

# Chapter 2

## Genetic Mechanisms of ADPKD

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**Abstract** Autosomal dominant polycystic kidney disease is caused by mutation of PKD1 (polycystic kidney disease-1) or PKD2 (polycystic kidney disease-2). PKD1 and PKD2 encode PC1 (polycystin-1) and PC2 (polycystin-2), respectively. In addition, the mutation of cilia-associated proteins is also a recognized major factor of pathogenesis, since PC1 and PC2 are located in primary cilium. Abnormalities of PC1 or PC2 lead to aberrant signaling through downstream pathways, such as the negative growth regulation, G protein activation, and canonical and non-canonical Wnt pathways. According to the “second hit” model, an additional somatic mutation results in the expansion of cyst growth. In this chapter we discuss the genetic mechanisms and signaling pathways involved in ADPKD.

**Keywords** Genetic mechanism • PKD • Mutation • PKD1 • PKD2 • Polycystin-1 • Polycystin-2 • Signaling pathways

### 2.1 Polycystin-1 and Polycystin-2

Autosomal dominant polycystic kidney disease (ADPKD) is caused by mutations of two genes, namely PKD1 (polycystic kidney disease-1) and PKD2 (polycystic kidney disease-2), which encode polycystin-1 (PC1) and polycystin-2 (PC2), respectively. Approximately 85% of ADPKD cases result from mutations in PKD1. PC1 is a 450-kD receptor-like protein with a large extracellular N terminus, 11 membrane-spanning domains, and a short cytoplasmic C terminus. The expression of PC1 was evaluated in epithelial cells during development (Ward et al. 1996), but its expression level is high in fetal renal tissue only and low in adult tissue (Chauvet et al.

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2002). PC1 localizes to the cilium, plasma membrane, and adhesion complex in polarized epithelial cells (Ibraghimov-Beskrovnyaya et al. 1997; Huan and van Adelsberg 1999). PC1 and PC2 form a complex through their C-terminal tails (CTTs) to play a role in intracellular  $\text{Ca}^{2+}$  regulation (Tsiokas et al. 1997; Qian et al. 1997). The N terminus of PC1 consists of 15 PKD repeat motifs, two leucine-rich motifs, and a C-type lectin domain (Harris et al. 1995; Bycroft et al. 1999). These domains play an important role in mediating the subcellular localization of PC1 within the plasma membrane and junctional complexes (Streets et al. 2009; Babich et al. 2004). The CTT of PC1 includes a G protein-binding domain, a coiled-coil domain, and residues associated with ubiquitin-mediated degradation (Low et al. 2006). The N- and C-terminal domains of PC1 can be cleaved. The N-terminal domain is cleaved at the G protein-coupled receptor proteolysis site (GPS) in the early secretory pathway (Wei et al. 2007; Yu et al. 2007). Generally, PC1 exists as a heterogeneous population of the full-length and N-terminal cleaved forms (Wei et al. 2007). However, one study suggested that N-terminal cleavage is necessary for the complete functional activation of PC1 (Qian et al. 2002). One interesting study revealed that cleaved CTT, which is assembled in the nucleus during reduced fluid flow in mouse kidney, was increased in the cyst-lining cells in ADPKD (Low et al. 2006).

