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Staphylococcus aureus Formyl Peptide Receptor–like 1 Inhibitor (FLIPr) and Its Homologue FLIPr-like Are Potent FcγR Antagonists That Inhibit IgG-Mediated Effector Functions

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To evade opsonophagocytosis, Staphylococcus aureus secretes various immunomodulatory molecules that interfere with effective opsonization by complement and/or IgG. Immune-evasion molecules targeting the phagocyte receptors for these opsonins have not been described. In this study, we demonstrate that S. aureus escapes from FcγR-mediated immunity by secreting a potent FcγR antagonist, FLIPr, or its homolog FLIPr-like. Both proteins were previously reported to function as formyl peptide receptor inhibitors. Binding of FLIPr was mainly restricted to FcγRII receptors, whereas FLIPr-like bound to different FcγR subclasses, and both competitively blocked IgG-ligand binding. They fully inhibited FcγR-mediated effector functions, including opsonophagocytosis and subsequent intracellular killing of S. aureus by neutrophils and Ab-dependent cellular cytotoxicity of tumor cells by both neutrophils and NK cells. In vivo, treatment of mice with FLIPr-like prevented the development of an immune complex–mediated FcγR-dependent Arthus reaction. This study reveals a novel immune-escape function for S. aureus–secreted proteins that may lead to the development of new therapeutic agents in FcγR-mediated diseases. The Journal of Immunology, 2013, 191: 000–000.

The commensal bacterium Staphylococcus aureus is a leading cause of a wide variety of infections in humans and animals worldwide, ranging from mild superficial skin infections to fatal deep-seated infections that entail spread through the bloodstream and body (1). Its great success with regard to infection is explained by the numerous strategies that this commensal has developed to breach host immune responses (2, 3).

The principal line of defense against extracellular bacterial infection relies on phagocytes, including residential macrophages and immigrating neutrophils. These leukocytes recognize, remove, and destroy invading bacteria through phagocytosis. Bacterial recognition can occur directly via membrane-bound pattern recognition receptors, although many pathogens, including S. aureus, resist direct engulfment by phagocytes and require opsonization by complement (C3b, C3bi) or IgGs (IgA, IgG) for efficient phagocytosis. The phagocyte receptors for these opsonins, complement receptors CR1 and CR3, FcγRs, and leukocyte FcγRs, respectively, become activated upon ligand binding. They induce the initial uptake of the pathogen into a phagosome that subsequently fuses with lysosomes, resulting in the intracellular killing of the pathogen. An intracellular IgG receptor, the neonatal FcR (FcRn) (4), contributes to this process as well; however, mechanistic details remain to be elucidated.

To evade phagocytosis, S. aureus expresses a variety of both secreted and cell surface–associated immunomodulatory proteins. These proteins bind to key elements in this process and inhibit their proper function. Several of these abrogate effective bacterial opsonization by complement and/or IgG (5). SCIN (6), Efb, and its C-terminal homolog Ecb (7) are secreted proteins that target complement deposition on the bacterial surface by direct and indirect inhibition of C3 convertases. Sbi is an excreted and cell wall–anchored protein with a dual function, disturbing both complement and IgG opsonization (8, 9). Sbi binds to fragment C3d of complement factor C3 and to the constant domain (Fc) of IgG, thereby blocking interactions with FcγR and complement factor C1q. A similar inhibition of IgG Fc tail function, although targeting IgG1...
exclusively, is provided by the secreted SSL10 (10). Staphylococcal protein A (SpA) is a cell wall–anchored IgG-binding (11) and anti-phagocytic protein expressed by most strains of *S. aureus*. Its inhibitory effect on phagocytosis is explained by the concept that SpA captures IgG onto the bacterial surface in a maloriented position, thereby preventing recognition by neutrophil FcyR. In addition to these blocking proteins, *S. aureus* also expresses an enzymatic inhibitor of bacterial opsonization, staphylokinase, which degrades the bacterium-bound opsonins, C3b and IgG, by activation of plasminogen into plasmin, an active serine protease (12). Staphylococcal immunomodulatory molecules that directly target the phagocyte opsonin receptors have not been described. In this study, we focus on FcyRs, the receptors for IgG.

Through binding of the Fc domain of IgG, FcyRs activate immune effector cells on which they are broadly expressed (13–15). FcyRs are members of the Ig superfamily. They possess an extracellular ligand–recognizing α-chain consisting of two or three Ig-like domains, a transmembrane region, and an intracellular tail. Cross-linking of FcyRs by IgG-opsonized particles or immune complexes induces several cell type–dependent immune responses, ranging from phagocytosis, respiratory burst, and Ab-dependent cellular cytotoxicity (ADCC) to secretion of inflammatory mediators, enhancement of Ag presentation, and regulation of Ab production. Based on structural and biochemical differences they are divided in three distinct, but closely related, classes of FcyR, the major histocompatibility complex (MHC) class II homologs (FcR). Based on their expression on different cell types, FcR have been divided in three classes: FcyR I (CD64), FcyRIIa, and FcyRIIb (CD32), and FcyRIII (CD16) – containing 12 isomers that differ in cellular distribution and affinity for IgG. Monocytes and macrophages express members of all three FcyR classes: FcyRI, FcyRIIa/b/c, and FcyRIIIa (on monocyte subtype). The most abundant phagocyte, the neutrophil, constitutively expresses only two members of the FcyR classes: FcyRIIa and FcyRIIib. FcyRIIa is the predominant receptor involved in phagocytosis and binds IgG only in complexed or polymeric form. The FcyRIIa gene demonstrates allelic variation (16), resulting in two allotypes with different affinity for IgG: FcyRIIa-H131 (E27) and FcyRIIa-R131 (Y27). Human neutrophils also express limited amounts of the inhibitory FcyRIib (17, 18). FcyR class III contains two isoforms: the medium-affinity receptor FcyRIIlia, which is expressed on NK cells, macrophages, and some monocytes, and the GPI-anchored FcyRIIib, with a low affinity for IgG, which is constitutively expressed on neutrophils. For FcyRIIa, two functionally different allelic variants are known that differ at position 158 (V158 and F158) (16). FcyRIIib bears a polymorphism (16) at four positions in the extracellular region, resulting in different allotypes, neutrophil Ag (NA) 1 (R18 N47 D64 V88) and NA2 (S18 S47 N64 I88), which have different glycosylation patterns and interaction with IgG. The high-affinity IgG FcγR, which is expressed on monocytes, macrophages, and activated neutrophils, is structurally unique in that it contains three extracellular Ig-like domains, in contrast to the two found in FcyRI and FcyRII.

