°C with opsonizing reagent (E2870, ThermoFisher, Illkirch,
France), according to manufacturer instructions.

129 Reactive oxygen species and mitochondrial superoxide quantification

130 Reactive oxygen species and mitochondrial quantification was performed by labelling fresh CD45+

131 CD11b+ Ly6G+ neutrophils for 20 min at 37°C, using CellRox Orange reagent (ref. C10443) and

- 132 Mitosox reagent (ref. M36008) respectively, following the manufacturer's instructions (Molecular
- 133 Probes, ThermoFisher Scientific).

134

135

136 RNA extraction and RNA-seq data processing

137 Total RNA was isolated using TRIzol reagent (Fisher Scientific, Illkirch, France), as described by the 138 manufacturer. RNA integrity and quality were verified using RNA ScreenTape kit and Tapestation 139 2200 apparatus from AGILENT (Les Ulis, France). cDNA libraries were synthesized using 140 NEBNext® rRNA Depletion and UltraTM II Directional RNA Library Prep Kit (New England Biolabs, 141 Evry-Courcouronnes, France). Library quality was checked on Tapestation 2200 apparatus from 142 AGILENT (Les Ulis, France) with DNA 1000 ScreenTape. Samples were sequenced on Novaseq 143 6000 (Illumina) with an average sequencing depth of 30 million of paired-end reads. Length of the 144 reads was 150 bp. Each 24 Plex Samples was sequenced on one Illumina SP FlowCell (2*800 million 145 of 150bases reads). Raw sequencing data was quality-controlled with the FastQC program. Low 146 quality reads were trimmed or removed using Trimmer (minimum length: 120 bp). Reads were aligned 147 to the mouse reference genome (mm10 build) with the Star tool. Gene counts were obtained by read 148 counting software Htseq. Normalization and differential analysis were performed with the DESeq2 149 package with Benjamini-Hochberg FDR multiple testing correction (p < 0.05; 1.5-fold or higher 150 change) comparing WT and KO animals. The data discussed in this publication have been deposited 151 in NCBI's Gene Expression Omnibus (31) and are accessible through GEO Series accession number 152 GSE209860 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE209860).

153 **Bioinformatic analysis**

To assess biological interpretation of the most differentially expressed genes, we used Gene ontology (GO) enrichment analysis. A gene set enrichment analysis (GSEA) was performed using signatures from GSEA collections. A normalized enrichment score (NES) was calculated for each gene set and only gene sets with an adjusted p value < 0.05 were selected.

158 Statistics

159 Statistical analyses were carried out using unpaired Mann-Whitney test.

161 **Results**

162 *Cxcr2* invalidation affects the maturation of neutrophils

- 163 To evaluate the impact of *Cxcr2* knockout on neutrophil distribution and function, we first measured
- 164 the presence of CD45+ CD11b+ Ly6G+ neutrophils in the BM and the spleen by flow cytometry
- 165 (Fig.1A). Ly6G+ neutrophils were composed of two subpopulations with high (Ly6G^{hi}) or low
- 166 (Ly6G^{lo}) levels of Ly6 (Fig. 1A). In BM, the percentage of total Ly6G+ (Ly6G^{hi} + Ly6G^{lo})
- 167 neutrophils was increased by about 30% in *Cxcr2-/-* compared to WT animals, and this was much
- 168 more pronounced in the spleen, with more than 8 fold more neutrophils in *Cxcr2-/-* animals (Fig.
- 169 1B). Of particular note, the percentage of CD45+ cells was not different in WT and KO spleens,
- 170 whereas it slightly increased (88.7% vs 95.2%) in KO BM compared to WT BM (Supplemental Fig.
- 171 1). No major change in FSC and SSC distribution was observed for Ly6G+ neutrophils
- 172 (Supplemental Fig. 2). In terms of absolute numbers, we observed a 5-fold increase of the total
- 173 number of CD45+ cells and CD45+ CD11b+ Ly6G+ neutrophils in the spleen of Cxcr2-/- animals,
- 174 whereas minimal differences between and Cxcr2-/- and WT animals was seen in BM (no change of
- 175 the number of CD45+ cells and less than 30 % increase for CD45+ CD11b+ Ly6G+) (Supplemental
- 176 Fig. 3). This obviously creates a bias in the analysis of any type of subpopulation and for this reason,
- 177 we decided to continue to look at percentage of subpopulations of neutrophils among neutrophils, to178 avoid this.

