


BMJ Open Diagnostic yield of massively parallel sequencing in patients with chronic kidney disease of unknown etiology: rationale and design of a national prospective cohort study

Amber de Haan ¹, Mark Eijgelsheim,¹ Liffert Vogt,² Bert van der Zwaag,³ Albertien M van Eerde,³ Nine V A M Knoers,⁴ Martin H de Borst¹

To cite: de Haan A, Eijgelsheim M, Vogt L, *et al*. Diagnostic yield of massively parallel sequencing in patients with chronic kidney disease of unknown etiology: rationale and design of a national prospective cohort study. *BMJ Open* 2022;**12**:e057829. doi:10.1136/bmjopen-2021-057829

► Prepublication history and additional supplemental material for this paper are available online. To view these files, please visit the journal online (<http://dx.doi.org/10.1136/bmjopen-2021-057829>).

Received 29 September 2021
Accepted 16 March 2022



© Author(s) (or their employer(s)) 2022. Re-use permitted under CC BY-NC. No commercial re-use. See rights and permissions. Published by BMJ.

For numbered affiliations see end of article.

Correspondence to

Professor Martin H de Borst;
m.h.de.borst@umcg.nl

ABSTRACT

Introduction Chronic kidney disease (CKD) can be caused by a variety of systemic or primary renal diseases. The cause of CKD remains unexplained in approximately 20% of patients. Retrospective studies indicate that massively parallel sequencing (MPS)-based gene panel testing may lead to a genetic diagnosis in 12%–56% of patients with unexplained CKD, depending on patient profile.

The diagnostic yield of MPS-based testing in a routine healthcare setting is unclear. Therefore, the primary aim of the VARIETY (Validation of algoRithms and IdEnTification of genes in Young patients with unexplained CKD) study is to prospectively address the diagnostic yield of MPS-based gene panel testing in patients with unexplained CKD and an estimated glomerular filtration rate (eGFR) <60 mL/min/1.73 m² before the age of 50 years in clinical practice.

Methods and analysis The VARIETY study is an ongoing, prospective, nationwide observational cohort study to investigate the diagnostic yield of MPS-based testing in patients with unexplained CKD in a routine healthcare setting in the Netherlands. Patients are recruited from outpatient clinics in hospitals across the Netherlands. At least 282 patients will be included to meet the primary aim. Secondary analyses include subgroup analyses according to age and eGFR at first presentation, family history, and the presence of extrarenal symptoms.

Ethics and dissemination Ethical approval for the study has been obtained from the institutional review board of the University Medical Center Groningen. Study findings should inform physicians and policymakers towards optimal implementation of MPS-based diagnostic testing in patients with unexplained CKD.

INTRODUCTION

Chronic kidney disease (CKD) affects 11%–16% of the population worldwide,^{1–3} is associated with extensive comorbidity and an increased risk of premature mortality, and may ultimately result in end-stage kidney disease (ESKD) requiring dialysis or transplantation.^{4,5} CKD may be caused by a variety of systemic (eg, diabetes, hypertension) or

Strengths and limitations of this study

- First prospective study to examine the diagnostic yield of massively parallel sequencing in patients (age <50 at first presentation) with unexplained chronic kidney disease (CKD) in a routine healthcare setting.
- Nationwide study with relatively large sample size, allowing analyses of specific subgroups according to age and kidney function at first presentation.
- Study findings should inform physicians and policymakers in the implementation of gene panel testing in adults (age <50 at first presentation) with unexplained CKD.
- A potential limitation is that the definition of 'unexplained CKD' is not unequivocal.

primary renal diseases (eg, IgA nephropathy, membranous nephropathy). Current diagnostic approaches, including kidney biopsy, are often non-specific or inconclusive, contraindicated or omitted due to lack of clinical consequences.^{6,7} Therefore, the cause of CKD remains unknown in approximately 20% of patients with ESKD.^{8–10} However, knowledge of the underlying kidney disease can be pivotal as it may influence prognosis and medical treatment. In the setting of kidney transplantation, it may influence (living-related) donor selection and post-transplant recurrence risk. Approximately 27%–34% of patients with CKD report a positive family history of kidney disease (first or second degree relative with CKD)^{11,12} and a genetic cause can be identified in at least 10% of adults with CKD,^{13,14} indicating that in many cases a hereditary origin for the disease should be considered. Genetic testing could therefore be a valuable tool in the diagnostic process of CKD of unknown aetiology.

