

1 **Intestinal microbiota of mice influences resistance to *Staphylococcus***

2 ***aureus* pneumonia**

3

4 **Running title:** Microbiota and *S. aureus* pneumonia

5

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## 27 **ABSTRACT**

### 28 **Background**

29 Th17-immunity in the gastrointestinal tract is regulated by intestinal microbiota  
30 composition, particularly the presence of segmented filamentous bacteria (sfb), but the  
31 role of intestinal microbiota in pulmonary host defense is not well explored. We tested  
32 whether altering gut microbiota by acquiring sfb influences susceptibility to  
33 staphylococcal pneumonia via induction of type 17 immunity.

### 34 **Methods**

35 Groups of C57BL/6 mice, which differed in their intestinal colonization with sfb, were  
36 challenged with methicillin-resistant *Staphylococcus aureus* in an acute lung infection  
37 model. Bacterial burden, bronchoalveolar lavage fluid (BALF) cell counts, cell types, and  
38 cytokine levels were compared between mice from different vendors, mice from both  
39 vendors after co-housing, mice given sfb orally prior to infection, and mice with and  
40 without exogenous IL-22 or anti-IL-22 antibodies.

### 41 **Results**

42 Mice lacking sfb developed more severe *S. aureus* pneumonia than mice colonized with  
43 sfb, indicated by higher bacterial burden in lungs, lung inflammation, and mortality. This  
44 difference was reduced when sfb-negative mice acquired sfb in their gut microbiota  
45 through co-housing with sfb-positive mice or when given sfb orally. Type 17 immune  
46 effectors in the lung were higher after infection in sfb-positive mice and increased in sfb-  
47 negative mice after acquiring sfb, as demonstrated by higher levels of IL-22, higher  
48 numbers of IL-22+ TCR $\beta$ + cells, and of neutrophils in BALF. Exogenous IL-22 protected  
49 mice from *S. aureus* pneumonia.

## 50 **Conclusion**

51 The murine gut microbiota, particularly the presence of sfb, promotes pulmonary type  
52 17 immunity and resistance to *S. aureus* pneumonia, and IL-22 protects against severe  
53 pulmonary staphylococcal infection.

54

## 55 **Keywords**

56 *Staphylococcus aureus*

57 MRSA

58 Pneumonia

59 Segmented filamentous bacteria (sfb)

60 Gut microbiota

61 Th17 immunity

62 Type 17 immunity

63 IL-17

64 IL-22

65 ROR $\gamma$ t

66 Neutrophils

67 Innate lymphoid cells type 3 (ILC3s)

68

## 69 **INTRODUCTION**

70 *Staphylococcus aureus* continues to be one of the most common pathogens causing  
71 invasive life-threatening infections (1). Methicillin-resistant *S. aureus* (MRSA) currently  
72 accounts for 20-40% of hospital-acquired and ventilator-associated pneumonias (2) and

73 9% of community-acquired pneumonias (3), and MRSA pneumonia is associated with  
74 very high mortality rates (3, 4).  
75  
76 The Th17 pathway plays an important role in mucosal host defense against a wide  
77 range of bacterial pathogens (reviewed in (5)). Defects in human Th17 signaling (e.g. in  
78 hyper-IgE or Job's syndrome) are associated with immunodeficiency syndromes  
79 characterized by increased susceptibility to staphylococcal infections of the lung and  
80 skin, suggesting a specific role for Th17 immunity in host defense against *S. aureus* (6,  
81 7). Additionally, mice with defects in Th17 signaling have impaired bacterial clearance  
82 from the lung after infection with *Klebsiella pneumoniae* (8). More recently, the Th17  
83 pathway has been implicated in the defense against *S. aureus* pneumonia as well (9-  
84 11). Mice lacking the IL-17 receptor or IL-22, or mice that are coinfectd with influenza  
85 A and thereby deficient in type 17 immunity, displayed impaired bacterial clearance of  
86 *S. aureus* compared to wild type or influenza-free mice (10). Type 17 immunity has also  
87 been reported to contribute to mucosal vaccine responses against *P. aeruginosa* and *M.*  
88 *tuberculosis* (12-14).  
89  
90 The gastrointestinal (GI) tract of mammals is inhabited by thousands of species of  
91 commensal microorganisms that exist in a mutualistic relationship with the host. How  
92 the commensal microbiota influences the host immune system is poorly understood, but  
93 it appears clear that microbiota is a major regulator of the immune system and that  
94 bacterial signals have profound influences on antibacterial defenses in the GI tract and  
95 also in other organs (15, 16). Ivanov et al. showed that colonization of the GI tract of

96 mice with a commensal microbe, segmented filamentous bacterium (sfb), was sufficient  
97 to induce the appearance of Th17 cells in the small intestine, leading to increased  
98 expression of genes associated with inflammation and antimicrobial defenses, and  
99 resulted in enhanced resistance to the murine intestinal pathogen *Citrobacter rodentium*  
100 (17-19). The influence of the GI microbiota on lung immunity, the so-called gut-lung  
101 axis, has recently become the focus of more interest, but underlying mechanisms are  
102 still incompletely understood (20). Commensal organisms of the GI tract contribute to  
103 host defense in *Escherichia coli* pneumonia via toll-like receptor signaling (21), and  
104 germ-free mice have a strikingly higher mortality rate following *P. aeruginosa*  
105 pneumonia compared to conventional mice (22). Little is known regarding the role of  
106 specific organisms in modulating pulmonary immunity and whether the gastrointestinal  
107 microbiota has any influence on Gram-positive lung pathogens, or *S. aureus* in  
108 particular. We hypothesized that the intestinal microbiota can affect *S. aureus*  
109 pneumonia and that the presence of sfb in the mouse intestine specifically, influences  
110 type 17 immunity in the lung and increases resistance to *S. aureus* pneumonia. To test  
111 this hypothesis, we compared mice with differing intestinal microbiota in a murine  
112 staphylococcal pneumonia model.  
113  
114 C57BL/6 mice from Jackson Laboratory and Taconic Biosciences differ in their  
115 gastrointestinal microbiota and most notably in colonization with the commensal sfb,  
116 (with Jackson mice being sfb-negative and Taconic mice generally sfb-positive) (18).  
117 We demonstrate that mice from Jackson are more susceptible to intranasal challenge  
118 with the MRSA strain LAC compared to mice from Taconic. This difference in resistance

119 diminishes when mice from both vendors are co-housed, indicating an environmental  
120 rather than a genetic or inherent factor influencing the variation in pulmonary  
121 phenotype. Following co-housing, sfb are passed from sfb-positive mice to their sfb-  
122 negative cage-mates, leading to increased resistance to *S. aureus* pneumonia.  
123 Furthermore, when sfb-negative mice are given sfb via gavage two weeks prior to  
124 infection, they also become more resistant to *S. aureus* pneumonia. BALF from the  
125 more resistant sfb-positive mice as well as initially sfb-negative mice that acquired sfb  
126 via GI colonization contained more IL-22, more IL-22<sup>+</sup> TCR $\beta$ <sup>+</sup> cells, and more  
127 neutrophils, all indicators for increased type 17 immunity activation. We also show that  
128 neutralization of the Th17 cytokine IL-22 with anti-IL-22 antibody prior to challenge with  
129 *S. aureus* leads to increased susceptibility and conversely, intranasal administration of  
130 IL-22 at the time of infection with *S. aureus* renders mice more resistant to infection,  
131 suggesting that IL-22 is protective against *S. aureus* pneumonia.

132

## 133 MATERIALS AND METHODS

### 134 Bacterial strains.

135 *Staphylococcus aureus* strain LAC (a USA300 methicillin-resistant MRSA), initially  
136 isolated from a patient suffering from necrotizing pneumonia), was obtained from the  
137 Network on Antimicrobial Resistance in *S. aureus* (NARSA). To prepare bacterial  
138 inocula for in vivo challenge studies, frozen bacterial stocks of *S. aureus* were plated on  
139 Columbia agar (CBA) supplemented with 2% sodium chloride (Columbia salt agar,  
140 CSA) and grown at 37°C overnight. Subsequently, colonies were grown in Columbia  
141 salt broth (CSB, Columbia broth supplemented with 2% sodium chloride) at 37°C with

142 shaking at 200 rpm to an optical density at 650nm of 0.5. Bacteria were washed and  
143 resuspended in phosphate-buffered saline (PBS) to yield the intended calculated  
144 inoculum ( $2-4 \times 10^8$  per mouse for experiments measuring bacterial burdens and  $7.5-8 \times 10^8$   
145 per mouse for survival experiments). The inoculum was verified after serial  
146 dilution in TSB supplemented with 0.05% Tween and enumeration of growth on 5%  
147 sheep blood agar plates (BAP) after overnight incubation at 37°C. 20  $\mu$ L of bacterial  
148 suspensions were used for intranasal (IN) challenge in the mouse experiments.

