Description for the general public

Streptococcus pyogenes is a pathogen responsible for a wide range of infections with varying degrees of severity from relatively light, such as pharyngitis (sore throat, strep throat) or impetigo and severe (invasive) infections such as necrotizing fasciitis, or toxic shock syndrome and severe postinfectional sequelae.

According to the World Health Organization (WHO), *S. pyogenes* causes annually about 700 million infections worldwide, and the estimated number of deaths from invasive infections and complications is more than 500 000 cases per year. That positions *S. pyogenes* among ten most important and most deadly human pathogens. The global nature of infections, resistance to some classes of antibiotics or the presence of highly virulent groups of specialized strains (clones) among invasive isolates, makes *S. pyogenes* a subject of continued interest for physicians, microbiologists and epidemiologists. One of the main purposes of the research on this organism is to track changes in virulence and sensitivity to drugs used in therapy. Major topics in research on *S. pyogenes* are also epidemiological investigations on genetic diversity and clonality between strains and the relationship between groups of strains with specific characteristics and the types of infections and their severity.

Usually the treatment with penicillin is not fully effective for treating invasive deep tissue infections. For many years, macrolide antibiotics such as erythromycin, has been used as an important alternative to penicillin. Unfortunately, macrolides and similar lincosamides (clindamycin), cannot replace penicillin because of the emerging resistance to this class of drugs. Bacteria exhibiting such resistance are isolated in many countries around the world. The level of resistance varies from 3 to 40% in different countries, in Poland level of resistance to erythromycin of is estimated around 12%.

Analysis of *S. pyogenes* population shows a clonal proliferation of certain strains of groups (clones) which are resistant to macrolide antibiotics. Interestingly, groups dominating among resistant strains are different than groups predominantly circulating in the environment. The mechanism of such specialization of resistant clones is not known, but certainly has its source in a specific genetic makeup.

Our project involves a comparative genomic analysis of resistant and susceptible *S. pyogenes* clones. The analysis will try to precisely define a set of characteristics of *S. pyogenes* genetic markers, which are responsible for the selection and maintenance of a stable non-random population of clones resistant to macrolides.