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# Sticky connections: extracellular matrix protein recognition and integrin-mediated cellular invasion by *Staphylococcus aureus*

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*Staphylococcus aureus* is a leading cause of hospital-acquired and often persistent infections. A key feature of pathogenic *S. aureus* is the expression of an array of extracellular matrix-binding proteins. In particular, the fibronectin-binding proteins FnBP-A and FnBP-B afford the pathogen the ability to connect to cellular integrins and to trigger internalization into host cells. Recent work has highlighted the role of host cell invasion in the pathogenesis of *S. aureus*, the structure–function relationship of FnBPs, and the host factors required to allow bacterial uptake. Understanding the invasive capacity of *S. aureus* should open up new avenues to control this microorganism in diverse disease settings.

## Addresses

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## Introduction

*Staphylococcus aureus* is an extremely versatile pathogen, causing a wide spectrum of diseases ranging from mild, superficial skin infections to life-threatening septicaemia, endocarditis and pneumonia [1]. Currently, *S. aureus* is one of the leading nosocomial pathogens in hospitals around the globe. In particular, the extraordinary capacity of this microorganism to acquire antibiotic resistance determinants is regarded as a major reason for the increase of nosocomial infections caused by *S. aureus*. The pathogen has genes that encode several virulence factors, the expression of which is controlled by a complex regulatory network including the quorum-sensing *agr* system, transcriptional regulators of the Sar family, the two-component regulatory systems ArlRS and SaeRS, and the alternative sigma factor SigB [2]. During *in vitro* cultivation, bacterial surface-associated virulence factors are preferentially expressed in the logarithmic growth phase,

whereas secreted virulence factors are released in the post-logarithmic phase. It is assumed that this biphasic expression of virulence factors orchestrates the infection process. Initially, surface-bound adhesins recognize host surface structures, facilitating colonization, which is then followed by further growth of the microbes and secretion of toxins and enzymes, such as hemolytic toxins ( $\alpha$ -,  $\beta$ -,  $\gamma$ - and  $\delta$ -toxin), leucotoxins (e.g. Panton-Valentine leukocidin and LukFS), enterotoxins (e.g. EntB), toxic shock syndrome toxin-1, several proteases [e.g. metalloprotease aureolysin (Aur), serine proteases (SspA) and cysteine protease (SspB)], and lipases (e.g. Geh). Although in most cases the infection remains localized, the bacteria can also spread into deeper tissues and, importantly, are able to cause chronic diseases [1,3,4].

A characteristic feature of pathogenic *S. aureus* is the presence of adhesins that bind host extracellular-matrix (ECM) proteins and serum components. These proteins either remain associated with the surface of the bacteria or are released into the culture supernatant. Accordingly, the former have been collectively termed MSCRAMMs (microbial surface components recognizing adhesive matrix molecules), whereas the latter are referred to as SERAMs (secretable expanded repertoire adhesive molecules). Both types of protein are involved in colonizing host tissues and in the evasion of host immune response (Table 1) [5,6]. However, the contribution of isolated MSCRAMMs or SERAMs to the infection process *in vivo*, as analysed by experimental models, is often not clear. This ambiguity might be caused by the functional redundancy seen, for example, in the case of fibrinogen binding, where *S. aureus* strains express at least seven proteins with the ability to associate with this serum component (Table 1). Moreover, individual MSCRAMMs or SERAMs might only be important in particular pathological conditions that are not fully addressed by current experimental models.

One of the pathogenic properties of *S. aureus* that has been difficult to assess *in vivo* is the role of host-cell invasion during infection. Such behaviour might be necessary for the pathogen to escape from the host immune surveillance and the antibiotic pressure and might also contribute to the persistence of the microorganism. Recent *in vitro* studies have provided convincing evidence that *S. aureus* can invade non-professional phagocytes, including epithelial and endothelial cells, fibroblasts, osteoblasts, keratinocytes and kidney cells [7–11]. The molecular events guiding the uptake of *S. aureus* by host cells were the focus of numerous investigations

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Table 1

Major *S. aureus* surface proteins and secreted proteins that confer adherence to extracellular matrix components and serum proteins.