149

#### 150 **Mice**

151 All animal experiments were approved by the Harvard Medical Area Institutional Animal  
152 Care and Use Committee. Four to six week old C57BL/6 mice were purchased from  
153 Jackson Laboratories or Taconic Biosciences. All groups of mice were age-, gender-,  
154 and weight-matched for comparison experiments. Mice were housed under virus-free  
155 conditions in microisolator-topped cages.

156

#### 157 **Co-housing and sfb detection**

158 For co-housing experiments, two sfb-negative mice each and two sfb-positive mice  
159 were transferred into one common cage after ear tagging sfb-negative mice to enable  
160 identification. Prior to co-housing and 12-18 days into co-housing, fecal pellets (freshly  
161 produced after temporary transfer of mice to a new cage) were collected from each  
162 mouse group. DNA from feces was purified using the QIAamp DNA Stool Kit following  
163 manufacturer's instructions (Qiagen, Valencia, CA). The presence of sfb was examined  
164 by PCR using the primers 736F (GACGCTGAGGCATGAGAGCAT) and 844R



165 (GACGGCACGGATTGTTATTCA) and the following PCR conditions: 94° x 5 min, 30  
166 cycles of 94° x 30 sec, 52° x 40 sec, 72° x 90 sec, and 72° x 7 min. Sfb presence  
167 resulted in a ~150bp amplicon.

168

#### 169 **Sfb Acquisition**

170 Sfb-containing stool was obtained from initially germ-free mice that were mono-  
171 colonized with sfb (kindly provided by Dr. Neil Surana), suspended in PBS, and passed  
172 through a cell strainer to remove particulate matter. Fifty µL of this suspension was  
173 given orogastrically via gavage to four-week-old female C57BL/6 mice sedated with  
174 isoflurane. Control mice were given PBS. Prior to challenge with *S. aureus* two weeks  
175 later, stool from these mice was collected, bacterial DNA extracted, and the presence or  
176 absence of sfb confirmed by PCR.

177

#### 178 **Murine pneumonia model**

179 Mice were anesthetized per intraperitoneal (IP) injection with ketamine and xylazine.  
180 After inoculation with 10 µL of the *S. aureus* suspension into each nostril, mice were  
181 observed until recovered from anesthesia. For survival studies, mice were observed  
182 closely for signs of illness and impending death (i.e., a moribund state) at least three  
183 times daily. If appearing moribund (based on hunched posture, inability to move, eat, or  
184 drink, ruffled fur, labored breathing, and crusted eyes), mice were euthanized by carbon  
185 dioxide inhalation followed by cervical dislocation and considered non-survivors. For  
186 quantification of bacteria and analysis of cells and cytokines in bronchoalveolar lavage  
187 fluid (BALF), mice were euthanized by IP injection of pentobarbital at indicated time

188 points. For experiments with IL-22 administration, recombinant IL-22 (R&D systems)  
189 suspended in PBS+0.1% BSA was mixed with the bacterial inoculum and administered  
190 to anesthetized mice via intranasal (IN) inhalation. Control mice were given the bacterial  
191 inoculum mixed with PBS+0.1% BSA.

192

193 Mice given anti-IL-22 antibody IN were sedated with ketamine and xylazine and then  
194 given 25  $\mu$ L containing 25  $\mu$ g polyclonal anti-IL-22 goat IgG or polyclonal goat IgG (all  
195 from R&D systems) as a control 4 hours prior to bacterial challenge.

196

#### 197 **Bronchoalveolar lavage (BAL)**

198 The trachea of euthanized mice was cannulated with a 20-gauge angiocatheter and  
199 BALF was obtained following two instillations of 350  $\mu$ L of ice-cold PBS containing 0.5  
200 mM EDTA. BALF was centrifuged and the supernatant stored at -80°C before  
201 measurement of cytokines using the Magnetic Luminex Assay with the mouse cytokine  
202 20-plex panel (Life Technologies, Grand Island, NY) or, for IL-17 and IL-22  
203 concentration, by ELISA (R&D systems, Minneapolis, MN). Erythrocytes in the cell  
204 pellets were lysed using a mouse erythrocyte lysis kit (R&D systems) according to the  
205 manufacturer's instructions. Total cell counts were determined with trypan blue staining  
206 in a Countess Automated Cell Counter (Life Technologies, Grand Island, NY).

207

#### 208 **Determination of viable bacterial counts**

209 The right lung and the spleen were removed, weighed, and homogenized using an  
210 Omni TissueMaster homogenizer-125 (Omni International, Marietta, GA) in TSB with

211 0.05% Tween. Serial 10-fold dilutions of the lung and spleen homogenates were then  
212 plated onto 5% sheep agar plates and incubated overnight at 37°C prior to counting  
213 CFU and calculating CFU per gram tissue.

214

#### 215 **Flow cytometry**

216 BALF cells were washed with flow cytometry buffer (2% FCS (fetal calf serum) in PBS)  
217 and adjusted to a concentration of  $5 \times 10^5$ /mL. Cells were then treated with FcγR blocker  
218 (anti-CD16/32, clone 2.4G2) in flow cytometry buffer for 20 min on ice to block  
219 nonspecific staining, then stained with appropriate isotype-matched antibodies to the  
220 following cell surface markers: CD45 (30-F11), Ly6G (1A8) (all from Biolegend, San  
221 Diego, CA), and TCRβ (H57-597, eBioscience, San Diego, CA). For intracellular  
222 cytokine staining of IL-17A (using mAb TC11-18H10.1, Biolegend, San Diego, CA) and  
223 IL-22 (using mAb 1H8PWSR, eBioscience, San Diego, CA), cells were stimulated ex  
224 vivo for 6 hours with PMA (phorbol 12-myristate 13-acetate) and ionomycin in the  
225 presence of brefeldin A followed by fixation, permeabilization with saponin, and staining  
226 (all using a Cytofix/Cytoperm Fixation/Permeabilization Kit, BD Biosciences, San Jose,  
227 CA) and then analysis on a FACSCalibur flow cytometer.

228

#### 229 **Confocal microscopy**

230 Paraffin-embedded lung sections were de-paraffinized using EZ-Dewax as per  
231 manufacturer's protocol. De-paraffinized samples were blocked with 1% BSA/PBS  
232 overnight at 4°C followed by labeling with a dilution of 1:200 of rabbit anti-IL-22 antibody  
233 (Abcam), FITC-conjugated CD3e antibody (eBioscience), APC-conjugated RORγt

234 antibody (eBioscience) or the appropriate isotype control antibodies (Biolegend or  
235 eBioscience) in 0.5% BSA/PBS overnight in a humidified chamber at 4°C. The samples  
236 were washed and 1:400 of the secondary antibody, donkey anti-rabbit IgG Alexa Fluor  
237 568-conjugated (Invitrogen), was added to the relevant samples described above for 2  
238 hours at room temperature. Samples were washed, mounted, and analyzed by confocal  
239 microscopy with a Zeiss LSM5 Pascal instrument equipped with a krypton/argon laser.

240

## 241 **Histology**

242 The trachea was cannulated with an angiocatheter and Bouin's fixative solution was  
243 directly injected into the lung. The left lung was then removed and placed in Bouin's  
244 fixative solution prior to paraffin embedding, thin sectioning, and hematoxylin-eosin  
245 staining by the Harvard Rodent Histopathology Core. The lung tissue sections were  
246 scored for percentage of lung tissue affected by inflammation by a veterinary pathologist  
247 who was blinded to the experimental conditions.

248

## 249 **Data analysis and interpretation**

250 The significance of differences in lethal outcomes and bacterial burdens in lungs and  
251 spleens between groups of mice was analyzed by parametric or non-parametric ANOVA  
252 or t tests, as appropriate depending on whether the data were normally distributed,  
253 followed by post-hoc analyses for significant differences between paired groups. We  
254 considered  $p < 0.05$  as statistically significant and used the label \* for  $p < 0.05$  and \*\* for  
255  $p < 0.01$ . We performed survival analysis using the Kaplan-Meier method and the log-  
256 rank test. All analyses were performed using GraphPad's Prism software.

