Multicentre prospective validation of a urinary peptidome-based classifier for the diagnosis of type 2 diabetic nephropathy

Justyna Siwy1,2, Joost P. Schanstra1,3,4, Angel Argiles5,6,7, Stephan J.L. Bakker8, Joachim Beige9, Petr Boucek10, Korbinian Brand11, Christian Delles12, Flore Duranton5, Beatriz Fernandez-Fernandez13, Marie-Luise Jankowski2, Mohammad Al Khatib14, Thomas Kunt14, Maria Lajer15, Ralf Lichtinghagen11, Morten Lindhardt15, David M Maahs16, Harald Mischak1,12, William Mullen12, Gerjan Navis8,17, Marina Noutsou18, Alberto Ortiz13, Frederik Persson15, John R. Petrie12, Johannes M. Roob19, Peter Rossing15,20,21, Piero Ruggenenti22,23, Ivan Rychlik24, Andreas L. Serra25, Janet Snell-Bergeon16, Goce Spasovski26, Olivia Stojceva-Taneva26, Matias Trillini22,23, Heiko von der Leyen27, Brigitte M. Winklhofer-Roob28, Petra Zürbig1 and Joachim Jankowski2

1Mosaiques Diagnostics GmbH, Hanover, Germany, 2Charité-Universitätsmedizin Berlin, Medizinische Klinik IV, Berlin, Germany, 3Institut National de la Santé et de la Recherche Médicale (INSERM), U1048, Institut of Cardiovascular and Metabolic Disease, Toulouse, France, 4Université Toulouse III Paul-Sabatier, Toulouse, France, 5RD Néphrologie, Montpellier, France, 6Néphrologie Dialyse St Guilhem, Sète, France, 7Service de Néphrologie, Dialyse Péritoneale et Transplantation, Montpellier, France, 8Department of Internal Medicine, University Medical Center Groningen and University of Groningen, Groningen, The Netherlands, 9Department of Nephrology and KfH Renal Unit, Hospital St. Georg, Leipzig, Germany, 10Diabetes Centre, Institute for Clinical and Experimental Medicine, Prague, Czech Republic, 11Institut für Klinische Chemie, Medizinische Hochschule Hannover, Hannover, Germany, 12BHF Glasgow Cardiovascular Research Centre, Institute of Cardiovascular & Medical Sciences, University of Glasgow, Glasgow, UK, 13IIS-Fundacion Jimenez Diaz/UAM/IRSIN and REDIREN, Madrid, Spain, 14HealthPlus Diabetes & Endocrinology Center, Abu Dhabi, UAE, 15Steno Diabetes Center, Gentofte, Denmark, 16Barbara Davis Center for Childhood Diabetes, University of Colorado Denver, Aurora, CO, USA, 17Department of Clinical Pharmacology, University Medical Center Groningen, Groningen and University of Groningen, The Netherlands, 18Diabetes Center, Second Department of Medicine, Athens University Medical School, Hippokration Hospital, Athens, Greece, 19Clinical Division of Nephrology, Department of Internal Medicine, Medical University of Graz, Graz, Austria, 20HEALTH, University of Aarhus, Aarhus, Denmark, 21Faculty of Health, University of Copenhagen, Copenhagen, Denmark, 22IRCCS – Istituto di Ricerche Farmacologiche Mario Negri, Clinical Research Center for Rare Diseases ‘Aldo e Cele Daccò’, Bergamo, Italy, 23Unit of Nephrology and Dialysis, Azienda Ospedaliera Papa Giovanni XXIII, Bergamo, Italy, 24Second Department of Internal Medicine, Third Faculty of Medicine, Charles University, Prague, Czech Republic, 25Division of Nephrology, University Hospital, Zürich, Switzerland, 26Department of Nephrology, University of Skopje, Skopje, Macedonia, 27Hannover Clinical Trial Center, Hannover, Germany and 28Human Nutrition & Metabolism Research and Training Center, Institute of Molecular Biosciences, Karl-Franzens University of Graz, Graz, Austria