Abbreviation	Full protein name	Experimentally demonstrated ligands	Reference
<b>MSCRAMM</b>			
FnBP-A	Fibronectin binding protein A	Fibronectin Fibrinogen Elastin	[37–39]
FnBP-B	Fibronectin binding protein B	Fibronectin Elastin	[37,39]
ClfA	Clumping factor A	Fibrinogen $\gamma$ -chain Fibrin	[40,41]
ClfB	Clumping factor B	Fibrinogen $\alpha$ - and $\beta$ -chain Type I cyokeratin 10	[42–44]
Cna	Collagen binding protein	Collagen	[45]
EbpS	Elastin binding protein	Elastin	[46]
Spa	Protein A	Von Willebrand factor	[47]
Bbp	Bone sialoprotein binding protein	Bone sialoprotein	[48]
EbhAB	Extracellular matrix binding protein	Fibronectin	[49]
<b>SERAM</b>			
Eap	Extracellular adherence protein	Fibrinogen $\alpha$ -chain Fibronectin Prothrombin	[50]
Efb	Extracellular fibrinogen binding protein	Fibrinogen $\alpha$ -chain C3b	[51–52]
Emp	Extracellular matrix binding protein	Fibronectin Fibrinogen Vitronectin	[53]
vWbp	Von Willebrand factor binding protein	Von Willebrand factor	[54]
Coa	Coagulase	Prothrombin Fibrinogen	[55,56]

during recent years. Interestingly, and despite the presence of numerous adhesins in this microbe, the fibronectin-binding proteins A and B (FnBP-A and FnBP-B) were identified as major factors in initiating the internalization of *S. aureus*.

### ***In vivo* relevance of fibronectin recognition by *S. aureus***

FnBP expression and fibronectin (Fn) recognition are found in most clinical isolates of *S. aureus* [12]. Furthermore, evidence from several experimental models suggests that interfering with the ability of the bacteria to associate with Fn attenuates *S. aureus* virulence (for review, see [13]). Importantly, earlier studies did not address if the full pathogenic potential of *S. aureus* requires Fn recognition per se or if it depends on FnBP–Fn-mediated invasion into host cells. However, recent investigations suggest that *S. aureus* is indeed an invasive microorganism in different diseases settings and that FnBPs play a major role in this. For example, Brouillette *et al.* [14] detected the presence of intracellular *S. aureus*, when infecting the mouse mammary gland with this pathogen in an experimental model of mastitis. Importantly, an *fnbA/fnbB* double mutant was unable to colonize the lactating gland [14]. A more complex picture emerges from the study of Que *et al.* [15<sup>••</sup>], who investigated the ability of *S. aureus* to colonize damaged rat

heart valves. In this experimental endocarditis model, FnBP-expressing bacteria were detected in the fibrin deposits on the damaged tissue, but also within neighboring endothelial cells, by immunohistochemistry and electron microscopy. Furthermore, the bacteria spread to other organs and were re-isolated in high numbers from the spleen. The authors also employed recombinant *Lactococcus lactis* strains that expressed FnBP-A or derivatives thereof. This heterologous system allowed them to investigate which functional domains of FnBP are required to confer a virulent phenotype to non-pathogenic *L. lactis*. Interestingly, the fibrinogen-binding domain of FnBP or additional expression of Clumping factor A (ClfA) were essential to allow the colonization of fibrin deposits in the heart (Table 1). However, only an intact Fn-binding site of FnBP was necessary the infection to proceed and spread to the endothelium or other organs such as the spleen [15<sup>••</sup>]. These results highlight the complex interplay between different virulence factors, or even between distinct domains within single proteins; they also clearly provide *in vivo* proof that FnBP expression is sufficient to confer an invasive phenotype to non-pathogenic *L. lactis* [15<sup>••</sup>]. Additional clinical evidence that cell invasion by *S. aureus* occurs *in vivo* comes from a recent study in which intracellular *S. aureus* was detected in the endonasal mucosa of patients suffering from recurrent rhino-sinusitis [16<sup>•</sup>]. These studies clearly

