

# Urinary Proteomics for Early Diagnosis in Diabetic Nephropathy

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Diabetic nephropathy (DN) is a progressive kidney disease, a well-known complication of long-standing diabetes. DN is the most frequent reason for dialysis in many Western countries. Early detection may enable development of specific drugs and early initiation of therapy, thereby postponing/preventing the need for renal replacement therapy. We evaluated urinary proteome analysis as a tool for prediction of DN. Capillary electrophoresis-coupled mass spectrometry was used to profile the low-molecular weight proteome in urine. We examined urine samples from a longitudinal cohort of type 1 and 2 diabetic patients ( $n = 35$ ) using a previously generated chronic kidney disease (CKD) biomarker classifier to assess peptides of collected urines for signs of DN. The application of this classifier to samples of normoalbuminuric subjects up to 5 years prior to development of macroalbuminuria enabled early detection of subsequent progression to macroalbuminuria (area under the curve [AUC] 0.93) compared with urinary albumin routinely used to determine the diagnosis (AUC 0.67). Statistical analysis of each urinary CKD biomarker depicted its regulation with respect to diagnosis of DN over time. Collagen fragments were prominent biomarkers 3–5 years before onset of macroalbuminuria. Before albumin excretion starts to increase, there is a decrease in collagen fragments. Urinary proteomics enables noninvasive assessment of DN risk at an early stage via determination of specific collagen fragments. *Diabetes* 61:3304–3313, 2012

**C**hronic kidney disease (CKD) is usually characterized by a slow and asymptomatic but progressive impairment of renal function. It generally takes several years from the onset of clinically detectable disease until end-stage renal disease occurs. Patients suffering from end-stage renal disease require renal replacement therapy (dialysis or renal transplantation) for the rest of their lives. Owing to organ shortage, renal transplantation is not an option for all patients. The most common cause of CKD in North America, Europe, and Asia today is diabetic nephropathy (DN), followed by hypertension and glomerulonephritis (1).

DN represents a major and growing public health problem, which may be improved upon by more accurate detection at an early stage (2,3). Early detection may

enable development of specific drugs and early initiation of appropriate preventive therapy that can delay or prevent progression to later stages of disease.

In clinical practice, DN is diagnosed by presence of proteinuria and/or changes in serum creatinine indicating decline in the glomerular filtration rate (4). Although these tests are appropriate in patients with advanced DN, high interindividual variability and, as a consequence, moderate specificity and sensitivity at early stages of disease are major limitations for early diagnosis with these standard tests (5). In general, development of DN is characterized by a progressive increase of urinary albumin excretion rate (UAER) from normo- to micro- to macroalbuminuria (6). Microalbuminuria is considered a risk marker indicating possible onset of DN and is today the best predictor of DN available in the clinic (7,8). However, microalbuminuria may be a marker rather than a predictor of DN. It is not specific for DN and is highly variable within an individual, further compromising its specificity (9,10). Originally, it was reported that 80% of patients with type 1 diabetes and microalbuminuria would develop DN, but our previous results show that only ~34% of type 1 diabetic patients with microalbuminuria progress further to macroalbuminuria and 15–20% even regress to normoalbuminuria (11). In addition, the onset of impaired renal function in the absence of overt albuminuria has been reported in almost one-half of a cohort of type 1 diabetic patients (12), indicating also a lack of sensitivity. Significant reduction of glomerular filtration rate is certainly a clear indicator of DN but only at a late stage of disease, when success of treatment is severely compromised by the presence of advanced structural damage (13).

Therefore, new markers are needed for early diagnosis to allow early treatment of DN. A number of urinary proteins were analyzed in the last years for investigation of their role as predictors of DN (14–16). In comparison with other proteomic methods, capillary electrophoresis coupled to mass spectrometry (CE-MS) offers several advantages (for more details, see recent revs. in 17–19). A main advantage is the good reproducibility, which enabled the generation of >10,000 comparable individual datasets, substantially easing identification and validation of biomarkers. Hence, CE-MS has recently been used to analyze urine samples from healthy volunteers and patients with various kidney diseases in several studies at different centers (20–23).

In a previous study (24), 65 DN biomarkers were identified with a proteomic approach using CE-MS. In an independent validation cohort ( $n = 70$ ), DN was classified with 97% sensitivity and specificity. This DN biomarker classifier derived from 65 biomarkers was further validated in a multicenter study cohort ( $n = 145$ ) with 93.8% sensitivity and 91.4% specificity (25). However, only 34 of the 65 DN peptide biomarkers have been sequenced thus

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Received 20 March 2012 and accepted 30 May 2012.

DOI: 10.2337/db12-0348

This article contains Supplementary Data online at <http://diabetes.diabetesjournals.org/lookup/suppl/doi:10.2337/db12-0348/-/DC1>.

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See accompanying commentary, p. 3072.

far. Most of these were fragments of collagen down-regulated in the urine of patients with DN. We therefore speculated that changes in the collagen metabolism are closely linked with renal damage.

Good et al. (26) recently reported on a classifier based on a panel of 273 urinary biomarkers that was shown to be indicative with high specificity and sensitivity for CKD, irrespective of the underlying pathology, and thus different from the 65-marker DN classifier. In this multicenter effort, a total of 889 urine samples from 339 patients with various biopsy-proven CKDs and 550 control subjects were analyzed using CE-MS to establish a CKD-specific biomarker classifier. This support vector machine (SVM)-based CKD273 classifier showed satisfactory performance for the discrimination between presence and absence of CKD as indicated by specificity and sensitivity values of 97.8 and 85.5%. All 273 peptide biomarkers were identified by tandem mass spectrometry (27), and 74% of the biomarker peptides are collagen fragments. Furthermore, the biomarkers of the CKD273 classifier changed significantly after treatment (28), where the most prominent were changes of the collagen fragments. These changes were not observed in the placebo-treated individuals. It is tempting to speculate that this decrease in urinary collagen-derived peptides is related to an increase in extracellular matrix deposition, which is a major complication in diabetes. Therefore, urinary proteome analysis might enable noninvasive assessment of this process at an early stage via determination of specific collagen fragments.

Since the biomarkers of the CKD273 classifier were identified in an extensive cohort and all biomarkers have been sequenced, we applied this classifier to a longitudinal cohort for the diagnosis of DN to further validate it and to specifically examine whether the proteomic analysis can detect DN at early stages (before onset of microalbuminuria). In addition, we investigated which of the 273 biomarkers are most suitable for early diagnosis of DN.

## RESEARCH DESIGN AND METHODS

The local ethics committees approved the study, and all participants gave informed consent. The study was performed in accordance with the Declaration of Helsinki. From an inception cohort of type 1 diabetic patients followed from onset of diabetes at Steno Diabetes Center (11), samples from urine collection were available from 5 case subjects with normoalbuminuria later developing persistent macroalbuminuria and 9 matched control subjects remaining normoalbuminuric during follow-up and from a cohort of 21 normoalbuminuric diabetic patients (19 type 2 diabetic patients and 2 type 1 diabetic patients), of whom 11 progressed to macroalbuminuria from Austin Health Center. Samples were available almost yearly from each patient over a period of ~10–15 years (UAER: normoalbuminuria <20  $\mu\text{g}/\text{min}$ , microalbuminuria 20–200  $\mu\text{g}/\text{min}$ , and macroalbuminuria >200  $\mu\text{g}/\text{min}$ ). Patients are categorized based on urine samples' characteristics as shown in Supplementary Table 2.