Correspondence and offprint requests to: Joachim Jankowski; E-mail: joachim.jankowski@charite.de

ABSTRACT

Background. Diabetic nephropathy (DN) is one of the major late complications of diabetes. Treatment aimed at slowing down the progression of DN is available but methods for early and definitive detection of DN progression are currently lacking. The ‘Proteomic prediction and Renin angiotensin aldosterone system Inhibition prevention Of early diabetic ne-phropathy In TYpe 2 diabetic patients with normoalbuminuria trial’ (PRIORITY) aims to evaluate the early detection of DN in patients with type 2 diabetes (T2D) using a urinary proteome-based classifier (CKD273).
INTRODUCTION

In the year 2008; around 347 million people worldwide were suffering from diabetes mellitus, representing about 9.5% of the adult population [1]. In addition, the total number of people with diabetes mellitus is estimated to double by 2030 [2]. Improved treatment and disease management has reduced mortality, further contributing to increasing prevalence.

Diabetic nephropathy (DN) is one of the major late complications of diabetes and is associated with substantial cardiovascular morbidity and mortality [3]. A number of large-scale clinical studies have demonstrated nephroprotective effects by interfering with the renin-angiotensin-aldosterone system [4–6]. Although these treatments slow down the progression of renal disease, they do not halt its development.

Currently, microalbuminuria (30–300 mg/24 h or 20–200 μg/min) is considered a key risk factor for development of DN. However, the value of microalbuminuria as a predictor of DN is questioned since it is not specific and is highly variable [7, 8]. Furthermore, the onset of DN in the absence of overt albuminuria has been reported in up to 50% of type 1 diabetic patients [9], indicating a lack of sensitivity. Reduction of the estimated glomerular filtration rate (eGFR) in the context of diabetes is a clear indication of advanced DN, but at this late stage of the disease, the success of treatment is severely compromised by irreversible structural damage [6]. Thus, microalbuminuria lacks sensitivity/specificity and a significant reduction of eGFR is a late sign of DN.

We have previously established a urinary peptide-based classifier composed of 273 different urinary peptides termed ‘CKD273’, which detects with high sensitivity and specificity chronic kidney disease (CKD) in patients with different disease aetiologies [10]. In small-scale studies, this classifier predicted the progression from normoalbuminuria to macroalbuminuria in diabetic patients [11, 12], as well as progression of CKD in patients with renal disease originating from different aetiologies [13]. CKD273 was superior to urinary albumin in predicting DN, and also significantly improved prognosis based on currently used classical risk factors [11].

The performance of CKD273 suggests clinical use of the classifier in early detection and prediction of progression of CKD. Evaluation of CKD273 for selection of diabetic patients that will benefit from a low dose of aldosterone treatment in combination with ACEi or ARB blockade is the aim of the recently initiated multicentre interventional trial ‘Proteomic prediction and Renin angiotensin aldosterone system Inhibition prevention Of early diabetic nephropathy In T2 Diabetes patients with normoalbuminuria’ (the PRIORITY trial, www.eu-priority.org). In PRIORITY, n = 3280 patients with type 2 diabetes (T2D) will be assessed using the CKD273 classifier to detect individuals at ‘high risk’ of developing DN. This subset of patients will be randomized to receive low-dose spironolactone (25 mg/d) or placebo and followed up to assess time to onset of DN. If positive, the study will demonstrate the value of proteomics in guiding early targeted therapy with spironolactone in T2D.

In the present ancillary study, we assessed the ability of CKD273 to detect DN in prospectively collected urine samples from a total of 165 T2D patients originating from 9 different PRIORITY clinical centres.
Table 1. Sample cohorts