In this study, we investigated the hypothesis that *S. aureus* evades opsonophagocytosis via the secretion of an FcyRIIa inhibitory molecule. We describe the identification of two immunomodulatory homolog proteins secreted by *S. aureus* that target FcyR directly by recognizing epitopes in or near their IgG-binding domain. Both proteins were reported to be antagonists for the formyl peptide receptor (FPR) family. In this study, we demonstrate that these proteins are potent antagonists of FcyR-mediated effector functions in vitro, including opsonophagocytosis and ADCC, and in vivo.

Materials and Methods

**Abs and reagents**

The following anti-FcγR mAbs were used: PE-conjugated mAb 7.3 (FcyRII; Research Diagnostics), FITC-conjugated mAb FL18.26 (FcyRII; BD), FITC-conjugated mAb IV.3 (FcyRII; American Type Culture Collection), FITC-conjugated mAb 30G (FcyRIII; BD), PE-conjugated mAb B73.1 (FcyRIII; BD), FITC-conjugated mAb 10.1 (FcyRI; BD), and PE-conjugated mAb MIP8a (FcεR). HRP-conjugated anti-His mAb was from Invitrogen, anti-polystyreneHistidine mAb was from R&D Systems, and human IgG1κ (HuMab-KLH) was from Genlabe. Soluble fFcyRs of different subclasses –λ, ll, IIa (H131 and R131), llb, IIIa (V158 and F158), and llb (Na1 and Na2) – containing a polyhistidine tag were kindly provided by Genlabe (19). Additional soluble FcyRIIa, FcεR, and FcεR were from R&D Systems. Human αβ macromolecules (IgG1), panthymumab (IgG2), and lgA directed against the epidermal growth factor receptor were from the Department of Immunology, University Medical Center Utrecht.

**Bacterial supernatants and proteins**

Clinical and laboratory strains of *S. aureus* were grown overnight at 37°C in IMDM without Phenol Red (Invitrogen), and cell-free supernatant was harvested by centrifugation and filter sterilized. One liter of supernatant from *S. aureus* subsp. aureus strain ATCC 25923 (GenBank BA000018) was passed over a 25-ml “Reactive Red 120” ligand dyes (Sigma–Aldrich) attached to an Akta–FPLC system (GE Healthcare Life Sciences). After washing with PBS, the column was eluted into 2.5-ml fractions using 1 M NaCl. PMSF (1 mM) was added, and fractions were dialyzed in PBS for 18 h. Fractions were screened for activity by anti-FcγRIIB mAb 7.3 staining on fresh human neutrophils. Active fractions were pooled, concentrated using a 10-kDa Centricon (Amicon; Millipore), and separated on a GE Healthcare Superdex-75 gel filtration column into 2.5-ml fractions that were again screened for activity. Active fractions were pooled and concentrated using a 10-kDa Centricon and stored at −20°C in small aliquots. Different fractions were precipitated with 20% TCA for 30 min on ice and analyzed on 15% SDS-PAGE (Mini-Protein II; Bio-Rad) by silver staining.

For affinity isolation, magnetic Cobalt-chelating beads (TALON Dynabeads; Invitrogen) were coated with recombinant His-tagged human CD32a (the extracellular domain Ala 36–Ile 218 of human FcyRIIa; #1330-CD; R&D Systems). Fifty microliters of beads was washed twice with PBS containing 0.1% Triton X-100 (PBS-Triton) and incubated for 30 min with 100 μl 200 μg/ml His-tagged CD32a in PBS. Beads were washed three times with PBS-Triton and incubated with purified supernatant for 18 h at 4°C under gentle rotation in a total volume of 400 μl. Supernatant was discarded, and beads were washed three times with PBS-Triton, suspended in 30 μl SDS-PAGE sample buffer for 15 min, and heated for 2 min at 100°C. The sample was centrifuged briefly (10 s at 10,000 × g), and the supernatant was analyzed on 15% SDS-PAGE by silver staining. Bands were excised and sent for protein identification at the Department of Bio-molecular Mass Spectrometry, Utrecht Institute for Pharmaceutical Sciences, Utrecht, The Netherlands.

The recombinant staphylococcal proteins FLIPr, FLIPr-like, and CHIPS were expressed and purified from *Escherichia coli* as described (20–22).

