

Myeloid cell-specific deletion of $AMPK\alpha 1$ worsens ocular bacterial infection by skewing macrophage phenotypes

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2 skewing macrophage phenotypes

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23 Abstract

AMP-activated protein kinase (AMPK) plays a crucial role in governing essential cellular 24 functions such as growth, proliferation, and survival. Previously, we observed increased 25 vulnerability to bacterial (S. aureus) endophthalmitis in global AMPKα1 knockout (KO) 26 mice. In this study, we investigated the specific involvement of AMPKa1 in myeloid cells 27 using LysM^{Cre}; AMPKa1^{ff} mice. Our findings revealed that while endophthalmitis resolved 28 in wild-type (WT) B6 mice, the severity of the disease progressively worsened in 29 AMPKa1 deficient mice over time. Moreover, the intraocular bacterial load and 30 inflammatory mediators (e.g., IL-1 β , TNF- α , IL-6, and CXCL2) were markedly elevated 31 in the LvsM^{Cre}: AMPKα1^{fl} mice. Mechanistically, the deletion of AMPKα1 in myeloid cells 32 skewed macrophage polarization toward the inflammatory M1 phenotype and impaired 33 34 the phagocytic clearance of S. aureus by macrophages. Notably, transferring AMPKcompetent bone marrow from wild-type mice to AMPKa1 KO mice preserved retinal 35 function and mitigated the severity of endophthalmitis. Overall, our study underscores 36 the role of myeloid-specific AMPKa1 in promoting the resolution of inflammation in the 37 eye during bacterial infection. Hence, therapeutic strategies aimed at restoring or 38 enhancing AMPKa1 activity could improve visual outcomes in endophthalmitis and other 39 ocular infections. 40

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43 Keywords: Eye, Endophthalmitis, *S. aureus*, Inflammation, AMPK,
44 Immunometabolism, macrophages

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46 Introduction

Bacterial endophthalmitis is a serious eve infection that can lead to vision loss 47 due to severe intraocular inflammation and tissue damage [1-4]. Staphylococci, 48 especially Staphylococcus (S) aureus, are the primary culprits, and although they 49 account for only 10-15% of cases, they often lead to poor outcomes [5]. Typically, 50 during ocular surgeries, S. aureus gains entry into the eye, releasing virulence factors 51 such as toxins and cell wall components such as peptidoglycan and lipoteichoic acids 52 [6]. Host immune cells recognize these bacterial elements through pattern recognition 53 receptors and trigger a complex inflammatory immune response [3, 7]. Moreover, the 54 blood-retinal barrier, which is crucial for ocular defense, becomes compromised, 55 influx of immune cells, predominantly 56 allowing а large neutrophils and monocytes/macrophages, into the vitreous chamber [8, 9]. While this influx is necessary 57 to combat bacterial growth, it also leads to excessive inflammation, which, if unchecked, 58 59 damages intraocular tissues, especially the neurosensory retina, resulting in irreversible vision loss [2, 6, 10]. Unfortunately, there is no standardized treatment to control 60 intraocular inflammation, and visual outcomes often remain suboptimal even after 61 62 aggressive antibiotic treatments and vitrectomy surgeries [11, 12]. Moreover, the increase in antibiotic-resistant ocular pathogens poses a significant challenge in 63 managing these infections [13, 14]. Therefore, research aimed at understanding the 64 65 mechanisms governing inflammation initiation and resolution holds promise for identifying potential therapeutic targets to prevent and treat bacterial endophthalmitis. 66

67 Given the intricate nature of host-pathogen interactions, we employed an 68 integrated approach combining metabolomics and transcriptome analysis of *S. aureus*-

infected retina tissues to identify novel immunomodulatory and antimicrobial targets [15-69 17]. Our findings revealed significant impacts on various pathways durina 70 71 endophthalmitis, including inflammatory and immune responses, antimicrobial defense mechanisms against bacteria, endoplasmic stress, cell trafficking, and death, as well as 72 energy metabolism, notably involving disruptions in NAD+ and lipid biosynthesis [1, 15, 73 16, 18]. Within the realm of energy metabolism, AMP-activated protein kinase (AMPK) 74 has emerged as a key player in maintaining host energy balance [19]. AMPK not only 75 governs cellular energy metabolism but also regulates immune responses by 76 modulating immune signaling pathways [20-22]. This cross-talk between AMPK and 77 immune signaling pathways has crucial implications for reshaping the metabolic and 78 functional profiles of immune cells [23, 24]. 79

In our previous work, we demonstrated that both genetic (using AMPKa1 global 80 knockout mice) and pharmacological (with AICAR) activation of AMPK confer protection 81 82 against endophthalmitis [1]. However, a limitation of this study was the inability to discern the cell-specific contribution of AMPK to the pathogenesis of bacterial 83 endophthalmitis. Given that the primary immune cells involved in endophthalmitis are of 84 85 myeloid origin, we aimed to investigate the specific role of AMPKa1 in myeloid cells during endophthalmitis. In this study, employing myeloid-specific AMPKa1 knockout 86 mice (LysM^{Cre}; AMPK α1^{fl}) and bone marrow reconstitution chimera approaches, we 87 found that the loss of AMPKa1 in myeloid cells worsens bacterial endophthalmitis 88 89 highlighting the importance of myeloid-specific AMPK in bacterial endophthalmitis.