<table>
<thead>
<tr>
<th>Centre number</th>
<th>Centre Short name</th>
<th>Sample name</th>
<th>Sample cohort (cases/controls)</th>
<th>Age (mean) median (range)</th>
<th>Gender (male per case/control group) 4/1</th>
<th>Urinary albumin median (range) (mg/L) case 368 (11–8620)</th>
<th>Urinary albumin median (range) (mg/L) control 11 (11–11)</th>
<th>eGFR median (range) (mg/1.73 m²) case 72 (34–104)</th>
<th>eGFR median (range) (mg/1.73 m²) control 87 (60–117)</th>
<th>Area under the curve (AUC, 95% CI) 1.00 (0.815–1.000)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Charité-Berlin</td>
<td>CHA</td>
<td>9/9</td>
<td>57/61</td>
<td>4 (1)</td>
<td>11 (11)</td>
<td>87 (60–117)</td>
<td>0.95 (0.74–0.999)</td>
<td>34 (10–48)</td>
<td>85 (83–111)</td>
</tr>
<tr>
<td>2</td>
<td>Faculty University of Skopje</td>
<td>SKO</td>
<td>10/5</td>
<td>64/64</td>
<td>5 (0)</td>
<td>28 (10–48)</td>
<td>87 (63–111)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
<tr>
<td>3</td>
<td>Hospital St Georg Leipzig</td>
<td>STG</td>
<td>12/7</td>
<td>62/54</td>
<td>7 (4)</td>
<td>21 (7–50)</td>
<td>87 (63–111)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
<tr>
<td>4</td>
<td>Charles University</td>
<td>CUP</td>
<td>10/10</td>
<td>n.a.</td>
<td>n.a.</td>
<td>38 (19–48)</td>
<td>88 (66–160)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
<tr>
<td>5</td>
<td>Diabetes Centre Prague</td>
<td>DCP</td>
<td>10/10</td>
<td>63/60</td>
<td>5 (6)</td>
<td>28 (10–48)</td>
<td>87 (63–111)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
<tr>
<td>6</td>
<td>Mario Negri Institute</td>
<td>MAR</td>
<td>9/10</td>
<td>n.a.</td>
<td>n.a.</td>
<td>20 (10–48)</td>
<td>87 (63–111)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
<tr>
<td>7</td>
<td>Steno Diabetes Center</td>
<td>STE</td>
<td>9/10</td>
<td>n.a.</td>
<td>n.a.</td>
<td>20 (10–48)</td>
<td>87 (63–111)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
<tr>
<td>8</td>
<td>IIS-Fundación Jimenez Diaz</td>
<td>FJD-U TE</td>
<td>14/9</td>
<td>64/64</td>
<td>11 (5)</td>
<td>43 (16–102)</td>
<td>87 (63–111)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
<tr>
<td>9</td>
<td>Health Plus Abu Dhabi</td>
<td>Abu Dhabi</td>
<td>4/8</td>
<td>67/44</td>
<td>3 (5)</td>
<td>79 (19–123)</td>
<td>87 (63–111)</td>
<td>20 (7–50)</td>
<td>88 (66–160)</td>
<td>0.89 (0.670–0.984)</td>
</tr>
</tbody>
</table>

Given are the different centres with the number of collected samples and sample characteristics. In addition, the resulted AUC (area under the curve) values obtained using the CKD273 classification score for each centre are listed.

n.a., not available.

*P < 0.05 (for age the Mann–Whitney test, for gender Fisher’s exact test was used).

a: Albuminuria (mg/24 h).

b: Proteinuria (mg/24 h).

c: Albumin/creatinine ratio (mg/g).
using the CKD273 classifier [10]. The individual classification scores are listed in Supplementary Table S1. Combined abundance of all detected peptides and of the 273 CKD biomarkers are shown in Figure 1. A clear difference in the abundance of a large number of the 273 peptides of CKD273 can be observed between T2D patients with and without DN (Figure 1C and D).

As CKD273 was initially defined in a gender-balanced cohort [10], we studied the effect of gender and age on the classification score. An age bias was observed in one of the nine centres (Table 1, centre 9). Logistic regression was used to investigate if patient age and gender contributed to the proteome classifier-based prediction of the diagnosis. Samples for which no data on age were available (Table 1, centre 4, 6, 7) were excluded from these analyses. No significant contribution of age and gender to the score was observed (P = 0.269 for age and P = 0.312 for gender).