Recent studies suggest that massively parallel sequencing (MPS) techniques (previously referred to as next-generation sequencing)¹⁵ could be used as diagnostic tool in adults with unexplained CKD and should even be considered as first mode of diagnostics in patients with ESKD prior to the age of 50 years.¹⁶ Depending on patient selection, MPS led to a genetic diagnosis in 12%–56% of patients with unexplained CKD.^{14 17–19} However, most of these studies have been performed in a research setting, and therefore little is known about the diagnostic utility of MPS for adults with unexplained CKD in a routine healthcare setting. Moreover, currently available studies have been commonly based on subgroups of larger retrospective cohorts, and are heterogeneous in design and selection of genes used in MPS.²⁰ For this reason, it is difficult to define profiles of patients (eg, based on age and severity at disease onset, extrarenal manifestations, positive family history) that should preferentially undergo genetic testing. A recent joint publication by the ERA Working Group on Inherited Kidney Disorders and the Molecular Diagnostics Taskforce of the European Rare Kidney Disease Reference Network called for further research to explore the diagnostic yield of genetic testing in CKD of unknown origin in a clinical setting.²¹

Therefore, the objective of this national prospective cohort study is to determine the diagnostic yield, that is, the percentage of participants with a genetic diagnosis, using a large MPS-based multigene panel for kidney diseases in young patients (first presentation at age <50) with unexplained CKD (estimated glomerular filtration rate (eGFR) <60 mL/min/1.73 m²) in a routine healthcare setting. In addition, we aim to identify specific patient profiles with a high diagnostic yield. These findings can guide physicians and policymakers in implementing MPS-based diagnostic testing in patients with unexplained CKD.

METHODS AND ANALYSIS

Study design

The VARIETY (Validation of algoRithms and IdEnTification of genes in Young patients with unexplained CKD) study is a prospective nationwide observational cohort study designed to investigate the diagnostic yield of genetic testing in patients with unexplained CKD in a routine healthcare setting in the Netherlands. The study will collect and analyse data obtained during routine clinical practice and through a questionnaire. Participants will be included from both academic and non-academic hospitals throughout the Netherlands. The anonymised data are collected, stored and analysed in the University Medical Center Groningen (UMCG). All participants will give written informed consent on enrolment.

Study population

The targeted study population consist of all patients with unexplained CKD and an eGFR <60 mL/min/1.73 m²

before the age of 50 years. Unexplained CKD is defined as the absence of all the following criteria: a biopsy-proven diagnosis (eg, IgA nephropathy), a specific morphological renal diagnosis (eg, polycystic kidney disease suspected of autosomal/recessive polycystic kidney disease), or a specific or plausible renal diagnosis (eg, history of long-term insulin-dependent diabetes mellitus before the onset of CKD, lithium-induced nephropathy). Since hypertensive nephropathy is a nonspecific diagnosis and hypertension is also a very common consequence of CKD,²² patients with hypertensive nephropathy in the absence of a clear underlying disorder such as renal artery stenosis are considered to have unexplained CKD. Patients with renal hypoplasia, renal atrophy, and nonspecific histological conditions (such as secondary focal segmental glomerulosclerosis, glomerulonephritis of unknown cause, or interstitial nephritis) are also considered to have unexplained CKD.

Patients with a current age >50 years, but who presented with an eGFR <60 mL/min/1.73 m² before the age of 50 years, and renal transplant recipients who had a pre-transplant eGFR <60 mL/min/1.73 m² before the age of 50 years are also eligible for inclusion. In addition, genetic testing with a specific MPS-based gene panel (see ‘Genetic testing’) is required for participation. Exclusion criteria for participation in the VARIETY study are: age <18 years at time of inclusion or patients who do not give or are unable to give informed consent for genetic testing or for the current study.

Recruitment

To ensure a representative sample of CKD patients, patients are recruited from outpatient clinics in both academic and non-academic hospitals across the Netherlands. Depending on the hospital, patients will be screened by the primary treating nephrologists or by trained study investigators. In case of a study investigator, a list with potential participants will be sent to the treating nephrologist to confirm the diagnosis of unexplained CKD. Eligible participants will be informed about the study by the investigators or their treating nephrologists aware of the study protocol. A study investigator or treating nephrologist will ask for informed consent for this study. Information for patients has been made available in the form of a patient information folder and a website (in Dutch): www.onbegrepennierziekte.nl.

Data collection

Detailed clinical and demographic data are collected from patients’ electronic health record (EHR) and through a questionnaire following informed consent. The data will subsequently be entered into a secure electronic case report form.

Electronic health record

The following information will be collected from the EHR: age at inclusion, sex, primary renal disease diagnosis, age at CKD onset/presentation, dialysis or kidney

transplantation, age at start dialysis or kidney transplantation, presence of extrarenal features, medication use at inclusion, medical history, family history (including three-generation pedigree), blood pressure at CKD onset and at inclusion, presence of haematuria and/or nephrotic syndrome, laboratory results (serum creatinine, eGFR, total cholesterol, high-density lipoprotein (HDL), low-density lipoprotein (LDL), triglycerides, 24-hour urine albumin excretion, 24-hour urine creatinine excretion, 24-hour urine total protein excretion, haematuria) at CKD onset/presentation and inclusion, renal histopathology and imaging of the native kidneys, and results of genetic testing in relation to kidney disease. We will also collect information regarding the clinical consequences of a genetic diagnosis and if genetic counselling was performed by a nephrologist or clinical geneticist. If participants are referred to a clinical geneticist, we will also collect the results of any additional genetic testing.

Questionnaire

Data collected from the EHR will be expanded with a questionnaire to collect additional data on family history, medical history, current health complaints and extrarenal manifestations (online supplemental table 1).

