Scientific achievements

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My scientific career started in 2007 at mosaiques-diagnostics in Hanover (Germany), after my master degree in biotechnology from the University of Applied Science in Emden (Germany). In the first phase of my scientific career, I developed a new method for calibration and standardization of proteome data and was a member of international consortium, developing standards for urine proteome analysis. These standards allowed for the first time the comparison of peptidomics data between different laboratories. The applied standards enabled among others the development of the urinary peptide biomarker-based classifier CKD273 for the early detection of chronic kidney disease. The successful validation and application of this classifier in a multicenter study resulted in initiation of the prospective EU-PRIORITY (Proteomic prediction and Renin angiotensin aldosterone system Inhibition prevention Of early diabetic nephRopathy In TYpe 2 diabetic patients with normoalbuminuria) trial. In this study, we showed that CKD273 allows prediction of onset of CKD and detection of patients at high-risk for disease progression. Based on these data, I subsequently identified and validated urinary biomarkers that allow discriminate between different CKD etiologies. This work was also the background for the identification of specific urinary biomarkers for the progression of IgA nephropathy. Combined, the data demonstrated that urinary peptides enable not only early detection of disease, prediction of disease progression, but also to discriminate between the different renal damage courses and enable prognosis of response to specific therapy, in a non-invasive way. The successful application of the urinary biomarkers for the detection and discrimination of CKD in different studies resulted in registration as in-vitro diagnostic in Germany and in the application of urine proteomics/peptidomics in clinical decisions.

The availability of by now over 10000 datasets in the context of CKD enabled focusing on molecular pathophysiology and the initiation of efforts towards using the high-resolution urinary peptide data (typically 2000 – 5000 peptides and small proteins are assessed in a single sample) to guide personalized intervention. In efforts to understand molecular pathophysiology, I investigated among others the association of urinary peptides with fibrosis and could show an association of specific collagen fragments with the degree of

fibrosis. This resulted in the hypothesis that the fibrosis may be the result of attenuated collagen degradation, not of increased collagen synthesis, with major consequences for therapeutic intervention, that are now starting to be addressed in collaborative projects.