



Genetics of Biofilms Laboratory - URA CNRS 2172

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Annual Report

Biofilms are mixed communities of microorganisms developing on surfaces in all environments. Besides their positive ecological roles, biofilms formed on medical implants are difficult to eradicate due to a characteristic increased tolerance to biocides. Bacterial biofilms are therefore considered an important cause of chronic and nosocomial infections. From a fundamental point of view, growth on surfaces also results from or induces novel behaviors as compared to individual microorganisms and the study of biofilm lifestyle will likely reveal new or under-explored aspects of bacterial biology.

The studies undertaken in the Genetics of Biofilms Unit (GBU) essentially address 2 main questions: **how do bacteria form biofilms?** And **what particular physiological properties** do these bacteria express once the biofilm is formed? Most of these questions are addressed in commensal and pathogenic *Escherichia coli*, or in other microorganisms such as *Salmonella enteritidis*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* via collaborations.

We use genetic, genomic and molecular biology approaches combined with different biofilm models **i)** to identify several bacterial factors involved in biofilm formation promoting both initial surface contacts and bacterial-bacterial interactions. **ii)** to study gene expression and regulatory pathways associated with the biofilm lifestyle. **iii)** to investigate biofilm-specific physiological properties with particular emphasis on competitive bacterial interactions within mixed, multispecies biofilms. **iv)** to investigate biophysical aspects of bacterial contact with surfaces in collaboration with physico-chemists.

Selected activity in 2010

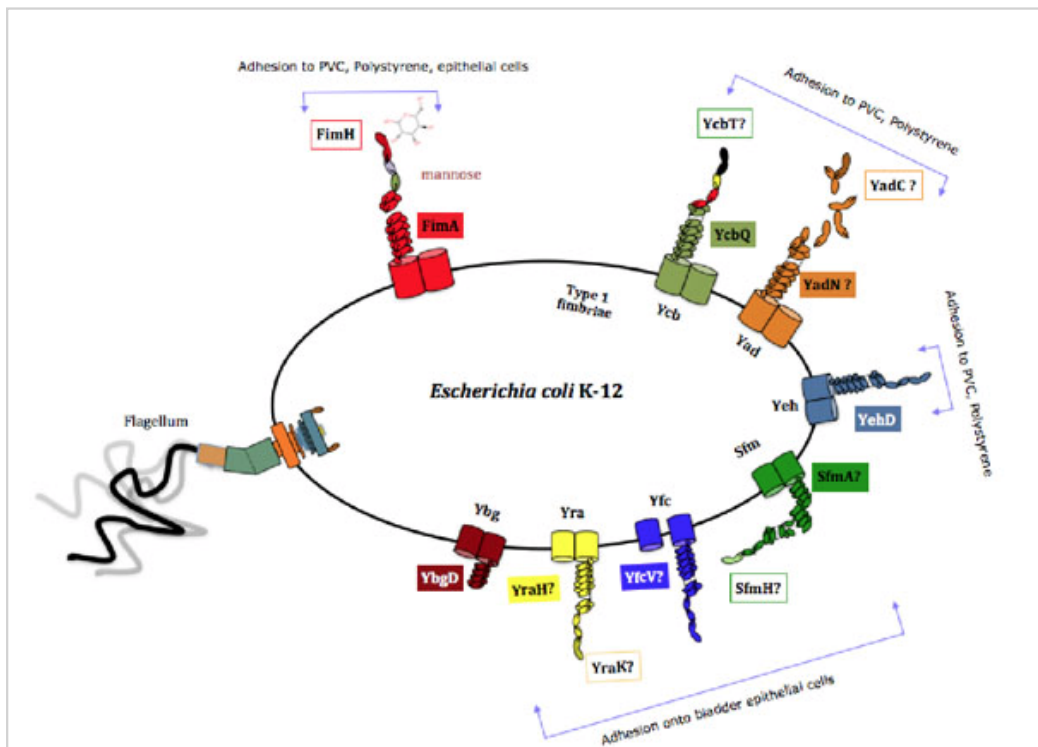
Characterization of cryptic but functional chaperone-usher fimbriae in *Escherichia coli*

Commensal and pathogenic *E. coli* (and probably all bacteria), possess a partly unexplored arsenal of potential surface adhesins with unassigned or poorly characterized functions. We hypothesized that some of these genes could correspond to adhesins contributing to colonization and biofilm maturation and expressed under specific physiological conditions, possibly in response to different environmental cues. We validated this hypothesis and characterized seven *E. coli* K-12 operons (*ycb*, *ybg*, *yfc*, *yad*, *yra*, *sfm* and *yeh*) encoding for type 1 fimbriae homologues. Type I fimbriae are surface filamentous structures secreted via the chaperone/usher pathway that were shown to contribute to bladder colonization. We showed that these cryptic fimbriae are fully functional and under the negative control of H-NS repressor. Moreover, these fimbriae have carbohydrate-binding specificities that are distinct from those described for type 1 fimbriae. These results further extend the known diversity of commensal and pathogenic *E. coli* adhesins. The distinct substrate specificities of the characterized cryptic fimbriae suggests that they could be involved in *E. coli* tissue tropism contributing to bacterial ability to adapt and colonize a variety of surfaces in different environments. (Figure)

Bacteriophage Mu contamination of random mutagenesis in Mu-sensitive bacteria

Random transposon mutagenesis is the strategy of choice for associating a phenotype with its unknown genetic determinants. It is generally performed by mobilization of a conditionally replicating vector delivering transposons to recipient cells using broad-host range RP4-conjugative machinery carried by the donor strain. We demonstrated that bacteriophage Mu could have contaminated random mutagenesis experiments performed on Mu-sensitive species with the widely used donor strains SM10 *lpir* and S17-1 *lpir*, leading to potential misinterpretation of the transposon mutant phenotype and therefore perturbing analysis of mutant screens. To circumvent this problem, we produced a new Mu-free donor strain, which be used with most of the available transposon-delivering plasmids and enable more efficient and easy-to-analyze mutant hunts in *E. coli* and other Mu-sensitive RP4 host bacteria.

Keywords: Biofilm, adhesion, *Escherichia coli*



Escherichia coli K-12 chaperone-usher fimbriae.

Schematic depiction of seven *E. coli* K-12 CU fimbriae, (*ycb*, *ybg*, *yfc*, *yad*, *yra*, *sfm* and *yeh*). Major pilus subunits are indicated in filled coloured boxes with a question mark when no formal demonstration of their function nor potential carbohydrate ligands were obtained.

Publications

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