Influence of sample storage
To assess the possible effect of different containers for urine collection on the classification scores obtained with the CKD273 classifier, freshly collected samples (n = 19) were stored in two different containers at −20°C: Nunc® Cryo-Tubes® and Urine-Monovette® and shipped on dry ice. Both replicates were analysed using CE/MS and classified using the CKD273 classifier. No significant difference in CKD273 classification was detected between samples from the two different storage containers (P = 0.623, paired Wilcoxon test).

Multicentre validation of CKD273 to detect DN in T2D patients
The classification scores of T2D patients were analysed using receiver operation curve (ROC) statistics (Table 1) for each individual centre. This resulted in AUC values for the individual centres ranging between 0.9 and 1.0. Comparison of areas under independent ROC curves did not show significant differences between the individual AUC values. Figure 2A shows these scores in the form of box and whisker plots for all T2D patients with and without DN. As previously described [10], a sample with a CKD273 score lower than 0.343 indicates absence of DN, while a score above 0.343 indicates presence of DN. When combining all 165 samples of the 9 centres the classification resulted in AUC of 0.95 (95% CI: 0.90–0.98).

**FIGURE 1:** Compiled urinary protein profiles. (A) All peptides detected in the combined T2D cohort with DN and (B) without DN. (C) The 273 CKD biomarkers in the combined T2D cohort with and (D) without DN. Normalized molecular weight (800–20 000 Da) in logarithmic scale is plotted against normalized migration time (18–45 min). The mean signal intensity of polypeptides is given as peak height.
In the present ancillary study of PRIORITY, we observed a high consistency of the CKD273 markers included in the individual centres. The present ancillary study of PRIORITY, as in any study using a proteomics approach, reproducible results are essential for successful implementation. Numerous issues need to be considered in applying proteome analysis to assess disease state, progression or response to drug treatment in the clinic.

One of the most relevant aspects is validation of the biomarker model in independent cohorts. Validation of biomarkers in independent test sets (i.e. not used for discovery) needs to be performed since most statistical approaches used for biomarker evaluation assume (i) an even distribution of features across the data (similar variance in control and disease groups, and the absence of covariates), (ii) that the findings can be generalized and (iii) that an association exists only with the investigated condition. As these assumptions do not generally hold in a ‘real world’ setting, most biomarkers with promising initial results have less promising results in independent data sets.

Here we investigated the stability of the CKD273 classifier for the first time in a multicentre setting using prospectively collected samples. We analysed 165 samples of T2D patients from 9 different centres. Although sample collection is described for each centre in a standardized sampling protocol, minor differences in sample collection and handling and in the patient population are expected. In addition, differences in diet and lifestyle, e.g. in different countries, may impact on the urinary proteome. However, all of these differences did not modify the performance of the CKD classifier, which was found to be similar between the centres, resulting in a consistently high AUC value of 0.89–1.00. Therefore, the present study complements previous single-centre studies employing the classifier either focusing on the detection of CKD.

Two hundred and seven of the 273 CKD markers (76%) could be verified in a minimum of one of the nine centres. These 207 markers are listed in Supplementary Table S2. This set of biomarkers included 94 collagen alpha-1 (I), 37 collagen alpha-1 (III), 18 alpha-1-antitrypsin, 10 uromodulin, 9 collagen alpha-2 (I), 7 serum albumin, 4 fibrinogen alpha, 3 polymeric-immunoglobulin receptor, 3 alpha-2-HS-glycoprotein, and 2 osteopontin, sodium/potassium-transporting ATPase gamma and transthyretin fragments.

To increase statistical power, we combined the data of T2D patients (n = 165) from all centres and investigated the distribution of the 273 biomarkers in this combined cohort. Because of the large number of samples used for this analysis, a P-value of 0.05 was used as significance threshold. When examining the 100 most significant biomarkers in the CKD273 classifier (based on the Good et al. [10], P-value <0.0001 in the training cohort and the lowest P-values in the validation cohort), 67 out of those 100 peptides could be verified in the current study (Supplementary Table S3, Figure 3). These were alpha-1-antitrypsin, serum albumin, transthyretin, alpha-2-HS-glycoprotein, polymeric-immunoglobulin receptor sodium/potassium-transporting ATPase gamma and uromodulin fragments, as well as fragments of collagen alpha-1 (I), alpha-1 (III) and collagen alpha-2 (I).