257

258 **RESULTS**

259 **Sfb-negative C57BL/6 mice are more susceptible to *S. aureus* pneumonia than**  
260 **sfb-positive C57BL/6 mice.**

261 Following intranasal challenge with the MRSA strain LAC, sfb-negative mice were found  
262 to have greater infectious bacterial burdens compared with age- and gender-matched  
263 sfb-positive mice. Sfb-negative mice had 21-fold higher bacterial burdens in their lungs  
264 18 hours after infection compared to sfb-positive mice (mean of  $1.4 \times 10^9$  CFU/gram lung  
265 tissue vs.  $6.6 \times 10^7$  CFU/gram lung tissue, respectively, **Figure 1a**). This was  
266 accompanied by higher rates of translocated bacteria, as the spleens of sfb-negative  
267 mice had about 70 times more bacteria compared to spleens of sfb-positive mice  
268 (**Figure 1b**).

269

270 Analysis of the lung histology in MRSA infected mice showed dense inflammatory cell  
271 infiltration as visualized by H+E staining, which was more pronounced in sfb-negative  
272 mice compared to sfb-positive mice (**Figures 1c and d and 1e and f**, respectively).  
273 These results indicate a higher susceptibility of sfb-negative mice to *S. aureus*  
274 pneumonia compared to sfb-positive mice.

275

276 **Resistance to *S. aureus* pneumonia is influenced by an environmental factor.**

277 To examine whether sfb-negative mice are more susceptible to *S. aureus* lung infection  
278 due to an environmental or genetic factor, we co-housed female age-matched sfb-  
279 negative (purchased from Jackson) and sfb-positive mice (from Taconic) in the same

280 cages for two weeks, from 4 to 6 weeks of age, prior to respiratory challenge with *S.*  
281 *aureus*. While the median levels of *S. aureus* in the lungs of the initially sfb-negative  
282 mice co-housed with sfb-positive mice were somewhat higher than bacterial levels in  
283 the continuously sfb-positive mice, this difference was no longer statistically significant  
284 (**Figure 2**). In addition, mice that became sfb-positive during co-housing were  
285 significantly more resistant to *S. aureus* lung infection than sfb-negative mice that were  
286 not co-housed. Co-housing of sfb-positive mice with sfb-negative mice did not alter their  
287 response to *S. aureus* lung infection as they showed the same bacterial levels, as did  
288 mice that were sfb-positive and not co-housed. To confirm the presence of sfb in the  
289 mice in the different groups, we examined the feces of the co-housed mice as well as  
290 mice from Taconic Biosciences reportedly supplied as sfb-positive for the presence of  
291 sfb by PCR. Initially sfb-negative mice sharing a cage with sfb-positive mice became  
292 positive for sfb, as were the mice from the supplier known to carry sfb (**Supplemental**  
293 **Fig. S1**). Stool samples from mice from Jackson Laboratories, reportedly negative for  
294 sfb, were confirmed by PCR to be sfb-negative.

295

#### 296 **Protective effect of sfb gut colonization on susceptibility to *S. aureus* pneumonia**

297 To determine whether the difference in susceptibility to *S. aureus* pneumonia was due  
298 to the presence of sfb in the murine intestine, we administered sfb-containing stool  
299 (obtained from initially germ-free mice that had been mono-colonized with sfb (23)) or  
300 PBS via gavage to 4-week-old sfb-negative mice 2 weeks prior to challenge with *S.*  
301 *aureus*. Sfb was detected by PCR in the stools of mice two weeks after the gavage with  
302 sfb. The PBS-gavaged mice were negative for sfb. When challenged with *S. aureus*,

303 mice that had acquired sfb were more resistant to infection, as demonstrated by  
304 significantly lower bacterial counts in lungs (4.9-fold difference, **Figure 3a**) and a trend  
305 ( $P=0.08$ ) towards lower bacterial counts in spleens (11-fold difference, **Figure 3b**).  
306 When challenged with a higher bacterial inoculum in a survival assay, initially sfb-  
307 negative mice that had become sfb-positive were also at much lower risk of succumbing  
308 to their MRSA lung infection compared to continuously sfb-negative mice. All sfb-  
309 negative mice died by 36 hours, while 70% of mice rendered sfb-positive survived  
310 (**Figure 3c**).

311

#### 312 **Sfb gut colonization is associated with differential pulmonary type 17 immunity.**

313 We measured levels of type 17-associated cytokines in the BALF after *S. aureus*  
314 challenge and tested whether acquisition of sfb via gut colonization alters type 17  
315 immunity in the lung comparing initially sfb-negative mice that became sfb-positive,  
316 either after co-housing with sfb-positive Taconic mice or after gavage with sfb-  
317 containing stool. As shown in **Figure 4a-4d**, we found that BALF levels of IL-22, one of  
318 the main Th17 effector cytokines, differed significantly between groups of mice with and  
319 without sfb-colonization. At 8 hours after intranasal challenge with MRSA, both sfb-  
320 negative and sfb-positive mice had similar IL-22 levels (**Figure 4a**), but by 18 hours post  
321 infection, all sfb-positive mice (whether initially sfb-positive or becoming sfb-positive  
322 mice after co-housing with sfb-positive mice or after sfb-gavage) had significantly higher  
323 IL-22 levels than sfb-negative mice (**Figure 4b-4d**).

324

325 We did not observe significant differences in IL-17 levels, another key cytokine in Th17  
326 immunity, between any group of mice (**Figures 4e-4h; and S2b and S2c**), except for a  
327 small increase in IL-17 in BALF of mice initially sfb-negative after becoming sfb-positive  
328 through co-housing (**Figure 4g**), indicating that this cytokine likely does not play a very  
329 important role in *S. aureus* pneumonia or at least not at the time points we examined.

330  
331 Consistent with the known role of IL-6 in promoting IL-22 expression (24), we also found  
332 that sfb-negative mice had significantly less IL-6 in BALF at an early time point (8 hours)  
333 after challenge with *S. aureus* (**Figure 4i**). At 18 hours, sfb-negative mice had  
334 significantly more IL-6 in BALF (**Figure 4j**), possibly due to the very high bacterial levels  
335 driving IL-6 production in the sfb-negative mice at this time point, while the sfb-positive  
336 mice were beginning to clear the infection.

337  
338 Th17 immunity leads to neutrophil attraction (25) and production of antimicrobial  
339 peptides (11). Sfb-positive mice (both initially colonized mice or initially sfb-negative  
340 mice after co-housing with sfb-positive mice or gavage with sfb) had higher numbers of  
341 Ly6G-positive cells (neutrophils) in BALF (**Figures 4k and 4l**), supporting their  
342 propensity towards Th17 pulmonary responses.

343  
344 In order to identify the types of cells capable of producing IL-22 in the lungs after  
345 infection with MRSA, we stained lung tissue sections of infected sfb-positive mice for  
346 ROR $\gamma$ t, IL-22, and CD3e (**Figure 4m-o**). We found two predominant populations of cells  
347 that were positive for IL-22. One group of cells was positive for ROR $\gamma$ t, IL-22, and CD3



348 and likely represents Th17 or Th22 cells or  $\gamma\delta$  T cells. Another population of cells was  
349 positive for ROR $\gamma$ t and IL-22, but negative for CD3, and possibly represents innate  
350 lymphoid cells type 3 (ILC3s). Although these images are not meant to quantify the  
351 exact number of cells present in lung tissue of sfb-negative and sfb-positive mice, IL-22-  
352 producing cells were qualitatively more prevalent in sfb-positive mice (**Figure 4m**)  
353 versus sfb-negative mice that recently acquired sfb (**Figure 4n**) and sfb-negative mice  
354 (**Figure 4o**). For control stains of images, please see **Supplemental Figure S2**.  
355 Since studies by other groups have reported that  $\gamma\delta$  T cells are the primary source of IL-  
356 17 in a similar murine model of *S. aureus* pneumonia (26) and we observed no  
357 difference in IL-17 levels, we predicted that  $\gamma\delta$  T cells were not likely to be involved in  
358 the sfb-induced responses and focused instead on  $\alpha\beta$  T cells (Th17 cells). Therefore,  
359 we quantified the numbers of IL-22-producing Th17 cells using intracellular staining with  
360 flow cytometry using cells isolated from BALF 8 hours after infection and found  
361 significantly higher numbers of IL-22+ TCR $\beta$ + cells in sfb-positive versus sfb-negative  
362 mice (**Figure 4p**).