**Sample preparation.** Urine samples were stored in the clinical centers. After arrival, they were prepared essentially as previously described (29). Briefly, for CE-MS analysis 0.7 mL aliquot was thawed immediately before use and diluted with 0.7 mL 2 mol/L urea and 10 mmol/L  $\text{NH}_4\text{OH}$  containing 0.02% SDS. For removal of high-molecular weight polypeptides, samples were filtered using Centriscart ultracentrifugation filter devices (20 kDa molecular weight cutoff; Sartorius, Goettingen, Germany) at 3,000g until 1.1 mL filtrate was obtained. Subsequently, filtrate was desalted using a PD-10 column (GE Healthcare, Stockholm, Sweden) equilibrated in 0.01%  $\text{NH}_4\text{OH}$  in high-performance liquid chromatography-grade water. Finally, samples were lyophilized and stored at  $-20^\circ\text{C}$ . This procedure results in an average recovery of sample in the preparation procedure of ~85% (22). Shortly before CE-MS analysis, lyophilisates were resuspended in high-performance liquid chromatography-grade water to a final protein concentration of 0.8  $\mu\text{g}/\mu\text{L}$  checked by BCA assay (Interchim, Montlucon, France).

**CE-MS analysis.** CE-MS analysis was performed as previously described (30,31). The limit of detection was ~1 fmol, and mass resolution was >8,000, enabling resolution of monoisotopic mass signals for  $z \leq 6$ . After charge

deconvolution, mass deviation was <25 ppm for monoisotopic resolution and <100 ppm for unresolved peaks ( $z > 6$ ). The analytical precision of the platform was assessed by 1) reproducibility achieved for repeated measurement of the same replicate and 2) reproducibility achieved for repeated preparation and measurement of the same urine sample; details on analytical precision have recently been reported (26). To ensure high data consistency, a minimum of 800 peptides/proteins had to be detected with a minimal mass spectrometry resolution of 8,000 in a minimal migration time interval of 10 min.

**Data processing.** Mass spectral ion peaks representing identical molecules at different charge states were deconvoluted into single masses using MosaiquesVisu software (32). Both capillary electrophoresis migration time and ion signal intensity (amplitude) showed variability, mostly owing to different concentrations of ions in the sample, and were consequently normalized. Reference signals of 1,770 urinary polypeptides were used for capillary electrophoresis time calibration by local regression. For normalization of analytical and urine dilution variances, mass spectrometry signal intensities were normalized relative to 29 internal standard peptides generally present in at least 90% of all urine samples with small relative SD. For calibration, linear regression was performed (33). The obtained peak lists characterized each polypeptide by its molecular mass (Da), normalized capillary electrophoresis migration time (minutes), and normalized signal intensity. All detected peptides were deposited, matched, and annotated in a Microsoft SQL database, allowing further statistical analysis.

**CKD273 classifier analysis.** CE-MS measurement of the urine samples and data processing resulted in a maximum of 5,010 distinct peptides, which described the human urinary low-molecular weight proteome (27,34). The CKD273 classifier is an SVM-based classification model (35–37), which allows the classification of samples in the high-dimensional parameter space using MosaCluster software (version 1.7.0) (38). When the CKD273 classifier was applied to CE-MS data of unknown samples, MosaCluster calculated classification scores based on the amplitudes of the 273 CKD biomarkers. Classification is performed by determining the Euclidian distance (defined as the SVM classification score) of the 273-dimensional vector to a 272-dimensional maximal margin hyperplane, which was defined previously (26). The cutoff of the classification score was determined with the result of the biomarker discovery cohort in the study by Good et al. (26). Patients with urine samples who had classification factors >0.343 were classified as CKD273 classifier-positive case subjects, and patients with urine samples scoring <0.343 were classified as CKD273 classifier control subjects.

**Statistical analysis.** Sensitivity, specificity, and area under the curve (AUC) of the previously defined CKD273 classifier and 95% CIs were calculated using receiver operating characteristic (ROC) plots (MedCalc version 12.1.0.0; MedCalc Software, Mariakerke, Belgium [www.medcalc.be]) (39). Furthermore, Mann-Whitney *U* test (for independent samples) was performed to develop Box-and-Whisker plots, and logistic regression was used to calculate the (adjusted) odd ratios (ORs) of the CKD273 classifier with this software. For analysis of differences of individual peptides between case and control subjects, statistical significance was assumed at  $P < 0.05$ .

## RESULTS

**Early identification of patients at risk for DN.** To systematically assess whether the CKD273 classifier allows identification of patients who develop DN in the future while clinical indicators like UAER are still normal, we retrospectively analyzed 316 urine samples collected in a cohort of initially normoalbuminuric diabetic patients. Samples were available from patients with type 1 ( $n = 16$ ) or type 2 ( $n = 19$ ) diabetes from two different centers (Steno Diabetes Center, Gentofte, Denmark, and Austin Health, Victoria, Australia). We analyzed mean  $\pm$  SD  $9 \pm 3$  urine samples from each patient over a period of  $9.1 \pm 3.3$  years. (Baseline patient data and *P* values are summarized in Table 1 and Table 2.) We defined patients who had an increase in UAER from <20  $\mu\text{g}/\text{min}$  (normoalbuminuric) at baseline to >200  $\mu\text{g}/\text{min}$  (macroalbuminuric) over the observed period as “progressors” and patients who retained a UAER of <20  $\mu\text{g}/\text{min}$  as “nonprogressors.” At baseline, most potential risk factors, i.e., UAER, estimated glomerular filtration rate (eGFR), age, diabetes duration, and blood pressure, showed no significant differences between progressors and nonprogressors. In type 1 diabetic patients (Table 1), only  $\text{HbA}_{1c}$  and systolic blood pressure

TABLE 1  
Patient characteristics at baseline of longitudinal study of type 1 diabetic patients

	<i>n</i>	Sex (male/ female)	Age (years)	Diabetes duration (years)	HbA <sub>1c</sub> (%)	Glucose (mmol/L)	Cholesterol (mmol/L)	Triglyceride (mmol/L)	UAER ( $\mu$ g/min)	eGFR (mL/min/ 1.73 m <sup>2</sup> )	SBP (mmHg)	DBP (mmHg)
Nonprogressors	10	8/2	41 $\pm$ 7	9 $\pm$ 3	7.4 $\pm$ 0.8	10.6 $\pm$ 4.9	n.d.	n.d.	5 $\pm$ 2	105 $\pm$ 13	123 $\pm$ 9	78 $\pm$ 6
Progressors	6	3/3	49 $\pm$ 12	11 $\pm$ 6	8.9 $\pm$ 1.3	7.0 $\pm$ 3.3	n.d.	n.d.	12 $\pm$ 9	102 $\pm$ 19	146 $\pm$ 14	81 $\pm$ 11
<i>P</i> ( <i>t</i> test)		0.299*	0.132	0.356	0.029	0.167			0.123	0.765	0.018	0.575

Data are means  $\pm$  SD unless otherwise indicated. DBP, diastolic blood pressure; n.d., no data available; SBP, systolic blood pressure. \*Fisher exact test.

were different, and in type 2 diabetic patients (Table 2) glucose concentrations were different between groups. However, observation of the clinical parameters at end point of the longitudinal study (data not shown) showed that no risk factor except UAER and eGFR showed significant differences between progressors and nonprogressors. Proteome analysis was performed without the laboratory having any knowledge of the clinical characteristics or outcome (single blinded).

In this longitudinal study, all urine samples from diabetic patients were measured with CE-MS. The calibrated CE-MS data of each urine sample was matched to the urinary database. Applying the CKD273 classifier to the CE-MS data of each urine sample resulted in a classification score defined by SVM-based analysis. The resulting classification factors are listed in Supplementary Table 1. The CKD273 classifier score was associated with CKD events in univariate analysis (OR 25.6 [95% CI 2.5–265.4], *P*=0.007). When adjustment was made for other known CKD risk factors and potential confounders, the CKD273 score remained significantly associated with CKD, as shown in Table 3.