**DISCUSSION**

In the present ancillary study of PRIORITY, we observed a high consistency of the CKD273 classification scores across centres, with areas under the curve (AUCs) for the separation between patients with and without DN ranging from 0.9 to 1.0. Moreover, absence of an effect of gender and age on the accuracy of the classifier and absence of effects due to different urine storage containers were established. These results support the feasibility of using CKD273 routinely in a multicentre setting for the detection of DN in T2D patients.

In PRIORITY, as in any study using a proteomics approach, reproducible results are essential for successful implementation. Numerous issues need to be considered in applying proteome analysis to assess disease state, progression or response to drug treatment in the clinic.

**FIGURE 2:** Classification results of the T2D patient cohort. (A) Classification of all T2D patients based on the CKD273 score divided per centre. The scores of patients with macroalbuminuria or and eGFR < 45 mL/min/1.73 m² (cases) are marked in gray and the scores of patients with normalalbuminuria and eGFR > 60 mL/min/1.73 m² (controls) are marked in black. The diagnosis cut-off of 0.343 is also shown. The centre number is given on the x-axis (Table 1). (B) Combined ROC curve for the CKD273-based prediction of all T2D patients (n = 165, AUC = 0.95).
or predicting progression of disease [11–13]. The data demonstrate that the CKD273 classifier is robust and can be applied to samples shipped to a central laboratory from different centres. Importantly, we ascertained that the use of different sample containers had no effect on the performance of the CKD273 classifier.

Additional basic issues, including temperature stability, freeze/thaw stability, post-preparation stability, reproducibility, intermediate precision and time course, have been studied for the CKD273 classifier, and have previously been described [10]. The relative intra- and inter-assay standard deviation of the classifier was below 7 and 10%, respectively [10]. Further technical validation of CKD273 included assessment of in vivo drug interference and inter-laboratory variability and resolution, mass accuracy and amplitude variability of individual peptides. These treatment interference experiments showed no significant modification of the classifier [28]. To address the inter-laboratory variability, the same 86 samples (45 cases and 41 controls) were analysed in three different laboratories in Germany, France and the UK. The individual results were correlated with each other and resulted in correlation coefficients of 0.881–0.904 [28]. The results of the current study demonstrate that CE/MS-based urinary proteome analysis can provide robust and accurate results when applied in multiple clinical centre studies.

Although we observed high accuracy in the classification of DN (AUC of 0.95), we also recorded a total of 10 false-positive and 8 false-negative classifications among the T2D case and control samples. From four of the apparently false-positive patients (i.e. controls classified as cases), follow-up data were available. One of the apparently false-positive controls developed microalbuminuria, and one developed macroalbuminuria after 1 year follow-up. The other two false-positive patients did not develop any sign of DN within the observation period (8 months – 1 year). These data indicate that the apparent false positives may in fact be true positives, but at an early stage of disease that is detectable by CKD273, but not based on albuminuria [12]. These observations are preliminary, need to be expanded to a longer observation period for all patients, but indicate that the results may, at least in part, be due to the prognostic capabilities of the classifier as previously suggested [11–13, 28].

We also investigated the distribution of individual CKD biomarkers in the single centres. As the cohort size in the single centres was significantly smaller (generally less than one tenth) than in the study for development of CKD273, we did not expect to confirm each biomarker. In addition, we did not observe each of the 273 CKD biomarkers in this cohort of diabetic patients, patients with different CKD aetiologies were used, not only patients with DN [10]. Therefore, in the complete biomarker set of peptides included in CKD273, peptides specific to, e.g. IgA-nephropathy, focal segmental glomerulosclerosis, membranous glomerulonephritis, or ANCA-associated vasculitis, are represented. As these are not associated with DN, they are not expected to be validated in this study.