363  
364 **IL-22 is critical for host defense against severe *S. aureus* pneumonia.**

365 To further define the role of IL-22 in *S. aureus* pneumonia, we tested whether antibody-  
366 mediated neutralization of IL-22 or administration of recombinant IL-22 impacted the  
367 clearance of *S. aureus* from the murine lung. Sfb-positive mice given monoclonal  
368 antibody to IL-22 intranasally 4 hours prior to infection with *S. aureus* subsequently  
369 exhibited a near 2-log increase in bacterial burdens in the lung compared to mice

370 receiving control IgG (**Figure 5a**), indicating significantly higher susceptibility to infection  
371 in the absence of IL-22.

372

373 Alternatively, administration of recombinant IL-22 intranasally simultaneously with  
374 challenge with *S. aureus* protected sfb-negative mice from development of severe  
375 pneumonia as indicated by significantly lower bacterial burdens in their lungs and  
376 spleens (**Figure 5b-5c**). Of note, intranasal administration of IL-22 led to an about 60-  
377 fold increase in BALF IL-22 concentrations (**Supplemental Figure S3a**). Exogenous  
378 administration of anti-IL-22 antibody did not lead to significant measurable differences in  
379 BALF IL-22 and IL-17 concentrations (**Supplemental Figure S3b and S3c**,  
380 respectively). Exogenous rIL-22 administration to sfb-positive mice simultaneously to  
381 challenge with MRSA strain LAC had no significant protective effect on susceptibility to  
382 MRSA pneumonia (**Supplemental Figure S4**), suggesting that there is no additional  
383 benefit of adding IL-22 (at least at this dose) in an sfb-positive setting.

384

## 385 **DISCUSSION**

386 Understanding the immune responses important for host defense against *S. aureus*  
387 pneumonia, which is a leading cause of death worldwide, is critical for the development  
388 of vaccines and immunotherapies. In this study, we examined whether the GI  
389 microbiota, particularly the presence of sfb has an effect on susceptibility to *S. aureus*  
390 pneumonia. Our findings indicate that sfb-positive mice are more resistant than sfb-  
391 negative mice when challenged in a *S. aureus* pneumonia model and this resistance  
392 was correlated with a type 17 innate immune response. Sfb-negative mice were much

393 more susceptible to *S. aureus* pneumonia with higher bacterial burdens in lungs and  
394 spleens and higher mortality after challenge with *S. aureus*. Co-housing sfb-negative  
395 mice with sfb-positive mice for 14 days, and thereby transferring sfb and likely other GI  
396 microbiota, significantly decreased susceptibility to *S. aureus* pneumonia and improved  
397 survival. Furthermore, we demonstrate that sfb accounts for most of this change in  
398 phenotype by showing that transfer of sfb to sfb-negative mice via orogastric lavage  
399 increases resistance to *S. aureus* lung infection. Overall, a strong case is made for a  
400 critical role of sfb-driven type 17 immunity in the ability to clear *S. aureus* from infected  
401 lungs, and, in particular, a role for IL-22, whose production is closely linked to the  
402 presence of sfb microbiota in the GI tract. Thus, even though the lung does not contain  
403 many GI organisms, these clearly influence innate immunity in this tissue, indicating a  
404 far-reaching role of GI microbiota-driven immune effectors in tissues beyond the GI  
405 tract.

406  
407 While the results implicate the sfb-component of the GI microbiota in susceptibility of  
408 C57BL/6 mice to *S. aureus* lung infection, there may still be some genetic variability  
409 contributing as co-factors in the experiments comparing mice from different vendors (i.e.  
410 Jackson and Taconic). The inbred mouse line C57BL/6 is widely used in animal models,  
411 and, often little attention is paid to the breeding facility from which mice are purchased  
412 for experiments. Although all C57BL/6 mouse strains originated from the same  
413 ancestor, separation in different laboratories over multiple decades and generations has  
414 resulted in the emergence of genetic and phenotypic differences. A recent study  
415 compared in detail the genomic and phenotypic differences of C57BL/6J (established at

416 the Jackson Laboratories in 1948) and C57BL/6N (passed on to the National Institutes  
417 of Health (NIH) in 1951 and later transferred to Taconic Biosciences in 1991) strains,  
418 finding 34 SNPs, 2 indels, and 15 structural variants, as well as a range of phenotypic  
419 differences (27), including physiologic, metabolic, and behavioral. Simon et al. found  
420 that male C57BL/6N mice, compared to male C57BL/6J mice, showed enhanced  
421 resistance to *Listeria monocytogenes* and an increased pro-inflammatory response  
422 (represented by increased plasma levels of IL-6, interferon-inducible protein (IP)-10,  
423 and chemokine ligand (CCL2) (27). Whether this difference was due to a genetic or an  
424 environmental factor (e.g. the GI tract microbiota) is not known. Nonetheless, it is  
425 possible that some of these genetic differences also contributed to the innate immune  
426 response of C57BL/6 mice to *S. aureus* in our experiments comparing mice from  
427 different sources. However, genetic variation is very unlikely to play a role in our  
428 experiments comparing mice from the same source with and without sfb-gavaging.  
429

430 The alteration of susceptibility to *S. aureus* pneumonia in our study is in accordance  
431 with a study by Fagundes et al. who demonstrated that colonization by indigenous  
432 microbiota alters the way a host reacts to infectious stimuli through activation of toll-like  
433 receptor (TLR)-dependent pathways (28). They showed that germ-free mice were more  
434 susceptible to *Klebsiella pneumoniae* pneumonia and that priming germ-free mice with  
435 LPS or other TLR agonists increased their inflammatory responsiveness and led to  
436 better bacterial clearance and survival (28). Two studies have recently demonstrated  
437 that the GI tract microbiota also regulates immune defenses in the respiratory tract  
438 against influenza infection via the TLR7 pathway (29) or inflammasome activation (30).

439 Gut microbiota are likely not only important in infections in the lung, as microbiota  
440 modulate tumoral immune surveillance in this tissue via the Th17 pathway, as well (31).  
441 In Cheng's study, mice treated with antibiotics had increased susceptibility to lung tumor  
442 development, which could be rescued by administration of  $\gamma\delta$ T17 cells or IL-17(31). It is  
443 generally well described that mice without a microbiota have a vastly immature immune  
444 system, which likely contributes to differences in susceptibility to infection. Our work is  
445 unique in regards to examining a specific commensal organism affecting susceptibility  
446 to a non-enteric infection.

447

448 The Th17 pathway has been shown to play an important role in mucosal host defense  
449 against several respiratory pathogens, including *Klebsiella pneumoniae* (8),  
450 *Pseudomonas aeruginosa*(32), *Chlamydia pneumonia* (33, 34), *Mycoplasma*  
451 *pneumonia* (35), and *Mycobacterium tuberculosis* (36) (reviewed in(5)). Type 17  
452 immunity has been described to be important in defense to *S. aureus* pneumonia in  
453 several other studies, although some with conflicting results (9-11). The *S. aureus*  
454 virulence factor  $\alpha$ -hemolysin leads to increased transcription of host cytokine and  
455 chemokine genes, including the p19 subunit of IL-23, producing a prominent cellular  
456 Th17 response (37). Mice lacking the IL-17 receptor or IL-22, or which are coinfectd  
457 with influenza A and thereby have an inhibited Th17 immunity, display impaired  
458 clearance of *S. aureus* compared to wild type or influenza-free mice (10). These results  
459 contrast to those of Choi et al. who reported that IL-17<sup>-/-</sup> and IL-22<sup>-/-</sup> mice showed no  
460 difference in MRSA clearance compared to wild type mice (9). Whether these

461 conflicting results are related to variable GI tract microbiota among mouse strains, or to  
462 different bacterial challenge strains, or other experimental variables, is unclear.