**Surface-enhanced laser desorption ionization time-of-flight mass spectrometry**

For identification by mass, a Ciphergen (Bio-Rad) IMAC30 ProteinChip (the extracellular domain Ala 36–Ile 218 of human FcyRIIa; #1330-CD; R&D Systems). Fifty microliters of beads was washed twice with PBS containing 0.1% Triton X-100 (PBS-Triton) and incubated for 30 min with 100 μl 200 μg/ml His-tagged CD32a in PBS. Beads were washed three times with PBS-Triton and incubated with purified supernatant for 18 h at 4°C under gentle rotation in a total volume of 400 μl. Supernatant was discarded, and beads were washed three times with PBS-Triton, suspended in 30 μl SDS-PAGE sample buffer for 15 min, and heated for 2 min at 100°C. The sample was centrifuged briefly (10 s at 10,000 × g), and the supernatant was analyzed on 15% SDS-PAGE by silver staining. Bands were excised and sent for protein identification at the Department of Bio-molecular Mass Spectrometry, Utrecht Institute for Pharmaceutical Sciences, Utrecht, The Netherlands.

For identification by mass, a Ciphergen (Bio-Rad) IMAC30 ProteinChip Array was used that incorporates nitritricatric acid groups forming stable complexes with metal ions. After loading the array with nickel salt, 10 μg/ml His-tagged soluble FcγR was added and subsequently incubated with semipurified concentrated staphylococcal supernatant. The array was washed with PBS, rinsed with water, air dried, and treated with a saturated solution of sinapinic acid, an energy-absorbing molecule that assists in desorption and ionization. After air drying, the array was analyzed using the Ciphergen ProteinChip System Series 4000 read at a setting optimized for protein/molecular mass range. Spectra were externally calibrated, baseline corrected, and normalized to total ion current within a mass/charge (m/z) range of 1,500–50,000 Da.

**Cells and flow cytometry staining**

The mouse P388D1 macrophage cell line was maintained in RPMI 1640 medium supplemented with 10% (v/v) FCS. Human neutrophils and mononuclear cells were isolated from heparinized blood as described (21). Cells were incubated with staphylococcal supernatants (30% v/v) or purified recombinant proteins for 0–10 min on ice, washed, and subsequently stained with fluorescent mAb. Fluorescent intensities were measured by flow cytometry and expressed relative to control cells not exposed to supernatant or recombinant protein. FLIPr and FLIPr-like were labeled with FITC, as described (21, 22), and incubated with leukocytes in the presence of specific markers for neutrophils (PE-labeled anti-CD14), T cells (allophycoerycian-labeled anti-CD3), B cells (PE-labeled anti-CD19), or NK cells (PE-labeled CD56 and allophycoerycian-labeled anti-CD56). Cells were gated by their scatter and marker profile.
**Evaluation of FcγR binding and Ig inhibition by ELISA**

To detect binding of staphylococcal proteins to FcγR subclasses, MaxiSorp plates (Nunc) were coated overnight at 4°C with 100 μl FLIPr, FLIPr-like, or chemotaxis inhibitory protein of *Staphylococcus aureus* (CHIPS) at 1 μg/ml in PBS. Plates were washed three times with PBS supplemented with 0.05% v/v Tween 20 and incubated with a serial dilution of different soluble FcγR proteins containing a polystyidene tag in PBS supplemented with 0.05% v/v Tween 20 and 0.2% w/v BSA. After 2 h of shaking (300 rpm) at room temperature, plates were washed and incubated for 90 min with HRP-conjugated anti-His mAb to detect FcγR binding. Inhibition of Ig binding to the different FcγR subclasses by staphylococcal proteins was measured with another ELISA. Plates were coated overnight with 4 μg/ml anti-polystyidene mAb, washed, and incubated with 2 μg/ml soluble His-tagged FcγR for 90 min. The plates were washed and incubated with a serial dilution of the staphylococcal proteins. After washing, the different subclasses of FcγR were probed with an optimal concentration of human monoclonal IgG1 (HuMab-KLH) that was detected with HRP-conjugated anti–human Fc. Statistical analysis was performed using a two-tailed Student *t* test.

**Phagocytosis and killing**

Phagocytosis was measured with FITC-labeled *Staphylococcus* (6). In a 96-well plate, bacteria were mixed with a concentration range of human serum (pooled from 15 donors), complement-inactivated serum (30 min at 56°C), or purified IgG (by Protein G affinity chromatography from the same serum pool) for 15 min at 37°C for opsonization. Subsequently, neutrophils or macrophages, with or without inhibitor, were added to a 10:1 bacteria/ cell ratio and incubated for 15 min at 37°C on a shaker (750 rpm). The reaction was stopped with ice-cold paraformaldehyde (1%), and cell- associated fluorescent bacteria were analyzed by flow cytometry. Phagocytosis is defined as the percentage of cells with a positive fluorescent signal. To compare the experiments, the values are expressed relative to the second highest opsonin concentration of control cells without inhibitor protein. Killing of *Staphylococcus* was determined by colony plate counting. Bacteria were opsonized for 15 min in 1% complement-inactivated serum, mixed with neutrophils at a 1:10 ratio, and incubated for 1 h at 37°C while shaking. A 50-μl sample was diluted into 2.5 ml ice-cold water [pH 11], vortexed, and incubated for 5 min on ice to lyse the neutrophils. The remaining viable bacteria in each reaction mixture were counted by plating 50 μl onto nutrient agar plates, followed by overnight incubation at 37°C. Controls consisted of nonopsonized bacteria and bacteria without neutrophils.