179 The level of Ly6G expression has been correlated with the degree of maturation of neutrophils with

180 Ly6G^{hi} neutrophils being the most mature (32). In BM, there was a slight reduction of the percentage

- 181 of immature Ly6G^{lo} neutrophils among total Ly6G+ in *Cxcr2-/-* animals, whereas there was an
- 182 increase by 2-fold of immature Ly6G^{lo} neutrophils in *Cxcr2-/-* spleen (Fig. 1C). To strengthen these
- 183 results, we used the CD101 marker, which characterizes mature neutrophils (8). Among neutrophils,
- 184 we observed a reduction of CD101+ mature neutrophils in the spleen, but an increase of mature
- 185 neutrophils in BM (Fig. 1D, F). Next, we also looked at Cxcr4 expression in neutrophils, which is

186 correlated not only to immaturity of neutrophils (8), but also to aged neutrophils (33). The percentage 187 of Cxcr4+ neutrophils increased twice in the spleen, but was unaffected in the BM (Fig. 1E, G), 188 confirming the increase of the proportion of immature neutrophils in the neutrophil fraction of the 189 spleen. To assess more precisely whether these neutrophils corresponded to immature or aged 190 neutrophils in the spleen of KO animals, we used the marker CD62L (L-Selectin), in addition to CXCR4 to identify "aged" CD62L^{lo}- CXCR4^{hi} neutrophils, as previously described (33). We 191 observed that the proportion of aged CD62L^{lo}- CXCR4^{hi} cells among neutrophils increased in KO 192 193 spleen compared to WT, but there was no significant change in BM (Supplemental Fig. 4). 194 To further assess the nature of neutrophils, we isolated by cell sorting CD45+ CD11b+ Ly6G+ 195 neutrophils from WT and KO BM and spleen and colored them with Giemsa (Supplemental Fig. 9). 196 WT BM neutrophils displayed a condensed round nucleus, with a small cytoplasm, whereas KO BM 197 neutrophils seem to have a larger ring-shaped nucleus, which could suggest that they are more 198 mature. In the spleen, WT neutrophils had a strongly colored ring-shaped nucleus. Spleen KO 199 neutrophils exhibited a larger nucleus with a less pronounced staining and also a cytoplasmic center, 200 which could be reminiscent of band neutrophils (34). These morphological differences suggest that 201 WT and KO neutrophils might have distinct features.

202 Cxcr2-/- neutrophils display altered phagocytic ability

203 Phagocytosis is one of the major function of neutrophils to eliminate infections. Thus, we analyzed

204 the phagocytic abilities of BM and spleen neutrophils. Kinetics of phagocytosis showed that BM

205 *Cxcr2-/-* neutrophils had an enhanced phagocytic ability compared to WT neutrophils (Fig.2A),

whereas spleen Cxcr2-/- neutrophils were less phagocytic than spleen WT neutrophils (Fig. 2B). We

- 207 have also performed an additional analysis, by separating Ly6G^{hi} and Ly6G^{lo} neutrophils
- 208 (Supplemental Fig. 5). Similar results were obtained for Ly6G^{hi} neutrophils as for Ly6G+
- 209 neutrophils, which is an increase of phagocytosis for BM KO neutrophils and a decrease of

phagocytosis for spleen KO neutrophils. Concerning Ly6G^{lo} neutrophils, they were less phagocytic
than Ly6G^{hi} neutrophils, both in the spleen and BM. Moreover, BM KO Ly6G^{lo} were also more
phagocytic than BM WT Ly6G^{lo} neutrophils. On the other hand, no difference was seen for spleen
Ly6G^{lo} neutrophils between WT and KO animals. In addition, when using opsonized bioparticles
(Supplemental Fig. 6), we obtained the same trend of difference between WT and KO neutrophils as
for non-opsonized particles.

