



From Basic to Translational Research in Oncology

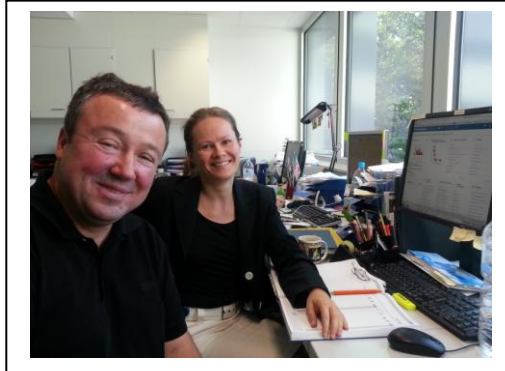


**Report on the 2<sup>nd</sup> twinning visit of Tomasz Stokłosa in the Department of Internal Medicine III, University of Ulm, Germany within 7PR21/BASTION/WP1 in August 22-26, 2015**

Major aim of this short visit (August 22<sup>nd</sup> – 26<sup>th</sup> 2015) to the Department of Internal Medicine III in University of Ulm, Germany was to summarize the effects of previous twinning visits between my group and Prof. Lars Bullinger group with special regard to analyze new RNA sequencing (RNAseq) data obtained in May/June by Marcin Machnicki during his twinning visit in Ulm (see separate report) and combine them with the results obtained in 2013 (by Eliza Glodkowska-Mrowka, see separate report). All visits were coordinated under the twinning agreement between the Medical University of Warsaw and the University of Ulm in WP1 (Task 1.3)

Recent progress in targeted therapy in chronic lymphocytic leukemia (CLL) is related to the use of tyrosine kinase inhibitors (TKI). Recently published observations with ibrutinib (Bcr-1 tyrosine kinase inhibitor) showed that although this therapy is effective in a large cohort of patients, significant portion of them develop resistance to this drug. TKIs might be effective in CLL, however detailed mechanisms of action and potential markers of sensitivity to these drugs are missing. Major aim of our project is to characterize genes involved in response to these promising novel drugs for CLL with special focus on dasatinib in order to define group of patients who may benefit from such treatments. Libraries from CLL samples for RNAseq on Illumina platform were prepared by Marcin Machnicki during his visit, but since sequencing experiments have been done in late June (after he left) it was not possible during his visit to perform the analysis. Thanks to experience and potential of Prof. Lars Bullinger group (a special thanks to Dr. Anna Dolnik, who is a postdoc experienced with RNA seq both in the terms of libraries preparation and the analysis of data), during this visit we

were able perform most of the analysis. Moreover it was possible to combine samples from 2013 experiments and 2015 experiments into the RNAseq analysis pipeline. This time, I could also learn how to use a new tool, to find out if genes with differential expression between samples fall into specific pathway (iPathway tool)



**Dr. Tomasz Stokłosa with Dr Anna Dolnik, postdoc and expert in RNAseq data analysis during discussion on the results obtained with Partek platform and iPathway tool in the laboratory of the University Hospital, University of Ulm**

Although the visit was short it was very fruitful. Not only we were able to sum up work which had been done but also we discussed future plans and new projects, since our collaboration will definitely be continued after completion of the BASTION project.



**Dr. Tomasz Stokłosa with Professor Lars Bullinger and his Team at the farewell lab meeting on August 25th at the local beer garden**