90 Materials and Methods

91 Mice and ethical statement

B6.SJL-Ptprca Pepcb/BoyJ (Pep Boy) mice were obtained from the Jackson 92 Laboratory (Bar Harbor, ME), while wild-type (WT) and AMPKa1 global knockout (KO) 93 (B6/129 background) were used as described [1]. AMPKa1^{fl} mice were purchased from 94 Jackson laboratory (#014141) and crossed with LysM^{Cre} (#004781) to generate a 95 myeloid-specific loss of AMPKa1 referred to as LysM^{Cre}; AMPKa1^{fl}. Six- to eight-week-96 old mice of both male and female sex were utilized. They were housed in a controlled-97 access Division of Laboratory Animal Resources (DLAR) facility at the Kresge Eye 98 Institute, maintained under a 12-hour light/12-hour dark cycle at a temperature of 22°C, 99 and provided ad libitum access to water and LabDiet rodent chow (PicoLab; LabDiet, St. 100 Louis, MO). All procedures were conducted per the Association for Research in Vision 101 and Ophthalmology (ARVO) Statement for the Use of Animals in Ophthalmic and Vision 102 Research and were approved by the Institutional Animal Care and Use Committee 103 (IACUC) of Wayne State University (protocol # IACUC-22-04-4557). 104

105 Bacterial strain and induction of endophthalmitis

The S. aureus strain RN6390 was cultured in tryptic soy broth and on agar plates 106 (TSB/TSA; Sigma-Aldrich, St. Louis, MO). Bacterial endophthalmitis was induced in 107 108 mice, as described previously [3, 25]. Briefly, mice were anesthetized and intravitreally injected with S. aureus (500 CFU/eye) using a 34G needle under a dissecting 109 microscope within a biosafety cabinet. Contralateral eyes received sterile PBS injections 110 111 and served as controls. Disease progression was monitored through slit lamp examination and other modalities. Scotopic electroretinography (ERG) was used to 112 determine retinal function using the Celeries ERG system (Diagnosis LLC, Lowell, MA), 113

114 as per the manufacturer's recommendation and standardized in our prior studies [16,115 26].

116 Isolation of bone marrow-derived macrophages (BMDMs)

Mouse bone marrow-derived macrophages (BMDMs) were isolated according to 117 previously established protocols [27]. Briefly, mice were euthanized, and bone marrow 118 was flushed from the tibias and femurs using RPMI media supplemented with 10% FBS 119 and 0.2 mM EDTA. The cells were then centrifuged at 400xg for 5 minutes at 4°C to 120 pellet them. Red blood cells (RBCs) were lysed by adding 0.2% NaCl (hypotonic) 121 solution for 20 seconds, followed by the addition of 1.6% NaCl (hypertonic) and 122 subsequent centrifugation. The cell pellets were rinsed with RPMI media, re-suspended, 123 seeded in RPMI media supplemented with 10% FBS, 100 U/ml penicillin, 100 mg/mL 124 streptomycin, and 10 ng/ml M-CSF for macrophage differentiation and cultured at 37°C 125 in 5% CO2. Six days post-differentiation, BMDMs were seeded at a concentration of 126 4×10^{6} cells/mL in 60 mm Petri dishes for *in vitro* experiments. 127

128 Bacterial burden estimation

The eyes were enucleated following *S. aureus* infection at 24 h, 48 h, and 72 h post-infection. Whole-eye lysates were prepared in 250 μ L of PBS by beating with stainless steel beads in a tissue lyser (Qiagen, Valencia, CA). A 50 μ L aliquot of the tissue homogenate was serially diluted and plated on Tryptic Soy Agar (TSA) to quantify the viable bacterial load. The colonies were counted the next day, and the results are reported as the mean number of CFU/eye.

135 Cytokine ELISA

For *in-vivo* samples, eyes were enucleated, and lysates were prepared using a 136 tissue lyser as described above. The tissue homogenates were then centrifuged at 137 10,000 x g for 20 minutes at 4°C, and the resulting supernatant was utilized for cytokine 138 estimation. In the in vitro studies, conditioned media from both the S. aureus-infected 139 and drug-treated groups, as well as the vehicle control group, were collected and 140 preserved for cytokine measurements. Mouse ELISA was conducted to quantify the 141 inflammatory cytokines IL-1 β , IL-6, TNF- α , and CXCL2 according to the manufacturer's 142 instructions (R&D Systems, Minneapolis, USA). 143

144 Histological analysis

The eyes were enucleated and preserved in modified Davidson's fixative for subsequent histopathological analysis. The embedding, sectioning, and staining with hematoxylin & eosin (H&E) were carried out by Excalibur Pathology, Inc. (Oklahoma City, OK, USA).

149 **RNA extraction and qPCR analysis**

Total RNA was extracted from both the neural retina and BMDMs using TRIzol 150 according to the manufacturer's guidelines (Thermo Scientific, Rockford, IL). 151 152 Subsequently, the RNA was reverse transcribed using a Maxima first-strand cDNA synthesis kit following the manufacturer's protocol (Thermo Scientific, Rockford, IL). 153 Quantitative assessment of gene expression was conducted via SYBR green-based 154 155 qPCR, employing gene-specific primers, on the Step One Plus Real-Time PCR System (Applied Biosystems, Foster City, CA, USA). Data analysis was performed utilizing the 156 comparative ^{ΔΔ}Ct method, as previously described [28]. The expression levels of genes 157 158 in the test samples were normalized to endogenous β -actin controls.