463

464 IL-22 is a member of the IL-10 family of immune mediators that is expressed by a  
465 several lymphocytes, including those of the innate and adaptive immune system (38). It  
466 has multiple functions, among which is modulation of tissue response during  
467 inflammation and anti-microbial molecule production (i.e. beta-defensin, Reg3 $\gamma$ , and  
468 Lipocalin 2)(39-41). IL-22 has been shown to mediate early host defense against  
469 bacterial pathogens (41) and appears to prevent bacterial dissemination in the GI tract,  
470 e.g. after infection with *Citrobacter rodentium* (41) or *Salmonella enterica* serotype  
471 *Typhimurium* (39). In the lung, IL-22 has been shown to mediate mucosal host defense  
472 against pneumonia with *Klebsiella pneumoniae* (8), and IL-22 expressing  $\gamma\delta$ T cells were  
473 protective in a model of *Bacillus subtilis*-induced pulmonary fibrosis (42).

474

475 Given our observation that increased resistance to *S. aureus* pneumonia was  
476 associated with higher IL-22 levels, we tested its role directly and found that antibody-  
477 mediated neutralization of IL-22 led to increased susceptibility to *S. aureus* pneumonia  
478 in sfb-positive mice. Importantly, we also found that exogenous administration of IL-22  
479 to sfb-negative mice rescued their defense against *S. aureus* pneumonia to a resistance  
480 level similar to sfb-positive mice, which further supports the protective role of IL-22 in *S.*  
481 *aureus* pneumonia. These findings suggest that therapeutic administration of  
482 recombinant IL-22 is a potential new approach to treatment of *S. aureus* pneumonia.

483

484 We did not observe significant differences in IL-17 levels, another key cytokine in Th17  
485 immunity, between any group of mice, except for a slight increase in MRSA-infected  
486 mice after sfb-acquisition through co-housing, indicating that this cytokine likely does  
487 not play a very important role in *S. aureus* pneumonia or at least not at the time points  
488 we examined. It is possible that modulation of the pulmonary immune response by the  
489 enteric microbiota only affects specific cytokines. We observed at least two populations  
490 of cells capable of producing IL-22 in the lung after challenge with MRSA. The first  
491 population was comprised of cells positive for IL-22, CD3, and ROR $\gamma$ t likely representing  
492 Th17 or Th22 cells (43), while the second group was negative for CD3, but positive for  
493 IL-22 and ROR $\gamma$ t, possibly representing ILC3s (44).

494

495 Our data also highlight the importance of choosing an appropriate control mouse strain  
496 in these types of experiments and might explain the conflicting results seen in prior  
497 studies. Another explanation for reported conflicting results might relate to the finding  
498 that different pathogens can induce different cytokine production and effector function in  
499 Th17 cells (45).

500

501 Protective responses to *S. aureus* pneumonia were associated with IL-6 increase, a  
502 Th17-associated cytokine, at an early time point. Previous studies have shown that IL-6  
503 is a pleiotropic cytokine involved in the cross talk between immune cells and stromal  
504 cells, activates the STAT3 signaling axis, is one of the main regulators of Th17 cell  
505 differentiation (46), and promotes IL-22 expression (24). IL-6 deficient mice showed  
506 impaired defense against pneumococcal pneumonia (47). Interestingly, IL-6 and IL-1b

507 levels are elevated in mice orally treated with antibiotics resulting in commensal  
508 depletion compared to untreated mice and are associated with more severe illness (21).  
509 This is in accordance to our findings that sfb-negative mice have lower IL-6 levels  
510 compared to sfb-positive mice at 8 hours after infection and that sfb-negative mice after  
511 acquisition of sfb had markedly increased IL-6 expression. Sfb-negative mice in our  
512 study had higher IL-6 levels at 18 hours post-infection, possibly reflecting a delayed  
513 response or a response due to the continuing high levels of *S. aureus* in the lungs. IL-6  
514 produced by macrophages during MRSA infection stimulates the pulmonary epithelium  
515 via STAT3 signaling to produce the antimicrobial protein Reg3 $\gamma$ , which has  
516 bacteriostatic and bactericidal effects against MRSA (9). Further studies are needed to  
517 examine the link between GI microbiota and production of certain antimicrobial proteins  
518 in the lung.

519

520 We found increased susceptibility of sfb-negative mice to *S. aureus* lung infection and  
521 could demonstrate this was related to IL-22 production. In human disease *S. aureus*,  
522 and particularly MRSA, can rapidly progress towards a fatal infection over a short time  
523 period, indicative of the importance of the innate response to infection. We do not know  
524 at this time whether humans who get these invasive *S. aureus* pneumonias have or lack  
525 organisms in their GI microbiota predisposing them to increased susceptibility, but as  
526 progress in understanding the interaction of the microbiota and the immune system  
527 ensues, it might be possible to insure that individuals carry organisms that can  
528 maximize their innate resistance to infection. Our findings also suggest exogenous IL-22



529 could be a therapy for *S. aureus* pneumonia, a disease process in desperate need for  
530 improved therapies.

531

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541

542 **Figure 1. Sfb-negative mice exhibit increased susceptibility to MRSA pneumonia**  
543 **compared to sfb-positive mice.**

544

545

546 C57BL/6 mice from Jackson (sfb-negative) and Taconic (sfb-positive) were challenged  
547 with  $5 \times 10^8$  CFU of MRSA intranasally and sacrificed after 18 hours for determination of  
548 bacterial CFU/gram lung (**A**) and spleen (**B**) tissue. Symbols represent individual  
549 animals; bars represent the medians. *P* values were determined by Mann Whitney U  
550 tests.

551 Histological appearance of lung tissue of a representative sfb-negative (**C and D**) and  
552 sfb-positive (**E and F**) mouse 18 h after infection with MRSA Lac. The sfb-negative mice  
553 showed higher percentages of lung tissue involved by inflammation (60% affected (**C**  
554 **and D**) vs. 10% affected (**E and F**)). 40-fold magnification (**C and E**) and 100-fold  
555 magnification (**D and F**). The black bar represents 1mm.

556

557 **Figure 2. Sfb-negative mice acquire increased resistance to *S. aureus* pneumonia**  
558 **after co-housing with sfb-positive mice.**

559

560 Female sfb-negative C57BL/6 mice and age-matched, female sfb-positive C57BL/6  
561 mice were housed together in isolated cages for 2 weeks prior to bacterial challenge. All  
562 of the co-housed mice were sfb-positive at the time of bacterial challenge. Eight  
563 additional sfb-negative or sfb-positive mice were not co-housed for the same time  
564 period, and remained sfb-negative and sfb-positive, respectively. After 2 weeks, mice  
565 were challenged with  $5 \times 10^8$  CFU of MRSA IN and sacrificed after 18 hours for  
566 determination of bacterial CFU/gram lung tissue. Symbols represent individual animals;  
567 bars represent the medians. *P* values were determined by Kruskal-Wallis test (overall  
568 ANOVA,  $P < 0.01$ ) and *P* values depict the Dunn's multiple pair-wise comparisons for  
569 nonparametric distributions.

570

571 **Figure 3. Sfb-negative mice acquire increased resistance to *S. aureus* pneumonia**  
572 **after colonization with sfb in their GI tract.**

573

574 Sfb-negative C57BL/6 mice were either gavaged with PBS (sfb-negative+PBS, n=5) or  
575 with sfb-containing stool (sfb-negative + sfb, n=6) 2 weeks prior to intranasal challenge  
576 with MRSA strain LAC at a dose of  $5 \times 10^8$  CFU (**A and B**) or  $2 \times 10^9$  CFU for a survival  
577 experiment (n=10 in each group) (**C**). Bacterial CFU/gram lung tissue (**A**) and spleen  
578 tissue (**B**) at 18 h post-infection. (**C**) Kaplan-Meier survival curves. Symbols represent  
579 individual animals; bars represent the medians. *P* values were determined by Mann  
580 Whitney U tests (**A and B**) or by logrank test (**C**).

581

582 **Figure 4. Type 17 immunity differs in the lungs of sfb-negative and sfb-positive**  
583 **mice.**

584

585 At 8 and 18 h post-infection with MRSA, mice were euthanized and BALF was obtained  
586 for (removed: cellular and) cytokine analysis. Bars represent the means and error bars  
587 represent standard deviations (SD). *P* values were determined by Mann Whitney U  
588 tests for 2-group comparisons or Kruskal-Wallis test with Dunn's multiple comparison.

