

ARTICLE

Chromosomal abnormalities in hepatic cysts point to novel polycystic liver disease genes

Edgar S Wills^{1,2,9}, Wybrich R Cnossen^{1,2,9}, Joris A Veltman^{2,3}, Rob Woestenenk⁴, Marloes Steehouwer², Jody Salomon¹, René HM te Morsche¹, Meritxell Huch^{5,6,7}, Jayne Y Hehir-Kwa², Martijn J Banning², Rolph Pfundt², Ronald Roepman^{2,8,10}, Alexander Hoischen^{2,8,10} and Joost PH Drenth^{*,1,8,10}

Autosomal dominant polycystic liver disease (ADPLD) is caused by variants in *PRKCSH*, *SEC63*, and *LRP5*, whereas autosomal dominant polycystic kidney disease is caused by variants in *PKD1* and *PKD2*. Liver cyst development in these disorders is explained by somatic loss-of-heterozygosity (LOH) of the wild-type allele in the developing cyst. We hypothesize that we can use this mechanism to identify novel disease genes that reside in LOH regions. In this study, we aim to map abnormal genomic regions using high-density SNP microarrays to find novel PLD genes. We collected 46 cysts from 23 patients with polycystic or sporadic hepatic cysts, and analyzed DNA from those cysts using high-resolution microarray ($n=24$) or Sanger sequencing ($n=22$). We here focused on regions of homozygosity on the autosomes (>3.0 Mb) and large CNVs (>1.0 Mb). We found frequent LOH in *PRKCSH* (22/29) and *PKD1/PKD2* (2/3) cysts of patients with known heterozygous germline variants in the respective genes. In the total cohort, 12/23 patients harbored abnormalities outside of familiar areas. In individual ADPLD cases, we identified germline events: a 2q13 complex rearrangement resulting in *BUB1* haploinsufficiency, a 47XXX karyotype, chromosome 9q copy-number loss, and LOH on chromosome 3p. The latter region was overlapping with an LOH region identified in two other cysts. Unique germline and somatic abnormalities occur frequently in and outside of known genes underlying cysts. Each liver cyst has a unique genetic makeup. LOH driver gene *BUB1* may imply germline causes of genetic instability in PLD. *European Journal of Human Genetics* (2016) 24, 1707–1714; doi:10.1038/ejhg.2016.97; published online 24 August 2016

INTRODUCTION

Polycystic liver disease (PLD) is part of the phenotype of two inherited disorders; autosomal dominant PLD (ADPLD) and autosomal dominant polycystic kidney disease (ADPKD). In 83–94% of ADPKD patients, polycystic livers are seen.^{1,2} Variants in *Protein Kinase C Substrate 80 K-H* (*PRKCSH*), *SEC63* homolog (*Saccharomyces cerevisiae*; *SEC63*), and *Low-density lipoprotein Receptor-related Protein 5* (*LRP5*) cause ADPLD, and are present in ~25% of cases,^{3,4} whereas variants in *Polycystic Kidney Disease 1* (*PKD1*) and *Polycystic Kidney Disease 2* (*PKD2*) are responsible for ADPKD in virtually all cases.⁵ Protein products of genes underlying PLD are located in the endoplasmic reticulum (ER) or primary cilium.^{6,7} Experimental data favor a genetic interaction network between ER-localized protein products of *PRKCSH* and *SEC63*, and cilium-localized *PKD1* and *PKD2*.^{7,8} The finding of *LRP5* variants in PLD suggests that Wnt signaling may be disrupted downstream of this interaction network. Genes that underlie PLD thus function in distinct organelles and pathways, despite a final common cystogenic effect. Furthermore, ciliopathy-associated genes act outside of the *PKD1/PKD2* genetic interaction network,^{7,9} and may also cause liver cysts. The search for new genes should therefore not be limited to currently known genomic sites. At a tissue level, PLD

appears to be a recessive disease. Complete loss of cyst gene expression from diseased epithelium follows loss-of-heterozygosity (LOH),^{10–15} which may be related to cyst genetic instability.^{16,17} The proportion of somatic variants varies with the gene that is affected in the germline. Recent studies found that second, somatic variants or LOH occurred in 56/71 liver cysts (79%) from patients with *PRKCSH* variants,¹¹ in 4/5 (80%) *PKD2* variant carriers,¹⁸ but only 1/14 cysts (7%) from a patient with a *SEC63* variant.¹⁰ This indicates LOH incidence depends upon the genetic and phenotypic background. We hypothesize that a ‘two-hit model’ is a general principle for the development of hepatic cysts. Therefore, somatic LOH regions in cyst epithelium may harbor novel candidate PLD-causing genes, which harbor heterozygous germline variants in the respective cases. Considering the genetic interaction network in PLD,^{7,8} digenic or transheterozygous variants at two genetic loci may also have a role. Transheterozygous *PKD1/PKD2* variants have been described in renal cysts,^{14,15} whereby a variant in one cyst gene is succeeded by a variant in a second cyst gene. Cysts with heterozygous variants in *PRKCSH* and *SEC63* continue to express the relevant proteins.^{10,11} It is reasonable to hypothesize that transheterozygosity may be another mechanism in hepatic cyst formation. This study aims to determine novel genetic loci that are

