Keywords: phenazine biosynthesis, domain swapping, substrate channelling

FA1-MS12-P06

The secretome of parasitic nematodes: Analysis of host-parasite cross-talk. Markus Perbandt[a,c], Raphael Eberle[a], Kai Lüersen[b], Eva Liebau[b], Christian Betzel[a]. [a]*University of Hamburg, Department of Chemistry, Laboratory for Structural Biology of Infection and Inflammation, c/o DESY, Germany.* [b]*University of Münster, Institute of Animal Physiology, Department of Molecular Physiology, Germany.* [c]*University Medical Center Hamburg-Eppendorf, Department of Medical Microbiology, Virology and Hygiene, Germany.*
E-mail: perbandt@chemie.uni-hamburg.de

We analyse functional macromolecular systems in filarial nematode worms causing major infectious diseases like river blindness and lymphatic filariasis. These helminths parasitize for long periods their immunocompetent hosts, provoking only restricted pathology in their tissue habitats although the pathogens can accumulate to large essemblies. Because of their size, helminths cannot sequester in niches like many bacteria, fungi and protozoa. By co-evolution, these "king-sized" pathogens have developed other strategies to secure survival. Recent research on the interaction between helminths and vertebrate hosts has provided information and insights about evasion, immunomodulation and protection mechanisms [1]. Here, molecules are most important that are secreted into the host tissue or are associated with the surface of the parasite. They represent the first molecules exposed to and affecting the host immune apparatus and are thus likely to be involved in the establishment and maintenance of the parasite within the host and in the avoidance, modulation and skewing of the host immune response. Immune modulation is suggested to be beneficial to both, the human host and the parasite, as it protects the worm from being eradicated, and at the same time protects the host from excessive inflammatory responses that may lead to tissue damage.
We analyse the composition of excretory-secretory products (ESPs) and selected surface proteins of parasitic nematodes, since these are likely to present the principle players in parasite-host cross-talk and have the capacity to actively shape the immunological environment [2,3].
We presently analyse the structures of all important and identified key proteins and here we present the structural insights of the first targets like the OvGST1 from Onchocerca *volvulus*, the causative agent of river blindness.

[1] Allen J.E, Adjei O., Bain O., Hoerauf A., Hoffmann W.H., Makepeace B.L., Schulz-Key H., Tanya V.N., Trees A.J., Wanji S., Taylor D.W., *PLoS Negl Trop Dis.*, 2008, 2, 217. [2] Maizels R.M., Yazdanbakhsh M., Nat Rev Immunol., 2003, 3, 733. [3] Maizels R.M., Balic A., Gomez-Escorbar N., Nair M., Taylor M.D., Allen J.E., *Immunol Rev.*, 2004, 201, 89-116.

Keywords: river blindness, immunmodulation, host-parasite cross-talk

FA1-MS12-P07

Crystal structure of *Enterococcus faecalis* Thymidylate synthase. C. Pozzi[a], M. Benvenuti[a], S. Ferrari[b], R. Luciani[b], A. Catalano[c], R.M. Stroud[d], M.P. Costi[b], S. Mangani[a]m [a]*Department of Chemistry,University of Siena, Italy.* [b]*Department of Pharmaceutical Sciences, University of Modena and Reggio Emilia, Italy.* [c]*Department of Pharmacy and Chemistry, University of Bari, Italy.* [d]*University of California at San Francisco, USA.*
E-mail: Mangani@unisi.it

Thymidylate synthase (TS) is an enzyme that catalyzes the reductive methylation of 2'-deoxyuridine 5'-monophosphate (dUMP) to thymidyne 5'-monophosphate (dTMP), using the cofactor 5,10-methylene-5,6,7,8-tetrahydrofolate (mTHF) as a one–carbon donor and reductant [1]. This reaction is the only the novo source of thymidylate for the cells [2]. The inhibition of TS leads to pronounced changes in cellular protein and RNA, cessation of DNA replication and eventually cell death [3]. Because of its critical function, considerable effort has been focused on the design of TS inhibitors for the treatment of cancer [4]. Less attention has been directed towards the design of species-specific TS inhibitors aimed at treating diseases caused by bacterial, fungal or opportunistic pathogens. However, taking into account the rise in antibiotic resistant bacteria, the relative toxicity of treatments for fungal infections and the poor therapies available for several opportunistic infections in immunocompromised patients, the successful development of pathogen-specific TS inhibitors may offer an important alternative to current antibiotic, antiparasitic and antifungal drugs [5,6]. TS enzymes show an highly conserved structure, but some differences of the active site may be exploited for the design of inhibitors able to discriminate pathogen TSs vs. human TS [7].
In the effort to increase our knowledge about bacterial TS, we have determined the 2.18 Å crystal structure of *Enterococcus faecalis* TS (EfTS), which is the first structure determination of this enzyme, as prepared and in complex with a specific inhibitor.
EfTS is a homodimer showing subunit heterogeneity as only one of the subunits brings bound a derivative of the tetrahydrofolate intermediate of the catalyzed reaction. The binding of the inhibitor is accompanied by large rearrangement of the protein, determining the ordering of a mobile loop that appears disordered in the inhibitor free subunit. The designed inhibitor replaces the naturally occurring inhibitor while leaving the other subunit free.
The determination of the two crystal structures provides interesting clues about the catalytic mechanism of EfTS and its inhibition that might be relevant for the rational design of more powerful and selective inhibitors towards bacterial targets.

[1] K. Perry, E. Fraumann, et al. *Proteins* 1990, 8, 315. [2] C.W. Carreras, D.V. Santi *Annu. Rev. Biochem.* 1995, 64, 721. [3] J. Phan, S. Koli, et al. *Biochemistry* 2001, 40, 1897. [4] M.P. Costi *Med. Res. Rev.* 1998, 18, 21. [5] T.M. File *Jr. Chest* 1999, 115, 3S. [6] R.E. Chaisson, J.E. Gallant, et al. *Aids* 1998, 12, 29. [7] T.A. Fritz, D. Tondi, et al. *Chemistry & Biology* 2001**,** 8, 981.

Keywords: macromolecular crystallography drug design, thymidylate synthase, drug discovery and design

FA1-MS12-P08

Binary complex of 14-3-3σ/p53 pT387-peptide and implications for stabilization. Benjamin Schumacher, Justine Mondry, Philipp Thiel, Michael Weyand[a], Christian Ottmann[a,*]. *Chemical Genomics Centre of the*