

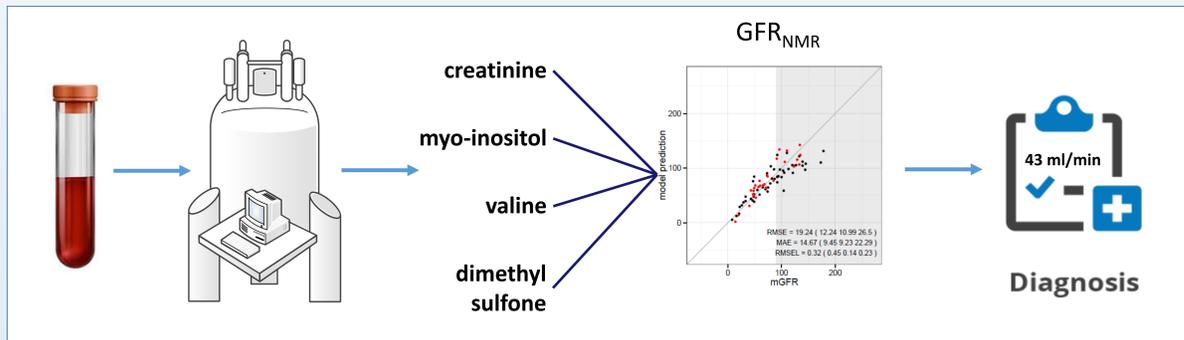
A NMR-BASED BIOMARKER CONSTELLATION FOR GFR PREDICTION ENABLES METABOLIC PHENOTYPING

Jochen Ehrich¹, Laurence Dubourg², Sverker Hansson³, Jens Drube¹, Lars Pape¹, Katharina Schäffler⁴, Tobias Steinle⁴, Jana Fruth⁴, Sebastian Höckner⁴, Eric Schiffer⁴

¹Children's Hospital, Hannover Medical School, Hannover, Germany, ²Service d'Explorations Fonctionnelles Rénales et Métaboliques, Hôpital Edouard Herriot, Lyon, France, ³Department of Pediatrics, Sahlgrenska University Hospital, Gothenburg, Sweden, ⁴numares AG, Regensburg, Germany

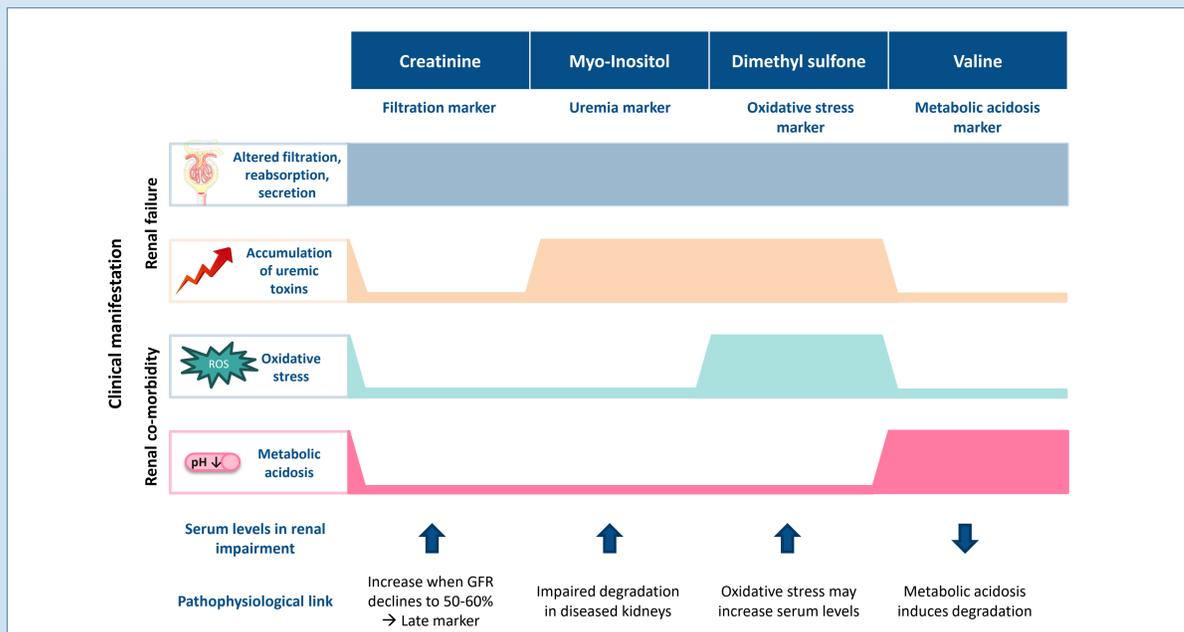
BACKGROUND

Assessment of kidney function by radioactive clearance measurements (mGFR) or estimated GFR by moderately-performing equations (eGFR) is integral to management of kidney disease. Recently, we developed a novel method for accurate prediction of GFR, based on a serum biomarker constellation of creatinine, myo-inositol, valine and dimethyl sulfone analyzed by nuclear magnetic resonance (NMR) spectroscopy. This metabolite constellation was tested and validated in three separate cohorts in a multi-center study.