**IgG transcytosis**

Twelve-millimeter polycarbonate Transwell filters (0.4 μm pore size; Costar/Corning) were inoculated with 3 × 10^5 human choriocarcinoma cells (JAR), grown overnight to confluence, and washed with PBS; medium was replaced with 1.5 ml fresh medium basolaterally and 0.5 ml apically (IMDM [pH 7.4], supplemented with L-glutamine, 10% FCS, and penicillin/streptomycin). Mixtures of IgG contained 125 pg/ml streptavidin-HRP (Protosyn) to assess background transport. Apical to basolateral transport was replaced with 1.5 ml fresh medium basolaterally and 0.5 ml apically. Supernatant of sequenced FLIPr-like was ad- ded to the reaction. The peritoneal cavity was lavaged with 6 ml ice-cold PBS/Rs. Different recombinant soluble FcγR isoforms and block IgG binding

**Results**

Identification of a putative staphylococcal FcγRIIa inhibitor

To investigate potentially secreted staphylococcal FcγRIIa antagonists, culture supernatants of various clinical and laboratory *S. aureus* strains were screened for their ability to competitively inhibit specific neutrophil FcγRIIa staining by flow cytometry. The anti-FcγRII a mAb clone 7.3 was used because of its specificity for an epitope in the IgG binding site of the receptor (26). Several staphylococcal supernatants inhibited mAb 7.3 binding to FcγRIIa on neutrophils (data not shown). Supernatant of sequenced *S. aureus* strain N315 was among the most potent (Fig. 1A) and was selected for purification of the inhibitor compound. Using a chip coated with soluble FcγRIIa, with mass detection in a surface-enhanced laser desorption/ionization time-of-flight system, identified a 12.3-kDa mass peak in the semipurified staphylococcal supernatant (Fig. 1B). Affinity isolation on magnetic beads, coupled with soluble FcγRIIa, was used to obtain a final active preparation containing one single nearly homogeneous protein band ~13 kDa on SDSPAGE (Fig. 1C). Gel extraction and subsequent mass spectrometry identified the protein as FLIPr. FLIPr, a secreted staphylococcal protein of 105 aa with a mass of 12.3 kDa, is a potent inhibitor of the chemotaxis receptor FPR2 (formerly annotated as formyl peptide receptor-like 1 or FPR1L) (21). Initially, FLIPr was discovered based on its 49% homology with CHIPS (20).

To confirm that FLIPr was the active FcγRIIa inhibitory compound present in the staphylococcal supernatant, recombinant FLIPr was tested for its effect on neutrophil FcγRIIa staining. Like the supernatant, recombinant FLIPr inhibited binding of mAb 7.3 to neutrophils, with an IC50 of 48.4 ng/ml (range, 33.5–69.8 ng/ml) (Fig. 1D). The recombinant homolog of FLIPr, FLIPr-like (104 aa with ~72% identity) (22), was ~10-fold more active in FcγRIIa blocking compared with FLIPr, with an IC50 of 4.9 ng/ml (range, 3.7–6.5 ng/ml). The related staphylococcal protein CHIPS did not affect FcγRIIa staining. Because of its structural and functional similarities, CHIPS was used as control protein in further experiments.

**FLIPr and FLIPr-like bind different FcγR isoforms and block IgG binding**

A capture ELISA was performed to confirm that FLIPr and FLIPr-like directly interact with FcγRIIa, as well as to analyze the specificity for other FcγR isoforms. Different recombinant soluble FcγRs and their polymeric isoforms containing a polystyidene tag (Ia, Ia-H131 and Ia-R131, Ibb, Ibb-V158 and Ibb-F158, and Iibb-NA1 and Iibb-NA2) were evaluated for their relative binding to the coated
staphylococcal proteins FLIPr, FLIPr-like, and CHIPS. Both FLIPr and FLIPr-like bound to soluble FcγRIIa in ELISA (Fig. 2B, 2C). In contrast to FLIPr-like, FLIPr demonstrated differential binding to the two allelic variants of FcγRIIa that differ at position 131, which is located in the ligand-binding region and is crucial for IgG binding (15). FLIPr bound preferentially to the high-affinity isoform FcγRIIa-H131, whereas binding to the low-affinity R131 isoform was almost negligible. The highly homologous inhibitory receptor FcγRIIb, whose ectodomain differs at 10 positions from FcγRIIa (11 for the FcγRIIa-H131 variant) (27), including two (or three for FcγRIIa-H131) amino acids involved in IgG binding, was bound equally well by FLIPr and FLIPr-like (Fig. 2D). With regard to the other FcγR subclasses, FLIPr did not bind significantly to FcγR class I and III receptors (Fig. 2A, 2E–H) and could be considered class II specific. In contrast, FLIPr-like bound to FcγRIIa (Fig. 2A) and differentially to FcγRIIIa-V158 and FcγRIIIa-F158, an amino acid also involved in IgG binding (Fig. 2E, 2F). The two isoforms of FcγRIIib, differing by six ectodomain amino acids from FcγRIIIa-F158 (and 5 aa from FcγRIIIa-V158), of which two are located in IgG-binding regions (23, 24, 28), were both bound by FLIPr-like, but only minimally in the case of FcγRIIIb-NA1. CHIPS did not bind to any of the soluble FcγRs. Furthermore, none of the staphylococcal proteins bound to soluble FcεRI and FcαRI, the receptors for IgE and IgA, respectively, in ELISA (data not shown). Because all FcγRs are composed of Ig-like domains strongly resembling the domains of IgG, we used ELISA to test whether FLIPr and FLIPr-like bound to IgG molecules, as well. In contrast to Mac-1, a streptococcal FcγR-binding protein that does bind IgG (29), neither FLIPr nor FLIPr-like bound IgG in ELISA (data not shown).