216 To better understand the mechanisms underlying these changes in phagocytic ability, we looked at 217 ROS production and to actin-tubulin cytoskeleton organization of neutrophils, which are essential for 218 phagocytosis (35). We observed a strong reduction in the production of cytoplasmic ROS (Fig 3A, B) 219 and mitochondrial superoxide (Fig. 3C, D) of spleen Cxcr2-/- neutrophils, whereas no difference 220 could be measured between BM WT and Cxcr2-/- neutrophils. Spleen Cxcr2-/- neutrophils had also 221 lower levels of F-Actin (Fig. 4A, B) as well as tubulin (Fig. 4C, D) compared to WT, but BM 222 neutrophils were unaffected by Cxcr2 impairment. These results of decreased levels of F-actin and 223 tubulin were also confirmed, when comparing MFI values for F-actin and tubulin for the different 224 types of neutrophils (Supplemental Fig. 7). Altogether, these results could account for the lower 225 phagocytic ability of spleen *Cxcr2-/-* neutrophils, which is in agreement with a lower maturity.

226

227 Spleen *Cxcr2-/-* neutrophils have a higher viability

228 Neutrophil are short term living cells, so we wondered whether Cxcr2 could modulate their survival

ability. We observed that the percentages of apoptotic or dead cells were reduced for spleen Cxcr2-/-

- 230 neutrophils (Fig. 5B and 5C, respectively), whereas it was similar for WT and Cxcr2-/- BM
- 231 neutrophils. So, this suggests that the reduced phagocytic ability of spleen *Cxcr2-/-* neutrophils is not
- a consequence of an impaired survival. We have also measured apoptosis and death after a 2h
- 233 incubation at 37°C, and obtained similar results (Supplemental Fig. 8), which suggests that an

- 234 increased apoptosis or death after 2h incubation does not affect the phagocytosis ability of
- 235 neutrophils.

236	Transcriptomic analysis confirms the impaired maturation of spleen Cxcr2-/- neutrophils
237	We next focused on spleen neutrophils to decipher whether and how Cxcr2 deficiency impacts their
238	molecular identity. RNAseq analyses of WT and Cxcr2-/- spleen neutrophils showed that more than
239	2,500 transcripts were up-regulated and about the same number down-regulated in Cxcr2-/- spleen
240	neutrophils (Fig. 6A, B). We then focused on their maturation using the neutrophil maturation
241	signature reported by Xie and collaborators (36). GSEA analysis confirmed that spleen Cxcr2-/- were
242	less mature than their WT counterparts (Fig. 6D, E), with down regulation of genes encoding
243	Cathepsin D (Ctsd), JunB or IL-1ß involved in Netosis (2), Arginase-2 (Arg2) controlling extra-urea
244	cycle arginine metabolism and nitric oxide synthesis (12), C-type lectin receptor Clec4d crucial for
245	bacteria elimination (37) or Selplg (CD162), important for the rolling of neutrophils (38).
246	In addition, there was a cluster of GSEA Biological process (BP) signatures showing a down-
247	regulation of the chemotaxis and migration of spleen Cxcr2-/- neutrophils (Fig. 6F), suggesting a
248	decrease in the migration ability of these neutrophils.
249	ERK and p38 MAPK pathways are down-regulated in spleen Cxcr2-/- neutrophils
250	To look at the signaling that were affected in spleen Cxcr2-/- neutrophils, we first focused on ERK
251	and p38 MAPK signaling, which are known to modulate the migration and adhesion of neutrophils
252	(39, 40). RNAseq data showed that both ERK1 and ERK2 cascade (Fig. 7A and C), as well as
253	p38MAPK cascade (Fig. 7B and D), were down regulated in spleen Cxcr2-/- neutrophils. Concerning
254	ERK1/2 cascade, there is in particular a down-regulation of the AP-1 Transcription Factor Jun, of the
255	Cyclic AMP-Dependent Transcription Factor Atf-3, IL1β, growth factors such as TGFβ1 and IGF1,
256	multiple chemokines such as Ccl3, 4, 15, 18, 23 and of a number of kinases such as Ptk2b (Protein
257	Tyrosine Kinase 2 Beta), the tyrosine-protein kinase Syk, Csk (C-Terminal Src Kinase) or the

- 258 serine/threonine protein kinase BRAF (Fig. 7C). For p38MAPK cascade, we observed in particular a
- down regulation of Mitogen-Activated Protein Kinase 14 (Mapk14), Mitogen-Activated Protein
- 260 Kinase Kinase 3 (Map3k3), Map3k5, and cytokines such as IL1β, HGF.
- 261 To confirm these results, we measured by flow cytometry the intracellular content of Phospho-p42/44
- 262 MAPK ERK1/2 and phospho-p38 MAPK (Thr 180/ Tyr 182). The mean of fluorescence (MFI) of p-
- 263 ERK1/2 and p-p38 were down-regulated by about 50% in spleen *Cxcr2-/-* neutrophils compared to
- 264 WT neutrophils (Fig. 7E and 7F, respectively) confirming the alterations of these pathways.

