Abstract of the PhD research

Protein phosphorylation is an essential and efficient mechanism by which cells can transduce signals and regulate different processes. Its existence in the three domains of life is well-established and the process is thoroughly studied in **Eucarya** and **Bacteria**. However, in **Archaea** little is still known about the process of protein phosphorylation.

A phosphoproteomic study revealed that protein phosphorylation occurs widely in the model archaeon **Sulfolobus acidocaldarius**, of which numerous targeted proteins are involved in central cellular processes including respiration, motility and transcription regulation. Intriguingly, tyrosine was the most targeted residue for phosphorylation. The prominent abundance of phosphorylation in **Sulfolobus** is associated with lack of reliable information about it. More specifically, very little is known about the cognate kinases and/or phosphatases responsible for specific phosphorylation events and the effects on cellular processes in which they are involved.

In this work, the role of phosphorylation for the functioning of two transcription regulators was studied in **S. acidocaldarius**: one involved in cellular motility (AbfR1) and one in fatty acid metabolism (FadR_{Sa}). The effect of phosphorylation on DNA binding and ligand binding was studied. Moreover, I identified a novel protein kinase with tyrosine phosphorylation activity, which is the first of its type to be described in **Archaea**. The enzymatic activity of this representative of a novel archaeal family of kinases was analyzed in addition to the identification of protein substrates using a phosphoproteomic approach. In summary, this work contributes to a better understanding of signal transduction mechanisms in **S. acidocaldarius** by means of phosphorylation of transcription factors.