PC2 (968 aa; ~110 kDa) is a six-transmembrane protein with intracellular N and C termini (Mochizuki et al. 1996). PC2 acts as a  $\text{Ca}^{2+}$ -responsive cation channel of the transient receptor potential family (Gonzalez-Perrett et al. 2001). Although PC2 is co-localized with PC1 to the cilium and plasma membrane (Yoder et al. 2002; Yu et al. 2009), the major portion of cellular PC2 is observed in the intracellular compartment and functions to release calcium from the intracellular store (Vassilev et al. 2001). The channel formed by PC1 and PC2 in complex is activated in response to ciliary bending, and it leads to signal transduction by chemical or mechanical stimuli (Nauli et al. 2003). The calcium-conducting pore consists of the loop between the fifth and sixth transmembrane domains, and a missense mutation in the conducting pore was shown to cause ADPKD (Koulen et al. 2002). PC2 also functions as an indirect regulator of the cytoplasmic calcium level together with two other intracellular  $\text{Ca}^{2+}$  channels, namely the inositol 1, 4, 5-triphosphate receptor (IP3R) and ryanodine receptor. The C-terminus of PC2, which directly interacts with IP3R, results in IP3-induced  $\text{Ca}^{2+}$  flux. PC2 also binds to the ryanodine receptor channel and regulates calcium-induced calcium release (Anyatonwu et al. 2007; Li et al. 2009). The largest pools of PC2 appear in the ER and the early Golgi body among the subcellular compartments (Cai et al. 1999; Koulen et al. 2002). PC2's subcellular localization requires specific signal transduction and trafficking proteins that bind to PC2's C terminus (Chapin and Caplan 2010). The movement of PC2 from the ER to the Golgi is modulated by polycystin-2 interactor (PIGEA-14), which causes a redistribution of PC2 (Hidaka et al. 2004).

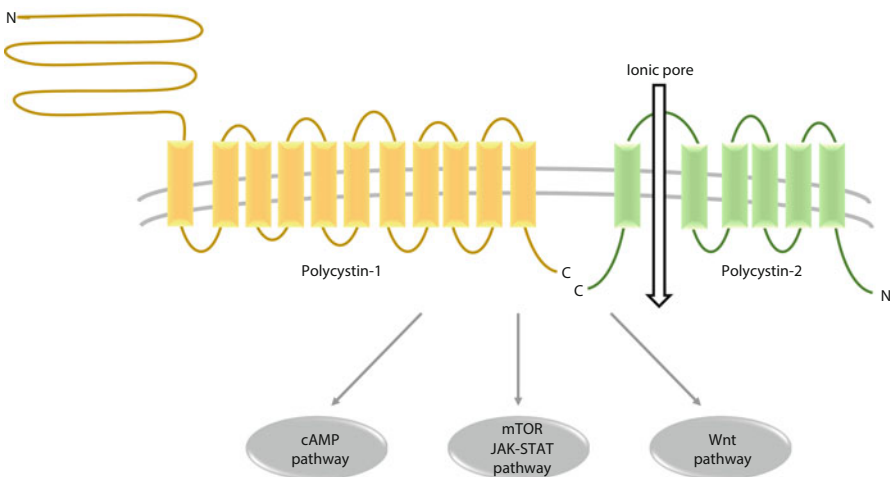
The PC1 and PC2 proteins are co-located in the primary cilium and ER (Yoder et al. 2002); however, they are also found in other locations depending on their functions (Hanaoka et al. 2000; Grimm et al. 2003). Especially, many studies have suggested that PC1 and PC2 reciprocally influence each other's localization. One study confirmed that impairing the function of PC1 prevents GPS cleavage in ADPKD

cyst cells, which leads to a decreased co-localization and amount of both PC1 and PC2 in primary cilia (Xu et al. 2007). The interaction between PC1 and PC2 has been recognized as an important factor for creating a functional ion channel through the intrinsic channel formed by activated PC2 alone or the emergent channel formed by the PC1-PC2 complex (Hanaoka et al. 2000). A physical connection between PC1 and PC2 is mediated by the CTTs of PC1 and PC2 (Qian et al. 1997; Tsiokas et al. 1997; Casuscelli et al. 2009). Through this interaction, PC2 prevents the ability of PC1 to activate G proteins (Delmas et al. 2002).

## 2.2 Signaling Pathways of PKD1 and PKD2

Although the complete pathologic mechanisms remain to be elucidated, the loss of function of the PC1 and/or PC2 proteins leads to ADPKD pathogenesis through a myriad of signaling pathways, including planar cell polarity (PCP), Wnt, mammalian target of rapamycin (mTOR), cyclic adenosine monophosphate (cAMP), G-protein coupled receptor (GPCR), cystic fibrosis transmembrane conductance regulator (CFTR), epidermal growth factor receptor (EGFR), mitogen-activated protein kinase (MAPK), cellular  $\text{Ca}^{2+}$ , and the cell cycle (Gallagher et al. 2010). As explained above, PC1 and PC2 form a complex that functions as a transient receptor potential channel to maintain intracellular calcium homeostasis (Vassilev et al. 2001; Anyatonwu and Ehrlich 2005) and as a calcium release channel (Koulen et al. 2002). Disruption of PC1/PC2 results in a decreased level of intracellular  $\text{Ca}^{2+}$ , leading to upregulated cAMP signaling and increased cell proliferation (Masyuk et al. 2006) (Fig. 2.1).