¹Department of Gastroenterology and Hepatology, Radboud University Medical Centre, Nijmegen, The Netherlands; ²Department of Human Genetics, Radboud University Medical Centre, Nijmegen, The Netherlands; ³Department of Clinical Genetics, Maastricht University Medical Centre, Maastricht, The Netherlands; ⁴Department of Hematology, Radboud University Medical Center, Nijmegen, The Netherlands; ⁵Wellcome Trust/Cancer Research UK Gurdon Institute, Henry Wellcome Building of Cancer and Developmental Biology, University of Cambridge, Cambridge, UK; ⁶Wellcome Trust/Medical Research Council Stem Cell Institute, University of Cambridge, Cambridge, UK; ⁷Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK; ⁸Radboud Institute for Molecular Life Sciences, Radboud University Medical Center, Nijmegen, The Netherlands

*Correspondence: Dr JPH Drenth, Department of Gastroenterology and Hepatology, Radboud University Medical Center, PO Box 9101, 6500 HB Nijmegen, The Netherlands. Tel: +31 24 361 4760; Fax: +31 24 354 0103; E-mail: joostphdrenth@cs.com

⁹These authors contributed equally to this work.

¹⁰These authors contributed equally to this work.

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involved in cystogenesis both at germline and somatic level. To this end, we followed an unbiased approach and assessed copy-number variations (CNVs) and LOH regions in PLD cyst epithelium using a genome-wide high-resolution cytogenetic array analysis.

METHODS

Patient material

We obtained DNA from liver cyst cholangiocytes of 23 newly included patients who underwent either laparoscopic cyst fenestration or aspiration sclerotherapy from 2011–2014 because of large cysts. All patients except one were females, and had single or multiple liver cysts. All patients had severe symptoms and the mean age was 54 (range 42–83) years. Seventeen patients had ADPLD, three had ADPKD, and three had solitary or sporadic cysts. Use of this tissue for research was reviewed and approved by the regional ethics review board 'Commissie Mensgebonden Onderzoek regio Arnhem-Nijmegen'.

Cyst work-up

We isolated cholangiocytes by four methods (Supplementary Figure S1; Table 1). First, as described from 23 previously studied laparoscopy-derived liver cysts (six patients) obtained from 2010 to 2012,¹⁸ we collected cells from fresh tissue by ethylenediaminetetraacetic acid detachment. Keratin (KRT)-19 staining indicated the purity of each sample. Second, we collected cells from 30 laparoscopy-derived liver cysts of eight patients from 2012 to 2014. These cells expanded into adult liver organoids using conditions suitable for their expansion.¹⁹ Under these conditions, only stem cells with a cholangiocyte-like phenotype expressing KRT19 persisted. DNA from one cyst per patient was studied using high-density SNP microarrays (Affymetrix Cytoscan HD, Santa Clara, CA, USA). DNA from the remaining 22 cysts was used to assess somatic loss of the wild-type allele of heterozygous *PRKCSH* germline variants by Sanger sequencing. Third, symptomatic cyst patients were referred to our hospital for aspiration sclerotherapy. We collected 68 cyst fluid aspirates from 50 patients in 2011 and 2012. We subjected all samples to centrifugation, KRT19 staining, and fluorescent-activated cell sorting (FACS) of cholangiocytes (Supplementary Methods). This yielded eight additional samples for single-nucleotide variant (SNP) microarray studies. Fourth, we grew eight cultures from 30 aspiration sclerotherapy fluids collected from 2012 to 2014, using conditions suitable for the expansion of adult liver stem cells.¹⁹ We obtained cyst fluid and epithelium samples, and stored them in the course of treatment following the Dutch Code for the proper secondary use of human tissue. Use of this tissue for research was reviewed and approved by the regional ethics review board 'Commissie Mensgebonden Onderzoek regio Arnhem-Nijmegen'.

DNA isolation from cyst cholangiocytes

We isolated DNA from the cyst cholangiocytes using the QIAamp DNA Micro kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. For samples with low DNA yields (which included all FACS obtained samples), whole-genome amplification (WGA) using the Qiagen REPLI-g Mini kit (Qiagen) was performed.