Owing to the fact that proteomic analysis of body fluids may be troubled by sample degradation/proteolysis over time, it is instructive to demonstrate that the classification score of the CKD273 classifier is irrespective of the storage time. Long-term stability was analyzed with a standard sample (40) over 35 months. With the regression analysis of these 1,229 data, we extrapolated a possible shift of the CKD273 classifier owing to the long-term storage of the samples in the clinical centers (Supplementary Fig. 1). The longest storage time (analysis date minus sampling date) was calculated to be 259 months. The potential shift of  $-0.286$  was within the intermediate precision of the CKD273 classifier ( $10 \pm 0.300\%$ ), which has been analyzed before (26).

Progression was defined as change in UAER from normo- to microalbuminuria (Supplemental Fig. 2). Of type 2 diabetic patients who progressed to microalbuminuria during follow-up (*n* = 10), seven had classification factors above the cutoff before they developed microalbuminuria. Of the type 1 diabetic patients who progressed to microalbuminuria during follow-up (*n* = 6), four showed classification factors above the cutoff before developing microalbuminuria. In contrast, only two of nine type 2 diabetic patients (and none of the type 1 diabetic patients) who did not progress to microalbuminuria had classification factors above the cutoff.

To determine how many years before the development of macroalbuminuria the CKD273 classifier showed a positive result and to compare this with microalbuminuria, we performed paired *t* tests for all progressors (*n* = 16). With use of the CKD273 classifier, the diagnosis of macroalbuminuria were  $4.9 \pm 2.2$  years earlier compared with  $3.4 \pm 2.1$  years for microalbuminuria (*P* = 0.016) (Fig. 1). The difference of 1.5 years means a relative improvement of 44% for the urinary proteomic analysis compared with the commonly used microalbuminuria.

To investigate the predictive value of the CKD273 classifier in comparison with UAER with respect to diabetic nephropathy, we analyzed UAER and CKD273 classifier of each patient at  $-5$ ,  $-4$ ,  $-3$ ,  $-2$ , and  $-1$  year before onset of macroalbuminuria (Fig. 2). In Fig. 2A, progressors are on average around the cutoff (0.343) and nonprogressors are lower. In Fig. 2B, the mean of the classification factors is above the cutoff except at  $-5$  years before onset of

TABLE 2  
Patient characteristics at baseline of longitudinal study of type 2 diabetic patients

	<i>n</i>	Sex (male/female)	Age (years)	Diabetes duration (years)	HbA <sub>1c</sub> (%)	Glucose (mmol/L)	Cholesterol (mmol/L)	Triglyceride (mmol/L)	UAER ( $\mu$ g/min)	eGFR (ml/min/1.73 m <sup>2</sup> )	SBP (mmHg)	DBP (mmHg)
Nonprogressors	9	1/8	56 $\pm$ 11	n.d.	8.9 $\pm$ 1.6	15.6 $\pm$ 3.1	6.1 $\pm$ 1.5	2.2 $\pm$ 2.9	8 $\pm$ 5	77 $\pm$ 16	131 $\pm$ 13	83 $\pm$ 10
Progressors	10	6/4	63 $\pm$ 10	n.d.	8.6 $\pm$ 1.1	11.5 $\pm$ 3.2	5.5 $\pm$ 1.2	2.0 $\pm$ 1.0	10 $\pm$ 3	72 $\pm$ 27	142 $\pm$ 13	79 $\pm$ 10
<i>P</i> ( <i>t</i> test)		0.057*	0.192		0.728	0.038	0.462	0.906	0.357	0.635	0.149	0.471

Data are means  $\pm$  SD unless otherwise indicated. DBP, diastolic blood pressure; n.d., no data available; SBP, systolic blood pressure. \*Fisher exact test.

macroalbuminuria, where the SD of progressors and non-progressors overlap. The UAER showed a good separation of progressors and nonprogressors at  $-1$  and  $-2$  years before onset of macroalbuminuria (Fig. 2C and D). Furthermore, as depicted in Fig. 2D, the mean UAER of the progressors is below the cutoff (20  $\mu$ g/min) from  $-4$  and  $-5$  years, and the SD overlaps from  $-3$ ,  $-4$ , and  $-5$  years before onset of macroalbuminuria.

For the differentiation of progressors from non-progressors, an ROC analysis of all urine samples where 5-year follow-up resulted in either macroalbuminuria (progressor) or normoalbuminuria (nonprogressor) was performed using UAER or proteomic scoring as a continuous variable (Fig. 3A). Based on 214 urine samples, this ROC analysis resulted in an AUC of 0.93 (95% CI 0.89–0.96) for the proteomic scores compared with 0.86 (0.81–0.90) for the UAER in the same samples ( $P = 0.022$ ). To obtain more information on the predictive value of the CKD273 classifier, we examined only urine samples that were normoalbuminuric at the sampling date ( $n = 150$ ). The ROC analysis resulted in an AUC of 0.92 (95% CI 0.86–0.96) for the CKD273 classifier versus 0.67 (0.59–0.75) for UAER ( $P = 0.0001$ ) (Fig. 3B).

To examine the sensitivity of the CKD273 classifier in relation to type of diabetes, we performed a stratified ROC analysis. For urine samples ( $n = 128$ ) from type 2 diabetic patients, AUC values of 0.94 (95% CI 0.88–0.97) for the CKD273 classifier and 0.80 (0.72–0.86) for UAER were observed ( $P < 0.001$ ). For urine samples ( $n = 86$ ) from type 1 diabetic patients, ROC analysis resulted in AUC values of 0.91 (0.82–0.96) for the CKD273 classifier and 0.93 (0.86–0.98) for the UAER ( $P = 0.607$ ).

**Time course of urinary biomarker levels.** In the former section, we demonstrated that the urinary biomarkers enabled detecting development of DN with high sensitivity and specificity  $\sim 4$  years before clinical manifestation. The aim of the subsequent assessment was to examine which of the 273 biomarkers showed altered urinary excretion at this early time point. Therefore, we compared urinary biomarker levels at “early” ( $-5$  to  $-3$  years) and “late” ( $-2$  to 0 years) time points before clinical manifestation of DN. Subsequently, we examined the CKD273 classifier, UAER, and selected representative specific peptides (with the highest AUC values in their group) of the CKD273 classifier in patients at late and early stage before clinical manifestation of macroalbuminuria in type 1 (Supplemental Fig. 3) and type 2 (Supplemental Fig. 4) diabetic patients. This was done to assess the performance of each analysis/biomarker with respect to diagnosis over time. As previously demonstrated in type 1 diabetic patients, also at late and early stages, the CKD273 classifier showed AUC values ( $P = 0.0889$  and 0.9570) similar to those of UAER. In type 2 diabetic patients, the subdivision in late and early stages demonstrated significant higher AUC values ( $P = 0.0348$  and 0.0156) of the CKD273 classifier and UAER.

In urine of patients of both diabetes types, fragments of collagens, polymeric-immunoglobulin receptor, clusterin, CD99 antigen, and uromodulin had lower amplitude levels in progressors than in nonprogressors. In the majority of the case subjects, the AUC values at later stage were higher than in the early stage prior to clinical diagnosis of DN. In contrast, fragments of abundant blood proteins, such as  $\alpha$ -1-antitrypsin or serum albumin, had higher amplitude levels in progressors than in nonprogressors.