An increased level of cAMP has been identified in many animal models of polycystic kidney disease (PKD), not only in the kidney but also in other tissues, such as



**Fig. 2.1** Representative signaling pathways regulated by polycystin 1 and/or 2

cholangiocytes (Masyuk et al. 2007), vascular smooth muscle cells (Kip et al. 2005), and the choroid plexus (Banizs et al. 2007). cAMP levels are modulated by the activities of membrane-bound GPCRs, soluble adenylyl cyclases (ACs), and cAMP phosphodiesterases (PDEs). Several hypotheses have been proposed regarding the mechanisms by which the cAMP level is influenced in PKD. At first, reduced calcium directly inhibits PDE1, indirectly suppresses PDE3, and activates membrane bound AC6 (Gattone et al. 2003; Wang et al. 2010). Next, a defect in PC2-mediated calcium entry in the ciliary protein complex occurs, leading to the inhibition of AC5/6 and the activation of PDE4C (Choi et al. 2011). Also, depletion of the endoplasmic reticulum (ER) calcium store triggers the accumulation of stromal interaction molecule 1 to the plasma membrane and activates AC6 (Spirlì et al. 2012). Likewise, several factors can contribute to an increase in the intracellular level of cAMP—disrupted PC1 binds to heterotrimeric G proteins (Parnell et al. 1998), vasopressin V2 receptor is upregulated, and circulating vasopressin, forskolin, ATP, or other adenylyl cyclase agonists are increased (Putnam et al. 2007; Hovater et al. 2008). Certain ACs and PDEs are recognized as being important in PKD progression because of their influence on compartmentalized pools of cAMP (Torres and Harris 2014).

One of the most evident characteristics of ADPKD pathogenesis is elevated cellular growth and division. Polycystin proteins inhibit cell growth through interactions with several pathways including the mTOR (Shillingford et al. 2006) and Janus kinase (JAK)-signal transducers and activators of transcription (STAT) (Bhunia et al. 2002) pathways. PC1 inhibits mTOR activity by stabilizing the tuberous sclerosis 1-tuberous sclerosis 2 (TSC1-TSC2) complex, which is known as a negative regulator of the mTOR complex (Huang and Manning 2008; Distefano et al. 2009; Dere et al. 2010). PC1 stabilizes the TSC1-TSC2 complex through two distinct mechanisms. PC1 suppresses the ERK-dependent phosphorylation of TSC2 at S664 (Distefano et al. 2009) and Akt-dependent phosphorylation of TSC2 at S939 by binding to TSC2 at the plasma membrane (Dere et al. 2010). The influence of the PC1-TSC2 interaction allows the TSC1-TSC2 complex to inhibit the mTOR signaling pathway. PC1 also functions as a positive regulator of p21 (cyclin-dependent kinase inhibitor) by binding and activating members of the JAK-STAT pathway (Bhunia et al. 2002). Following the PC2-JAK2 interaction and the formation of the intact C terminus of PC1, PC1 can activate STAT1 and STAT3 and it allow to increase p21 and decrease cell growth (Bhunia et al. 2002). PC2 also reduces cell proliferation by binding both eukaryotic translation elongation initiation factor 2a (eIF2a) and pancreatic ER-resident eIF2a kinase (Liang et al. 2008).