Genetic analysis by microarray and genotyping

We assessed CNVs, LOH regions, and regions of homozygosity using genome-wide high-resolution cytogenetic array analysis (CytoScan HD, Affymetrix). We screened whole-blood PLD patient DNA for germline variants in *PKD1* (NG_008617.1, NM_001009944.2), *PKD2* (NG_008604.1, NM_000297.3), *PRKCSH* (NG_009300.1, NM_002743.3), *SEC63* (NG_008270.1, NM_007214.4), and *LRP5* (NG_015835.1, NM_002335.3) using direct sequencing as described previously.¹¹ Briefly, we isolated DNA from whole blood using the PureGene DNA isolation kit (Gentra Systems/Qiagen, Minneapolis, MN, USA) or High Pure Polymerase chain reaction (PCR) template preparation kit (Roche, Mannheim, Germany), and stored it at 4 °C. PCR amplified *PKD2*, *PRKCSH*, *SEC63*, and *LRP5*, exons and flanking intronic sequences with specific primers (Supplementary Table S1). Screening for germline variants in *PKD1* (NG_008617.1, NM_001009944.2) was carried out by a method adapted from Tan *et al.*²⁰ In short, primer sequences (Supplementary Table S1) for long range PCR were chosen on specific regions of the *PKD1* gene preventing the

amplification of the known duplications of the first 33 exons at the proximal side of the gene. PCR reactions were performed according to the manufacturer's manual using FastStart Taq DNA Polymerase System supplemented with GC-RICH solution (Roche) for exon 1 or GeneAmp High Fidelity PCR System (Life technologies, Carlsbad, CA, USA) supplemented with 5% DMSO for all other fragments. Annealing temperatures during PCR were carefully selected for each amplicon to amplify the desired regions. After purification of PCR amplicons from gel using the QIAEXII Gel Extraction Kit (Qiagen), a total of 500 ng of equimolar amounts of the PCR amplicons of each sample were sequenced in a single run using Ion Torrent Next-Generation Sequencing (Life Technologies).

All cysts from patients with *PRKCSH* variants were analyzed for LOH using direct sequencing of this variant. We screened the entire coding region of *BUB1 Mitotic Checkpoint Serine/Threonine Kinase (BUB1)* (NG_012048.1, NM_004336.4) in a cohort of unrelated patients with ADPLD ($n=100$) that met the Reynolds' criteria.^{21,22} We performed high-resolution melting curves (RotorGene-Q; Qiagen) to reveal differences in melting curve shape that correlate to *BUB1* genotype variants and validated these findings by Sanger sequencing. *Adenylate Cyclase 1 (ADCY1)* (NG_034198.1, NM_021116.2), *Insulin-Like Growth Factor Binding Protein (IGFBP) 1* (NC_000007.14, NM_000596.2), and *IGBPF3* (NG_011508.1, NM_001013398.1) were analyzed in a patient with cyst chromosome 7 copy-number loss. Exons and flanking intronic sequences were amplified using PCR with specific primers (Supplementary Table S1). We purified PCR amplicons from gel using the QIAEXII Gel Extraction Kit (Qiagen) and sequenced them with the BigDye terminator kit (Applied Biosystems, Foster City, CA, USA) and ABI3730, ABI310, or ABI3100 Genetic Analyzers (Applied Biosystems, Boston, MA, USA), or (from 2014 onwards) Ion Torrent sequencing (Life Technologies).

Data analysis

We considered large regions of homozygosity on the autosomes (>3.0 Mb) and large CNVs (>1.0 Mb) for further analysis. For samples not derived by FACS/WGA, we placed no limits for size of LOH or CNVs around known cyst genes. We only assessed X chromosomes for whole-chromosome abnormalities. For selected cases, we compared the array results derived from cyst cell DNA (somatic) and germline DNA (genomic) to ensure identification of somatic events. We selected cases for germline analysis based on FACS/WGA origin of cyst DNA or presence of non-mosaic >1.0 Mb CNVs. We used individual CytoScan HD data chromosome analysis suite (CHAS, Affymetrix) V2.1. For analysis involving multiple SNP array data, we used Nexus Copy Number (BioDiscovery, El Segundo, CA, USA) V6.0.

SNP array data

The data discussed in this publication have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO Series accession number GSE78808 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=kjipyeauhnbwzqv&acc=GSE78808>). Described variants have also been deposited at NCBI's database of genomic structural variations (Wills *et al*, 2016) and are accessible through dbVar (<http://www.ncbi.nlm.nih.gov/dbvar>) accession number nstd125.