The results of the statistical analysis of each CKD biomarker peptide per patient group (progressors or nonprogressors)

TABLE 3  
ORs of CKD273 predicted by CKD273 classifier at baseline

Factors adjusted for	OR for CKD273 classifier	95% CI	<i>P</i>
Univariate	25.6	2.5–265.4	0.007
Age (years)	17.9	1.5–217.0	0.024
Sex	27.0	2.7–274.1	0.005
Diabetes type	32.5	2.5–420.5	0.008
UAER ( $\mu\text{g}/\text{min}$ )	21.3	1.8–246.6	0.014
eGFR ( $\text{mL}/\text{min}/1.73 \text{ m}^2$ )	25.9	2.4–282.2	0.005
SBP (mmHg)	22.0	1.6–296.6	0.000
DBP (mmHg)	44.7	3.5–569.8	0.001
HbA <sub>1c</sub> (%)	48.1	2.6–878.0	0.001
Glucose (mmol/L)	30.8	2.8–343.2	0.003

DBP, diastolic blood pressure; SBP, systolic blood pressure.

at early and late stages stratified by diabetes type are shown in Supplementary Table 2. In the urine of type 1 diabetic patients, 66 of the 273 biomarkers were significant at early stages, whereas 69 biomarkers were significant at late stages. In type 2 diabetic patients, more biomarkers were significant: while 85 of 273 biomarkers showed significant alterations ( $P < 0.05$ ) at the early time point, urinary levels of 130 of 273 biomarkers were significantly altered at the late time point. As depicted in Fig. 4A and B, AUC values of collagen fragments were higher than those of other protein fragments in type 1 (late:  $P = 0.0166$ ; early:  $P = 0.0355$ ) and type 2 (late:  $P = 0.0001$ ; early: 0.0073) diabetic patients. Interestingly, urinary fragments of classical serum biomarker candidates showed almost no differences at early time points. While in urine of type 1 diabetic patients 1 of 18  $\alpha$ -1-antitrypsin fragments were significantly altered, no serum

albumin fragments were significantly elevated (Supplementary Table 2). In urine of type 2 diabetic patients, 2 of 9 serum albumin fragments and no  $\alpha$ -1-antitrypsin fragments were significantly changed.

Furthermore, we observed the best AUC values of the biomarkers at early and late stages in type 1 and 2 diabetic patients. Therefore, we searched for the highest AUC value of a protein fragment at late stage and compared it with the AUC value at early stage (Fig. 5A and C). This procedure was also performed with the highest AUC values at early stages (Fig. 5B and D). This assumption indicated that collagen peptides, especially collagen  $\alpha$ -1(I) and collagen  $\alpha$ -1(III) fragments, have the highest AUCs at both stages compared with peptides of other protein groups. In some cases (e.g., uromodulin, polymeric immunoglobulin receptor), the same peptides had the highest AUC values at late and early stages. Furthermore, almost all peptides with high AUCs at late stage also had AUC values  $>0.7$  at early stage and vice versa.

## DISCUSSION

In this study, we demonstrate that the previously generated CKD273 classifier, when applied to normoalbuminuric patients, identifies patients who will develop diabetic nephropathy during follow-up, performing better than or equal to UAER. In the investigated cohort, the CKD273 classifier was able to predict development of DN before patients developed microalbuminuria. The classification factors of the CKD273 classifier in patients who developed DN over the time showed consistently higher values than in patients who did not develop DN. Furthermore, the CKD273 classifier identified progressors in 65% of the case subjects earlier than the classical parameter UAER; on average, the CKD273 classifier was 1.5 years earlier than microalbuminuria. Interestingly, the performance of UAER

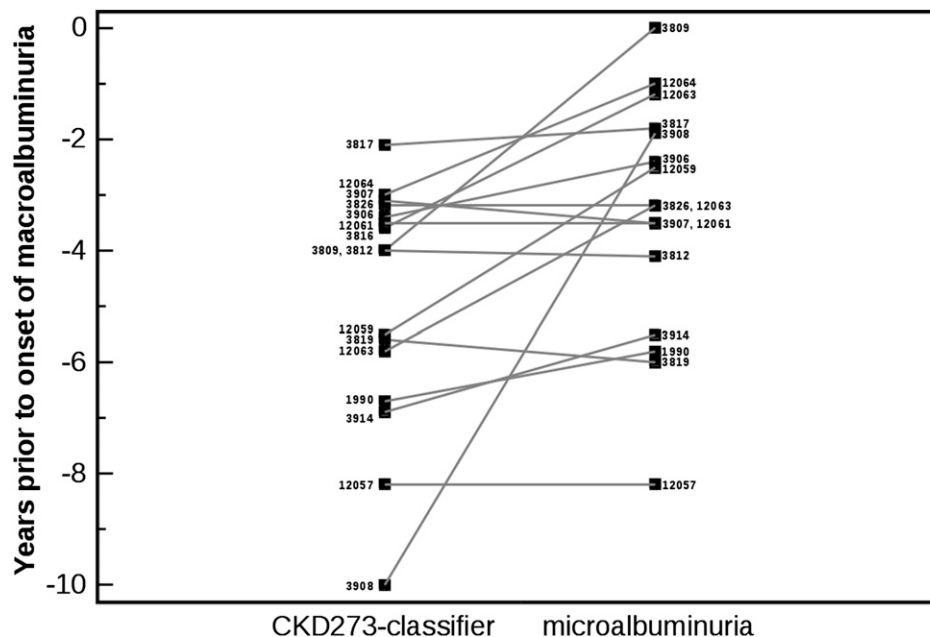
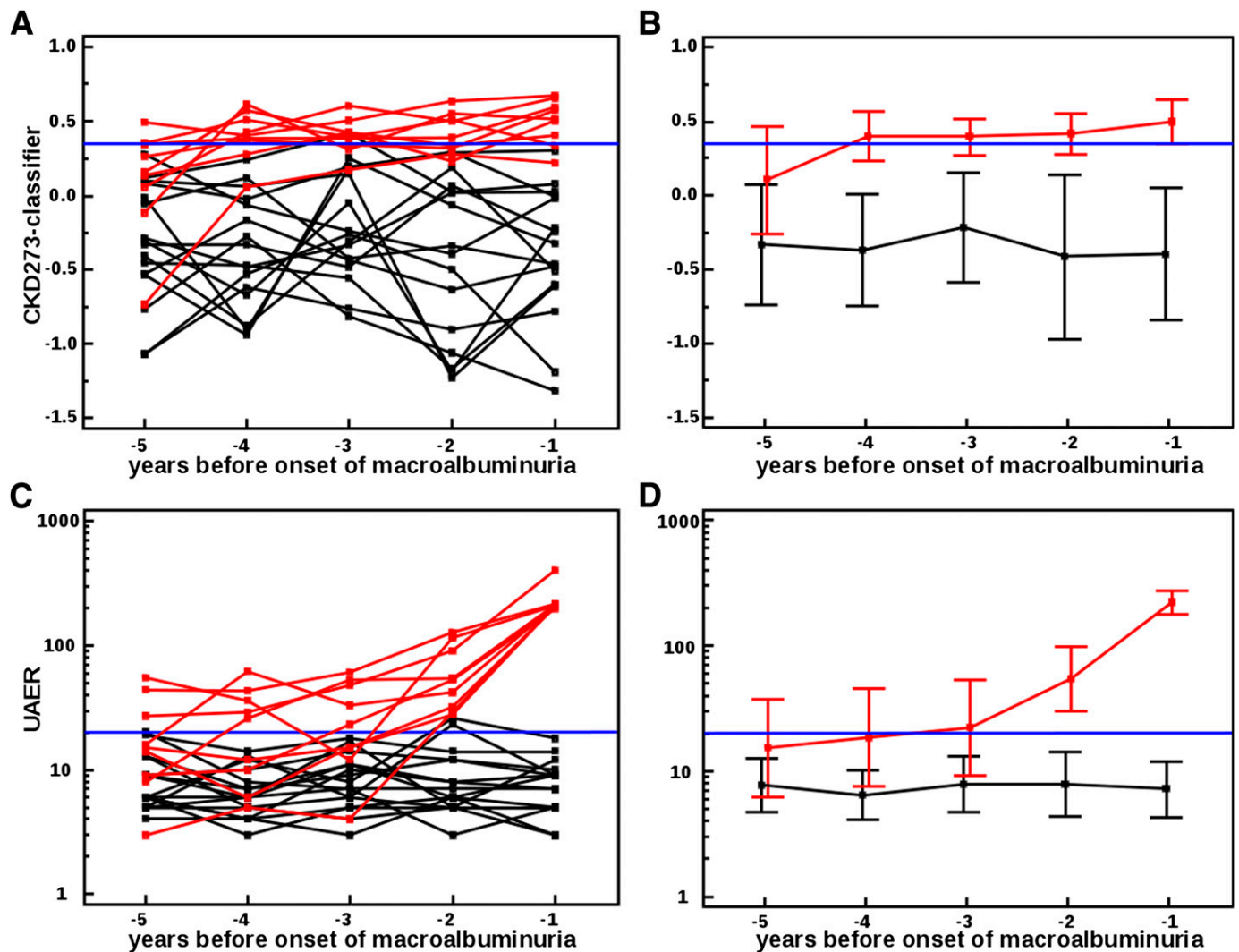