To investigate whether FLIPr and FLIPr-like interfere with FcγR–IgG interactions, an inhibition ELISA was performed. FcγRs were incubated with staphylococcal proteins, and relative

**FIGURE 1.** Identification of FLIPr as the secreted staphylococcal protein that inhibits FcγRIIa staining. (A) Inhibition of human neutrophil staining of FcγRIIa by serial dilutions of the supernatant from *S. aureus* strain N315. (B and C) Analysis of the protein(s) purified from *S. aureus* N315 culture supernatant using immobilized soluble FcγRIIa. (B) Surface-enhanced laser desorption/ionization time-of-flight profile of enriched active supernatant fraction on noncoated IMAC chip (upper panel) and IMAC chip coated with soluble FcγRIIa (lower panel). Mass of soluble FcγRIIa and the major specific peak are indicated. (C) Silver nitrate staining of the same active fraction captured with FcγRIIa-coated magnetic Talon beads resolved by SDS-PAGE. (D) Inhibition of neutrophil FcγRIIa staining by serial dilutions of the purified recombinant staphylococcal proteins FLIPr, FLIPr-like, and CHIPS. FcγRIIa staining of antagonist-treated cells by mAb 7.3 (A, D) is expressed relative to the fluorescence value of buffer-treated cells (mean ± SEM of three experiments).
binding of recombinant human IgG1 to FcyR was determined. FLIPr and FLIPr-like efficiently prevented binding of human IgG1 to the FcyRs (Fig. 3), in accordance with their specific binding. The control protein CHIPS did not inhibit FcyR–IgG binding. In summary, FLIPr seems to be class II restricted and preferentially inhibiting IgG binding to FcyRIIa-H131 (Fig. 3B), the predominant receptor in phagocytosis. In contrast, FLIPr-like displays a broader profile and inhibits FcyR–IgG interactions for all FcyRs, with the exception of FcyRIIIb (Fig. 3G).

**FLIPr and FLIPr-like bind to human FcyR-expressing leukocytes and recognize epitopes involved in ligand binding**

In earlier studies, we demonstrated concentration-dependent binding of FLIPrFITC and FLIPr-likeFITC to neutrophils and CD14+ monocytes (21, 22) (Supplemental Fig. 1A, 1B), cells known to express both FPRs and FcyRs. The binding of FLIPr-likeFITC could be inhibited by high-affinity FPR1 ligand, peptide WKYMVM, but only partially, suggesting unrecognized residual FcyR staining. Furthermore, FLIPrFITC and FLIPr-likeFITC bound to FPR but FcyR-expressing CD19+ B cells and CD3−/CD56+ NK cells (Supplemental Fig. 1D, 1E). Neither protein bound to FPR and FcyR−CD3+ T cells (Supplemental Fig. 1C).

To further investigate the binding site of FLIPr and FLIPr-like on the FcyR, additional mAb-competition studies were performed. In addition to anti-FcyRII mAb 7.3, FLIPr and FLIPr-like inhibited neutrophil binding of the more FcyRIIa-specific mAb IV.3, which also recognizes D2 epitopes involved in IgG interactions (26) (Fig. 4A, 4B). In contrast, neutrophil staining with the IgG-blocking anti-FcyRII mAb FLI8.26, which binds critical, although distinct, epitopes in D2 (26), was not affected by FLIPr and FLIPr-like (Fig. 4C). Similar patterns of competitive inhibition of FcyRII mAb staining by FLIPr and FLIPr-like were observed on human

**FIGURE 2.** FLIPr and FLIPr-like bind to different FcyR isoforms. Comparison of His-tagged soluble FcyRIa (A), FcyRIII isoforms (IIa-H131, Ila-R131 and Iib) (B–D), and FcyRIII isoforms (IIa-V158, IIIa-F158, Iib-NA1, and Iib-NA2) (E–H) for binding to FLIPr, FLIPr-like, and CHIPS by ELISA. Data are mean ± SEM of three independent experiments.