The Wnt signaling pathways regulate cell growth, differentiation, and planar cell polarity and are classified into the canonical ( $\beta$ -catenin dependent) and noncanonical ( $\beta$ -catenin independent) pathways. Both PC1 and PC2 affect the canonical Wnt pathway. In the case of PC1, the cleaved PC1 CTT directly or indirectly binds to  $\beta$ -catenin, translocates to the nucleus, and promotes T cell factor (TCF)-dependent transcription (Lal et al. 2008). PC2 also modulates the expression levels of some Wnt pathway components (Kim et al. 2009). In the noncanonical Wnt pathway, the function of PC1 is associated with the maintenance of planar cell polarity. Planar cell polarity is essential for oriented cell division and the establishment of kidney

tubule structure, and defects in this process trigger the expansion of renal tubules and cyst formation (Fischer et al. 2006).

### 2.3 Genetic Mechanisms of Pathogenesis

Approximately 85% of ADPKD patients have mutations in PKD1; thus, it is supposed that mutations in PKD1 cause a more severe disease than mutations in PKD2 do (Rossetti et al. 2007). Generally, patients with PKD1 mutations develop ADPKD symptoms at younger ages relative to patients with PKD2 mutations, but their disease phenotypes are influenced by mutations in both genes (Hateboer et al. 1999). A myriad of mutation types that can cause ADPKD have been revealed, and the position of each mutation determines the severity of the disease (Rossetti et al. 2002; Rossetti and Harris 2013). Recent studies revealed that the type of mutation is more important, because patients with truncating mutations showed more severe disease phenotypes than did those with non-truncating mutations (Pei et al. 2012; Cornec-Le Gall et al. 2013).

ADPKD is genetically dominant at the organismal level, but recessive at the cellular level (Chapin and Caplan 2010). Although a germ line mutation in PKD1 or PKD2 is necessary to induce cyst formation in ADPKD, cysts form in only part of the kidney tubules and hepatic bile duct. However, in adult tissues, both copies of the mutated polycystic gene undergo recessive loss of function, causing cyst formation to be accelerated in a subset of tubular epithelial cells. This paradox is explained by the occurrence of an additional somatic “second hit” mutation (Qian et al. 1996; Watnick et al. 1998; Pei et al. 1999). Although the somatic second hit mutation mechanism is generally applicable to human ADPKD, additional factors contribute to determining the extent of cyst formation, including non-cell autonomous effects on polycystins-expressing cells (Nishio et al. 2005), the timing of PKD1 in the developmental stages (Piontek et al. 2007), and hypomorphic mutations of PC1 compared to complete loss of function mutations (Rossetti et al. 2009; Hopp et al. 2012). Especially, reduced PC1 dosage is suggested to explain autosomal recessive PKD phenotypes, in which the degree of PC1 dysregulation is associated with the extent of tubule dilation and cyst formation (Hopp et al. 2012).

ADPKD is characterized by the formation of multiple fluid-filled kidney cysts. Thus, we need to focus on the mechanisms of cyst expansion. In the patient’s kidney, cells are organized in a circle and these lumens must fill with fluid. Subsequently, cysts increase by cell proliferation, leading to the dilation of the renal tubule and renal failure (Qian et al. 1996; Brasier and Henske 1997). One model involves a loss of oriented cell division in the cells of mouse models with kidney-specific PKD1 or PKD2 mutation, which does not initiate cyst formation. This model suggests that a defect of planar cell polarity is an important factor in the expansion of many cysts; however, this factor was not essential for the initiation of cyst formation (Nishio et al. 2010). According to other studies, ion absorption and secretion in cyst-lining epithelial cells are significant for cyst formation. cAMP can stimulate Cl<sup>-</sup> transport,

resulting in the rapid and progressive dilation of tubules (Grantham 1996). In addition, one research group reported that tubule enlargement is prevented by inhibitors of  $\text{Na}^+ - \text{K}^+ - 2\text{Cl}^-$  cotransporters and CFTR (Montesano et al. 2009). Therefore, cAMP signaling plays a key role in renal cyst formation by promoting  $\text{Cl}^-$  driven fluid secretion. Furthermore, polycystin proteins also function as regulators of cAMP signaling by modulating the expression, localization, and activity of  $\text{Cl}^-$  channels (Chapin and Caplan 2010).

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