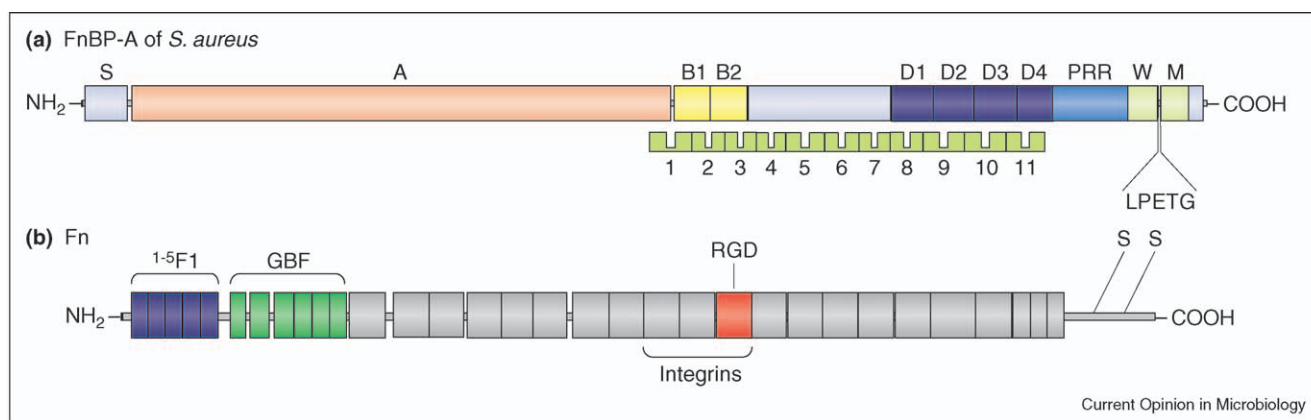
underline the importance of *S. aureus* host cell invasion during infection *in vivo*. Moreover, these findings support the concept that an ‘intracellular life-style’ protects *S. aureus* from attacks by the immune system and shelters it from the action of antibiotics. An invasive phenotype might not only create a reservoir of these pathogens in chronic infections, but also act as a prerequisite for invasive infections, such as sepsis, or the formation of metastatic abscesses in other organs.

### Structure-function relationship of *S. aureus* fibronectin-binding proteins

Most strains of *S. aureus* harbor two closely related genes, *fnbA* and *fnbB*, that are located in tandem on the chromosome. The proteins encoded by these two genes, FnBP-A and FnBP-B, are anchored by an LPXTG motif to the cell wall of *S. aureus* and therefore belong to the group of MSCRAMMs. Both FnBPs are crucial for invasion of eukaryotic cell types by *S. aureus* and mutants lacking FnBP-A and FnBP-B are severely impaired in host-cell invasion [11,17,18]. Moreover, heterologous expression of FnBPs in non-invasive gram-positive bacteria such as *L. lactis* or *S. carnosus*, as well as the coating of inert particles with FnBP-A, is sufficient to induce uptake by host cells [15,19]. Binding of Fn by FnBPs is crucial for the invasion process, as Fn serves as a bridging molecule that links FnBP, expressed by *S. aureus*, with integrin  $\alpha_5\beta_1$ , the principal Fn receptor on the surface of host cells [7,11,20]. Subsequently, the bacteria are engulfed by an active cellular process, which does not require further bacterial factors, as heat killed bacteria or FnBP-coated inert particles are also ingested [19]. The crucial role of integrin  $\alpha_5\beta_1$  for the uptake process is highlighted by the fact that cells lacking the integrin  $\beta_1$  subunit do not internalize *S. aureus* in significant numbers [20,21].