**FIGURE 3.** FLIPr and FLIPr-like compete for IgG1 ligand binding. Comparison of His-tagged soluble FcyRIa (A), FcyRIII isoforms (IIa-H131, Ila-R131, and Iib) (B–D), and FcyRIII isoforms (IIa-V158, IIIa-F158, Iib-NA1, and Iib-NA2) (E–H) for ligand inhibition by ELISA. Inhibition of human IgG1 binding to plates coated with FcyR in the presence of serial dilutions of FLIPr, FLIPr-like, and CHIPS is expressed as the percentage of buffer IgG1 binding. Data are mean ± SEM of three independent experiments.
monocytes and CD19+ B cells (Supplemental Fig. 2A–F). However, on B cells (expressing only FcyRIIb), binding of anti-FcyRII mAb FLI8.26 was inhibited by FLIPr (Supplemental Fig. 2C). Monocyte staining with the partially blocking anti-FcyRII mAb 10.1 (30, 31) was not affected by FLIPr or FLIPr-like (Supplemental Fig. 2G). Because FLIPr-like was shown to bind and block soluble FcyRIIa in ELISA, competitive inhibition of anti-FcyRIII mAb 3G8-mediated staining of human NK cells expressing FcyRIIIa (and FcyRIIc for some individuals) was analyzed. mAb clone 3G8, which does not distinguish between FcyRIIa and FcyRIIib, binds to the putative FG loop within D2 (32), the major binding site for IgG. FLIPr-like efficiently prevented the mAb 3G8-mediated FcyRIIIa staining on NK cells (Fig. 4D). In contrast to the ELISA results, FLIPr inhibited this mAb 3G8-mediated NK cell staining even more strongly. NK cell staining with the FcyRIII-specific mAb clone B73.1, which recognizes epitopes distinct from the IgG binding site restricted to the membrane distal domain 1 (D1) (32), was not inhibited by the staphylococcal proteins (Fig. 4E). Both FLIPr and FLIPr-like demonstrated inhibition of anti-FcyRII mAb 3G8-mediated staining of neutrophils (expressing FcyRIIIb and FcyRIIa) (Fig. 4F); this was in partial contrast to the ELISA results that indicated no binding of FLIPr to FcyRIIib. Binding of an IgA-blocking anti-FcεR mAb to monocytes and neutrophils was not affected by FLIPr or FLIPr-like (Supplemental Fig. 2H, 2I). The control protein CHIPS did not interfere with leukocyte anti-FcyR mAb binding in any of the experiments. Altogether, FLIPr and FLIPr-like inhibited anti-FcyR mAb from binding to epitopes involved in FcyR–IgG interactions, indicating that the staphylococcal proteins bind FcyRs in or near their IgG Fc-binding regions within D2.

Evasion of FcyR-mediated phagocytosis and killing

To test whether FLIPr and FLIPr-like could inhibit FcyR-mediated effector functions, we performed phagocytosis experiments. Fluorescently labeled staphylococci were opsonized with purified human IgG, complement-inactivated human pooled serum, or untreated human pooled serum with intact complement activity. Human neutrophils were incubated with the staphylococcal proteins at a concentration of 3 μg/ml, and phagocytosis was determined at increasing opsonin concentrations. Both FLIPr and FLIPr-like efficiently inhibited FcyR-mediated phagocytosis of staphylococci opsonized with purified IgG (Fig. 5A). Staphylococci opsonized with complement-inactivated serum were also fully protected from phagocytosis by FLIPr-like, whereas FLIPr did so less strongly (Fig 5B). In the presence of complement, the inhibitory effects of FLIPr and FLIPr-like on phagocytosis were only observed at the lower serum concentrations of 0.5 and 0.25% (Fig. 5C). The inhibitory proteins were both effective after a short preincubation with the neutrophils and when serum (or IgG), inhibitory protein, cells, and, finally, bacteria were immediately mixed together. Titration of staphylococcal protein concentrations demonstrated the 2-fold (2.3 ± 0.4) higher potency of FLIPr-like, which up to 0.75 μg/ml completely inhibited FcyR-mediated neutrophil phagocytosis in the presence of complement-inactivated serum (Supplemental Fig. 3). The reduced neutrophil bacterial uptake observed in the phagocytosis experiments was reflected by an increased S. aureus survival in bacterial-killing experiments in the presence of FLIPr and FLIPr-like (Fig. 5D). FLIPr-like did not interfere with the function of FcRn, the structurally distinct, other IgGR involved in phagocytosis (Fig. 5E).

Inhibition of FcyR-mediated tumor cell killing

Next, we tested whether FLIPr and FLIPr-like also inhibited additional FcyR-dependent cellular responses, such as ADCC, using specific human mAbs against tumor targets. Neutrophil FcyRIIa-mediated ADCC through panitumumab (IgG2; Fig. 6A) and cetuximab (IgG1; Fig. 6B), both directed against the epidermal growth factor receptor, were almost completely prevented by 3 μg/ml FLIPr and FLIPr-like, reaching the level of lysis in the absence of sensitizing mAb (no Ab). In agreement with ELISA and competitive mAb-staining data, human IgA-mediated neutrophil FcεRI-dependent ADCC was not affected by the staphylococcal FcyR inhibitors (Fig. 6C). NK cell FcyRIIIa (and FcyRIIc in some individuals)-mediated ADCC via IgG1 was inhibited by FLIPr-
like, but not by FLIPr (Fig. 6D), in accordance with their selective binding preferences to FcγRII and FcγRIII in ELISA (Fig. 2). CHIPS did not interfere with neutrophil- or NK cell–mediated ADCC. Taken together, FLIPr and FLIPr-like effectively inhibited phagocyte activation in vitro by preventing engagement and cross-linking of FcγR by IgG opsonized to target cells.

**FLIPr-like prevents Arthus reaction in mice**

To investigate the in vivo potency of the staphylococcal FcγR antagonists, the immune complex–mediated passive Arthus reaction model in mice was used (33). In this model, i.p. generation of immune complexes initiates a type III hypersensitivity reaction by FcγR-dependent influx of neutrophils. We confirmed that both proteins inhibited the murine FcγR-mediated phagocytosis using the mouse macrophage cell line P388D1. Similar to human neutrophils, mouse phagocytes were inhibited by FLIPr and FLIPr-like (Fig. 7A). Furthermore, FLIPr and FLIPr-like effectively inhibited phagocyte activation in vitro by preventing engagement and cross-linking of FcγR by IgG opsonized to target cells.