RESULTS

Patient characteristics

We included DNA from 24 liver cysts from 23 patients for Affymetrix CytoScan HD SNP array analysis in this study (Figure 1, Table 1; Supplementary Figure S1 for inclusion flow chart), together with 23 cysts from six previously described patients (Supplementary Table S2; Supplementary Figure S2). In the new cohort, all patients except one were females, and had single or multiple liver cysts. All patients had severe symptoms and the mean age was 54 (range 42–83) years. Seventeen patients had ADPLD, three had ADPKD, and three had solitary or sporadic cysts. Six carried *PRKCSH* variants, one carried a variant in *SEC63*, and two had *PKD1* variants.

Table 1 Patient characteristics

#	Patient & age	Source	Disease, germline mutation & SNP array CNV	Second hit mutation ^a	Additional events
1	Male, 61 years	Fluid	ADPLD Unknown Loss chr 9q (2.9Mb) CNN ROH chr 3p (12.7 Mb) CNN ROH chr 13q (5.4Mb)	None detected	None
2	Female, 58 years	Fluid	ADPLD Unknown	None detected	CNN LOH Chr 5q (3.6Mb)
3	Female, 60 years	Fluid	ADPLD Unknown	None detected	None detected
4	Female, 50 years	Fluid	ADPLD Unknown	None detected	None detected
5	Female, 59 years	Fluid	ADPLD Unknown	None detected	None detected
6	Female, 55 years	Fluid	ADPLD Unknown	None detected	None detected
7	Female, 83 years	Fluid	ADPKD <i>PKD1 hg38 chr16:g.2090007T>G</i>	CNN LOH chr 16p (34.6 Mb)	CNN LOH chr 1p (6.9Mb) CNN LOH chr 12q (4.4Mb)
8.1	Female, 44 years	Fluid	ADPLD <i>PRKCSH hg38 chr19:g.11437972G>C</i> Gain chr 2q13 (1.3Mb) Loss chr 2q13 (1.7Mb; including <i>Bub1</i>)	CNN LOH chr 19p (12.9 Mb)	None detected
8.2	Female, 44 years	Epith.	ADPLD <i>PRKCSH hg38 chr19:g.11437972G>C</i> Gain chr 2q13 (1.3Mb) Loss chr 2q13 (1.7Mb)	CNN LOH chr 19p (1.5Mb)	Loss chr 7p (1.7Mb)
9	Female, 54 years	Epith.	Sporadic cyst -	None	CNN LOH chr 2q (3.1Mb) CNN LOH chr 12q (3.7Mb)
10	Female, 57 years	Fluid	Sporadic cyst -	None	None
11	Female, 58 years	Epith.	ADPLD Unknown	CNN LOH chr 19p (1.7Mb)	Mosaic trisomy chr 7 CNN LOH chr 12q (3.6Mb)
12	Female, 47 years	Epith.	ADPLD <i>PRKCSH hg38 chr19:g.11449074A>G</i>	CNN LOH chr 19p (20Mb)	CNN LOH chr 6p (3.3Mb)
13	Female, 70 years	Fluid	ADPLD Unknown	Del chr 4q (39kb)	CNN LOH chr 5q (5.4 Mb)
14	Female, 52 years	Epith.	ADPLD Unknown	None	None
15	Female, 61 years	Epith.	ADPLD Unknown	None	CNN LOH chr 2q (3.2Mb) CNN LOH chr 5p (3.2Mb)
16	Female, 51 years	Fluid	ADPLD <i>SEC63 hg38 chr6: g.107904719del</i>	Del chr 6q (42 Mb)	None
17	Female, 50 years	Epith.	ADPLD <i>PRKCSH hg38 chr19:g.11449074A>G</i>	None	CNN LOH chr 5q (3.1Mb)
18	Female, 52 years	Fluid	ADPKD <i>PKD1 hg38 chr16 g.[2135508G>A(;) 2090517_2090558delinsGGAC], c.[182C>T(;) 2090517_2090558delinsGGAC], c.[182C>T(;)12171_12212 delinsGTCC], p.[Pro61Leu(;)Ser4057Argfs*87]</i>	<i>PKD1 hg38 chr16 g.[2135508G>A(;) 2090517_2090558delinsGGAC], c.[182C>T(;) 12171_12212delinsGTCC], p.[Pro61Leu(;)Ser4057Argfs*87]</i>	CNN LOH chr 3p (3.4Mb) CNN LOH chr 19 (1.2Mb) CNN LOH chr 11 (1.3Mb)
19	Female, 47 years	Epith.	ADPLD <i>PRKCSH hg38 chr19:g.11437972G>C 47XXX</i>	CNN LOH chr 19 (15.9Mb)	Trisomy X (entire) CNN LOH chr 3p (6.1 Mb)
20	Female, 43 years	Fluid	Sporadic cyst -	Gain CN 2.26 chr 16p (3.8Mb)	CNN LOH chr 1p (3.6Mb)

