Summary:

Bacteria from *Burkholderia cepacia* complex (Bcc) and bacteria *Pseudomonas aeruginosa* belong among the most serious pathogens causing lung infections in patients with cystic fibrosis (CF). These bacteria are highly resistant to almost all of the available antibiotics. Another serious problem is the ability of certain strains to spread among the patients, which can cause an epidemic infection.

Some of the Bcc strains are capable of entering the bloodstream and causing serious septic condition called cepacia syndrome. One of these strains is the Czech epidemic strain *B. cenocepacia* ST32, which spread among Czech patients with CF in the 90s of the 20th century.

The aim of this study was to compare transcriptome profiles of isolates gained from blood of patients with cepacia syndrome with transcriptome profiles of isolates gained from sputum of patients in the stable phase eventually exacerbation, and to choose the most appropriate genes with the different expression, which could be used as a possible marker for detection of arising cepacia syndrome. Another aim of this study was to do further study of function and influence on virulence of chosen marker (which is coding generally known virulence factor) in the time of cepacia syndrome. The last aim was to assess the epidemiologic situation of bacteria from *P. aeruginosa* in patients with CF in Prague CF centre and subsequent compilation of the best investigative procedure for the monitoring of these bacteria.

In the present thesis we:

a) based on the comparison of transcriptomic profiles of *B. cenocepacia* ST32 gained from blood (cepacia syndrome) with transcriptomic profiles of sputum (stabile phase/exacerbation) cultivated in different conditions, we chose appropriate genes with different expression for prospective monitoring of infection progression. We discovered that isolates obtained from blood are connected to higher expression of the type III secretion system as well as to lower expression of genes for motility.
b) verified genes with altered expression using qRT PCR. Monitoring of the gene expression was transferred to direct detection from the clinical material (sputum), without *in vitro* cultivation of isolates.
c) subjected the chosen factor of virulence, the type III secretion system, to deeper study using mutagenesis techniques. We supported the claim of its importance for survival in bloodstream.
d) excluded spreading the epidemic strain *P. aeruginosa* among patients from Prague CF centre. Furthermore, it was assembled the most appropriate procedure for monitoring the bacteria *P. aeruginosa* in a patient with cystic fibrosis.