589 **A)** BALF IL-22 8 h post-infection; **B)** BALF IL-22 18 h post-infection; **C)** BALF IL-22 18 h  
590 post-infection after co-housing; **D)** BALF IL-22 18 h post-infection in Jackson (sfb-  
591 negative) mice acquiring sfb after gavage two weeks prior to infection; **E)** BALF IL-17 8h  
592 post-infection; **F)** BALF IL-17 18h post-infection; **G)** BALF IL-17 18 h post-infection after  
593 co-housing; **H)** BALF IL-17 18 h post-infection in Jackson mice acquiring sfb after  
594 gavage two weeks prior to infection; **I)** BALF IL-6 8 h post-infection; **J)** BALF IL-6 18 h  
595 post-infection; **K-L)** Ly6G-positive cells (neutrophils) in BALF 18 h post-infection of co-  
596 housed mice (**K**) or sfb-colonized Jackson mice (**L**). **(M-P)** Mouse lung sections were  
597 stained with anti-ROR $\gamma$ t antibody (left upper squares, blue), anti-IL-22 (middle upper  
598 squares, red), and anti-CD3e (right upper square, green) and examined by confocal  
599 microscopy. Left lower squares depict phase contrast microscopy and right lower  
600 squares show merged confocal images. **(M)** Lung tissue sections of an sfb-positive  
601 mouse, showing many cells positive for ROR $\gamma$ t, IL-22, and CD3 (whitish-yellow cells in  
602 merged confocal image) likely representing Th17 or Th22 cells, as well as ROR $\gamma$ t and  
603 IL-22 positive, but CD3 negative cells (purple), possibly representing ILC3s. **(N)** Lung  
604 tissue sections of a previously sfb-negative mouse after acquisition of sfb 2 weeks prior

605 by nasogastric lavage showing also both ROR $\gamma$ t<sup>+</sup> IL-22<sup>+</sup> CD3<sup>+</sup> and ROR $\gamma$ t<sup>+</sup> IL-22<sup>+</sup>  
606 CD3<sup>-</sup> cell populations, but overall in less quantities, and very few CD3-positive cells. **(O)**  
607 Lung tissue sections of an sfb-negative mouse showing even less ROR $\gamma$ t<sup>+</sup> or IL-22<sup>+</sup>  
608 cells despite a denser cell infiltrate and no ROR $\gamma$ t<sup>+</sup> IL-22<sup>+</sup> CD3<sup>-</sup> cells. Isotype control  
609 stains for images **Figure 4m-o** are shown in supplemental **Figure S2a-c**. **(P)** Number  
610 of dually IL-22-and TCR $\beta$ -positive cells in BALF of mice at 8 hours after infection using  
611 intracellular staining by flow cytometry showed a significantly more IL-22<sup>+</sup> TCR $\beta$ -  
612 positive cells in sfb-positive versus sfb-negative mice.

613

614 Color key:

615 ROR $\gamma$ t – blue

616 IL-22 – red

617 CD3 – green

618

619 **Figure 5. Neutralization of IL-22 leads to more severe *S. aureus* pneumonia while**  
620 **exogenous IL-22 administration increases resistance of sfb-negative mice to**  
621 **infection.**

622 C57BL/6 mice from Taconic (sfb-positive) received monoclonal anti-IL-22 antibody or  
623 control IgG 4 h prior to challenge with  $5 \times 10^8$  CFU of MRSA intranasally. **(A)** Bacterial  
624 CFU/gram lung tissue 18 h post infection. **(B and C)** C57BL/6 mice from Jackson (sfb-  
625 negative) received exogenous recombinant IL-22 or control protein BSA during  
626 challenge with  $5 \times 10^8$  CFU of MRSA LAC intranasally. Bacterial CFU/gram lung **(B)** and  
627 spleen **(C)** at 18 h post-infection. Symbols represent individual animals; bars represent  
628 the medians. *P* values were determined by Mann Whitney U tests for 2-group  
629 comparisons or Kruskal-Wallis test with Dunn's multiple comparison.

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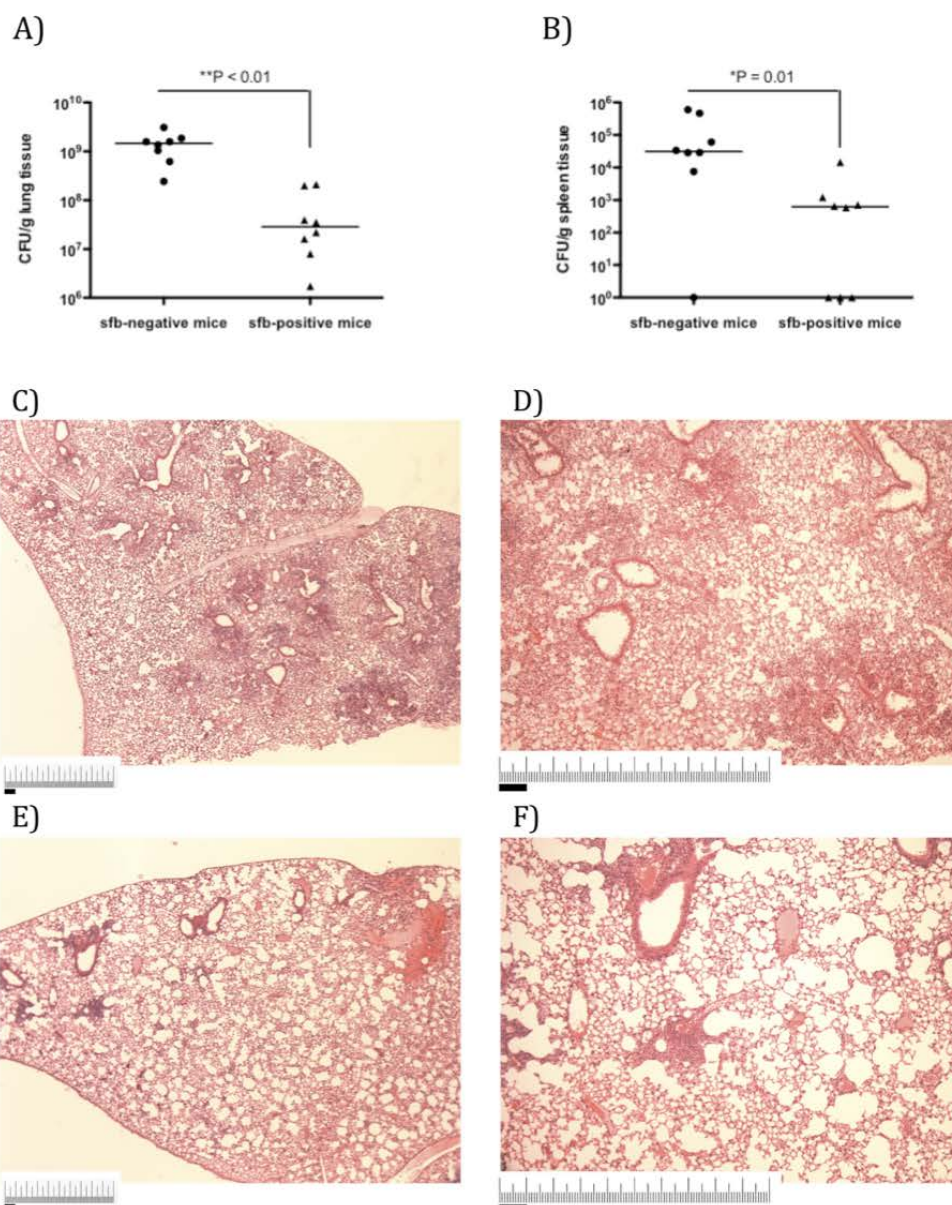
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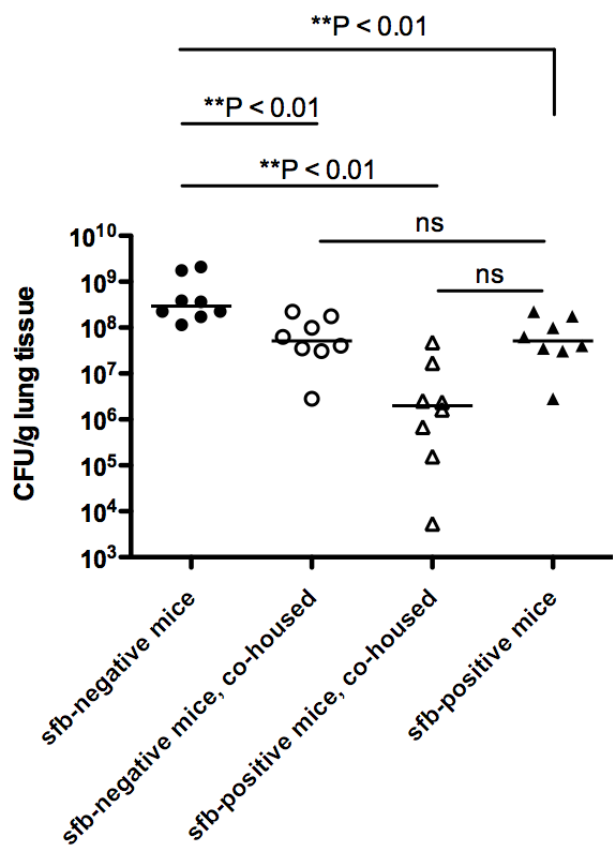
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**Figure 1. Sfb-negative mice exhibit increased susceptibility to MRSA pneumonia compared to sfb-positive mice.**



