Bacterial plasmids are an important group of mobile genetic elements. They are usually circular DNA molecules that, due to their own replication systems, occur in the cell in an autonomous form, not integrated with the chromosome. These replicons are the main natural carriers of genetic information involved in horizontal gene transfer. They often carry adaptive genes that allow bacteria for better adaptation to changing environmental conditions and survive in the presence of various stressors. Plasmids are highly diverse in terms of their size, structure, copy number, host range and the mechanisms that drive their replication, stability and transfer. Their genetic load also varies. Due to their mobility, these replicons can be transferred to different hosts, in which they may undergo numerous genomic rearrangements that shape their structure and specific properties.

Our analysis of bacterial plasmidomes has led to the identification of a group of plasmids that, in many ways, stand out from other bacterial replicons. These are so-called virulence plasmids (pVirCro), which determine the pathogenic properties of opportunistic bacteria of the genus *Cronobacter*. The plasmids are not transferable, occur in all species of this genus and are not found in other groups of bacteria. Interestingly, the results of phylogenetic analyses indicate that pVirCro have been accompanying *Cronobacter* spp. since the beginning of the evolutionary history of the entire taxonomic genus. It is therefore a unique model among plasmids, extremely useful for studying the mechanisms leading to the gradual domestication of exogenous replicons in bacterial cells, resulting in the transition of a mobile genetic element into an important component of the bacterial genome, undergoing, together with the chromosome, a common genetic regulation during the cell cycle.

A unique feature of pVirCro plasmids is also their extensive genetic load, a significant part of which has not been altered over the course of the evolution of the genus *Cronobacter*, thus over the past tens of millions of years. These plasmids carry approx. 40 common genes, however only a few of them, linked to the pathogenesis of *Cronobacter* spp., have been analyzed so far. We plan to conduct in-depth, comprehensive analyses of these replicons to investigate: (i) the potential regulatory coupling between the replication processes of pVirCro plasmids and bacterial chromosomes and the coordination of the segregation process of both types of replicons in the bacterial cell cycle, (ii) the influence of pVirCro on the 'fitness' of their host cells, and (iii) the biological role of the conserved genetic load of pVirCro plasmids, which, as we assume, may be involved in such important processes as biofilm formation, production of secretion of polysaccharides, generation of subpopulations of persisted cells (antimicrobial-tolerant by entering a state of dormancy), and (iv) their role in pathogenesis (analysis of novel pathogenicity determinants).

These will be the first such comprehensive, interdisciplinary studies devoted to a single group of bacterial plasmids. They will bring a wealth of valuable information on (i) the evolution of pVirCro plasmids, (ii) the mechanisms that led to the domestication of these replicons and their association with a single bacterial taxonomic genus, and (iii) genetic information of high adaptive importance that is relevant to *Cronobacter* spp. regardless of the ecological niche inhabited by these bacteria. The obtained results will also bring important new insights into the discussion of the evolution, structure and functioning and multi-replicon bacterial genomes.