FIG. 1. Dot-and-line plot of the comparison between early diagnoses of the CKD273 classifier and microalbuminuria in the longitudinal cohort. The *y*-axis depicts the years prior to onset of macroalbuminuria. The years prior to the onset of macroalbuminuria is the difference in examination date (Supplementary Table 1) of the first urine sample with UAER  $>200 \mu\text{g}/\text{min}$ , the examination date of the first sample with a classification factor  $>0.343$  in the case of the CKD273 classifier, and the examination date of the first sample with UAER  $>20 \mu\text{g}/\text{min}$  in the case of microalbuminuria, respectively. The numbers next to the dots correspond with the number of patients in the longitudinal cohort.



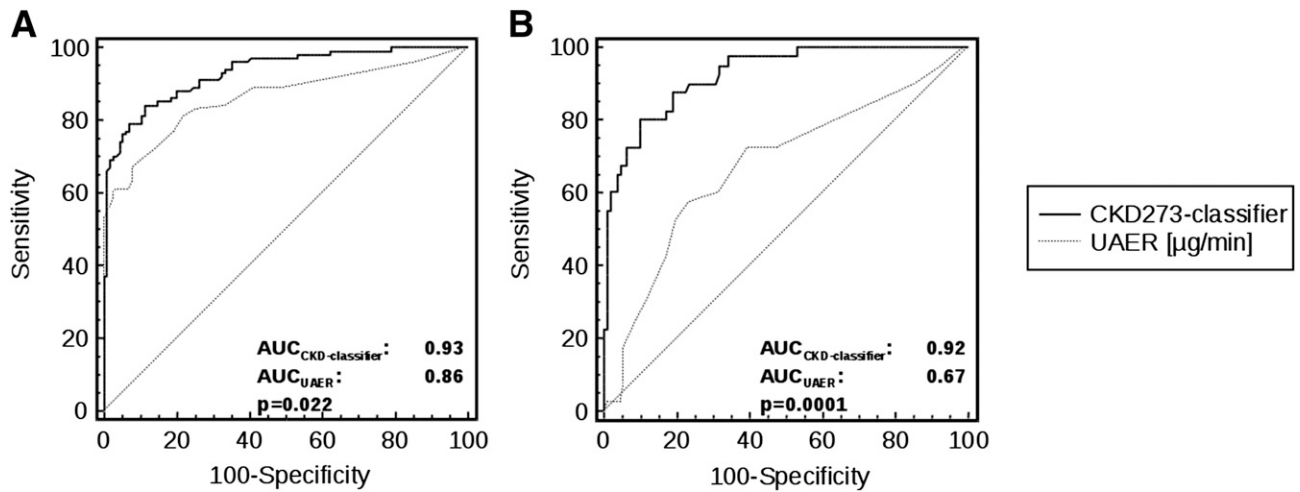
**FIG. 2.** Dot-and-line plots of the CKD273 classifier and UAER of progressors and nonprogressors of DN in the longitudinal data analysis. The x-axis shows the years prior to onset of macroalbuminuria. The blue line depicts the cutoff (0.343) of the CKD273 classifier and the cut off (20  $\mu\text{g}/\text{min}$ ) from normo- to microalbuminuria. The plots in the *left panel* show the progress of the CKD273 classifier and the UAER over the years prior to onset of macroalbuminuria. The *right panel* indicates the mean  $\pm$  SD of the CKD273 classifier and UAER.

was lower in type 2 diabetic patients, whereas the AUC values of the CKD273 classifier were similar with stratification for diabetes type. This effect may be due to the fact that albuminuria is a good predictor for development of CKD in younger patients, but its accuracy is compromised in the elderly.

Our data indicate that normoalbuminuric patients with the CKD273 classifier-positive pattern are at increased risk for development of DN and can be identified as such before patients develop microalbuminuria (at least in the type 2 diabetic patients). This suggests that the pattern could be used in the clinic to identify patients in need of optimal renoprotective treatment at an even earlier stage than is possible today. In clinical trials, the CKD273 classifier can potentially be used to identify high-risk normoalbuminuric subjects for intervention trials aiming for prevention of DN, thereby targeting intervention to those who need it and reducing the number of subjects needed for enrollment (41). Previous attempts at early prevention of development of microalbuminuria with blockade of the renin-angiotensin-aldosterone system have only shown limited (42) or no (43) beneficial effect,

perhaps because intervention has to be targeted at high-risk normoalbuminuric patients, such as CKD273 classifier-positive patients.

Statistical analysis of the 273 biomarkers depicted the regulation of each peptide in the urine with respect to diagnosis of DN over time. In the urine of diabetic patients, collagen fragments played the most important role even 3–5 years before onset of macroalbuminuria. Collagen fragments, especially fragments of the collagen  $\alpha$ -1(I) chain, are major constituents of the low-molecular weight urinary proteome (27). These peptides are likely the result of normal physiological turnover of the extracellular matrix. Hence, it has been assumed that diminished activity of matrix metalloproteinases may be responsible for the accumulation of proteins in the extracellular matrix and collagens that typify the fibrotic kidney (44). This effect may be interpreted as an indication of increased tissue levels of inhibitors of matrix metalloproteinases. Accumulation of extracellular matrix as predominantly observed in diabetic nephropathy was recently shown to be associated with decreased excretion of several specific collagen fragments (45). The data of this longitudinal study