159 Bacterial phagocytosis assay

BMDM cells (10⁶ cells/dish) were cultured in 60 mm Petri dishes in RPMI-1640 160 media. Subsequently, the cells were exposed to S. aureus at an MOI of 10:1 for 2 161 hours. After the incubation period, the cells were washed and treated with gentamicin 162 (200 µg/mL) for 2 hours to eliminate extracellular bacteria. The absence of extracellular 163 bacteria was confirmed through dilution plating and enumeration of CFUs. Two hours 164 post-gentamicin treatment, the cells were washed with RPMI-1640 and incubated with 165 fresh media containing gentamicin (200 µg/mL) for 1, 3, or 6 hours. To quantify 166 internalized bacteria, following the designated incubation periods, the cells were 167 washed three times with PBS and lysed using 0.01% Triton X-100. The lysed cells were 168 collected by scraping and centrifuged at 7500 x g for 5 minutes. The resulting cell 169 pellets were washed twice with PBS through centrifugation at 7500 x g for 5 minutes 170 each time. The pellets were then resuspended in 1 mL sterile PBS, serially diluted, and 171 172 plated onto TSA plates for enumeration of bacterial counts.

173 Immunostaining

BMDMs were cultured in a four-well chamber slide (Fisher Scientific, Rochester, 174 175 NY). Following treatment, the cells were infected with S. aureus at an MOI of 10:1 for 3 hours. At the specified time points, the infected cells were fixed with 4% PFA in PBS at 176 4°C. After washing with PBS, the cells were permeabilized and blocked with 1% (w/v) 177 178 BSA and 0.4% Triton X-100 in PBS for 1 hour at room temperature (RT). Subsequently, the cells were incubated overnight at 4°C with primary antibodies against iNOS and 179 Arg1 (1:100 dilution, Cell Signaling Technology, Danvers, MA). Following the removal of 180 the primary antibodies, the cells were thoroughly washed with PBS and then incubated 181

with anti-mouse/rabbit Alexa Fluor 485/594-conjugated secondary antibodies (1:200
dilution) for 1 hour at RT. Finally, the cells were washed four times (5 minutes each)
with PBS, and the slides were mounted in Vectashield antifade mounting medium
containing DAPI (Vector Laboratories, Burlingame, CA) before visualization using a
Keyence microscope (Keyence, Itasca, IL).

187 Western blotting

directly Protein samples obtained by lysing cells in 188 were radioimmunoprecipitation assay (RIPA) buffer containing protease and phosphatase 189 inhibitor cocktails. The total protein concentration of the cell lysates was determined 190 using a Micro BCA[™] protein assay kit (Thermo Scientific, Rockford, IL). Subsequently, 191 protein samples (30-40 µg) were separated via SDS-PAGE (8% or 12%) and 192 transferred onto a nitrocellulose membrane (0.45 µm) using a wet transfer system. The 193 membranes were then blocked in 5% (w/v) dry milk in Tris-buffered saline with Tween 194 195 (TBST) for 1 hour at room temperature. Following blocking, the membranes were incubated with primary antibodies against iNOS, Arg1, and HSP-90 (Cell Signaling 196 Technology, Danvers, MA) according to the manufacturer's instructions, followed by 197 198 incubation with appropriate horseradish peroxidase-conjugated secondary antibodies. After four TBST washes, the membranes were exposed to SuperSignal West Femto 199 200 chemiluminescent substrate and imaged using an iBright fluorescence imager (Thermo 201 Scientific, Rockford, IL). Densitometry analysis was carried out using ImageJ software (Rasband, W.S., ImageJ, U.S. National Institutes of Health, Bethesda, Maryland) 202

203 Flow cytometry

Flow cytometry was conducted following previously established methods to 204 assess the adoptive transfer and infiltration of neutrophils into the eyes [3]. In brief, 205 retinas from euthanized mice were isolated and digested with Accumax (Millipore) for 10 206 minutes at 37°C. A single-cell suspension was generated by gently triturating the cell 207 mixture with a 22G needle and subsequently passing it through a 40-µm cell strainer 208 209 (BD Falcon, San Jose, CA, USA). The cells were then blocked using Fc Block (BD Biosciences) for 30 minutes, followed by three washes with PBS containing 1% bovine 210 serum albumin (BSA). Subsequently, the cells were stained by incubating them with 211 CD45.1-APC, CD45.2-PE, and Ly6G-FITC conjugated antibodies (BD Biosciences) on 212 ice for 20 minutes in the dark. After incubation, the cells were washed and suspended in 213 PBS supplemented with 1% BSA. Flow cytometric analysis was performed using an 214 Accuri C6 flow cytometer and accompanying software (BD Biosciences), data analysis 215 was conducted using FlowJo[™] v8 Software (BD Life Sciences). 216

217 Bone marrow chimera

The adoptive transfer of naïve bone marrow cells into AMPKa1 KO mice (with the 218 CD45.2 allele) and B6. SJL-Ptprca Pepcb/BoyJ (Pep Boy, used as wild-type mice with 219 220 the CD45.1 allele) was carried out via the busulfan method [29]. Initially, recipient mice received a single preconditioning dose of 20 mg/kg busulfan (Cayman Chemicals, Ann 221 Arbor, MI) intraperitoneally daily until a cumulative dose of 100 mg/kg was achieved. 222 Subsequently, all mice were intravenously injected with 1x10⁷ donor bone marrow cells 223 obtained from the recipient mouse via tail vein injection in 200 µL of phosphate-buffered 224 saline (PBS). Starting at 2 weeks after transplantation, approximately 20-30 µL of blood 225 226 was collected from the lateral saphenous vein, and CD45.1 vs CD45.2 expression was assessed in peripheral blood using flow cytometry. Efficient engraftment of donor bone
 marrow (>80%) was observed at 6 weeks post-transplantation. Following successful
 engraftment, the mice were subjected to endophthalmitis as described above.

