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Proteomic analysis of AQP11-null kidney: Proximal tubular type polycystic kidney disease

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ABSTRACT

Autosomal Dominant Polycystic Kidney Disease (ADPKD) is caused by the mutation of polycystins (PC-1 or PC-2), in which cysts start from the collecting duct to extend to all nephron segments with eventual end stage renal failure. The cyst development is attenuated by a vasopressin V2 receptor antagonist tolvaptan which, however, will not affect proximal tubule cysts devoid of V2 receptor. Aquaporin-11 (AQP11) is expressed selectively in the proximal tubule of the kidney and AQP11-null kidneys have a disruptive PC-1 trafficking to the plasma membrane to develop polycystic kidneys. Here, we analyzed AQP11-null kidneys at the beginning of cyst formation by quantitative proteomic analysis using Tandem Mass Tag (TMT). Among ~ 1200 identified proteins, 124 proteins were differently expressed by > 1.5 or < 0.8 fold change. A pancreatic stone inhibitor or a growth factor, lithostathine-1 (Reg1) was most enhanced by 5 folds which was confirmed by western blot, while mitochondria-related proteins were downregulated. The identified proteins will be new target molecules for the treatment of proximal tubular cysts and helpful to explore the functional roles of AQP11 in the kidney.

1. Introduction

Human Autosomal Dominant Polycystic Kidney Disease (ADPKD) is caused by the mutation of polycystin-1 (PC-1) or polycystin-2 (PC-2) [1–3]. Cysts originate from the collecting duct in PC-1 null mice with defective cAMP signaling [1], which are marginally attenuated by a V2 receptor antagonist, tolvaptan [4]. Since V2 receptor is absent in the proximal tubule, tolvaptan will not affect the growth of proximal tubular cysts. Moreover, the mechanism for cyst development in the proximal tubule may not be same as in the collecting duct. The therapy against proximal tubular cysts will improve the suboptimal efficiency of tolvaptan therapy for ADPKD [4].

Aquaporin-11 (AQP11) is a new member of aquaporin family which is expressed at the membrane of intracellular organelles such as the endoplasmic reticulum (ER) [5–8]. Currently, the function of AQP11 is not clear even as a water channel due to its unusual location in the cell. However, AQP11-null mice revealed a striking phenotype of intracellular vacuole formation in the proximal tubule at one week old [5,9] indicating its critical role in the proximal tubule development. Surprisingly, these cells subsequently turn to cystic epithelia to develop polycystic kidney disease (PKD) at three week old and death at one month old [5]. The mechanism for the development of PKD in AQP11-null mice may not be related to its water channel function.

Our recent study on AQP11-null mice revealed a trafficking defect of PC-1 to the plasma membrane due to its abnormal glycosylation at the ER [10] possibly induced by abnormal environment of the ER with defective water and/or solutes transports. Irrespective of its mechanism, AQP11-null mice will be a good model for ADPKD affecting the proximal tubule selectively with intact collecting ducts, which will be useful to examine the proximal tubular cyst formation in ADPKD. As is the case with conditional knock-out mice of PC-1 [11], the effect of AQP11 deletion is also developmentally dependent as cysts were not observed with the disruption of AQP11 at ten days after birth [9]. Furthermore, these cysts may represent a very early stage of the cyst formation as they are in fact not cysts but dilated proximal tubules [9].

To expand our previous microarray studies [12], we employed a proteomic approach in this study to compare the differentially expressed proteins in AQP11-null kidney to identify key molecules for the development of proximal tubule specific cysts and functional role of AQP11 in the kidney.

2. Materials and methods

2.1. Animals

All procedures performed in animals were approved by the Meiji

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Pharmaceutical University Committee for Ethics of Experimentation and Animal Care (approved number: 2005). Homogenous AQP11-null mice {AQP11(-/-)} were generated as previously reported [5,12,13]. In short, AQP11(-/-) mice were produced by mating heterozygous AQP11-null mice {AQP11(+/-)} since AQP11(-/-) mice are fatal before matured enough to be mated. The genotypes for AQP11 gene mutation were determined by PCR as previously reported [5].

2.2. Protein isolation

Kidneys were isolated from three AQP11-null mice and three wild type mice anesthetized by barbiturate. The kidneys were frozen-powdered with liquid nitrogen by Cryo-Press (MICROTEC CO., LTD, Chiba, Japan), which were then homogenized in 20 volumes of 12 mM sodium deoxycholate (SDC), 12 mM sodium lauryl sulfate (SLS), and 50 mM triethylammonium bicarbonate. The homogenate was centrifuged at 19,000 × *g* at 4 °C for 15 min. The supernatant containing the mixture of proteins was collected, and the protein concentration was determined using a RCDC protein assay kit (Bio-Rad Laboratories, Hercules, CA, USA).

2.3. Trypsin digestion

The proteins were digested with trypsin essentially as previously described [14,15], with following modifications. 20 μL of 200 mM Triethylamonium bicarbonat/12 mM SDC/12 mM SLS and 2 μL of 200 mM tris (2-carboxylethyl) phosphine hydrochloride/ 120 mM TEAB were added and then the mixture was incubating at 50 °C for 30 min. After the addition of 2 μL of 375 mM iodoacetamide, the mixture was incubated in the dark for 30 min, to which 2 μL of 100 ng/μL trypsin was added with further incubation at 37 °C for indicated periods. Acetonitrile (ACN) and 5% trifluoroacetic acid, 50 μL each, were then added to the digest, followed by the centrifugation at 19,000 × *g* for 15 min. The supernatant was subjected to Tandem Mass Tag (TMT)-labeling as following.