Recent work has unraveled the structural details mediating the association of FnBP with Fn [22,23\*]. Importantly, the crystal structure of Fn in complex with the Fn-binding domain of FnBP from *Streptococcus dysgalactiae*, a domain that shows high homology to the Fn-binding domains of *S. aureus* FnBPs, highlights the extended binding interface between the two molecules that results in a model of extended tandem  $\beta$ -zipper formation [22]. Both FnBPs and Fn have a pronounced modular architecture (Figure 1). FnBPs of *S. aureus* are composed of an ~500 amino acid long N-terminal A domain that binds to fibrinogen, followed by a B-region of two 30-amino acid repeats, a short spacer termed C, and a D-repeat domain containing three ligand-binding repeats (D1–D3) and a shorter fourth repeat (for review, see [24]). Early studies suggested that only the D-repeats confer binding to Fn; however, further investigations revealed that the B-region also contains repetitive sequence units that mediate Fn binding [10,22,23\*]. The ligand-binding regions of FnBPs interact specifically with a 29 kDa N-terminal region of Fn encompassing the so-called Fn type I repeats (F1 region). The F1 region contains five sequential repeats: <sup>1</sup>F1–<sup>5</sup>F1. Each module is composed of five  $\beta$ -strands consisting of a double-stranded antiparallel  $\beta$ -sheet (strands A and B) and a triple-stranded antiparallel  $\beta$ -sheet (strands C, D and E). Upon association with FnBP, the E-strand within each of these F1 repeats interacts with a  $\beta$ -strand derived from the repetitive regions of the B and D repeats of FnBPs, resulting in an extended tandem  $\beta$ -zipper [12]. Interestingly, the ligand-binding regions of FnBPs lack a folded secondary structure [25]. A conformational change of the protein is induced after binding to Fn. Antibodies, from *S. aureus*-infected patients, that are mainly directed against immunodominant structures within the D-domain of FnBPs, only

Figure 1



Structural organization of *S. aureus* FnBP-A and Fn. (a) For FnBP-A, the location of the traditionally designated A, B and D regions, as well as the newly defined 11 segments (green) containing putative Fn-binding motifs are shown [22]. High affinity binding occurs through interaction of D1–D3 with the F1 modules of Fn. In addition, the seven green segments on the N-terminal side of D-region (1–7) of FnBP-A are also involved in Fn-binding [22,23\*]. The signal peptide (S), the C-terminal proline rich repeat domain (PRR), the cell wall-spanning W region, the membrane-spanning M region, and the Leu-Pro-Glu-Thr-Gly (LPETG) cell wall anchor are also indicated. (b) For Fn, the N-terminal F1-modules (<sup>1-5</sup>F1), the gelatine-binding fragment (GBF) and the integrin-binding RGD sequence are shown (modified from [24]).

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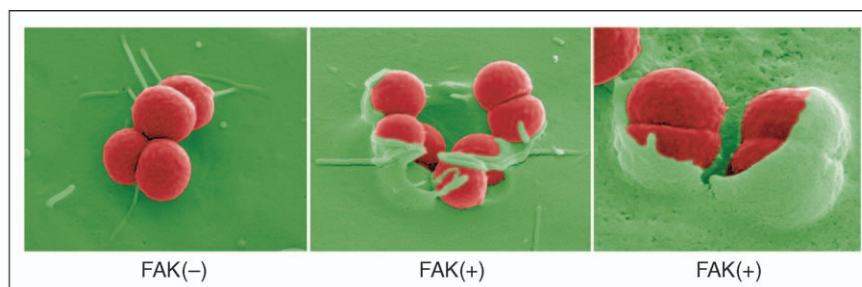
recognize FnBPs once they are bound to their ligand, but do not interfere with Fn binding [26] against immunodominant structures within the D-domain of FnBPs only recognize FnBPs once they are bound to their ligand, but do not interfere with Fn binding [26]. It has been discussed that this feature might be important for the infection process, as antibodies which recognize FnBPs, only after binding to their ligand, cannot block adhesion and subsequent invasion [27]. Whereas the association of Fn with FnBPs is mediated by the N-terminal F1 region, the centrally located 9th and the 10th type III repeats of Fn contain the well-characterized RGD (Arg–Gly–Asp) motif that is crucial for recognition by integrin  $\alpha_5\beta_1$ . These two binding entities of Fn allow the bacteria to employ Fn as a bridging molecule. Thus, Fn bound to FnBPs of *S. aureus* connects the bacteria to the host cell surface by integrin  $\alpha_5\beta_1$ .

