The ultimate goal of this project is to better understand mechanisms of endosymbiosis, which is one of the most interesting and important processes in the history of life on our planet. The endosymbiotic merger between an archaeon and proteobacterium triggered the evolution of the eukaryotic cell itself, and subsequently enabled some eukaryotes to perform photosynthesis upon the 'engulfment' of cyanobacteria by unicellular heterotrophic eukaryotes. These both types of endosymbiotic events resulted in bacteria-derived organelles: mitochondria and plastids, respectively, that specialize in energy conversion. In order to become cellular organelles, bacterial endosymbionts had to undergo tremendous transformation, including gene loss and their transfer to the host nuclear genome, and evolution of protein import machineries in the endosymbiont envelope for nuclear-encoded proteins. Mitochondria and plastids are surrounded by a double envelope membrane, and adapted prokaryotic and eukaryotic components to create their import machineries along with appropriate targeting signals and processing proteases. Interestingly, their targeting signals are similar to antimicrobial peptides (AMPs), small molecules that participate in host defense and/or microbial competition. AMPs are also a hopeful weapon to fight antibiotic-resistant bacteria.

In this research project, we would like to formulate a new model for plastid evolution which includes AMPs. We think that they are of immense importance for establishment of bacteria-derived organelles. Firstly, we will verify that targeting signals of mitochondria and plastids are derived from AMPs and indicate the potential AMP class from which they could have evolved. We will also ponder how to optimize AMPs with evolutionary information to design better AMPs to fight bacteria. Secondly, we plan to investigate the evolution of the plastid protein import machinery, especially enzymes responsible for removal of targeting signals, which have not been analyzed in this context yet. The obtained results and inferences drawn from the literature will be discussed in the light of our new **'AMP-based endosymbiosis hypothesis'**. The proposed model will also be relevant for explaining the evolution of other bacteria-derived organelles, including recently established photosynthetic bodies of *Paulinella*.