2.4. TMT-labeling

Each 6-plex TMT labeling reagent was re-dissolved with anhydrous ACN. A total of 12 μL of TMT solution was added to the eluate and then incubated for 1 h at the room temperature. The reaction was terminated by adding 2 μL of 5% hydroxyamine. Six samples labeled with TMT reagents were combined and desalted for SCX fractionation using 'stop and go extraction tips' (Stage tips) [16] filled with Empore™ C18 sealant and Cation Exchange (3 M, MN, USA).

2.5. LC-MS analysis

Sage tip SCX prefractionated samples were injected into a C18 0.075- × 20-mm trap column (Acclaim PepMap 100; Thermo Fisher Scientific) and then eluted into a C18 0.075- × 120-mm analytical column (Nano HPLC Capillary Column; Nikkyo Technos, Tokyo, Japan) configured to an EASY-nLC 1000 HPLC system (Thermo Scientific, San Jose, CA, USA). The flow rate of the mobile phase was 300 nl/min; mobile phase (A) consisted of 0.1% formic acid and mobile phase (B) with 0.1% formic acid/100% acetonitrile. Separated peptides were subjected to Q-ExactiveTM (Thermo Scientific) operated in data-dependent mode to switch automatically between full-scan MS and MS/MS acquisition. The ten most intense full-scan peaks were selected with an isolation window of 2.4 Da.

2.6. Protein identification and quantification

Database searches were performed using the SEQUEST algorithm incorporated in Proteome Discoverer 1.4 (Thermo Fisher Scientific). The search parameters were as follows: enzyme, trypsin; variable modification, oxidation of M residue; static modification, TMT labeling of N-terminal and K residues; peptide ion mass tolerance, 10 ppm; fragment ion mass tolerance, 0.02 Da. The identified peptides were searched against the decoy database with false discovery rate (FDR) set as 0.01 using Percolator scoring validated by posterior error probability. Peptide quantification was also performed using Proteome Discoverer 1.4. Both peptide identification and quantification were performed in an overall workflow in Proteome Discoverer. KEGG pathway and Swiss-Prot keywords of proteins were assigned by using the DAVID Bioinformatics Database.

2.7. Western Blotting

Protein of 20 μg in each lane was separated on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels (e-PAGEL 15%, ATTO CORPORATION, Tokyo, Japan) according to the manufacturer's protocol. After completion of electrophoresis, proteins were transferred onto PVDF membranes and detected with a mouse antibody against lithostathine-1 (Reg1) (1: 2000; R&D System, Minneapolis, MN, USA). Alkaline phosphatase conjugated secondary antibodies (Merck KGaA, Darmstadt, Germany) were diluted 1: 30,000. To calibrate the expression levels of Reg1, β- actin was used as an internal control with a rabbit anti-β-actin monoclonal antibody (Abcam, Cambridge, UK). Antigens on the membrane were detected with ProtoBlot® II AP Systems with Stabilized Substrate (Promega, Fitchburg, WI, USA). Gel images were converted to densitograms using Image J software 1.45I (http://rsb.info.nih.gov/ij/).

3. Results

3.1. Proteomic analysis of the kidney

Proteins from six kidneys (three AQP11-null mice and three wild type mice: SET1) were extracted and digested. Each sample was labeled with 6-plex TMT reagent and then mixed to be fractionated by C18-SCX STAGE-Tip and analyzed by LC-MS/MS. We also analyzed another set (SET2) of each three mouse kidneys by the same protocol. A total of 2044 proteins were identified by combining two LC-MS/MS analyses, 1420 and 1835 protein each, in which the proteins were mostly shared (~ 1200). The selected proteins whose average three reporter ion ratios of AQP11-null mouse were > 1.5 or < 0.80 were 126 (62 down-regulated and 162 up-regulated in AQP-null mouse) (Table 1 and Table 2, respectively)(see supplements Tables 1 and 2 in more details).

These proteins were functionally classified by Swiss-Prot Keywords. As shown in Table 3, phosphoproteins and acetylation-related proteins were predominant in both groups. Cytoplasm, metal-binding, and Ubl conjugation proteins were up-regulated, while mitochondrial, transporting and nucleotide-binding proteins were down-regulated (Table 3).

Fig. 1 and 2 illustrated SET2 proteins with altered expressions in AQP11-null and wild type mouse kidneys in Tables 1 and 2. Extracellular matrix proteins such as fibulin-5 (Fbln5), fibronectin (Fn1), and annexin A2 (Anexa2) were enhanced in AQP11-null kidneys, which agrees with the results of previous PKD mouse models [17,18]. Moreover, vimentin (Vim), prosaposin (Psap) and angiotensinogen (Agt) were also enhanced, which were unique to this study. On the other hand, mitochondrial-function-related proteins including L-xylulose reductase (Dcxr) and sodium/potassium-transporting ATPase subunit alpha-1 (Atp1a1) were depressed in AQP11-null kidneys, suggesting a mitochondrial defect of the cyst epithelium.

3.2. Expression of Reg1 transcript in the kidney

Notably, a pancreatic growth factor, lithostathine-1 (Reg1) was most increased by 8 folds. To further verify the identified proteins, western blotting analysis was performed to determine the increase of