## **Urinary Biomarkers Identify Autosomal Dominant Polycystic Kidney Disease** Patients With a High Likelihood of Disease Progression

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Introduction: The variable disease course of autosomal dominant polycystic kidney disease (ADPKD) makes it important to develop biomarkers that can predict disease progression, from a patient perspective and to select patients for renoprotective treatment. We therefore investigated whether easy-to-measure urinary biomarkers are associated with disease progression and have additional value over that of conventional risk markers.

Methods: At baseline, inflammatory, glomerular, and tubular damage markers were measured in 24-hour urine collections (albumin, IgG, kidney injury molecule-1 (KIM-1), N-acetyl-β-D-glucosaminidase (NAG), β2 microglobulin ( $\beta$ 2MG), heart-type fatty acid binding protein (HFABP), macrophage migration inhibitory factor (MIF), neutrophil gelatinase-associated lipocalin (NGAL), and monocyte chemotactic protein-1 (MCP-1). Disease progression was expressed as annual change in estimated glomerular filtration rate eGFR (Chronic Kidney Disease EPIdemiology equation), measured glomerular filtation rate (mGFR) (using <sup>125</sup>I-iothalamate), or height-adjusted total kidney volume (htTKV). Multivariable linear regression was used to assess associations of these markers independent of conventional risk markers.

**Results:** A total of 104 ADPKD patients were included (40  $\pm$  11 years, 39% female, eGFR 77  $\pm$  30, mGFR 79  $\pm$  30 ml/min per 1.73 m<sup>2</sup> and htTKV 852 [510–1244] ml/m). In particular,  $\beta$ 2MG and MCP-1 were associated with annual change in eGFR, and remained associated after adjustment for conventional risk markers (standardized  $\beta = -0.35$ , P = 0.001, and standardized  $\beta = -0.29$ , P = 0.009, respectively). Adding  $\beta$ 2MG and MCP-1 to a model containing conventional risk markers that explained annual change in eGFR significantly increased the performance of the model (final  $R^2 = 0.152$  vs. 0.292, P = 0.001). Essentially similar results were obtained when only patients with an eGFR  $\ge$  60 ml/min per 1.73 m<sup>2</sup> were selected, or when change in mGFR was studied. Associations with change in htTKV were less strong.

Discussion: Urinary β2MG and MCP-1 excretion were both associated with GFR decline in ADPKD, and had added value beyond that of conventional risk markers. These markers therefore have the potential to serve as predictive tools for clinical practice.

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he age at which patients with autosomal dominant polycystic kidney disease (ADPKD) will reach endstage kidney disease (ESKD) shows large interindividual

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variability,<sup>1</sup> even between family members that share the same mutation.<sup>2</sup> Predicting the rate of disease progression has become important, now that the first therapeutic options for ADPKD have emerged.<sup>3,4</sup> Especially patients with a high likelihood of rapid disease progression should be selected for treatment, because in such patients the benefit-to-risk ratio of treatment is expected to be optimal.<sup>5,6</sup>

Currently, several variables are available to predict disease progression in ADPKD. Glomerular filtration

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103 rate (GFR) indexed for age is a strong predictor but is 104 less sensitive in early stages of this disease, when GFR 105 can remain in the normal range due to compensatory 106 hyperfiltration, while cysts are progressively formed.<sup>1</sup> Therefore, much attention has been focused on total 107 kidney volume (TKV) as a predictor.<sup>1,7</sup> Furthermore 108 disease progression is influenced by the ADPKD 109 110 genotype, with patients with a PKD1 mutation, especially truncating mutations, progressing faster toward 111 ESKD compared to patients with a PKD2 mutation.<sup>2</sup> 112 113 However, assessment of TKV and genotype is labo-114 rious and expensive, and their associations with the 115 rate of disease progression are limited at an individual 116 patient level. Therefore, new risk markers need to be 117 developed that, either alone or in combination with 118 conventional risk markers, can predict the rate of 119 disease progression in ADPKD.

120 Because ADPKD is a tubular disease with an 121 inflammatory component, measurement of urinary 122 tubular damage and inflammation markers is of 123 interest, especially because these markers are rela-124 tively inexpensive and easy to measure. Several 125 cross-sectional studies have shown that these 126 markers are associated with ADPKD severity, assessed as GFR and TKV.<sup>8-11</sup> In this study, we aimed 127 128 to determine, in a longitudinal setting, whether 129 urinary tubular damage and inflammation markers 130 are associated with rate of ADPKD progression assessed as annual change in GFR and TKV, and 131 132 whether these markers have added value beyond that 133 of currently used risk markers.