265 Several pathways are impaired in spleen *Cxcr2-/-* neutrophils

266 To further investigate the mechanisms involved in the changes observed in spleen Cxcr2-/-

- 267 neutrophils, we explored the main pathways that were affected at the transcriptomic level. GSEA
- 268 analysis showed a reduction of PI3K-AKT signaling (Fig. 8A), TNFα signaling via NFκB (Fig. 8B),
- 269 NIK-NFκB signaling (Fig. 8C), as well of the cellular response to IL-1 (Fig. 8D) and TGFβ signaling
- 270 (Fig. 8E) and signaling by IFNγ (Fig. 8F) signatures in spleen Cxcr2-/- neutrophils compared to WT
- 271 neutrophils. Among the genes involved in PI3K-AKT pathway, we observed a down-regulation of
- 272 Phosphatidylinositol-4,5-Bisphosphate 3-Kinase Catalytic Subunit Alpha, Delta and Gamma (Pik3ca,
- 273 Pik3cd and Pik3cg), and Phosphoinositide-3-Kinase Regulatory Subunit 1, 2 and 5 (Pik3r1, Pik3r2,
- 274 Pik3r5), Janus Kinase 1 (Jak1), Glycogen Synthase Kinase 3 Beta (GSK3b), and Kras, which are
- crucial for this pathway.
- 276 NF-κB pathway was also impaired with in particular down-regulation of genes such as NF-κB
- 277 Subunits p52 (Nfkb2), Relb, C-Rel (Rel), TNF Alpha Induced Protein 2 and 3 (Tnfaip2 and Tnfaip3),
- 278 Tnfaip3 Interacting Protein 1 (Tnip1), TNF Receptor-Associated Factor 1, 3 and 5 (Traf1, Traf3,
- 279 Traf5) or TNF Receptor Superfamily Member 10b (Tnfrsf10b).
- 280 Upstream of NF-κB activation, cellular response to IL-1 was also altered, with a down-regulation of
- 281 IL-1 itself, but also of Interleukin 1 Receptor Type 1 (Il1r1). Two other pathways were also linked to

282	PI3K/Akt, ERK	, p38 and NF-кЕ	3 signaling,	namely TGFβ	and IFN _y	[,] signaling.	TGFβ	signaling	, was
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283 impaired with a decrease in Transforming Growth Factor Beta 1 (Tgfb1), Transforming Growth

- 284 Factor Beta Receptor 1 and 2 (Tgfbr1 and Tgfbr2), and Smad2, 3, and 4. IFNγ signaling is also acting
- 285 through ERK and MAPK and PI3K signaling and exhibits in particular a down-regulation of Janus
- 286 kinase 2 (Jak2), suppressor of cytokine signaling protein 1n and 3 (Socs1, Socs3), Signal transducer
- and activator of transcription 4 (Stat4), Intercellular adhesion molecule-1 (ICAM-1) and Integrin
- 288 Subunit Beta 7 (ITGB7).