**Figure 2. Sfb-negative mice acquire increased resistance to *S. aureus* pneumonia after co-housing with sfb-positive mice.**



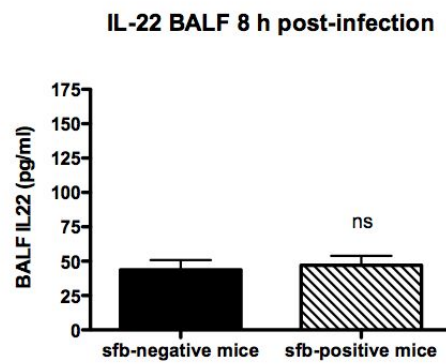
**A)** Scatter plot showing bacterial load (CFU/g lung tissue) at 24h post-infection. The y-axis is logarithmic, ranging from  $10^7$  to  $10^9$ . Two groups are compared: sfb-negative + PBS (filled circles) and sfb-negative + sfb (open circles). The sfb-negative + PBS group has a mean CFU of approximately  $2.5 \times 10^8$ , while the sfb-negative + sfb group has a mean CFU of approximately  $4 \times 10^7$ . A horizontal line with asterisks indicates  $*P < 0.05$ .

**B)** Scatter plot showing bacterial load (CFU/g spleen tissue) at 24h post-infection. The y-axis is logarithmic, ranging from  $10^0$  to  $10^6$ . Two groups are compared: sfb-negative + PBS (filled circles) and sfb-negative + sfb (open circles). The sfb-negative + PBS group has a mean CFU of approximately  $4 \times 10^3$ , while the sfb-negative + sfb group has a mean CFU of approximately  $10^3$ . A horizontal line indicates  $P = 0.08$ .

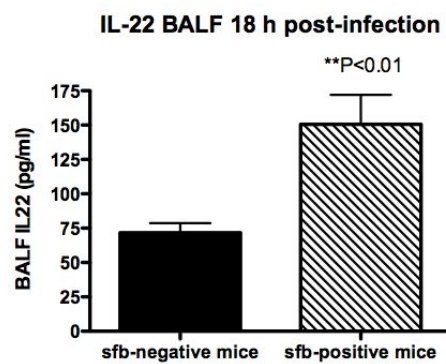
**C)** Kaplan-Meier survival curve showing percent survival over time after infection (hours). The y-axis ranges from 0 to 100. The x-axis ranges from 0 to 72 hours. Two groups are compared: sfb-negative + sfb (dashed line) and sfb-negative + PBS (solid line). The sfb-negative + PBS group shows a rapid decline in survival, reaching 0% by 36 hours. The sfb-negative + sfb group shows a slower decline, reaching approximately 70% survival by 72 hours. A horizontal line with asterisks indicates  $**P < 0.01$ .

**Figure 4. Type 17 immunity differs in the lungs of sfb-negative and sfb-positive mice.**

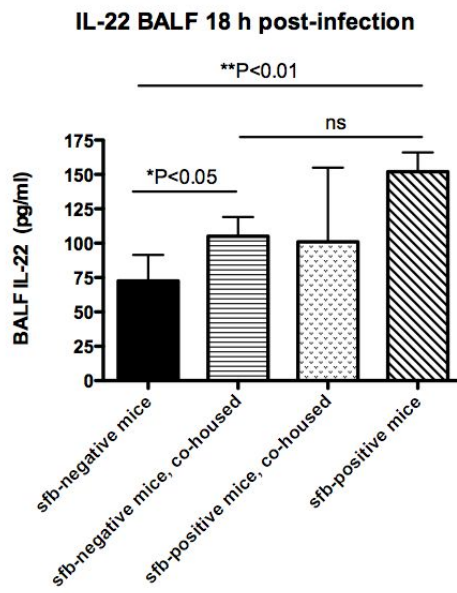
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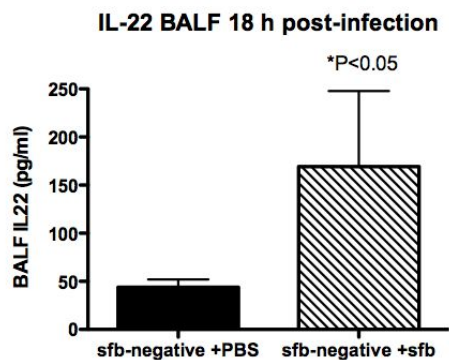
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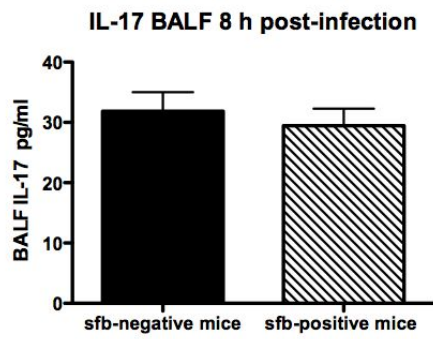
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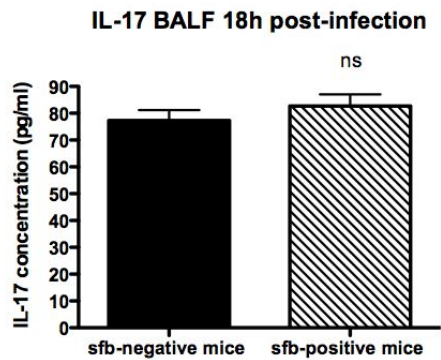
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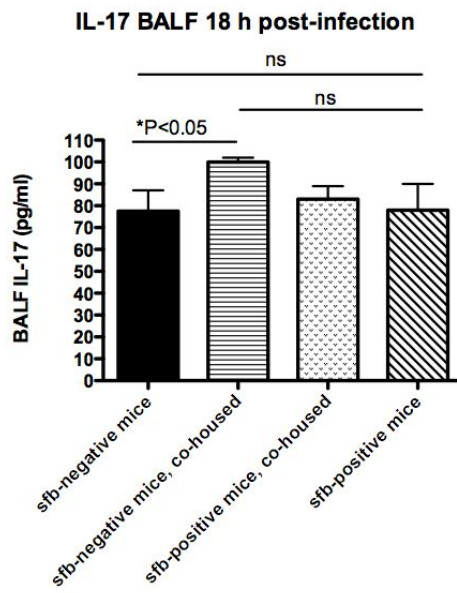
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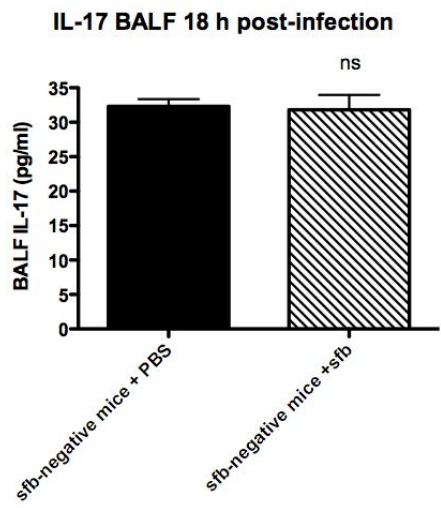
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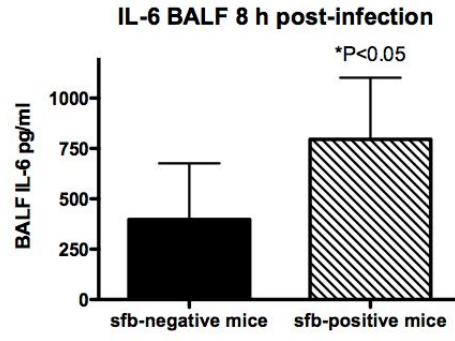
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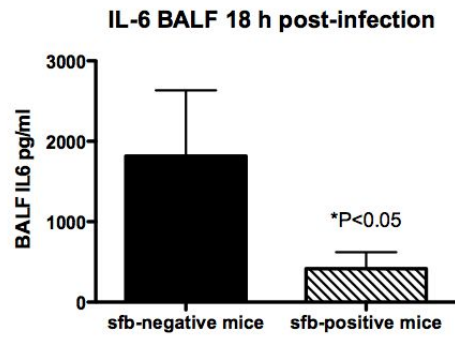
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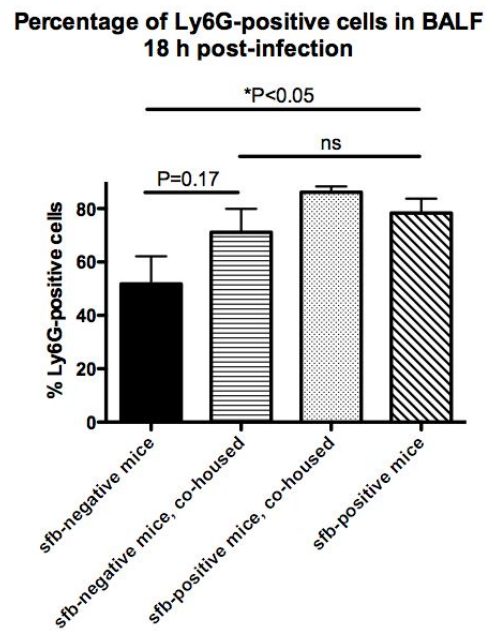