#### METHODS

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#### Setting and Subjects

138 From January 2007 until September 2012, a total of 133 139 ADPKD patients from the University Medical Center Groningen were included in an observational study. 140 The diagnosis of APDKD was made based upon the 141 revised Ravine criteria.<sup>12</sup> Patients were considered 142 ineligible if they received kidney replacement therapy, 143 144had undergone kidney surgery, were unable to undergo magnetic resonance imaging, or had other 145 systemic diseases or used treatments or medications 146 147 potentially affecting kidney function, such as calcineurin inhibitors or nonsteroidal 148 antiinflammatory drugs (NSAIDs).9,10 For the present 149 150 study, 29 patients were excluded because they had a follow up time < 1 year, leaving 104 patients for 151 152 Q2 analysis. The study was performed in adherence to the 153 Declaration of Helsinki, and all participants gave written informed consent. The institutional review 154 155 Q3 board deemed this study exempt from assessment 156 because of its post hoc exploratory nature.

#### Measurements

At the baseline visit, a physical examination was 158 performed, including blood pressure measurements. 159 Fasting blood samples were drawn for the measurement 160 of creatinine and PKD mutation analyses. The esti-161 mated GFR (eGFR) was calculated using the 2009 162 Chronic Kidney Disease EPIdemiology (CKD-EPI) 163 equation.<sup>13</sup> The *PKD* mutation analysis was performed 164 with DNA isolation using PUREGENE nucleic acid 165 purification chemistry on the AUTOPURE LS 98 plat-166 form (Qiagen), followed by sequencing of amplified Q4 167 coding exons directly (exons 34-46), or on long-range 168 polymerase chain reaction products (exons 1-33).<sup>14</sup> In 169 addition, measured GFR (mGFR) was determined by a 170 constant infusion method with <sup>125</sup>I-iothalamate, and 171 magnetic resonance imaging was performed to assess 172 TKV, using a standardized abdominal magnetic reso-173 nance imaging protocol without the use of intravenous 174 contrast. TKV was measured on T2-weighted coronal 175 images using Analyze direct 9.0 (AnalyzeDirect, Inc., 176 Overland Park, KS) by classical volumetry (i.e., manual 177 tracing) and adjusted for height (htTKV). 178

The day before the baseline visit, patients collected a 179 24-hour urine, of which samples were stored frozen 180 at  $-80^{\circ}$ C that were used to measure albumin as a 181 general kidney damage marker; immunoglobulin G 182 (IgG) as a glomerular damage marker; and  $\beta$ 2 micro-183 globulin ( $\beta$ 2MG), kidney injury molecule-1 (KIM-1), 184 and N-acetyl- $\beta$ -D-glucosaminidase (NAG) as proximal 185 tubular damage markers; heart-type fatty acid binding 186 protein (HFABP) as a distal tubular damage marker; and 187 macrophage migration inhibitory factor (MIF), neutro-188 phil gelatinase-associated lipocalin (NGAL), and 189 monocyte chemotactic protein-1 (MCP-1) as inflam-190 mation markers.<sup>15–23</sup> 191

Urinary albumin was determined by immunone-192 phelometry (BNII; Dade Behring Diagnostics, www. 193 dadebehring.com). Urinary IgG, HFABP (Hytest, 05 194 www.hytest.fi),  $\beta$ 2MG (Anogen, www.yesbiotech. 195 com), KIM-1, MIF, NGAL, and MCP-1 (R&D Systems, 196 www.rndsystems.com) were measured by enzyme-197 linked immunosorbent assay. NAG was measured 198 with a modified enzyme assay according to Lockwood 199 and corrected for nonspecific conversion (HaemoScan, 200 www.haemoscan.com). Urine samples were diluted 201 twice for KIM-1,  $\beta$ 2MG, MCP-1, and MIF, 5 times for 202 HFABP, and 100 times for NGAL and IgG. Detection 203 limit for albumin was 0.003 mg/ml, for IgG 220 ng/ml, 204 for  $\beta$ 2MG 18 ng/ml, for KIM-1 0.087 ng/ml, for HFABP 205 0.38 ng/ml, for MIF 0.06 ng/ml, for NGAL 22 ng/ml, 206 and for MCP-1 0.04 ng/ml. The intra- and interassay 207 coefficients of variation were 2.2% and 2.6% for 208 albumin, 6.3% and 8.5% for  $\beta$ 2MG, 7.4% and 14.5% 209 for KIM-1, 3.1% and 13.7% for NAG, 9.3% and 17.6% 210

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