230

231 **RNA sequencing**

For RNA sequencing, total RNA was extracted from the BMDMs of the AMPKα1 232 KO and WT mice in biological triplicates using RNeasy Mini Kits (Qiagen, Hilden, 233 Germany). The sequencing procedures were conducted by Novogene Co., Ltd. RNA 234 sequencing (RNA-seq) libraries were constructed from high-guality RNA using NEBNext 235 Ultra[™] II RNA Library Prep kits (New England BioLabs, Ipswich, MA, USA) following 236 the manufacturer's instructions. Sequencing was performed on the NovaSeq 6000 237 platform as paired-end 150-bp reads (Illumina), with a sequencing depth of 238 approximately 30 million reads per sample. Differential gene expression analyses were 239 240 conducted using DESeq2, while GO enrichment analysis was carried out using PANTHER and KEGG pathways analyses. 241

242 Statistical Analysis

Statistical analyses were conducted using Prism version 9.2 (GraphPad, San Diego, CA). Group comparisons were assessed using one-way ANOVA followed by Tukey's Multiple Comparison post-hoc tests, and data were presented as mean ± SD. A confidence interval of 95% was applied for all statistical tests. A p-value of <0.05 was considered statistically significant. Unless specified otherwise, all experiments were performed at least three times.

249 **Results**

250 Myeloid-specific AMPKα1 deficiency exacerbated bacterial endophthalmitis

The hallmark of bacterial endophthalmitis is the infiltration of myeloid cells such 251 as neutrophils and monocytes into the eye [6]. To investigate the role of AMPK in these 252 cells during ocular infections, we induced S. aureus endophthalmitis in both AMPK $\alpha 1^{fl}$ 253 (Wt) and LysM^{Cre}; AMPKα1^{fl} mice using a low-dose infection model, in which 500 254 colony-forming units (CFUs) of S. aureus were administered. Although this dosage 255 resolved in wild-type mice, it led to severe endophthalmitis in LysM^{Cre}; AMPKa1^{fl} mice 256 [3, 16]. We monitored the progression of endophthalmitis through daily eye exams, 257 retinal function testing, histopathological analysis, and estimation of intraocular bacterial 258 burden and inflammation. Compared to AMPKa1^{fl} mice, endophthalmitis worsened in 259 LysM^{Cre}; AMPKa1^{fl} mice, indicated by a time-dependent increase in corneal haze, 260 opacity, and hypopyon formation (Fig. 1A). Histopathological analysis revealed 261 increased retinal folding, tissue disintegration, and significant cellular infiltrates in the 262 vitreous chamber of LysM^{Cre}; AMPKα1^{fl} mouse eyes (**Fig. 1B**). Electroretinography 263 (ERG) demonstrated a notable decrease in both a- and b-wave amplitudes in LysM^{Cre}; 264 AMPKα1^{fl} eves at various time points (Fig. 1C). Additionally, the bacterial burden was 265 relatively greater in LysM^{Cre}; AMPKα1^{fl} mice (**Fig. 1D**). Overall, a greater percentage of 266 eyes exhibited damage due to *S. aureus* endophthalmitis in LysM^{Cre}; AMPKa1^{fl} mice 267 compared to AMPKα1^{fl} (**Fig. 1E**). 268

Furthermore, in addition to direct retinal damage caused by bacterial toxins, uncontrolled inflammation resulting from excessive infiltration and activation of innate immune cells such as neutrophils contributes to bystander tissue damage. To evaluate intraocular inflammation, we analyzed the expression of inflammatory cytokines at both

the mRNA (Fig. 2A) and protein (Fig. 2B) levels at various time points. Notably, 273 myeloid-specific deletion of AMPKa1 led to higher expression of inflammatory cytokines. 274 For instance, the transcript levels of *II-6* and *Cxcl2* were elevated at 72 hours, while the 275 protein levels increased at both 48 and 72 hours. Conversely, AMPKa1-deficient 276 macrophages exhibited consistently increased transcript levels of the inflammatory 277 278 cytokines *IL-1* β and *TNF-* α at all time points, with protein levels peaking at 48 or 72 hours. Additionally, we investigated the inflammatory response of bone marrow-derived 279 macrophages (BMDMs) from both AMPKa1^{fl} and LysM^{Cre}; AMPKa1^{fl} mice. revealing 280 increased levels of inflammatory mediators in AMPKa1 KO BMDMs consistent with the 281 *in vivo* data (**Fig. S1**). Taken together, these findings suggest that AMPKa1 deficiency 282 in myeloid cells enhances inflammation and exacerbates endophthalmitis. 283

