MS5-P10 Structural investigations of purine nucleoside phosphorylase from *Helicobacter pylori* II

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Helicobacter pylori is a well-known human pathogen involved in the development of many diseases. Due to the ever-growing infection rate and increase of *H. pylori* antibiotic resistance, it is of utmost importance to find a new way to attack and eradicate *H. pylori* . The purine metabolism in *H. pylori* is solely dependent on the salvage pathway and one of the key enzymes in this pathway is purine nucleoside phosphorylase (PNP). Therefore, PNP could be a promising drug target for inhibiting *H. pylori* growth. Like most bacterial PNPs, *H. pylori* PNP is a homohexameric protein that can be regarded as a trimer of dimers. The active site conformation of each monomer can be either open or closed (Koellner et al., 2002). In accordance with our hypothesis, substrate binding takes place in open, and catalytic action occurs in the closed conformation. In the crystal structures of the very similar *E. coli* PNP complexed with its ligands we have found the following distributions of the closed and open active sites: 3 open + 3 closed (Koellner et al., 2002), 4 open + 2 closed sites (Mikleušević et al., 2011). In the frame of this meeting in the presentation "Structural investigations of purine nucleoside phosphorylase from *Helicobacter pylori,* two crystal structures of the PNP from the *H. pylori* clinical isolate in complex with ligands will be described. To our surprise, in both crystal structures 5 open + 1 closed conformations were found. To the best of our knowledge, this is first such case among homohexameric PNP enzymes. Very recently, we have obtained also first crystals of the PNP from a referent strain of this bacterium, *Helicobacter pylori* 26695 in complex with ligands and data collection as well as crystal structure determination is under way. It is important to stress out that in the clinical isolate very important catalytic amino acid Asp204 is mutated in Asn, which, very likely, has implications to the catalytic mechanism. Differences in the active site conformations between PNP enzymes from two different *H. pylori* strains will be discussed, as well as possible implications on the PNP mechanism of action.

Koellner, G., Bzowska, A., Wielgus-Kutrowska, B., Luić, M., Steiner, T., Saenger, W., & Stepiński, J. (2002). *J. Mol. Biol.* **315**, 351–371.

Mikleušević, G., Štefanić, Z., Narczyk, M., Wielgus-Kutrowska, B., Bzowska, A., & Luić, M. (2011). *Biochimie*. **93**, 1610–1622.

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MS5-P11 Structural insights into fatty acid metabolism in *Bacillus subtilis* sporulation

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Bacillus subtilis is the model Gram-positive bacterium. Its genetic and physiological characterisation is of value not only for elucidating its basic biology, but also that of related pathogenic microorganisms. Similarly to other *Bacilli*, *B. subtilis* undergoes sporulation, a process of cellular differentiation producing metabolically dormant endospores. Studies of this process have important implications for understanding the life cycle and infectivity of related pathogenic *Bacilli* e.g. *B. anthracis,* responsible for anthrax. Despite the medical importance of sporulation questions still remain regarding the metabolic pathways involved in this process. As well as being integral components of phospholipid membranes fatty acids can also be metabolised and used as a source of energy by microorganisms. The mother cell metabolic operon (*mmg*) consists of genes with sequence similarity to those involved in fatty acid metabolism. Although exact roles for the enzymes encoded for by the *mmg* genes remain cryptic, they appear to play an important role in energy production during sporulation. Here I present recent progress in the structural and functional characterisation of the Mmg proteins, and explore their ability to form a single functional enzymatic complex. I highlight the implications of these findings for our understanding of *B. subtilis* sporulation.

Keywords: Multiprotein Complex, Metabolism, Structure.