### Host cell factors involved in integrin-mediated uptake of *S. aureus*

The engagement and clustering of integrin  $\alpha_5\beta_1$  by Fn-coated bacteria triggers characteristic signaling pathways in the host-cell. A crucial outcome of these signaling events is the reorganization of the actin cytoskeleton, which is essential for integrin-initiated uptake [28<sup>••</sup>,29]. Under physiological conditions, a similar clustering can be observed when integrins are bound to ECM proteins and cluster in ‘focal contacts’ at the cell-ECM interface. Focal contacts integrate the binding of integrins to the ECM with the organization of the intracellular actin cytoskeleton. This is achieved with the help of integrin-associated cytoplasmic proteins that indirectly link integrin cytoplasmic domains with actin filaments. Proteins that are functionally important at focal contact sites include adaptor molecules such as talin, paxillin, vinculin, tensin,  $\alpha$ -actinin and zyxin, as well as signaling molecules such as protein and lipid kinases and phosphatases [30]. With the use of pharmacological inhibitors, protein tyrosine kinases (PTKs) have been shown to be essential for integrin-mediated internalization of staphy-

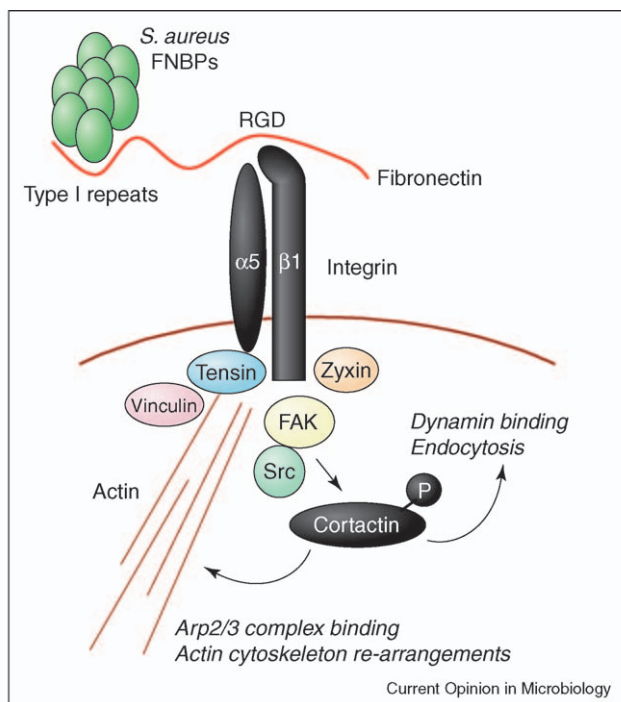
lococci [17]. A more detailed analysis employing dominant-negative mutants, as well as knockout cell lines, has demonstrated a crucial role for PTKs of the Src family [7,31]. These findings already highlight similarities between the physiological engagement of integrins and the bacterial exploitation of integrins as a means to enter cells. Interestingly, integrin  $\alpha_5\beta_1$  has been reported to be predominantly associated with fibrillar adhesions, a subtype of focal contacts involved in the assembly of the extracellular network of Fn fibrils [32]. Another characteristic component of fibrillar adhesions is tensin, an actin-binding adaptor molecule [32]. In addition, signaling enzymes such as PTKs of the Src family and focal adhesion kinase (FAK) have been implicated in the establishment of fibrillar adhesions and the integrin  $\alpha_5\beta_1$ -mediated assembly of a fibrillar Fn network [33,34]. Using confocal laser scanning microscopy, the assembly and composition of host-cell protein complexes at the site of bacterial invasion has been addressed recently. Not surprisingly, f-actin is transiently associated with the invading bacteria [28<sup>••</sup>]. Furthermore, engagement of integrin  $\alpha_5\beta_1$  by Fn-binding staphylococci induces the formation of fibrillar adhesion-like protein complexes at the site of bacterial attachment, as characterized by the recruitment of tensin, FAK, zyxin and vinculin [28<sup>••</sup>]. In addition to Src family PTKs, FAK also seems to be crucial in regulating both the turnover of these bacteria-induced ‘adhesion’ sites and the internalization of integrin-associated *S. aureus*. In particular, FAK tyrosine phosphorylation is increased upon infection, and over-expression of functionally compromised, or dominant negative FAK mutants block the uptake of *S. aureus*. Similarly, FAK-deficient cells are severely impaired in their ability to internalize *S. aureus*. This is reversed upon re-expression of FAK (Figure 2) [28<sup>••</sup>]. FAK deficiency not only abrogates the internalization of bacteria, but also prevents the increase in tyrosine phosphorylation at bacterial attachment sites, suggesting that FAK activation might be one of the initial signaling events upon integrin engagement by *S. aureus* [28<sup>••</sup>].