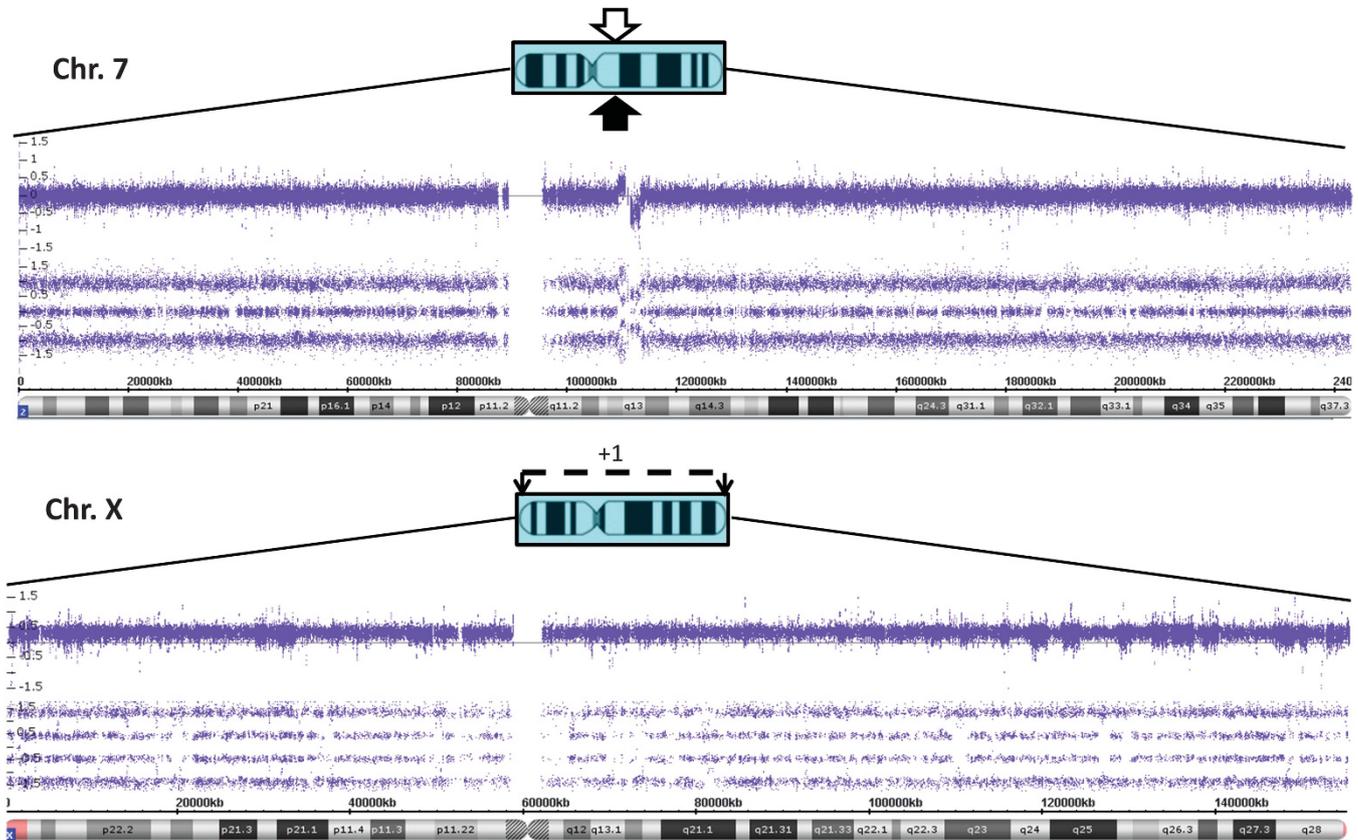


Figure 2 Upper panel: 2q13 complex rearrangement present in genomic blood DNA of PRKCSH variant patient (#8). Lower panel: presence of three X chromosomes in genomic blood DNA of blood of another PRKCSH variant patient (#19).