Cxcr2 function in neutrophils

290 **Discussion**

291 Although the role of neutrophils in general inflammation but also tumor microenvironment 292 inflammation is growing, the factors controlling their function are still not completely identified. In 293 particular, the involvement of Cxcr2 in neutrophil physiology and features, as well as its impact on 294 signalization in neutrophils is still a matter of debate. In this study, we report that impairment of 295 *Cxcr2* leads to a modest increase of the percentage of neutrophils in the BM, but a strong one in the 296 spleen, in agreement with previous studies (29). We also show that Cxcr2 differentially affects the 297 maturation state of neutrophils in the spleen and the BM. More precisely, based on the maturation markers Ly6G (32) and Cd101 (8) expression, Cxcr2 deletion led an increase of Ly6G^{lo} or CD101-298 299 immature neutrophils in the spleen, but to a decrease of immature neutrophils in the BM. The 300 presence of resident immature neutrophils in the spleen is thought to serve as a reservoir of 301 neutrophils, which will undergo a rapid proliferation and mobilization in case of infection to increase 302 the number of active mature neutrophils (18, 32). Spleen is also a site of accumulation and 303 destruction of neutrophils in human (41), so the presence of a high number of immature neutrophils 304 could correspond to both resident and recruited neutrophils. On the other hand, considering that the 305 BM is the main site of production of neutrophils, this would suggest that Cxcr2 impairment does not 306 alter the maturation process on neutrophils in the BM, or that there could be a retention of mature 307 neutrophils in BM. This latter hypothesis is unlikely, as we did not see any difference in the 308 percentage Cxcr4+ neutrophils in the BM. Cxcr4 is indeed crucial for the retention of neutrophils in 309 the BM (17), even though other studies have shown that the CXCR4 antagonist plerixafor did not 310 mobilize neutrophils from the BM, but rather enhanced the release of neutrophils in the circulation 311 from the marginated pool present in the lung (42). In contrast, the percentage of Cxcr4+ neutrophils 312 was increased 2-fold in the spleen, which could account for several features: this could be the sign of 313 more immature, since Cxcr4 expression is high in proliferating immature neutrophils (8). However, 314 high levels of Cxcr4 can also be seen in senescent or aging neutrophils (17, 43). To clarify this point,

315	we analyzed the presence of aged $CD62L^{lo} - CXCR4^{hi}$ neutrophils as defined previously (33). This
316	shows that there is an increase of aged $CD62L^{lo} - CXCR4^{hi}$ neutrophils in the spleen of KO animals,
317	but no change in BM. In addition, we also observed that the percentage of apoptotic or dead
318	neutrophils was reduced among spleen Cxcr2-/- neutrophils compared to WT, whereas no difference
319	was seen in BM. Overall, our data suggest that spleen Cxcr2-/- neutrophils are distinct from BM
320	neutrophils, as they are healthier and have more immature features (Ly6Glo Cd101- Cxcr4+) than
321	their WT counterparts.
322	To go further in the understanding of the effects of Cxcr2 impairment, we have observed that spleen
323	<i>Cxcr2-/-</i> neutrophils exhibited a reduced phagocytic ability than WT neutrophils. On the other hand,
324	BM Cxcr2-/- neutrophils had a higher phagocytic ability than the WT. This difference between
325	spleen and BM neutrophils might be explained by their difference of maturation mentioned above.
326	This is also true for basal phagocytic ability of WT neutrophils, which is higher in the spleen than in
327	the BM. This might be due to a higher proportion of mature CD101+ neutrophils in WT spleen
328	compared to WT BM (Fig. 1F), as we have also shown that Ly6G ^{hi} neutrophils had a better
329	phagocytic ability than Ly6G ^{lo} neutrophils (Supplemental Fig. 5).
330	To explore the difference in phagocytic ability of WT and Cxcr2-/- neutrophils more thoroughly, we
331	looked at ROS production and actin and tubulin cytoskeleton, which are key elements in
332	phagocytosis (35, 44). The percentage of cells with high cytoplasmic ROS, mitochondrial
333	superoxide, F-actin and α -tubulin was reduced among spleen <i>Cxcr2-/-</i> neutrophils compared to WT,
334	but was not modified in BM neutrophils. This reduction could explain part of the reduced phagocytic
335	ability of spleen Cxcr2-/- neutrophils, although one can also notice that decreased phagocytic ability
336	of WT BM neutrophils compared to WT spleen neutrophils is not correlated to their actin levels,
337	suggesting that other parameters might be involved. It is interesting to notice that aged neutrophils
338	are resistant to infections and display also a reduction of actin levels (43). Moreover, it has also been
339	shown that in some cases, immature neutrophils could produce less ROS (8).