284 AMPKa1 deficient BMDMs exhibit distinct transcriptomic profiles

To elucidate the mechanisms underlying the heightened inflammatory response 285 of S. aureus-infected AMPKa1-deficient mice, we performed RNA-seq analysis. This 286 analysis revealed ~3,516 differentially expressed genes (DEGs) in S. aureus-infected 287 AMPKa1 KO BMDMs compared to Wt, with 1,665 genes showing upregulation and 288 289 1,848 displaying downregulation (Fig. 3A). Gene set enrichment analysis indicated significant alterations in pathways associated with inflammation, metabolism, 290 291 endoplasmic reticulum stress, and cholesterol biosynthesis, with notable downregulation 292 of bacterial defense pathways in AMPKα1-deficient macrophages (Fig. 3B). Further analysis of DEGs based on the encoded proteins corroborated these findings, i.e., a 293 reduction in pathways related to inflammation resolution and responses 294 to 295 lipopolysaccharide and bacteria (Fig. 3C). A heat map was constructed to visualize the

highly downregulated and upregulated genes involved in inflammatory and antimicrobial
 immune defense (Fig. 3D).

Given the increased bacterial burden observed in S. aureus-infected LysM^{Cre}; 298 AMPKα1^{ff} mice, we hypothesized that this might stem from the downregulation of 299 antimicrobial genes such as S100a7, a8, and a10 in the RNAseg data. To verify this, we 300 examined their expression via gPCR and found that their levels were significantly lower 301 in AMPKa1 KO BMDMs (Fig. S2A). Consistently, AMPKa1 KO BMDMs exhibited 302 reduced intracellular phagocytic killing of *S. aureus* in the gentamicin protection assay 303 (Fig. S2B). Collectively, these findings underscore the role of AMPKa1 in regulating 304 antibacterial activity by enhancing phagocytic killing and the induction of antimicrobial 305 molecules during bacterial infection. 306

307 AMPKa1 deficiency promotes the M1 milieu during S. aureus endophthalmitis

Our RNAseq analysis revealed that a diminished response to bacterial infection 308 corresponds with the exacerbated endophthalmitis observed in AMPKa1-deficient mice. 309 Given the pivotal role of macrophages in inflammation resolution via the transition from 310 a pro-inflammatory (M1) to an anti-inflammatory (M2) phenotype, we examined the 311 expression of these markers in infected retinal tissue and cultured BMDMs. Our data 312 demonstrated relatively higher transcript levels of the classical M1 markers Cox2, iNos, 313 and *II23*, in the retinas of LysM^{Cre}; AMPKa1^{fl} mice compared to Wt mice (**Fig. 4A**). 314 Conversely, the levels of M2 phenotype markers (Arg1, Fizz1, and Yam1/2) were 315 downregulated in LysM^{Cre}; AMPK $\alpha 1^{fl}$ mice retinas. To corroborate these findings, we 316 assessed the pro-inflammatory (M1) and anti-inflammatory (M2) signatures in BMDMs 317 isolated from LysM^{Cre}; AMPKa1^{fl} and AMPK^{fl} mice, challenging them with *S. aureus*. 318

Immunostaining of *S. aureus*-infected LysM^{Cre}; AMPKα1^{fl} macrophages revealed increased levels of iNos (**Fig. 4C**) and decreased expression of Arg1 (**Fig. 4D**). Similarly, western blot analysis also demonstrated increased protein levels of iNos (**Fig. 4E&F**) and decreased Arg1 levels (**Fig. 4G&H**) in AMPKα1-deficient macrophages. These results further support the notion that AMPKα1 regulates the balance between the M1 and M2 phenotypes, whereby its deficiency promotes the inflammatory phenotype in the eye.

Bone marrow reconstitution of AMPKα1-deficient mice ameliorated endophthalmitis

To illustrate the protective function of myeloid AMPKa1 during endophthalmitis, 328 we used a bone marrow chimera approach, in which bone marrow from donor PepBoy 329 mice (CD45.1 allele) were transferred to recipient AMPKa1-deficient mice (CD45.2 330 allele) (Wt > KO) and vice versa (KO > Wt) (Fig. 5A- schematic). This adoptive transfer 331 yielded greater than 80% efficiency of bone marrow transfer in the recipient mice. Once 332 stable bone marrow chimeras were established. S. aureus endophthalmitis was 333 induced, and a time-course study was conducted. Eye imaging revealed decreased 334 opacity and corneal haze in the bone marrow of AMPKa1 KO mice with Wt (PepBoy) 335 336 bone marrow compared to those with AMPKα1 KO bone marrow in Wt mice (Fig. 5B). Electroretinography analysis demonstrated better retention of a- and b-wave amplitudes 337 in AMPKa1 KO mice with Wt bone marrow (Fig. 5C). Furthermore, transfer of Wt 338 chimera in AMPKa1 KO mice mitigated disease severity, as evidenced by decreased 339 corneal opacity (Fig. 5D) and reduced intraocular bacterial burden (Fig. 5E). 340

Subsequently, we assessed intraocular inflammation and found that Wt > KO chimera exhibited significantly lower levels of inflammatory markers such as IL-1 β , IL-6, TNF- α , and CXCL2 (**Fig. 5F**). This reduction correlated with a decrease in neutrophil infiltration in AMPK α 1 KO chimera (**Fig. 5G**) compared to PepBoy mice with AMPK α 1deficient bone marrow (**Fig. 5H**). Thus, myeloid-specific AMPK α 1 contributes to inflammation resolution and mitigates bacterial endophthalmitis.