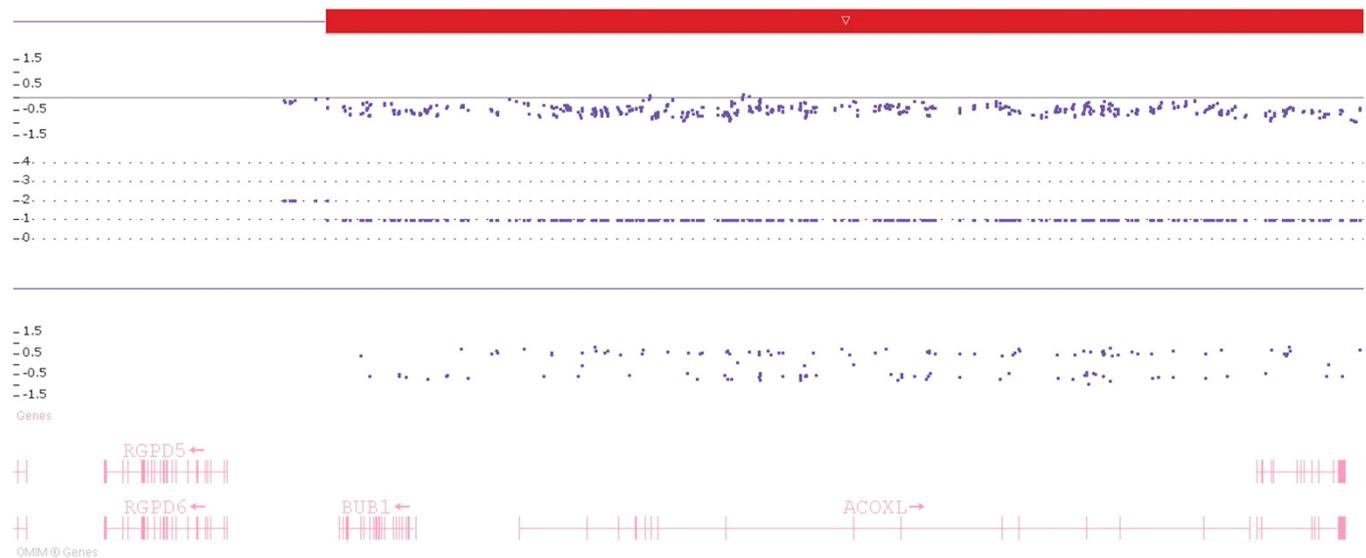


Figure 3 BUB1 is present at the centromeric part of the 2q13 loss region.

displayed LOH or allelic imbalance (AI) across *PRKCSH*, whereas >25% of cysts had *PKD1* LOH or AI. *PKD2*, *SEC63*, and *LRP5* all had lower percentages of LOH/AI ~15, ~15 and ~10%, respectively. Copy-number losses and gains in ADPLD occurred less frequently.

Novel, digenic abnormalities in cysts

As described above, patient #8 presented with two germline events. We identified a *PRKCSH* variant and a complex rearrangement resulting in *BUB1* haploinsufficiency. DNA from her second cyst