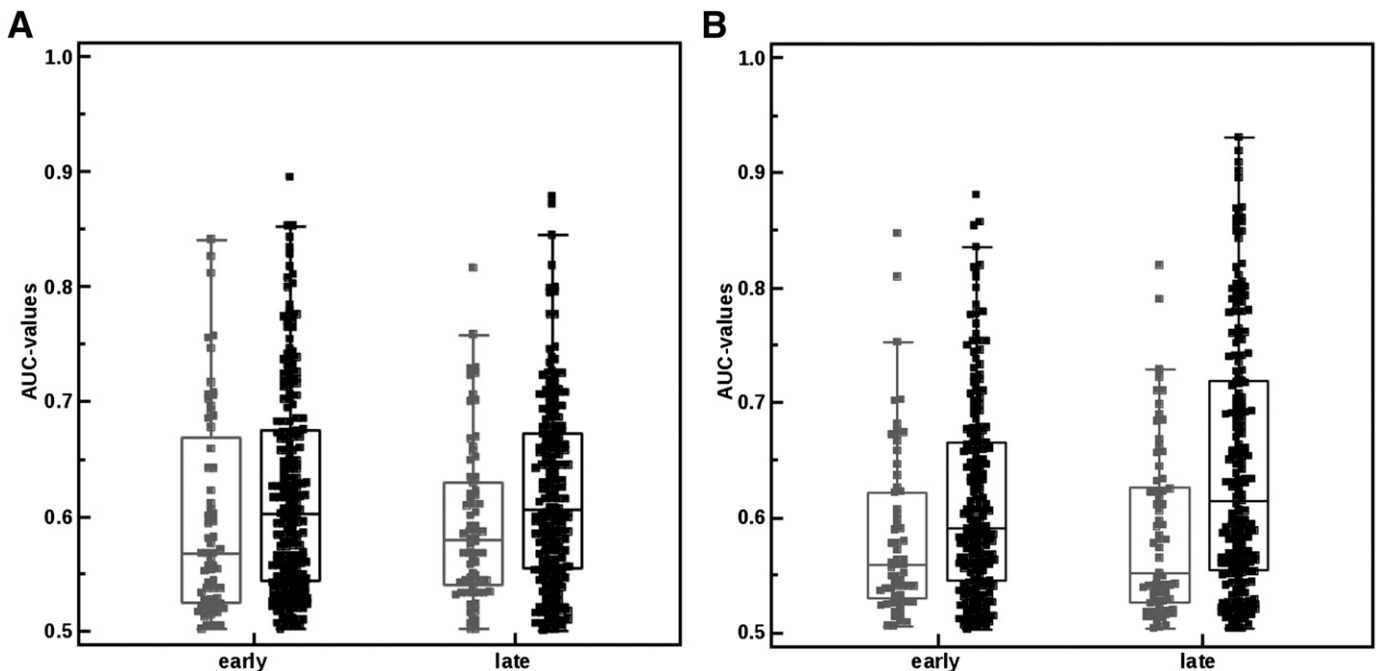


**FIG. 3.** Comparison of ROC curves of the classification results from longitudinal collected urine samples. **A:** ROC analysis of all urine samples of diabetic patients at sampling date up to 5 years prior to onset of macroalbuminuria (DN). **B:** ROC analysis of all samples of diabetic patients who are normoalbuminuric at sampling date up to 5 years prior to onset of DN. The black line shows the ROC curve from the CKD273 classifier and the dashed line from the UAER.

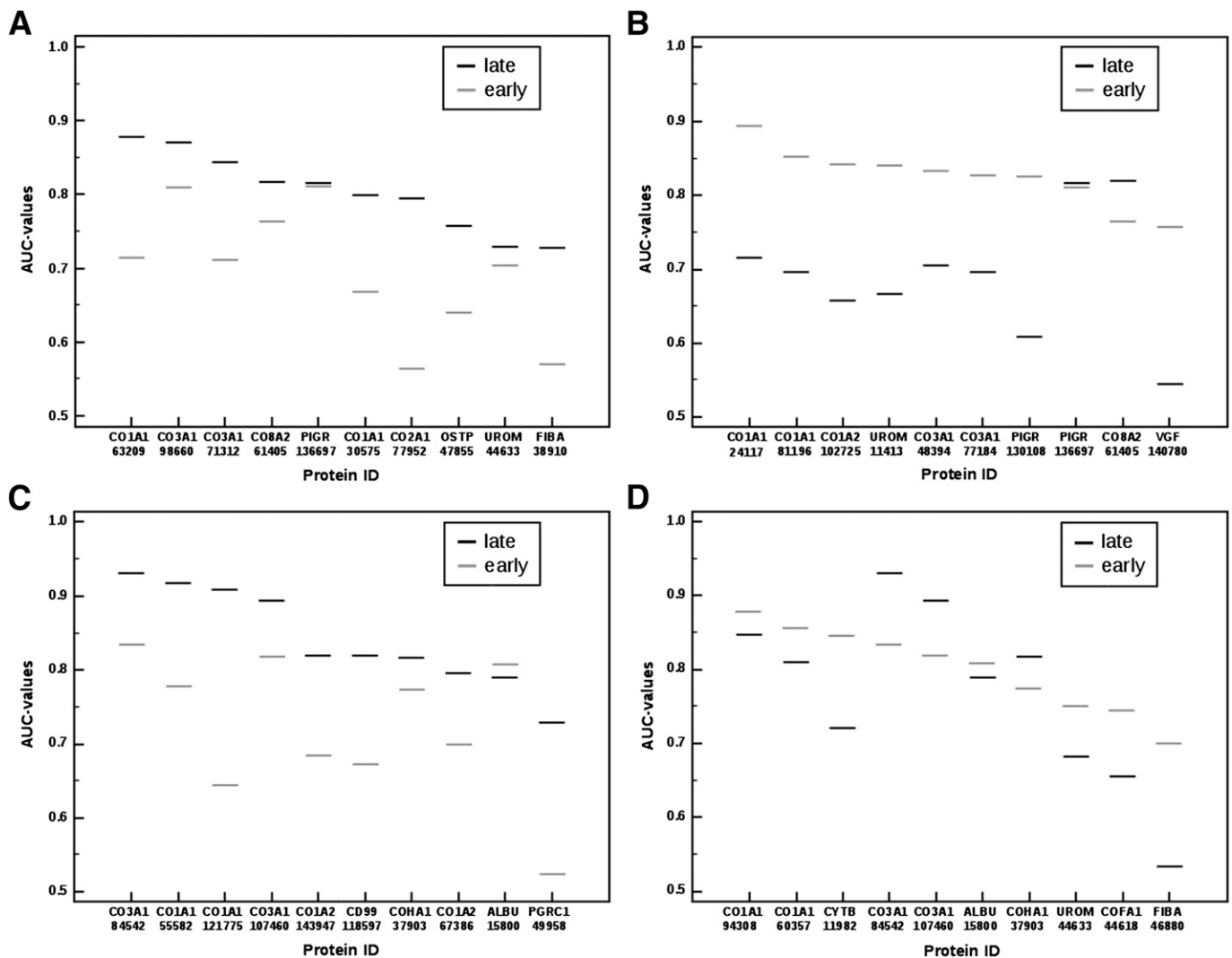
support the hypothesis that collagens play an important role in the development of diabetic nephropathy and may be suitable targets for therapeutic effects of novel drugs. It seems obvious that the use of a mass spectrometry-independent validation approach with available antibody reagents will allow the assessment of the concentration of full-length collagen versus collagen fragments. This would support the conclusion that the change in urinary collagen fragment concentration is generated by a disease process with decreased protease activity in urine. Unfortunately, the generation of antibodies for collagen fragments is difficult. Owing to the fact that almost all collagen fragments

are modified with several hydroxylated proline residues, the use of an immuno-based assay would typically only allow the detection of either the modified or the unmodified form—not the comparison of the abundance of each form when using only a single antibody (46). However, the next step will be to provide any evidence of alteration in protease activity, e.g., in experimental models.

Furthermore, other protein fragments show changes in the urine at an early stage of diabetic nephropathy: uromodulin expression is essentially restricted to the tubules. Excretion of uromodulin has been reported to be down-regulated in diabetic nephropathy (24,47,48), and reduced



**FIG. 4.** Box-and-Whisker plots of AUC values from biomarkers of the CKD273 classifier in type 1 (**A**) and type 2 (**B**) diabetic patients separated in collagen-derived and non-collagen-derived peptides. The black plot and dots depict the AUC values of the collagen fragments, and the gray plot and dots depict the AUC values of the noncollagen fragments.