METHODS

In order to characterize the role of these biomarkers in renal dysfunction and pathogenesis of CKD and to test their value for metabolic phenotyping, biomarker profiling was applied to sets of three age-, and mGFR-matched male patients with CKD stage II during end-stage liver disease. In order to compare the obtained profiles, measured biomarker concentrations were transformed into z-scores. This allows a direct comparison of the observed fold-changes from one marker to the other. The obtained z-scores were plotted in a chart with one axis for creatinine (as a marker of filtration), a second for dimethyl sulfone (as a marker of oxidative stress), a third axis for myo-inositol (as a marker of uremia), and a fourth axis for valine (as a marker of metabolic acidosis).

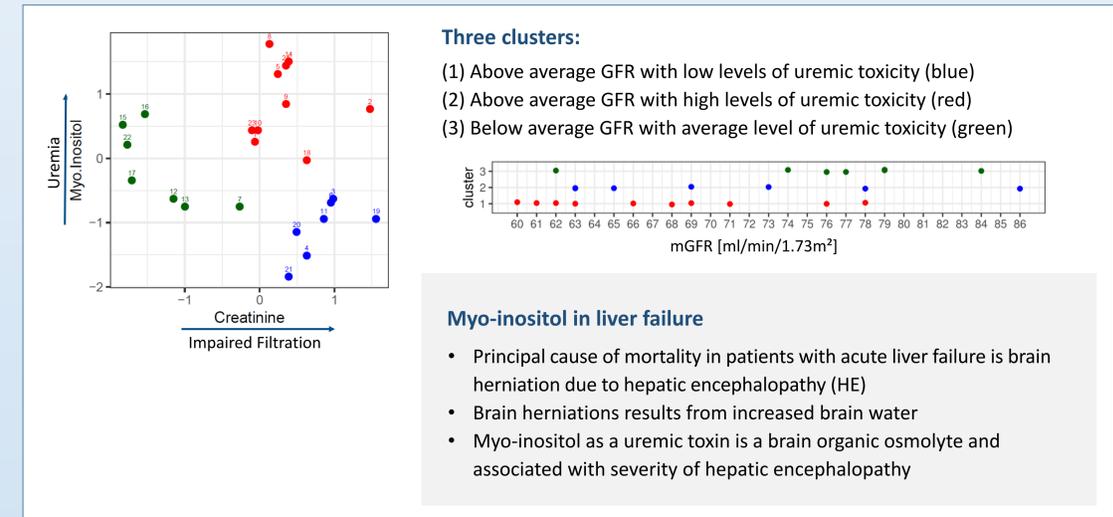
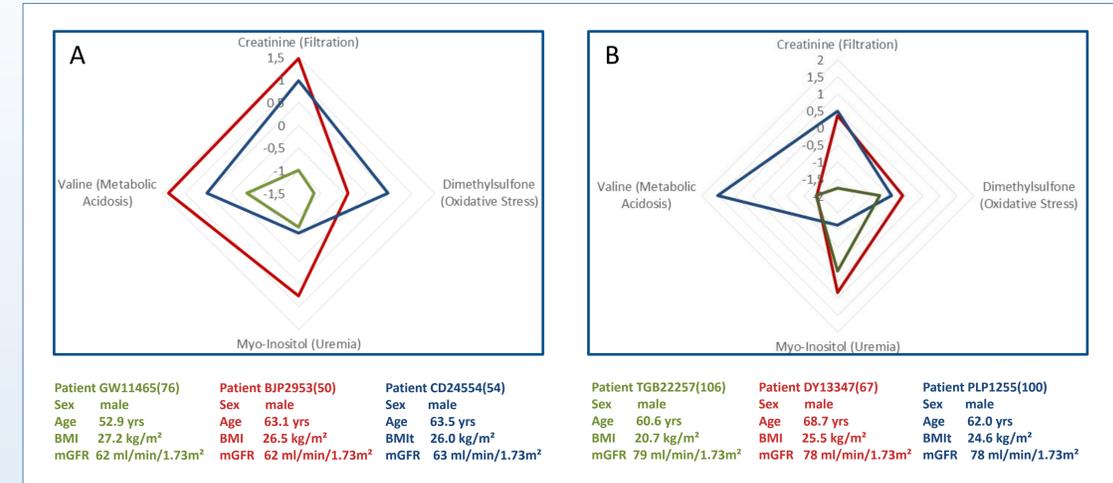


RESULTS

Within two age- and mGFR-matched sets, the metabolic profiles of these clinically similar patients differed significantly concerning single markers reflecting filtration, uremic toxins, oxidative stress, and acidosis.

Patients depicted in red and blue showed above average z-scores for creatinine and valine, while the patient depicted in green had below average z-scores for creatinine, dimethyl sulfone, myo-inositol, and valine (panel A). This observation would be compatible with the conclusion that the patient depicted in green had only minimal levels of oxidative stress, whereas patients in red and blue showed average or increased levels.

The three matched patients with measured GFR of 78 ml/min/1.73m² had very similar and average levels of oxidative stress (panel B). The patient depicted in blue showed a higher level of valine reflecting metabolic acidosis and a lower level of myo-inositol reflecting uremia if compared to the matched patients depicted in green and red.



CONCLUSIONS

These observations suggest that the set of renal biomarkers enables molecular phenotyping of clinically highly selected age-, sex-, and mGFR-matched patients of homogenous clinical etiology providing further insights into their individual renal comorbidities based upon complex design thinking and a single diagnostic method using one serum sample.

CONTACT DETAILS

maulik.shah@numares.com

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