**Discussion**

In this article, we describe a previously unrecognized role for the two homologous staphylococcal immune evasion proteins FLIPr and FLIPr-like. They bind FcγR and abrogate their IgG-recognizing function. FcγR-bearing immune cells that are involved in crucial antibacterial defense mechanisms lose their capacity to specifically recognize pathogenic targets. *S. aureus* demonstrates a novel strategy to evade host immunity. Mac-2 is an FcγR-binding protein secreted by *Streptococcus pyogenes*. It bound soluble FcγRII and FcγRIII and competed with IgG binding (29), as well as prevented the generation of reactive oxygen species by opsonized latex beads. However, in a whole-blood survival assay of *S. pyogenes*, only Mac-2 with intact IgG endopeptidase activity facilitated bacterial survival (35). To our knowledge, no other bacterial FcγR antagonist has been described; therefore, this is the first study to demonstrate a bacterial FcγR-binding protein...
that inhibits FcγR-mediated effector functions in vitro, as well as in vivo.

FLIPr and FLIPr-like are secreted proteins encoded by genes that cluster with other immune-evasion molecules, including SCIN, Ebf, and Ecb, in the immune evasion cluster II (7). The genomes of cluster with other immune-evasion molecules, including SCIN, in vivo.

logs is essential to FLIPr or FLIPr-like, suggesting that the function of these homo-

ment of two (A–C) or triplicates of one representative exper-

iment of two (D). Mean percentage (± SEM) of neutrophil-mediated lysis

of A1207 coated with IgG2a was 49.8% ± 6.4 (A), with IgG1 54.1% ± 7.6 (B), and with IgA 97.9% ± 10.5 (C). NK cell-mediated lysis of A1207 coated with IgG1 was 26.2% ± 0.2 (D). *p < 0.05, versus mAb-dependent lysis by buffer-treated cells, two-tailed Student t test.

that signaling of FcγRIIib might involve FPR and that activation

of FcγRIIib on human neutrophils modulates fMLF binding and migration (41). It is not known whether FLIPr and FLIPr-like can bind to both FPR2 and FcγR on phagocytes simultaneously, thereby inducing colocalization.

Despite their high degree of homology, FLIPr was almost exclusively restricted to class II receptors, with a preference for the high-affinity polymorphic allotype of the receptor FcγRIIa-H131. FLIPr-like bound to most FcγR isoforms tested, including FcγRI, which is expressed on monocytes, macrophages, and transiently on neutrophils during infection (42). FcγRIIIa is the predominant receptor in ADCC by NK cells, although it is involved in phago-

cytosis by mononuclear cells, as well. FcγRIIIa is also solely bound by FLIPr-like.

All FcγRs have similar modes of binding to IgG via sites that are structurally conserved (15, 43). X-ray crystallography, together with mutagenesis studies and homology modeling, demonstrated that the FcγR surface, which interacts with IgG, is primarily located in the extracellular D2 of all FcγRs, including FcγRI, which contains three (instead of two) extracellular domains. The FcγR binding site on IgG is primarily formed by residues in the lower hinge region and three segments of the CH2 domain. The fact that FLIPr and FLIPr-like bind to the FcγR, as well as antagonize FcγR–IgG interactions, was already indicated by the fact that both proteins competitively inhibited neutrophil staining with mAb clone 7.3, which was characterized as recognizing epitopes within the IgG binding site of FcγRII (26). Subsequently, other mAbs, binding to distinct epitopes in or near the IgG binding site of both

FIGURE 6. FLIPr and FLIPr-like inhibit Ab-dependent cellular cyto-
toxicity of tumor cells. Neutrophil-mediated (A–C) and NK cell-mediated (D) killing of IgG2 (A), IgG1 (B, D), or IgA (C) mAb-coated glioblastoma cell line A1207 in the presence of 3 μg/ml FLIPr, FLIPr-like, or CHIPS. No Ab is target cell lysis without mAb coating. Data are the mean (± SEM) relative lysis compared with buffer-treated cells of two to four in-
dependent experiments (A–C) or triplicates of one representative experi-

ine by FLIPr and FLIPr-like, in the immune evasion cluster II (7). The genomes of

that inhibits FcγR-mediated effector functions in vitro, as well as in vivo.

FIGURE 7. FLIPr and FLIPr-like inhibit FcγR-mediated phagocytosis by mouse macrophages and prevent the development of Arthus reaction in mice. (A) Phagocytosis of fluorescent staphylococci opsonized with purified human IgG by the mouse macrophage cell line P388D1 in the presence of 3 μg/ml FLIPr or FLIPr-like. Data are percentage of cells containing fluorescent bacteria. (B) Induction of the Arthus reaction in BALB/c mice treated with FLIPr-like; the i.p. influx of neutrophils was elicited by the injection of OVA and anti-OVA Ab. Data are the mean ± SEM of two experiments (A) and of eight mice from two independent experiments (B). *p < 0.05, versus Arthus reaction in buffer-treated mice, ANOVA.
FcγRIIa (mAb IV.3) and FcγRIII (mAb 3G8), also were inhibited. mAb clone B73.1, which binds epitopes on D1 outside of the IgG-ligand binding domain of FcγRIII, was not inhibited by FLIPr or FLIPr-like on NK cells. The lack of inhibition of ligand-blocking anti-FcγRII mAb FLI8.26 can be explained by the fact that this mAb is a member of another cluster (II) of mAb that binds the receptor via distinct D2 epitopes. The inhibition of anti-FcγRIII mAb 3G8 from binding to neutrophils and NK cells by FLIPr, without any binding to class III receptors by ELISA, is difficult to explain. It may be that this mAb (mouse IgG1) binds with its Fc tail to FcγRIIc, also expressed by NK cells (donor dependently) (44). This discrepancy correlates with binding of fluorescent FLIPs to NK cells that do not express FPR2, the other FLIPr-binding surface receptor (21). A second indication that both proteins bind to or near the IgG-recognizing region of the FcγR was reflected in the fact that the binding of FLIPr and FLIPr-like was influenced by single polymorphic differences in the FcγR ectodomain IgG-binding amino acids (FcγRIIa-131 and FcγRIIa-158). The ELISA data with regard to recombinant expressible soluble receptor variants show a good correlation between protein binding and functional inhibition of IgG1–ligand interactions. However, a disadvantage is the variation in affinity between the FcγRs for monomeric IgG (45), although the IgG1 concentration was optimized for each FcγR class.