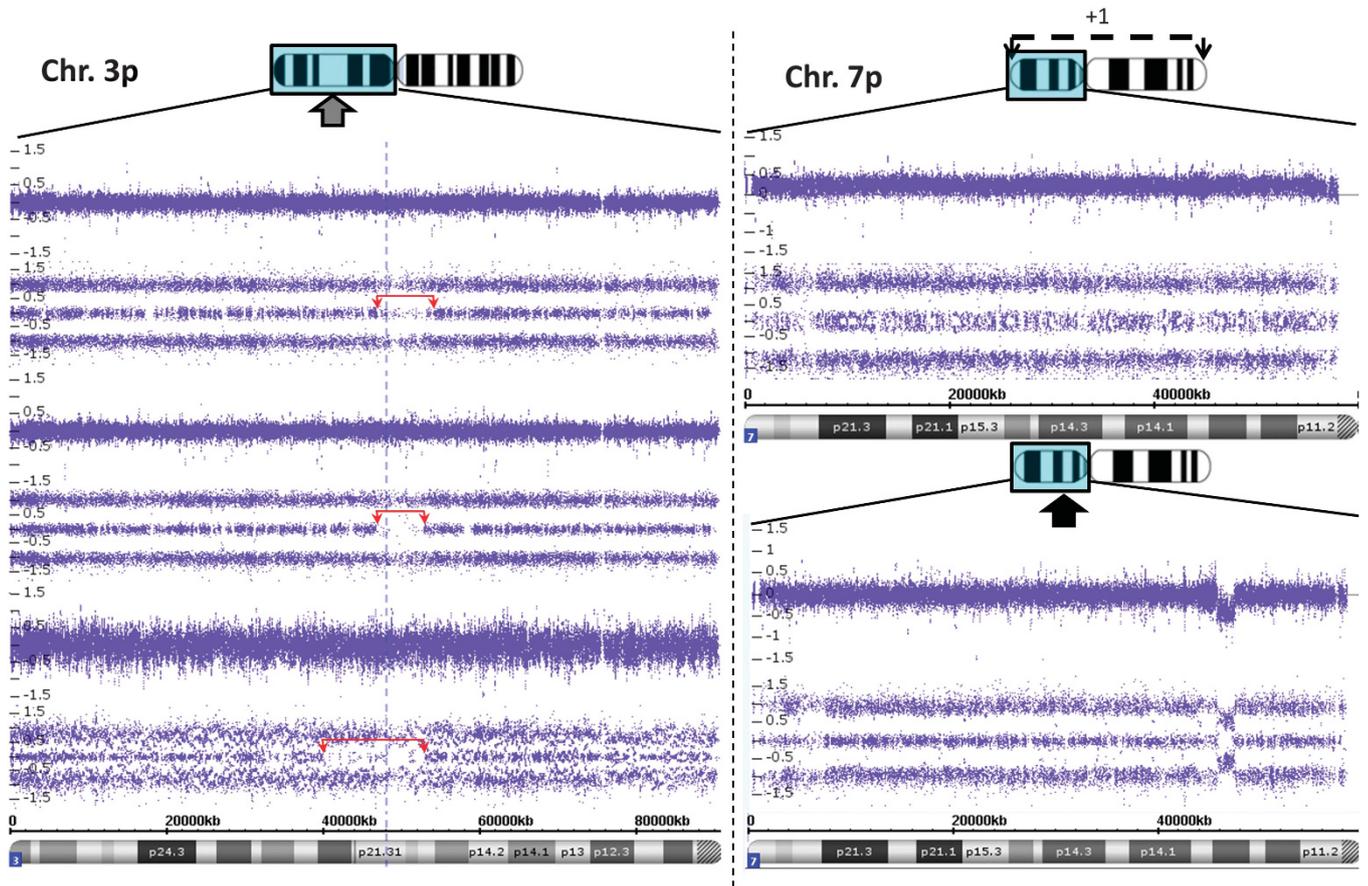


Figure 4 Left: CNN LOH on chromosome 3p of patient #18, 19, and 1, from above to below in that order. Right upper panel: mosaic whole-chromosome 7 gain in an ADPLD patient (#11) with unknown variant, chromosome 7p shown. Right lower panel: 1.7 Mb loss on chromosome 7p of a PRKCSH patient cyst (#8.2).

displayed multiple second hits when compared with peripheral blood. A 1.7 Mb copy-number loss region on chromosome 7 was present as well as CNN LOH surrounding *PRKCSH* on chromosome 19 (Figure 4). The loss region includes the genes *ADCY1*, *IGFBP1*, and *IGFBP3*, as well as the pseudogene *Septin 7B2* (*SEPT7B2*). It was not detected in the SNP array profile of germline DNA, nor were germline variants detected in any of these genes using Sanger sequencing. Sanger sequencing also did not reveal variants in these genes in the cyst. Another *PRKCSH* mutant cyst displayed mosaic trisomy 7 (#11), although only present in a subset of cells. Copy-number-neutral LOH of chromosome 19 (1.2 Mb), encompassing *PRKCSH*, and chromosome 11 (1.3 Mb), encompassing *LRP5*, was present in cyst DNA of an ADPKD patient (#18, germline *PKD1* variant). In this patient, an additional copy-number-neutral LOH region was detected on chromosome 3p (hg19 chr3:g.49,735,745_53,133,526), partially overlapping with a region of a *PRKCSH* variant carrier (#19; hg19 chr3:g.46,715,645_52,852,488). Notably, patient #1 with a larger copy-number-neutral LOH on chromosome 3p on germline and cyst DNA also had overlap (hg 19 chr 3:g.39,874,567_52,653,645). The minimal region of LOH contained >60 genes, containing multiple tumor suppressor genes (Supplementary Table S4).

Sporadic cysts

Two sporadic cysts of the same patient showed novel chromosomal LOH (patient #28; Supplementary Table S2). These cysts had

been previously described without abnormalities encompassing the then known cyst genes *PRKCSH*, *SEC63*, *PKD1*, or *PKD2*. Copy-number-neutral LOH (2.0 Mb) was found around *LRP5*, a novel cyst gene (Supplementary Figure S5). Germline DNA revealed no variant in *LRP5*, and the presence of two germline heterozygous *LRP5* SNPs (hg38 chr.11:g.68403545T>C, rs545382; hg38 chr.11:g.68425222G>A, rs556442) indicated that LOH was only present at a somatic level. Unfortunately, no cyst DNA remained, and it could not be confirmed whether this copy-number-neutral LOH led to loss of wild-type alleles by variant. Finally, the sporadic cyst from patient 20 displayed a 3.8 Mb mosaic copy-number gain at the telomeric part of chromosome 16p on cytoscanner. The signal was relatively weak, yet may suggest presence of a cellular subpopulation of this cyst with *PKD1* gain.