It was essential to analyze the mechanisms underlying the differences between spleen Cxcr2-/- and 340 341 WT neutrophils. RNAseq analysis of both types of isolated neutrophils confirmed the defect in 342 maturation of spleen Cxcr2-/- neutrophils, with in particular a down regulation of genes involved in 343 Netosis (Cathepsin D, JunB or IL-1 β) (45), of Arginase-2 controlling extra-urea cycle arginine 344 metabolism and nitric oxide synthesis, of Clec4d implicated in bacteria elimination (46) or Selplg 345 (CD162), essential for the rolling of neutrophils (47). Several GO pathways of migration and 346 chemotaxis constituted a down-regulated cluster, suggesting also an impairment of spleen Cxcr2-/-347 chemotaxis. This could explain an accumulation of neutrophils in the spleen, with a weak ability to 348 migrate to other tissues. Earlier studies have shown that in inflammatory conditions, Cxcr2 was 349 essential for the recruitment of neutrophils (48). 350 In terms of signaling, we report a down regulation of ERK and p38 MAPK pathways, both at the 351 transcriptomic level, but also when assessing the phosphorylation of ERK and p38 at the protein 352 level. The ERK and p38 MAP kinases are strongly stimulated in neutrophils upon activation by G-353 protein coupled receptors agonists. Moreover, p38 MAPK is critical for the release of primary and 354 secondary granules, but not that of secretory vesicles by neutrophils (49). p38 inhibition has been 355 shown to delay apoptosis of neutrophils (50), which is in agreement of the reduced rate of apoptosis 356 that we observed in spleen Cxcr2-/- neutrophils. Moreover, p38 MAPK promotes chemotaxis 357 towards fMLP by interfering with GRK2-mediated desensitization, whereas ERK MAPK is 358 inhibiting it (51, 52). However, the role of ERK MAPK pathway in neutrophil functions remains 359 unclear, due to contradictory studies (37). 360 In addition, PI3K-Akt, TNFα signaling and NF-κB signaling, were also altered. TNFα is essential to 361 trigger neutrophil activation and phagocytic activity (53). It is interesting to note that in neutrophils, 362 the production of ROS is dependent on PI3K and ERK (54). Moreover, PI3K, ERK and p38 are 363 necessary for efficient phagocytosis (55). It has also been reported that PI3K γ -/- neutrophils display a

- defect in migration towards fMLP, C5a, Cxcl8 or Ccl3 and respiratory burst upon activation by C5a
- 365 or fMLP (56), but another study suggests that PI3K is not required for chemotaxis towards fMLP366 (51).
- 367 Cellular response to IL-1 was also reduced. IL1α and IL1β are very potent mediators of
- 368 inflammation response, but their role in neutrophils remains poorly understood. Their main effect on
- 369 neutrophils could be to increase their survival (37).
- 370 We also observed a down-regulation of TGF β and IFN γ pathways. In the steady state situation, the
- 371 role of TGFβ on neutrophil function is poorly understood. However, in cancer context, TGFβ is
- 372 responsible for promoting the generation of pro-tumoral type N2 neutrophils (57), whereas type IFNβ
- and IFNγ might favor anti-tumoral type N2 neutrophils (58, 59). In non-cancerous situation, IFNγ has
- also been shown to enhance, or prime, increased ROS production in combination with a secondary
- 375 stimulus and to promote phagocytosis (60), which could account for the decrease in ROS and
- 376 phagocytosis that we observed in spleen Cxcr2-/- neutrophils. As treatment of PMNs with IFNy
- 377 increases the production of TNF α and IL-1 β (61), this could also account for the down-regulation of
- 378 TNF α and IL1 β signaling that we report.
- 379 In conclusion, this work highlights the multiple roles played by the chemokine receptor Cxcr2 in
- 380 neutrophils and reinforces the importance of localization of neutrophils in terms of action and
- 381 features. The identification of the pathways that are dependent on Cxcr2 and their further
- investigation will be essential to understand the roles of Cxcr2 in neutrophils in the steady state or
- 383 inflammatory situation but also in the tumoral context.
- 384

Cxcr2 function in neutrophils

385 386	1 Conflict of Interest
387	The authors declare that the research was conducted in the absence of any commercial or financial
388	relationships that could be construed as a potential conflict of interest.
389	
390	2 Author Contributions
391	P.B., B.G., E.R. and have contributed to the investigation. K.B. participated to writing review and
392	editing. GL was in charge of the conceptualization, investigation and supervision of the project,
393	funding acquisition and writing original draft preparation. All authors have read, revised and agreed
394	to the published version of the manuscript.
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403 404	

