



## Shedding light on *Streptococcus* pathogenesis with comparative molecular analysis

### Project Coordinator



**Dr. Patrick Trieu-Cuot**

Institut Pasteur  
Unité de Biologie des Bactéries  
Pathogènes à Gram-Positif  
28, Rue du Dr Roux  
75724 Paris Cedex 15  
France  
Tel.: +33-1-45689592  
E-Mail: [ptrieu@pasteur.fr](mailto:ptrieu@pasteur.fr)

### Project Description

Bacteria of the *Streptococcus* genus are common inhabitants of the human mouth, skin, intestine and upper respiratory tract. The name derives from the Greek streptos, meaning easily bent or twisted, like a chain, describing its means of cellular division, which occurs along a single axis and results in the growth of chains or pairs. Several *Streptococcus* species are characterised into groups based on specific carbohydrates in the bacterial cell wall. The most important from a medical perspective are *Streptococcus pyogenes*, also known as "Group A Strep" (GAS) and *Streptococcus agalactiae*, known as "Group B Strep" (GBS). These two groups are responsible for about a third of all human bacterial infections: Whereas GAS is responsible for health issues ranging from mild superficial skin infections to life-threatening systemic diseases, GBS is especially dangerous for babies, who are at risk of developing neonatal sepsis, meningitis or pneumonia.

Six researcher teams from three different countries have now come together under the roof of the *ERA-NET Pathogenomics* to shed some light on how these two closely related *Streptococcus* species have been able to evolve into highly successful human pathogens. The scientists are focusing on the bacterial surface molecules and hope to uncover the role that they play in infection processes. Based on a genomewide analysis, a range of mutants with specifically altered surface components will be created. These genetically engineered bacteria will then be studied in cell lines and animal models during their interaction with parts of the immune system to find the key factors that promote the development of diseases. Furthermore, the researchers will be utilising powerful bacterial bioimaging techniques with the aim of characterising *in vivo* formation of microcolonies and following disease progression in animal models in real time. By comparing the data of both *Streptococcus* species, the scientists hope to be able to identify shared factors, which could lead to the discovery of new fundamental disease-causing mechanisms and the development of novel therapeutics.