The most important FcγR-mediated immune response in the battle against S. aureus infection is phagocytosis and subsequent killing. FcγRIIa-mediated phagocytosis of IgG-opsonized bacteria by human neutrophils was efficiently prevented by FLIPr and FLIPr-like. FLIPr-like inhibition was stronger than that of FLIPr, which could be due, in part, to the (unknown) variation in donor FcγRIIa genotype. FLIPr is a more efficient FcγRIIa-H131 inhibitor. FcγR polymorphisms have been associated with susceptibility to or severity of autoimmune and infectious disease (16), van Mirre et al. (46) showed that the ratio of activating FcγRIIa/ inhibitory FcγRIIb mRNA in neutrophils varies among individuals, is associated with FcγR2b promoter haplotypes, and is accompanied by differences in the responsiveness of these cells to IgG complexes. However, the same investigators showed that, in contrast to the much smaller IgG dimers and aggregates, no significant difference was observed for phagocytosis of IgG-opsonized FITC-labeled S. aureus.

The inhibition of phagocytosis in serum-containing active complement was only observed at low serum concentrations. This could indicate that, under conditions with sufficient serum (>1%), the phagocytic process operates mainly via the complement receptors, and only at low serum concentrations is the process dependent on FcγR. Therefore, one could argue that these proteins contribute minimally to the immune-evasion arsenal of staphylococci. However, the relative amounts of individual complement components and IgG levels in the interstitial tissue outside of the blood vessels are unknown and could be very different, consequently skewing toward FcγR dependency. In addition, S. aureus secretes several potent inhibitors of the complement system (5). In contrast to SpA, SSL10, and Sbi, which bind to IgG and inhibit phagocytosis, FLIPr and FLIPr-like directly target the relevant receptor of the phagocytosis process.

The ability of FLIPr and FLIPr-like to block FcγR-mediated functions was also shown in the ADCC experiments that used well-defined monoclonal human subclass IgG molecules to inhibit tumor cell killing. Both FLIPr and FLIPr-like completely blocked neutrophil-mediated ADCC without interfering with the IgA-dependent killing of the same tumor cell target. The NK cell FcγRIIa-mediated ADCC was completely abolished by FLIPr-like, whereas FLIPr was ineffective. This correlates with the ELISA data demonstrating lack of binding of FLIPr to the soluble extracellular part of FcγRIIa. In addition to its role in antitumor immunity, ADCC is an important immune response against virally infected cells. Although speculative, by inhibiting ADCC and consequently suppressing local antiviral immunity, FLIPr-like might play a pathogenic role in the observed coinfections of S. aureus and influenza virus (47).

In vitro, FLIPr-like proved to be an effective inhibitor of mouse FcγR-mediated phagocytosis. Mouse and human FcγR are structurally very similar and exhibit identical modes of interaction with IgG (15). FcγRs play a central role in the pathogenesis of immune complex–based inflammation and disease, such as Ab-induced arthritis, immune anemia, and immune complex glomerulonephritis (25, 48). The reverse passive Arthus reaction in mice is a well-established in vivo model of immune complex–mediated inflammatory disease that relies on C5a/C5aR and the activating FcγR (33, 49). FcγR-γ-chain−/− mice, as well as C5aR−/− mice, exhibited abolished neutrophil influx in the peritoneum (25). Intervention with C5 activation by the staphylococcal protein Ecb or SSL7 also completely inhibited neutrophil accumulation in the peritoneum (7, 50). In this study, we demonstrate that administration of FLIPr-like blocked neutrophil influx in the peritoneum by inhibition of the other arm of this inflammatory model.

S. aureus secretes a set of two homologous proteins that effectively bind and neutralize FcγR-mediated effector mechanisms. Because these proteins bind several FcγR isoforms expressed on different leukocytes, these proteins are a valuable tool in dissecting the general contribution of FcγR to inflammation and infection. Whether FLIPr and FLIPr-like contribute to the virulence of S. aureus needs to be addressed in an appropriate in vivo infection model. Effective IgG-mediated phagocytosis targeting FcγR in mice is hampered by the lack of sufficient levels of naturally occurring anti–S. aureus Abs, as shown for several surface expressed and secreted proteins by multiplex assay (51) and proteome array (52). However, the purified proteins proved to be effective as an FcγR inhibitor in mice.

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Disclosures

The authors have no financial conflicts of interest.

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