DISCUSSION

Here, we show that germline and somatic abnormalities outside of known cyst genes frequently occur in PLD, and many cysts of PLD patients have a unique genetic signature. LOH in known regions was confirmed for *PRKCSH* (22/29) and *PKD1/PKD2* (2/3) variants. In the SNP array cohort of 23 new patients (24 cysts), we detected 12 cysts with sizable copy-number losses or LOH outside of earlier identified genomic regions. In three patients, we found the presence of unique germline aberrations in PLD. In addition, a patient with a primary liver phenotype had a germline *PKD1* variant. Cyst DNA showed

recurrent copy-number loss on chromosome 3, with overlap between three patients. On chromosome 7, a 1.7 Mb copy-number loss and a mosaic whole-chromosome gain were found. Sporadic cysts displayed LOH around *LRP5* and a mosaic gain surrounding *PKD1* at a somatic level.

Although many genomic abnormalities were present beyond genomic regions known for second hits, most were unique. Chromosomal mapping suggests that each cyst follows an independent genetic pathway, similar to mosaicism observed in tissues of other somatic second-hit disorders.^{24,25} This likely reflects significant heterogeneity that is at the genomic root of cyst development. It also reflects that general genomic instability presumably precedes cyst development.^{16,17} *BUB1* haploinsufficiency is a known driver of chromosomal instability resulting in LOH and tumorigenesis,^{23,26} and a 2q13 microdeletion has previously been described.^{26,27} Although we show that it is unlikely that this specific gene is generally involved in LOH in PLD, other drivers of genetic instability may be present in the disease. Wnt signaling abnormalities appear to be common in PLD. Wnt signaling abnormalities are associated with tumorigenesis in the liver and kidney, and cause aberrant cyst development in mice.^{28,29} *CTNNB1* deletions and *APC* variants are also frequently found in hepatoblastoma.^{30,31} Variants in canonical Wnt signaling component *LRP5* causes ADPLD in man,⁴ whereas the c-terminal tail of polycystin-1 might interact with beta-catenin.³² In the same vein, our finding of copy-number-neutral LOH around *CTNNB1* and with copy-number loss of *ROR2*³³ in the germline of an ADPLD patient, together with copy-number-neutral LOH around *LRP5* in two sporadic cysts of another patient, further implicates this pathway as crucial for cystogenesis.

Trisomy X, the final germline abnormality we found, is unlikely to be involved in cystogenesis. Although female gender is a risk factor for cyst development and complications,³⁴ this is most likely owing to the sex hormones.^{35,36} Furthermore, gene expression of triple-X cells is largely limited to one copy by X-inactivation, excluding 5–10% of genes on the X chromosome located in pseudoautosomal regions.³⁷ We see this as a chance finding, considering its prevalence of 1 in 1000 females. On a somatic level, possible digenic or transheterozygous variants, and a *PKD1* gain were present on cysts. The 1.7 Mb chromosome 7 copy-number loss of a *PRKCSH* variant carrier might point toward a novel transheterozygous modifier region. Haploinsufficiency of genes such as *IGFBP1*, *IGFBP3*, and *ADCY1* might be relevant in cyst development, as these genes are related to the IGF and adenylyl cyclase pathway that the anti-cystogenic somatostatin analogs are involved in.^{38–41} Surprisingly, another cyst displayed a mosaic gain over the whole of chromosome 7, indicating that overexpression of these or other genes may also be relevant for cyst development. More difficult is the recurrent, overlapping LOH region on chromosome 3 (49,735,745–52,653,645). Although two cysts display clear LOH, the third may have had a partially normal cellular subpopulation. Over 60 genes are present at this location, none of which are known cyst-related genes. This 3p21.3 region does contain a cluster of tumor suppressor genes,⁴² such as tumor susceptibility gene *Rassfla*.⁴³ The cluster frequently undergoes LOH in early formation of different tumors,⁴² including hepatocarcinomas and cholangiocarcinomas.⁴⁴ The mosaic gain of *PKD1* in one cyst may be consistent with overexpression of *Pkd1* in mice leading to cystogenesis.⁴⁵ The mosaicism of this region was relatively low however, and may represent an artifact. Given the substantial investment that went into genotyping this cohort, we express our disappointment that we found no more specific leads to clarify the origination of multiple cysts in the liver. Concluding, our chromosomal mapping indicates significant

genetic heterogeneity outside of known second-hit regions of liver cysts. We identified unique cystogenic regions, as well as characteristics of general genomic instability in hepatic cyst DNA. These findings may explain the large number of ADPLD cases without a known variant, as well as phenotypic dissimilarities between similar cyst germline variants.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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