Figure 2



Lack of *S. aureus* internalization by FAK-deficient cells. FAK-deficient cells [FAK(-)] or FAK re-expressing cells [FAK(+)] were infected for 60 min with *S. aureus* and analyzed by scanning electron microscopy. Pseudocolored images depict bacteria in red and the cell surface in green. Although *S. aureus* is able to firmly attach to FAK-deficient cells, membrane protrusions surrounding the bacteria and membrane invaginations forming below the bacteria are only observed in FAK-expressing cells. Magnification x20 000. (Reproduced with permission from [28<sup>••</sup>]).

Figure 3



Schematic summary of host cell signaling events induced by *S. aureus* engagement of integrin  $\alpha_5\beta_1$ . *S. aureus* associates through FnBP with the type I repeats of host-derived Fn. Fn deposited on the pathogen surface is recognized by the cellular Fn receptor, integrin  $\alpha_5\beta_1$ , that binds to the RGD motif contained within this matrix protein. Bacteria-induced clustering of integrins leads to the local recruitment of structural proteins such as tensin, vinculin and zyxin, as well as signaling enzymes such as Src family PTKs and FAK, to the site of bacterial attachment. The combined activity of FAK and Src results in tyrosine phosphorylation (P) of multiple downstream effectors including cortactin. Cortactin is functionally involved in bacterial internalization most likely by its influence on cytoskeleton rearrangements by the Arp2/3 complex or the regulation of endocytosis by dynamin.

One of the effectors of activated FAK and Src kinases during integrin-mediated internalization has been identified as cortactin, an actin-binding protein [28<sup>••</sup>]. Cortactin can also associate with the Arp2/3 complex to promote actin polymerization, and bind to dynamin-2, a regulator of membrane endocytosis [35,36]. Together, these investigations support the view that Fn-coated staphylococci induce fibrillar adhesion-like contact sites, which are regulated by PTK signaling. The recruitment of this protein complex to cell-attached microbes indirectly links the bacteria-occupied integrins with the intracellular actin cytoskeleton, and mediates the uptake of the pathogen (Figure 3).

## Conclusions

Considerable progress has been made in our understanding of ECM recognition by *S. aureus* and on the role that Fn recognition plays in these bacteria. From several *in*

*vitro* and *in vivo* studies, it appears that Fn-binding is a major virulence trait that enables this pathogen to cause invasive forms of disease and to persist within host cells. Approaches to target FNBPs of *S. aureus* and, thereby, to inhibit binding to Fn *in vivo* are being explored and initial results are encouraging [13]. An advanced molecular understanding of the invasive behavior of *S. aureus* should lead to novel treatment options to control this microorganism in diverse disease settings.

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