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C. R. Biologies 329 (2006) 849–857
COMPTES RENDUS BIOLOGIES
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Immunology / Immunologie

Biofilm-associated proteins

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Received 14 March 2006; accepted after revision 12 July 2006

Available online 21 August 2006

Presented by Gérard Orth & Philippe Sansonetti

Abstract

Although exopolysaccharides are important and often essential compounds of the biofilm matrix, recent evidences suggest that a group of surface proteins plays a leading role during the development of the microbial communities. The first member of this group of proteins was described in a *Staphylococcus aureus* bovine mastitis isolate and was named Bap, for biofilm-associated protein. Later on, other surface proteins homologous to Bap and involved in biofilm development have been described in many gram-positive and gram-negative bacteria. In this review, we have summarized our knowledge about three members of this group of proteins: Bap of *S. aureus*, Esp of *Enterococcus faecalis* and BapA of *Salmonella enterica* ser. Enteritidis. ***To cite this article: C. Latasa et al., C. R. Biologies 329 (2006).***

Keywords: Biofilms; Bap; BapA; Esp; Surface proteins

1. Introduction

Whilst the end of the 19th century and the beginning of the 20th century coincided in microbiology with the recognition of the microbial role in disease and the existence of the immune system, the new millennium will be associated with the availability of the complete bacterial genomes and the recognition that outside the laboratory flask bacteria grow attached to surfaces and embedded in a self-produced extracellular matrix, referred to as biofilms (Fig. 1). Although the synthesis of the matrix is energy consuming, the life in the community protects bacteria against environmental insults, the immune system or the action of biocides. Since most of all the bacterial species are able to produce biofilms, it seems reasonable that unrelated bacteria make use of common elements for biofilm development. In the last ten years, many groups have dedicated great efforts to identify factors involved in biofilm development. As a consequence, it has been discovered that different unrelated bacteria produce: (*i*) the same exopolysaccharides (cellulose, poly-β-1,6-*N*-acetylglucosamine) to build the matrix, (*ii*) the same secondary messenger, c-di-GMP, to regulate the production of biofilm matrix exopolysacharides, and (*iii*) a group of surface proteins that exhibit homology with Bap of *Staphylococcus aureus* (Biofilm-associated protein) to promote adhesion to biotic and/or abiotic surfaces (listed in Table 1).

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1631-0691/$ – see front matter
doi:10.1016/j.crvi.2006.07.008

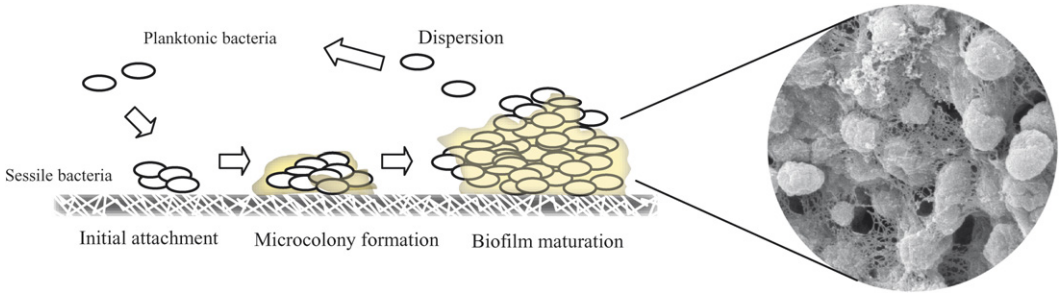

Fig. 1. Schematic figure showing biofilm formation process. Visualization of the biofilm formed by *Salmonella* through Scanning Electron Microscopy.

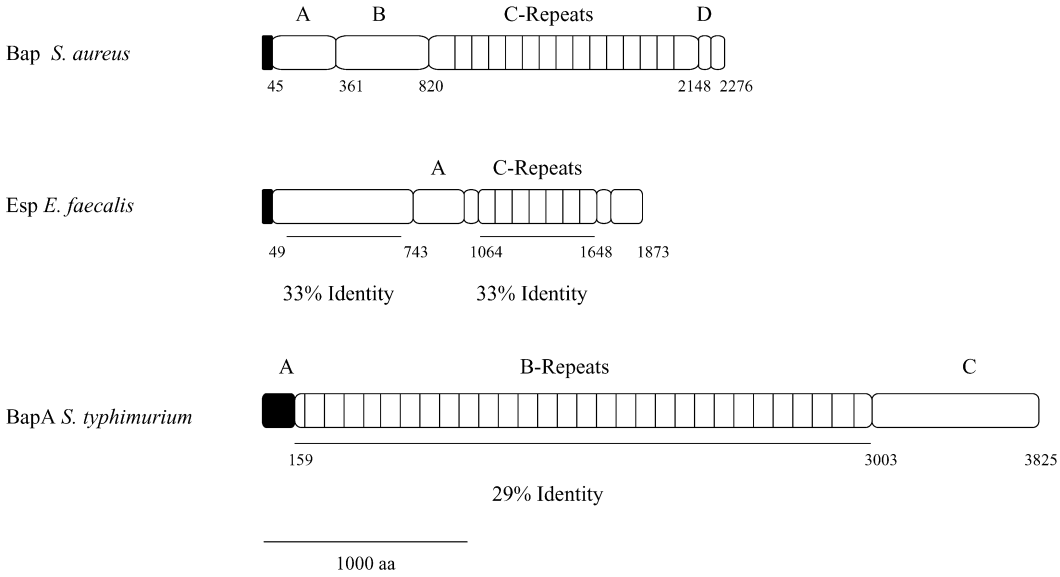

Fig. 2. Structural analysis of Esp and BapA and identity to Bap from *S. aureus*.

In this review, we will focus on these surface proteins and describe three representative members that mediate biofilm formation in three unrelated bacterial species.

2. Bap in *Staphylococcus aureus*

The first member of the BAP family was described during a previous investigation carried out by our group focused on the development of the *Staphylococcus aureus* biofilm. This study, based on a standard screening of transposon mutants unable to adhere to a polystyrene surface, identified a novel 6831pb open reading frame involved in biofilm development [1]. This gene is carried in a putative composite transposon inserted in the SapIbov2 pathogenicity island [2] and encodes for a 2276-amino acids surface protein, named Bap (Biofilm-associated protein). The gene *bap* has also been detected in isolates of several coagulase-negative staphylococcal species, like *S. epidermidis, S. chromogenes, S. xylosus, S. simulans*, and *S. hycus* [3]. However, up today, none of the human *S. aureus* isolates tested harbour the *bap* gene, suggesting that ruminant and human staphylococcal strains differ in their host-specific pathogenic strategies.

3. Bap structure

Bap shows structural characteristics typical from cell-wall-anchored proteins present in gram-positive bacteria. The N-terminus domain contains a signal sequence for extracellular secretion (first 44 aa), followed by two separated repeats of 32 aa (aa 45 to 360), which were designated as region A. The remaining amino terminal sequence up to amino acid 818 was designated as region B. According to the Coiled-Coil prediction program, a dimerization domain can be distinguished both in region A (aa 227 to 309) and region B (aa 528 to 548) [4]. This fact suggests that two Bap molecules,