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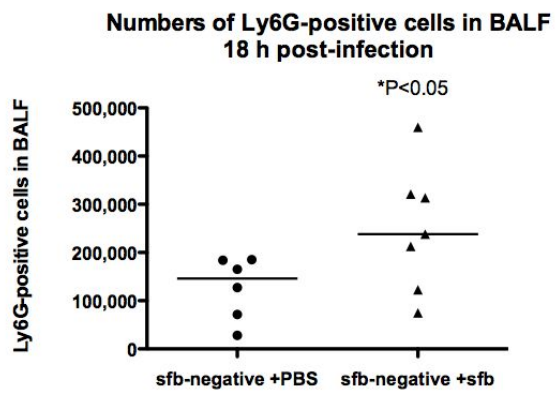


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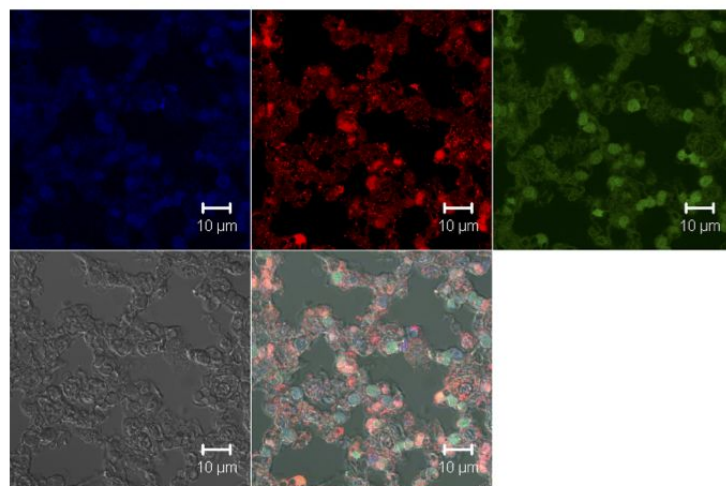


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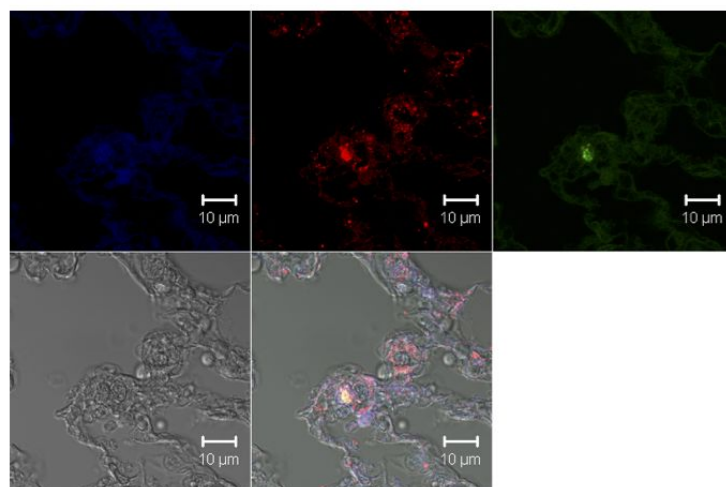


**Figure 4. Type 17 immunity differs in the lungs of *sfb*-negative and *sfb*-positive mice.**

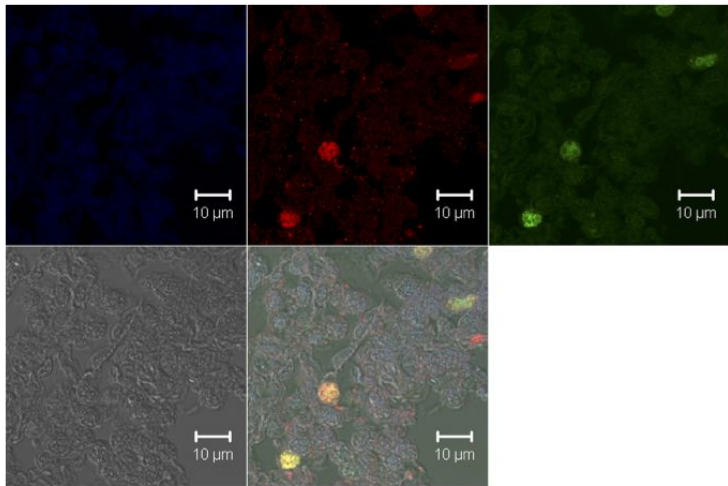
**M)**



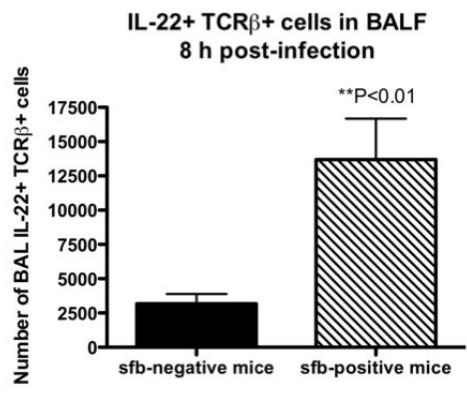
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O)

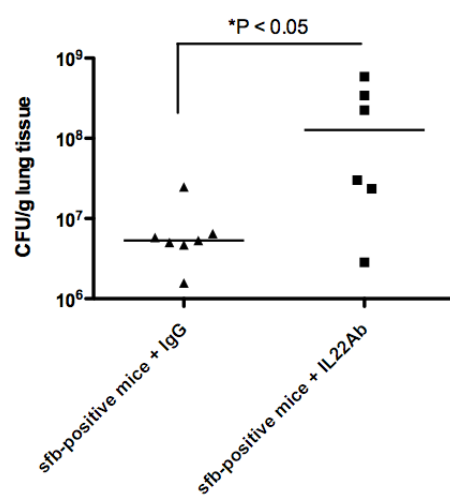


P)

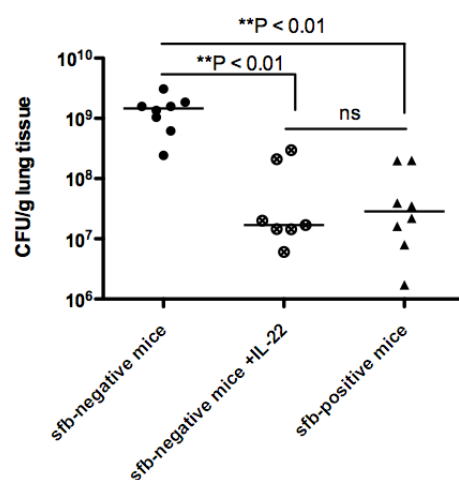


**Figure 5. Neutralization of IL-22 leads to more severe *S. aureus* pneumonia while exogenous IL-22 administration increases resistance of sfb-negative mice to infection.**

A)



B)



c)