**FIG. 5.** Distribution of highest AUCs of CKD273 classifier biomarkers for type 1 diabetic patients at late stage ( $-5$  to  $-3$  years prior to onset of macroalbuminuria) (A) and early stage ( $-2$  to  $0$  years prior to onset of macroalbuminuria) (B) and for type 2 diabetic patients at late stage (C) and early stage (D). For this figure, best AUCs ( $>0.7$ ) were selected at late and at early stage in type 1 and 2 diabetic patients, respectively (Supplementary Table 2). In case subjects in whom more than two peptides of a protein were identified, only two peptides are depicted. The AUC values of late stage are depicted with black lines and of early stage with gray lines. The markers are characterized by protein ID and the SwissProt name.

excretion of specific uromodulin fragments has also been observed in other forms of CKD (22). Clusterin (apolipoprotein J) has been known to be associated in diabetes (49), and a number of papers have been published on the possible use of urinary clusterin concentration analysis in the assessment of proteinuria and renal function disorders (50,51).  $\alpha$ -1-antitrypsin seems to be a good marker for the differentiation between DN case and control subjects (26), but for the early diagnosis of DN the amplitude levels are not significantly different in the progressors compared with nonprogressors.

A shortcoming of the study reported here is the relatively low number of patients included. Unfortunately, it is very difficult to obtain longitudinal collected samples over a large period. However, the results were consistent within each group and statistically significant. The ultimate proof of the benefit of urinary proteomics in management of DN would be a clinical trial that aims at identification of patients at risk for developing DN at an early stage (before microalbuminuria) based on urinary proteomics, followed by a targeted intervention (41). Such a proteomics-driven

intervention trial has started in Europe with the use of the CKD273 classifier (<http://eu-priority.org>).

In summary, collagens showed the major role in the initiation of DN, even at an early time point. The progress in urinary proteomics and the use of multiple biomarker classifiers, like the CKD273 classifier, open the possibility of establishing new tools adapted to different clinical needs. Some of them have been built up to differentiate etiology and others to screen for DN and DN progression. Although not routinely available, urinary proteomics is becoming more and more accessible with increasing automation, easing application, and reducing costs. In our study, urinary proteomics enabled identification of new biomarkers for early detection of DN with promising clinical value.

#### ACKNOWLEDGMENTS

This work was supported in part by European Union funding through SysKID (HEALTH-F2-2009-241544) and by grant 0315896B (NephAge) from Bundesministerium für Bildung und Forschung (BMBF).



P.Z. is employed by mosaïques diagnostics, and H.M. is cofounder and coowner of mosaïques diagnostics, the company that developed and established the CE-MS proteome analysis of human urine. P.R. has received speaker's honorarium from Novartis, sanofi-aventis, Boehringer Ingelheim, and Merck (MSD) and research grants from Novartis. F.P. has received speaker's honorarium and research grants from Novartis. No other potential conflicts of interest relevant to this article were reported.

P.Z. wrote the manuscript and researched data. G.J. contributed urine samples and reviewed and edited the manuscript. P.H. contributed urine samples and reviewed and edited the manuscript. R.J.M. reviewed and edited the manuscript. H.M. contributed to discussion and reviewed and edited the manuscript. S.E.N. reviewed and edited the manuscript. S.P. reviewed and edited the manuscript. F.P. reviewed and edited the manuscript. P.R. contributed urine samples and reviewed and edited the manuscript. P.Z. is the guarantor of this work and, as such, had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

The authors gratefully acknowledge the excellent technical assistance of Annika Krons, Marco Schiemann, and Julia Franke—all of mosaïques diagnostics. The authors are grateful to Dilek Cansiz of mosaïques diagnostics, as well as Jane Wilmot and Karey Cheong of Austin Health for review of the medical records.

