Bacterial genomes have a remarkable plasticity and variability. Their evolution is very fast, mainly due to the phenomenon of horizontal gene transfer (HTG), which enables bacteria to incorporate exogenous genetic material into their genomes. The main carriers of genetic information transmitted via HTG are mobile genetic elements, especially plasmids, which are extrachromosomal DNA molecules capable of self-replication in a host cell.

In the bacterial cell more than one plasmid may occur. Every additional (in relation to chromosome) replicon is an energy expenditure to the host, but very often benefit from having another plasmid is greater than the cost of its maintenance. This is because very often plasmids carry genes of adaptive potential.

The analysis conducted by our research group showed that bacteria of the genus *Psychrobacter*, isolated from polar environments, often have multi-replicon genomes. This is also the case of the strain ANT_AH3 from Antarctica, which carries as many as eleven plasmids. Most of these plasmids carry at least one gene encoding hypothetical protein of unknown function. Therefore, it is worth to check if these replicons have any influence on physiology or metabolism of their host. This could gave the answer to the question why so many plasmids are maintained in this strain. Moreover, during analysing the sequence of the ANT_AH3 plasmids we have identified two novel type II restriction-modification systems (R-M), which protect the cell against penetration of foreign DNA, and the gene encoding the DprA protein, which may increase the ability to uptake the foreign DNA by the host. This means that in one cell there are plasmids carrying the genetic modules, with a potentially opposite functions regarding to the exogenous DNA.

R-M systems are responsible for protecting the host cell against the invasion of exogenous DNA (e.g. phage or plasmid). Their operation is based on methyltransferase activity that methylates host's DNA within a specific sequences, thus protecting it from the action of the endonuclease, responsible for the destruction of unmodified DNA. In this case, the chromosomal and plasmid genetic material of the host is protected, in contrast to newly introduced one, which is destroyed.

DprA protein is described in the literature as a factor affecting the ability of the host to uptake exogenous DNA. This protein can bind to both single- and double-stranded DNA and protect it from nucleases. Moreover, the DprA protein has been shown to interact with other competence (involved in DNA uptake) proteins. Strain ANT_AH3 is unique because it is the first known example having the gene encoding the DprA protein within the plasmid. To date, *dprA* homologs have been identified only within bacterial chromosomes. By means of molecular methods we want to investigate the impact of the DprA protein on the ANT_AH3 ability to retrieve exogenous DNA, and thereby assess whether the plasmid carrying the *dprA* gene may become a kind of "key" opening the cell to other plasmids.

In summary, we assume that this project will allow us to clarify whether plasmids and plasmid-encoded genes can influence the cell biology and shaping of host genome, and especially creating a multi-replicon strain.