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Cxcr2 function in neutrophils

600 Figure legends

601 Fig.1: Cxcr2 knock-out decreases the percentage of mature neutrophils in the spleen

A. Representative dot plots of the gating strategy of CD45+ CD11b+ Ly6G^{hi} and CD45+ CD11b+
Ly6G^{lo} neutrophils among CD45+ cells in WT and *Cxcr2-/-* bone marrow (BM) and spleen (SP). B.
Quantification of the percentage of the total neutrophils (CD11b+ Ly6G+: sum of Ly6G^{hi} and Ly6G^{lo})
in the CD45+ fraction. C. Quantification of CD11b+ Ly6G^{hi} cells (left panel) and CD11b Ly6G^{lo}

606 (right panel) in the CD11b+ Ly6G+ (Ly6G^{hi} and Ly6G^{lo} fractions) population. **D.** Gating strategy to

identify CD101+ neutrophils in the CD45+ CD11b+ Ly6G+ fraction. E. Gating strategy to identify

- 608 CXCR4+ neutrophils in the CD45+ CD11b+ Ly6G+ fraction. F. Percentage of mature CD101+

609 neutrophils in the CD11b+ Ly6G+ fraction. G. Percentage of CXCR4+ neutrophils in the CD11b+

- 610 Ly6G+ fraction. Data represent the mean \pm SEM of at least 6 animals (Mann-Whitney test, NS: non-
- 611 significant, * p<0.05, ** p<0.01, *** p<0.001).
- 612

607

613 Fig. 2: spleen *Cxcr2-/-* neutrophils have an impaired phagocytosis ability

A. To measure phagocytosis, BM CD11b+ Ly6G+ neutrophils were incubated with Red E. coli Phrodo bioparticles at 37°C for 0, 30 min, 1h or 2h and analyzed by flow cytometry. Upper panel: Gating strategy to identify phagocytic neutrophils (Phago+) in the CD11b+ Ly6G+ fraction at 2h time. Lower panel: Percentage of phagocytic Ly6G+ neutrophils. **B.** Same experiment with spleen neutrophils. Results are expressed as the percentage of phagocytic neutrophils in the CD11b+ Ly6G+ population and represent the mean \pm SEM of at least 6 animals (Mann-Whitney test, NS: nonsignificant, * p<0.05, ** p<0.01, *** p<0.001).

621

622 Fig. 3: spleen *Cxcr2-/-* neutrophils display reduced ROS and superoxide levels

623 A. Gating strategy to measure cytoplasmic Ros levels using CellRox Orange in CD11b+ Ly6G+

624 neutrophils. B. ROS levels were quantified in spleen and BM CD11b+ Ly6G+ neutrophils using

625 CellRox Orange probe. Results are expressed as the percentage of ROS-positive neutrophils in the

626 CD11b+ Ly6G+ population and represent the mean \pm SEM of at least 6 animals (Mann-Whitney test,

627 NS: non-significant, ** p<0.01). C. Gating strategy to measure Mitochondrial superoxide levels using

628 Mitosox in CD11b+ Ly6G+ neutrophils. **D.** Measure of the percentage of mitochondrial superoxide

629 –positive CD11b+ Ly6G+ neutrophils using Mitosox reagent. Data represent the mean \pm SEM of at

630 least 6 animals (Mann-Whitney test, NS: non-significant, ** p<0.01).

631

632 Fig. 4: Decrease of Actin⁺ and Tubulin⁺ levels in spleen *Cxcr2-/-*

633 A. Gating strategy to measure F-Actin levels (Actin⁺) in CD11b+ Ly6G+ neutrophils. **B.** Percentage

634 of CD11b+ Ly6G+ expressing Actin (mean ± SEM of at least 6 animals; Mann-Whitney test, NS:

635 non-significant, ** p<0.01). C. Gating strategy to measure α -Tubulin levels (Tubulin⁺) in CD11b+

636 Ly6G+ neutrophils. **D.** Percentage of CD11b+ Ly6G+ expressing Tubulin. (mean ± SEM of at least

637 6 animals; Mann-Whitney test, NS: non-significant, ** p<0.01).