As expected, the correlation of individual biomarkers with CKD was lower than the correlation of the biomarker model with CKD, further supporting the application of a composite biomarker for the identification of complex diseases such as DN. When all data were combined, the majority of the 273 CKD markers could be verified in this combined multicentric cohort of diabetic patients. The most consistent biomarkers were fragments of alpha-1-antitrypsin, collagen alpha-1 (I) and (III), serum albumin, uromodulin, alpha-2-HS-glycoprotein, sodium/potassium-transporting ATPase gamma, polymeric-immunoglobulin receptor and transthyretin. We hypothesize that serum albumin and transthyretin are most likely derived from the circulation, while the different collagen fragments...
most likely originate from the kidney. The increased urinary excretion of alpha-1-antitrypsin by patients with CKD has already been reported [29–32].

The increased urinary abundance of circulating peptides may reflect structural damage to the glomerular filtration barrier and/ or impaired tubular absorption, which is well known to occur in CKD [10]. In the current study, all fragments of alpha-1-antitrypsin, serum albumin, uromodulin, alpha-2-HS-glycoprotein, sodium/potassium-transporting ATPase gamma, polymeric-immunoglobulin receptor and transthyretin, included in the 100 most significant markers from the Good et al. study [10], were verified. The number of consistent collagen alpha-1 (I) fragments was also high, but not all of the collagen alpha-1 (I) fragments included in the top 100 CKD273 marker set were replicated. These results also support the hypothesis that collagen degradation is significantly reduced in DN, resulting in accumulation of collagen in the kidney [33]. The accumulation of collagen results in fibrosis, a well-known hallmark of CKD [34]. The stability among the different centres in circulation- versus kidney-derived proteins such as collagens suggests that disturbances in the glomerular filtration barrier or tubular reabsorption may be earlier and more general events in the establishment of DN than albuminuria. This supports the hypothesis of a common pathway for the development of DN initiated by impaired glomerular filtration, leading to protein overload into glomerular and tubular epithelial cells in later stages to fibrosis [35, 36].

In summary, the results presented in this study and previous data obtained in the validation process of CKD273 set the stage for the PRIORITY trial and demonstrate the suitability of the classifier to be used in such a multicentre study to select patients for intervention, aiming at implementing the first steps towards personalized medicine.

SUPPLEMENTARY DATA

Supplementary data are available online at http://ndt.oxfordjournals.org.

ACKNOWLEDGMENTS

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CONFLICT OF INTEREST STATEMENT

H.M. is co-founder and a shareholder of mosaiques diagnostics GmbH (Hannover, Germany). J.S. and P.Z. are employees of mosaiques diagnostics GmbH. J.P.S. is temporarily employed by mosaiques diagnostics GmbH.

REFERENCES

A pilot study to determine the dose and effectiveness of adrenocorticotropic hormone (H.P. Acthar® Gel) in nephrotic syndrome due to idiopathic membranous nephropathy

Michelle A. Hladunewich¹, Daniel Cattran¹, Laurence H. Beck², Ayodele Odutayo¹, Sanjeev Sethi³, Rivka Ayalon², Nelson Leung⁴, Heather Reich¹ and Fernando C. Fervenza⁴

¹Division of Nephrology, University of Toronto for the Toronto Glomerulonephritis Registry, Toronto, ON, Canada, ²Division of Nephrology, Boston University School of Medicine, Boston, MA, USA, ³Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, MN, USA and ⁴Division of Nephrology and Hypertension, Mayo Clinic, Rochester, MN, USA

Correspondence and offprint requests to: Fernando C. Fervenza; E-mail: fervenza.fernando@mayo.edu

ABSTRACT

Background. H.P. Acthar® Gel is currently the only Food and Drug Administration therapy approved for the treatment of nephrotic syndrome. Active drug ingredients include structurally related melanocortin peptides that bind to cell surface G-protein-coupled receptors known as melanocortin receptors, which are expressed in glomerular podocytes. In animal models of membranous nephropathy, stimulation has been demonstrated to reduce podocyte injury and loss. We hypothesized that H.P. Acthar® Gel would improve symptoms of the nephrotic syndrome in patients with idiopathic membranous nephropathy.

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