347

348 **Discussion**

Bacterial endophthalmitis remains the most common vision-threatening 349 complication of eye surgeries and ocular trauma [4]. Owing to the rapid progression and 350 poor prognosis of endophthalmitis, early treatments with intravitreal injections of 351 empirical antibiotics remain the main treatment option for bacterial endophthalmitis [30]. 352 Antibiotics, while destroying bacteria, may release lipopolysaccharides [31, 32] 353 lipoteichoic acid, and peptidoglycan from bacterial cell walls, including that of S. aureus 354 (SA)[32], and evoke an inflammatory response [2, 33]. To suppress inflammation, 355 intravitreal injections of corticosteroids are recommended, but the usage of steroids 356 along with antibiotics for endophthalmitis has been marred with controversial outcomes 357 in humans [34-38] and animal studies [39-43]. Moreover, steroid-related side effects, 358 including elevated intraocular pressure (IOP), cataract formation, and retinal 359 detachment, further hamper their inclusion in the management of endophthalmitis [44]. 360 Thus, there is an urgent need to develop non-immunosuppressive anti-inflammatory 361 therapies. In this study, we demonstrated an anti-inflammatory and protective role of 362 myeloid-specific AMPK in bacterial endophthalmitis. 363

AMPK is an evolutionarily conserved heterotrimeric kinase with α , β , and γ 364 subunits that primarily regulate cellular energy homeostasis [23]. The AMPK complex is 365 activated either by increases in cellular AMP or ADP or by phosphorylation on Thr172 366 by upstream kinases, such as CaMKK-B, LKB1, or TAK1 [45-50]. This enhanced 367 activity, in turn, controls signaling pathways that regulate protein synthesis, cell division, 368 and intracellular membrane trafficking. Recent studies on AMPK regulation indicate that 369 it not only functions as an intracellular energy sensor but also functions as a stress 370 sensor to maintain intracellular homeostasis during infectious, autoimmune diseases 371 and skeleton muscle regeneration [51-53]. Previously, using global AMPKa1 KO mice, 372 we reported that loss of AMPKa1 increased the severity of bacterial endophthalmitis. 373 However, the cell-specific role of AMPKa1 was not determined. Here, our data showed 374 that myeloid cell-specific AMPKa1 plays a protective role during endophthalmitis as 375 evidenced by worse disease outcomes in LysM^{Cre}; AMPKa1^{fl} mice (**Fig. 6**). Moreover, the 376 377 protective effects of AMPKa1 on myeloid cells are exhibited via several potential mechanisms. 378

379 Here, we observed that the bacterial burden was greater in myeloid-specific 380 AMPKa1 deficient mice. As we reported that activation of AMPKa and its downstream ACC in retinal Müller glia regulate autophagy-mediated clearance of S. aureus [17], we 381 hypothesized that lack of AMPKa will impair pathogen clearance. Notably, phagocytosis 382 383 of the pathogen activates the host autophagy initiation complex and the upstream 384 regulatory components LKB1 and AMPK α 1, which regulate autophagy induction through their kinase activities [54]. Deletion of AMPKα1 in myeloid cells results in susceptibility 385 386 to exacerbated bacterial infection and host tissue cell death. In support of these

findings, our data showed that BMDMs from LysM^{Cre}; AMPKa1^{fl} mice had reduced 387 phagocytic killing of S. aureus. Moreover, AMPKa1 deficiency led to a significant 388 decrease in the bacterial infection-induced expression of antimicrobial peptides which 389 might also contribute to greater bacterial burden in the eyes. Our results corroborate 390 previous studies reporting the increased phagocytic activity (E. Coli and L. 391 pneumophila) of macrophages upon pharmacological activation of AMPK via AICAR or 392 metformin treatment [55, 56]. Moreover, the defect in phagocytosis following AMPKa1 393 ablation in macrophages is associated with their inability to undergo phenotypic 394 transition, explaining the defect in bacterial clearance. A recent study has shown that 395 restoring AMPK activity accelerates recovery from bacterial pneumonia [57]. Similarly, 396 we also reported that AMPK activation inhibits viral replication in retinal cells [58]. These 397 studies highlight the multifaceted roles of AMPK in viral and bacterial infections [59] 398 through the regulation of cellular metabolism [60, 61]. 399

400 Macrophages are also highly plastic innate immune cells, and environmental stimuli or bacterial infection can generate macrophages with a range of different 401 phenotypes and functions [62]. The classical activation of macrophages generates M1 402 403 macrophages with pro-inflammatory properties, while alternative activation generates M2 macrophages with anti-inflammatory properties [63]. M1 macrophages exacerbate 404 405 tissue injury whereas M2 macrophages promote the resolution of inflammation upon tissue injury [63, 64]. A careful examination of LysM^{Cre}; AMPKa1^{fl} revealed impaired 406 inflammation resolution, leading to a subtle but significant increase in the expression of 407 M1 macrophage phenotype markers (*iNos* and *II23* expression) with the endophthalmitis 408 409 progression. In contrast, the same mice showed a decrease in M2 macrophage

phenotype markers (*Arg1* and *Fizz1*), corresponding to an anti-inflammatory state, resulting in accelerated inflammation and endophthalmitis. Interestingly, a previous study showed that AMPK α 1 mediated the regulation of macrophage skewing at the time of inflammation resolution during skeletal muscle regeneration [53]. Our data showing higher levels of inflammatory mediators in LysM^{Cre}; AMPK α 1^{fl} mice eyes indicate the predominance of the M1 milieu which results in inflammation mediated retinal tissue damage.