638

639 Fig. 5: spleen *Cxcr2-/-* neutrophils exhibit a reduced apoptosis and mortality

640 **A.** Gating strategy to identify alive, dead and apoptotic cells based on Annexin V and PI staining. 641 Control plot corresponds to cells labelled with cell surface markers, but not with Annexin V and PI 642 **B.** Measure of the percentage of apoptotic neutrophils in the spleen and BM of WT and *Cxcr2-/-*643 animals by annexin V staining. **C.** Same measure of dead cells by PI staining. Results are expressed 644 as the percentage of CD11b+ Ly6G+ neutrophils and represent the mean \pm SEM of 6 animals; Mann-645 Whitney test, NS: non-significant, ** p<0.01.

646

647 Fig. 6: Cxcr2-/- neutrophils display decreased maturity at the transcriptomic level

648 A. Volcano plot showing the global changes in RNA expression patterns for spleen neutrophils

649 isolated from Cxcr2-/- (SP KO) versus WT (SP WT) animals. Data represent analysis of cpm

650 estimates with a log of fold change of more than 1.5 fold and p < 0.05 of 4 animals per group. Grey 651 dots: NR: non-regulated genes; Green dots: genes with a log of fold change of more than 1.5 fold; 652 blue dots: genes with a p-value <0.05; red dots: genes with a log of fold change of more than 1.5 fold 653 and p < 0.05. **B.** Number of differentially regulated genes for the spleen neutrophils. Up: genes up-654 regulated in spleen isolated from Cxcr2-/- versus WT animals. Down: down-regulated genes. NR: non 655 regulated genes. C. Simplified Heatmap of spleen Cxcr2-/- versus WT neutrophils. D. Normalized 656 enrichment score (NES) after GSEA analysis of the transcriptome of spleen neutrophils isolated from 657 *Cxcr2-/-* versus WT animals according to Neutrophil maturation of Xie et al. (36). E. Heatmap of the 658 significantly regulated genes (p < 0.05) of Neutrophil maturation signature. F. Cluster of chemotaxis 659 and migration GSEA analysis from Cxcr2-/- versus WT animals according to Biologic process GO: 660 Cell-chemotaxis (NES= -1.64; q= 0.0002), Leukocyte-chemotaxis (NES= -1.62; q= 0.001), 661 Granulocyte chemotaxis (NES = -1.53; q = 0.029), Regulation of Chemotaxis (NES = -1.46; q = 662 0.013), Granulocyte migration (NES= -1.54; q=0.025), Myeloid-leukocyte-migration (NES= -1.50; 663 q=0.012), leukocyte-migration (NES = -1.48; q=0.003).

664

Fig. 7: ERK and p38 pathways are down-regulated in Spleen *Cxcr2-/-* **neutrophils.**

666 A. NES after GSEA analysis of the transcriptome of spleen neutrophils isolated from Cxcr2-/- versus 667 WT animals according to ERK1 and ERK2 cascade signature. **B.** Same analysis for p38-MAPK 668 signature. C. Heatmap of the significantly regulated genes (p<0.05) of GO-BP ERK1 and ER2 cascade 669 signature. **D.** Heatmap of the significantly regulated genes (p<0.05) of GO-BP p38 MAPK cascade 670 signature. E. Phospho-p42/44 MAPK ERK1/2 (Thr 202/ Tyr 204) was analyzed by flow cytometry in 671 spleen CD11b+ Ly6G+ neutrophils. Left panel: representative Mean of Fluorescence (MFI) of WT 672 (red line) and KO (blue line) Ly6G+ neutrophils. Results are expressed as MFI of phospho-ERK 673 positive neutrophils in the CD11b+ Ly6G+ population and represent the mean \pm SEM of at least 6

- 674 animals (Mann-Whitney test, * p<0.05). F. Phosphorylation of p38MAPK on Thr180/Tyr182 was
- analyzed by flow cytometry in the same conditions (Mann-Whitney test, *** p<0.001).
- 676

677 Fig. 8: Multiple pathways are down-regulated in Spleen *Cxcr2-/-* neutrophils

- 678 GSEA analysis of the following signatures: A. WIKI-PI3K-AKT signaling. B. Hallmark-TNFα
- 679 signaling via NFκB. C. GO-BP NIK-NFκB Signaling D. GO-BP Cellular response to IL-1 E. WP-
- 680 TGF β signaling pathway **F**. Hallmark IFNγ-response
- 681