## REFERENCES

1. Alebiosu CO, Ayodele OE. The global burden of chronic kidney disease and the way forward. *Ethn Dis* 2005;15:418–423
2. Levey AS, Atkins RC, Coresh J, et al. Chronic kidney disease as a global public health problem: approaches and initiatives - a position statement from Kidney Disease Improving Global Outcomes. *Kidney Int* 2007;72:247–259
3. Remuzzi G, Macia M, Ruggenenti P. Prevention and treatment of diabetic renal disease in type 2 diabetes: the BENEDICT study. *J Am Soc Nephrol* 2006;17(Suppl. 2):S90–S97
4. Levey AS, Eckardt KU, Tsukamoto Y, et al. Definition and classification of chronic kidney disease: a position statement from Kidney Disease: Improving Global Outcomes (KDIGO). *Kidney Int* 2005;67:2089–2100
5. Miller WG, Bruns DE, Hortin GL, et al.; National Kidney Disease Education Program-IFCC Working Group on Standardization of Albumin in Urine. Current issues in measurement and reporting of urinary albumin excretion. *Clin Chem* 2009;55:24–38
6. Parving HH, Hommel E, Mathiesen E, et al. Prevalence of microalbuminuria, arterial hypertension, retinopathy and neuropathy in patients with insulin dependent diabetes. *Br Med J (Clin Res Ed)* 1988;296:156–160
7. Mogensen CE. Microalbuminuria predicts clinical proteinuria and early mortality in maturity-onset diabetes. *N Engl J Med* 1984;310:356–360
8. Rossing P. Prediction, progression and prevention of diabetic nephropathy. The Minkowski Lecture 2005. *Diabetologia* 2006;49:11–19
9. Caramori ML, Fioretto P, Mauer M. The need for early predictors of diabetic nephropathy risk: is albumin excretion rate sufficient? *Diabetes* 2000;49:1399–1408
10. Macisaac RJ, Jerums G. Diabetic kidney disease with and without albuminuria. *Curr Opin Nephrol Hypertens* 2011;20:246–257
11. Hovind P, Tarnow L, Rossing P, et al. Predictors for the development of microalbuminuria and macroalbuminuria in patients with type 1 diabetes: inception cohort study. *BMJ* 2004;328:1105
12. Perkins BA, Ficociello LH, Roshan B, Warram JH, Krolewski AS. In patients with type 1 diabetes and new-onset microalbuminuria the development of advanced chronic kidney disease may not require progression to proteinuria. *Kidney Int* 2010;77:57–64
13. Brenner BM, Cooper ME, de Zeeuw D, et al.; RENAAL Study Investigators. Effects of losartan on renal and cardiovascular outcomes in patients with type 2 diabetes and nephropathy. *N Engl J Med* 2001;345:861–869
14. Matheson A, Willcox MD, Flanagan J, Walsh BJ. Urinary biomarkers involved in type 2 diabetes: a review. *Diabetes Metab Res Rev* 2010;26:150–171
15. Jerums G, Premaratne E, Panagiotopoulos S, Clarke S, Power DA, MacIsaac RJ. New and old markers of progression of diabetic nephropathy. *Diabetes Res Clin Pract* 2008;82(Suppl. 1):S30–S37
16. Steinke JM. The natural progression of kidney injury in young type 1 diabetic patients. *Curr Diab Rep* 2009;9:473–479
17. Fliser D, Novak J, Thongboonkerd V, et al. Advances in urinary proteome analysis and biomarker discovery. *J Am Soc Nephrol* 2007;18:1057–1071
18. Mischak H, Coon JJ, Novak J, Weissinger EM, Schanstra JP, Dominiczak AF. Capillary electrophoresis-mass spectrometry as a powerful tool in biomarker discovery and clinical diagnosis: an update of recent developments. *Mass Spectrom Rev* 2009;28:703–724
19. Mischak H, Delles C, Klein J, Schanstra JP. Urinary proteomics based on capillary electrophoresis-coupled mass spectrometry in kidney disease: discovery and validation of biomarkers, and clinical application. *Adv Chronic Kidney Dis* 2010;17:493–506
20. Decramer S, Wittke S, Mischak H, et al. Predicting the clinical outcome of congenital unilateral ureteropelvic junction obstruction in newborn by urinary proteome analysis. *Nat Med* 2006;12:398–400
21. Julian BA, Wittke S, Novak J, et al. Electrophoretic methods for analysis of urinary polypeptides in IgA-associated renal diseases. *Electrophoresis* 2007;28:4469–4483
22. Haubitz M, Good DM, Woywodt A, et al. Identification and validation of urinary biomarkers for differential diagnosis and evaluation of therapeutic intervention in anti-neutrophil cytoplasmic antibody-associated vasculitis. *Mol Cell Proteomics* 2009;8:2296–2307
23. Kistler AD, Mischak H, Poster D, Dakna M, Wüthrich RP, Serra AL. Identification of a unique urinary biomarker profile in patients with autosomal dominant polycystic kidney disease. *Kidney Int* 2009;76:89–96
24. Rossing K, Mischak H, Dakna M, et al.; PREDICTIONS Network. Urinary proteomics in diabetes and CKD. *J Am Soc Nephrol* 2008;19:1283–1290
25. Alkhalaf A, Zürbig P, Bakker SJ, et al.; PREDICTIONS Group. Multicentric validation of proteomic biomarkers in urine specific for diabetic nephropathy. *PLoS ONE* 2010;5:e13421
26. Good DM, Zürbig P, Argilés A, et al. Naturally occurring human urinary peptides for use in diagnosis of chronic kidney disease. *Mol Cell Proteomics* 2010;9:2424–2437
27. Siwy J, Mullen W, Golovko I, Franke J, Zürbig P. Human urinary peptide database for multiple disease biomarker discovery. *Proteomics Clin Appl* 2011;5:367–374
28. Andersen S, Mischak H, Zürbig P, Parving HH, Rossing P. Urinary proteome analysis enables assessment of renoprotective treatment in type 2 diabetic patients with microalbuminuria. *BMC Nephrol* 2010;11:29
29. Zürbig P, Renfrow MB, Schiffer E, et al. Biomarker discovery by CE-MS enables sequence analysis via MS/MS with platform-independent separation. *Electrophoresis* 2006;27:2111–2125
30. Kolch W, Neustüss C, Pelzing M, Mischak H. Capillary electrophoresis-mass spectrometry as a powerful tool in clinical diagnosis and biomarker discovery. *Mass Spectrom Rev* 2005;24:959–977
31. Theodorescu D, Wittke S, Ross MM, et al. Discovery and validation of new protein biomarkers for urothelial cancer: a prospective analysis. *Lancet Oncol* 2006;7:230–240
32. Neuhoff N, Kaiser T, Wittke S, et al. Mass spectrometry for the detection of differentially expressed proteins: a comparison of surface-enhanced laser desorption/ionization and capillary electrophoresis/mass spectrometry. *Rapid Commun Mass Spectrom* 2004;18:149–156
33. Jantos-Siwy J, Schiffer E, Brand K, et al. Quantitative urinary proteome analysis for biomarker evaluation in chronic kidney disease. *J Proteome Res* 2009;8:268–281
34. Coon JJ, Zürbig P, Dakna M, et al. CE-MS analysis of the human urinary proteome for biomarker discovery and disease diagnostics. *Proteomics Clin Appl* 2008;2:964–973
35. Girolami M, Mischak H, Krebs R. Analysis of complex, multidimensional datasets. *Drug Discov Today Technol* 2007;3:12–19
36. Yang ZR. Biological applications of support vector machines. *Brief Bioinform* 2004;5:328–338
37. Yang ZR, Chou KC. Bio-support vector machines for computational proteomics. *Bioinformatics* 2004;20:735–741
38. Wittke S, Fliser D, Haubitz M, et al. Determination of peptides and proteins in human urine with capillary electrophoresis-mass spectrometry, a suitable tool for the establishment of new diagnostic markers. *J Chromatogr A* 2003;1013:173–181
39. DeLeo JM. Receiver operating characteristic laboratory (ROCLAB): software for developing decision strategies that account for uncertainty. College Park, MD, Second International Symposium on Uncertainty Modeling and Analysis, 25 April 1993, p. 318–325

40. Mischak H, Kolch W, Aivaliotis M, et al. Comprehensive human urine standards for comparability and standardization in clinical proteome analysis. *Proteomics Clin Appl* 2010;4:464–478
41. Mischak H, Rossing P. Proteomic biomarkers in diabetic nephropathy—reality or future promise? *Nephrol Dial Transplant* 2010;25:2843–2845
42. Haller H, Ito S, Izzo JL Jr, et al.; ROADMAP Trial Investigators. Olmesartan for the delay or prevention of microalbuminuria in type 2 diabetes. *N Engl J Med* 2011;364:907–917
43. Bilous R, Chaturvedi N, Sjølie AK, et al. Effect of candesartan on microalbuminuria and albumin excretion rate in diabetes: three randomized trials. *Ann Intern Med* 2009;151:11–20, W3–4
44. Cheng S, Pollock AS, Mahimkar R, Olson JL, Lovett DH. Matrix metalloproteinase 2 and basement membrane integrity: a unifying mechanism for progressive renal injury. *FASEB J* 2006;20:1898–1900
45. Rossing K, Mischak H, Rossing P, Schanstra JP, Wiseman A, Maahs DM. The urinary proteome in diabetes and diabetes-associated complications: New ways to assess disease progression and evaluate therapy. *Proteomics Clin Appl* 2008;2:997–1007
46. Good DM, Thongboonkerd V, Novak J, et al. Body fluid proteomics for biomarker discovery: lessons from the past hold the key to success in the future. *J Proteome Res* 2007;6:4549–4555
47. Chakraborty J, Below AA, Solaiman D. Tamm-Horsfall protein in patients with kidney damage and diabetes. *Urol Res* 2004;32:79–83
48. Sejdiu I, Torffvit O. Decreased urinary concentration of Tamm-Horsfall protein is associated with development of renal failure and cardiovascular death within 20 years in type 1 but not in type 2 diabetic patients. *Scand J Urol Nephrol* 2008;42:168–174
49. Aronis KN, Kim YB, Mantzoros CS. Clusterin (apolipoprotein J): wither link with diabetes and cardiometabolic risk? *Metabolism* 2011;60:747–748
50. Ghiggeri GM, Bruschi M, Candiano G, et al. Depletion of clusterin in renal diseases causing nephrotic syndrome. *Kidney Int* 2002;62:2184–2194
51. Hidaka S, Kränzlin B, Gretz N, Witzgall R. Urinary clusterin levels in the rat correlate with the severity of tubular damage and may help to differentiate between glomerular and tubular injuries. *Cell Tissue Res* 2002;310:289–296



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**Title:**

Urinary Proteomics for Early Diagnosis in Diabetic Nephropathy

**Date:**

2012-12-01

**Citation:**

Zuerbig, P., Jerums, G., Hovind, P., Maclsaac, R. J., Mischak, H., Nielsen, S. E., Panagiotopoulos, S., Persson, F. & Rossing, P. (2012). Urinary Proteomics for Early Diagnosis in Diabetic Nephropathy. *DIABETES*, 61 (12), pp.3304-3313.  
<https://doi.org/10.2337/db12-0348>.

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