To further confirm the role of AMPKα1 in ocular infection, we generated bone-417 marrow chimeras and showed the ability of AMPKa1-competent bone marrow-derived 418 cells to rescue AMPKa1 KO from severe endophthalmitis. Consequently, impaired 419 inflammation resolution was observed in KO -> Wt chimera where Wt macrophages 420 were replaced with macrophages lacking AMPKa1 expression, whereas a benefit was 421 observed in Wt -> KO chimera expressing AMPK α 1 in macrophage. Moreover, the 422 extent of endophthalmitis resolution in the AMPKa1 KO recipients was similar to those 423 in Wt mice. This indicated that AMPKa1 expressed in infiltrating/residential myeloid cells 424 contributes to endophthalmitis resolution. 425

In summary, our study demonstrated the protective role of myeloid cell-specific
 AMPKα1 during bacterial endophthalmitis. These effects are mediated by enhanced
 phagocytic clearance of bacteria and the promotion of inflammation resolution via
 inducing M2 macrophage phenotype. Therefore, AMPKα1 activation can be targeted
 therapeutically to treat bacterial endophthalmitis.

431

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441 **Conflict of Interest.**

442 The authors declare no competing interests.

443 Data availability

- 444 All data are contained within the article.
- 445
- 446 **References**
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604 Figure Legends

Fig. 1: Myeloid-specific AMPKα1 deficiency exacerbates endophthalmitis severity 605 in mice. (A-B) Endophthalmitis was induced in AMPKa1^{fl} (Wt mice) or LysM^{Cre};a1^{fl} 606 (myeloid-specific AMPKa1 deficient) n = 6 per time point: 24, 48, and 72 h) by 607 intravitreal inoculation of S. aureus RN6390 (5,00 CFUs/eye). Eyes injected with PBS 608 609 were used as controls. Representative slit-lamp micrograph showing corneal haze/opacity and H&E staining of enucleated eyes showing retinal damage and immune 610 cell infiltration. C, cornea; AC, anterior chamber; L, lens; VC, vitreous chamber; R, 611 612 retina. (C) Scotopic ERG response as measured by the percentage of a-and b-wave amplitudes retained in comparison to uninfected control eyes with values maintained at 613 614 100%. (D) Quantitation of intraocular bacterial burden by serial dilution and plate count represented as CFUs/eye (n=6). (E) Corneal opacity was measured using ImageJ and 615 616 is represented as the integrated pixel intensity. The data represent the culmination of two independent experiments and are shown as the mean ± SD. Statistical analysis was 617 performed using one-way ANOVA with Tukey's multiple comparisons test (panels C, D, 618 & E). ns = not significant; *P< 0.01; **P< 0.001; ***P< 0.0001. 619

Fig. 2: Myeloid cell-specific AMPKα1 deletion enhances inflammation in *S. aureus*-infected eyes. (A-B) Endophthalmitis was induced in AMPKα1^{fl} (WT mice) or

LysM^{Cre}; AMPK α 1^{fl} (n = 6 per time point: 24, 48, and 72 h) by intravitreal inoculation of 622 S. aureus RN6390 (5,00 CFUs/eye). Eyes injected with PBS were used as controls. At 623 624 the indicated time points, the eyes or retinas were harvested, and ELISA or gPCR was performed to measure the levels of the indicated inflammatory cytokines or chemokines 625 in whole eye lysates or retinas (n = 6). The data represent the culmination of two 626 independent experiments and are shown as the mean ± SD. Statistical analysis was 627 performed using one-way ANOVA with Tukey's multiple comparisons test (panels A & 628 B). ns = not significant: *P< 0.01: **P< 0.001: ***P< 0.0001. 629

3: S. aureus-infected BMDMs lacking AMPKα1 exhibit a distinct Fig. 630 transcriptomic signature profile and attenuated phagocytosis. BMDMs from WT or 631 AMPKa1 knock-out (KO) mice were infected with S. aureus (MOI 10:1) for 6 h 632 (n=3/condition). RNA was extracted, and RNA sequencing was performed using the 633 Illumina platform. (A) Volcano plot showing the overall distribution of differentially 634 expressed genes (DEGs). The points represent genes, blue dots indicate no significant 635 difference in genes, red dots indicate upregulated differentially expressed genes, and 636 green dots indicate downregulated differentially expressed genes. The Y-axis shows the 637 adjusted p-value (log₁₀) and the X-axis shows the log₂ fold change. (B) Gene Ontology 638 639 enrichment analysis shows the significantly enriched downregulated pathways in KO BMDMs compared to the Wt BMDMs. (C) Bubble plot showing enrichment scores for 640 downregulated pathways in KO BMDMs. The size of the sphere is based on the positive 641 enrichment score. (D) Heatmap showing DEGs in S. aureus (SA)-infected KO vs WT 642 BMDMs. 643

Fig. 4: AMPKα1 deficiency promotes M1 macrophage phenotypes in S. aureus-644 infected eves and BMDMs. (A-B) Endophthalmitis was induced in AMPKa1^{fl} or 645 LvsM^{Cre}: AMPK α 1^{fl} (n = 6 per time point: 24, 48, and 72 h) by intravitreal inoculation of 646 S. aureus RN6390 (500 CFUs/eye). Eyes injected with PBS were used as controls. At 647 the indicated time points, the retinas were harvested, and gPCR was performed to 648 649 measure the expression profiles of M1 and M2 macrophage phenotype markers (n=6). (C-D) BMDMs from AMPKa1^{fl} (WT mice) or LysM^{Cre}; AMPKa1^{fl} (AMPKa1 deficient) 650 mice were infected with S. aureus (MOI 10:1) for immunostaining (3 h). Immunostaining 651 was performed for iNOS (red) or Arg1 (Green) expression and images were captured at 652 the original magnification of 60X. (E-F & G-H) BMDMs from AMPKα1^{fl} (WT mice) or 653 LysM^{Cre}; AMPKa1^{fl} mice were infected with *S. aureus* (MOI 10:1) for western blotting (3 654 h). Western blot was performed to detect iNOS, Arg1, and HSP90 proteins. 655 Densitometry analysis was performed using ImageJ and data are expressed as relative 656 fold changes normalized to the loading control, HSP90. The data are representative of 657 two independent experiments and are shown as the mean ± SD. Statistical analysis was 658 performed using one-way ANOVA with Tukey's multiple comparisons test (panels A & 659 B, E & G). ns = not significant; *P< 0.01; **P< 0.001; ***P< 0.0001. 660

Fig. 5: Adoptive transfer of wild-type myeloid cells to AMPKα1 deficient mice rescues *S. aureus-induced endophthalmitis.* (A) Schematic of experimental design for bone marrow transplant and endophthalmitis. (B-C) Endophthalmitis was induced in AMPKα1 KO (recipient), and B6.SJL-*Ptprc^a Pepc^b*/BoyJ (PepBoy, donor) (B6 background, n = 4, time point: 72 h) by intravitreal inoculation of *S. aureus* RN6390 (5,00 CFUs/eye). Eyes injected with PBS were used as controls. Representative slit-

lamp micrograph showing corneal haze/opacity. (C) Scotopic ERG response as 667 measured by the percentage of a-and b-wave amplitudes retained in comparison to 668 uninfected control eyes with values kept at 100%. (D) Corneal opacity was measured using 669 ImageJ and represented as integrated pixel intensity. (E) Quantitation of intraocular bacterial 670 burden by serial dilution and plate count represented as CFUs/eye (n=4). (F & G) At the 671 672 indicated time points, the eyes or retinas were harvested and ELISA or flow cytometry was performed to measure the levels of inflammatory cytokines or chemokines from 673 whole eye lysates or neutrophile infiltration from the retinas (n=4). (H) Bar graph 674 showing the frequency of neutrophil infiltration in chimeric mice. The data represented 675 are the culmination of two independent experiments and are shown as the mean ± SD. 676 Statistical analysis was performed using one-way ANOVA with Tukey's multiple 677 comparisons (panels B, & E) or unpaired t-test (C & D). ns = not significant; *P< 0.01; 678 **P< 0.001: ***P< 0.0001. 679

Fig. 6. Effect of myeloid cell-specific AMPKα1 deletion on *S. aureus*-induced endophthalmitis. Mechanistically, myeloid-specific AMPKα1 inactivation impairs the phagocytic clearance of *S. aureus* and the resolution of inflammation by skewing toward the M1 macrophage phenotype. The adoptive transfer of AMPK-competent bone marrow from WT mice to AMPKα1 deficient mice preserved retinal functions and attenuated disease severity.

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694 Supplementary Figures.

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Fig. S1: Myeloid cell-specific AMPKa1 loss enhances the inflammation in S. 697 *aureus*-infected BMDMs. BMDMs from AMPKa1^{fl} or LysM^{Cre}; AMPKa1^{fl} (n=4/condition) 698 were infected with S. aureus (MOI 10:1) for 6h. The expression of inflammatory 699 cytokines was measured by (A) qPCR and (B) ELISA. The data represent the 700 culmination of two independent experiments and are shown as the mean ± SD. 701 Statistical analysis was performed using one-way ANOVA with Tukey's multiple 702 comparisons test (panels A & B). ns = not significant; *P< 0.01; **P< 0.001; ***P< 703 0.0001. 704

Fig. S2: AMPK α deficient **BMDMs** exhibit attenuation of antimicrobial gene expression and phagocytosis. (A) BMDMs from AMPK α 1^{fl} or LysM^{Cre}; AMPK α 1^{fl} (n=4/condition) were infected with *S. aureus* (MOI 10:1) for 6 h. The expression profiles of genes (e.g., *S100a7, S100a8,* and *S100a10*) with antimicrobial functions were assessed by qPCR. (B) BMDMs from AMPK α 1^{fl} or LysM^{Cre}; AMPK α 1^{fl} (n=4/condition) were challenged with *S. aureus* (MOI 10:1) for 2 h. After 2 h of infection, the cells were rinsed to remove extracellular bacteria and incubated with fresh medium containing gentamicin (200 µg/mL) for the indicated time points. At the desired time point, the cells were lysed, and the viable bacterial counts were quantitated via serial dilution and counting. Statistical analysis was performed using one-way ANOVA with Tukey's multiple comparison test (panels A, & B). The data represents mean \pm SD from three independent experiments. ns = not significant; ***P* < 0.01; ***P* < 0.001.







Fig 4



AMPK^{fl} LysM^{Cre};a1^{fl}





Fig 1S