Genetic testing

We will include patients who have undergone MPS-based multigene panel testing, initiated by a clinical geneticist or nephrologist following pretest counselling as part of clinical care in patients with unexplained CKD, in accordance with guidelines in the Netherlands.²³ Figure 1 shows the suggested flowchart for genetic testing in the VARIETY study, based on these recommendations. The

criteria as shown in this flow chart are slightly more liberal than the published recommendations, which will help to define the optimal age and eGFR ranges where genetic testing is still of clinical benefit. To stimulate the implementation of the guideline, we made a website for the VARIETY study (www.onbegrepennierziekte.nl) where nephrologists can find information about genetic testing and pretest genetic counselling.

In order to reduce heterogeneity in the diagnostic approach, we will assess the diagnostic yield of a specific MPS-based gene panel, namely the ‘CKD-Y’ (‘CKD in Young patients’) targeted exome sequencing (ES) panel available at the University Medical Center (UMC) Utrecht, The Netherlands. The older version of this panel (v18) contains 141 different genes associated with early-onset CKD, including *PKD1* and *PKD2* (figure 2). On 8 March 2021, the CKD-Y panel was updated (v21) and the number of genes changed from 141 to 256 (figure 3). This panel was chosen as it is an ES-based panel and contains all the current genes associated with early-onset CKD. In addition, this panel can be ordered by nephrologists without referral to the clinical geneticist. Alternatively, the hereditary kidney disease panel from UMC Utrecht was allowed. This is another targeted ES panel, consisting of 379 genes in the v18 version and 495 genes in the updated v21 version (online supplemental figures 1-2). Since this panel contains some kidney cancer oncogenes, it may only be ordered by a clinical geneticist. The hereditary kidney disease panel includes all genes of the CKD-Y panel, making it possible to determine if a variant could also have been identified with the CKD-Y panel. Potential findings from the hereditary kidney disease

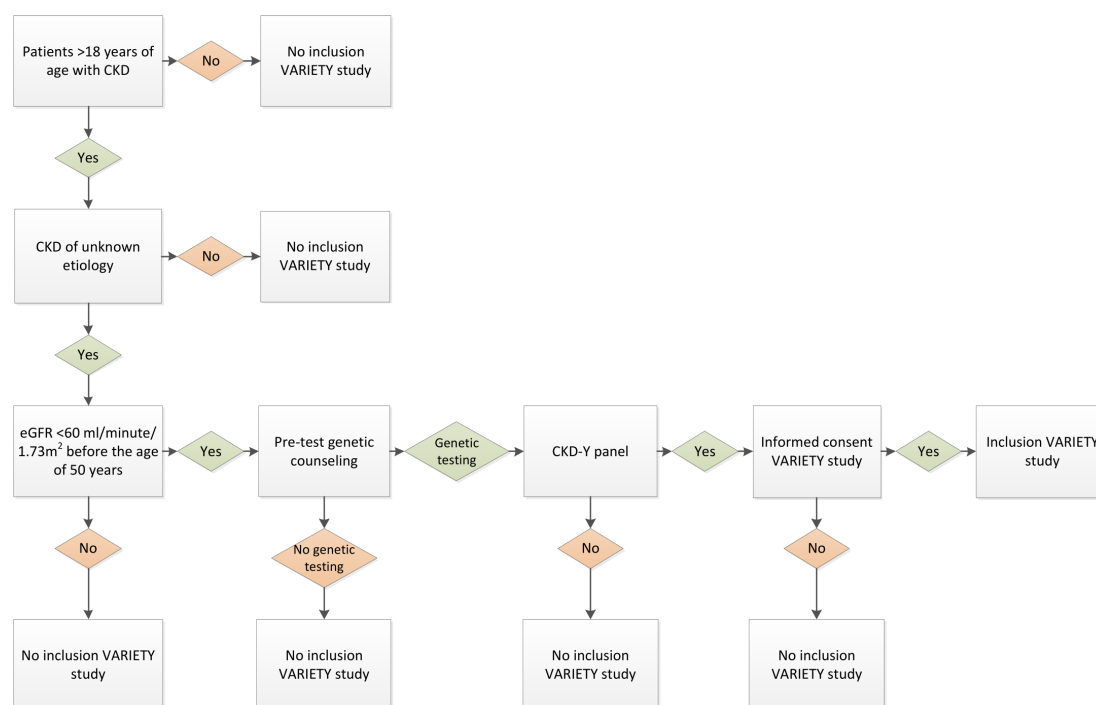


Figure 1 Flow chart for inclusion in the VARIETY study. CKD, chronic kidney disease; eGFR, estimated glomerular filtration rate; VARIETY, Validation of algoRithms and IdEnTification of genes in Young patients with unexplained CKD.

141 genes in the Chronic Kidney Disease in Young patients (CKD-Y) panel						
ACE	CEP290	EMP2	INF2	MYH11	PKD1	TBX18
ACTN4	CFB	EYA1	INVS	MYH9	PKD2	TMEM67
ADCK4	CFH	FAN1	IQCB1	MYO1E	PKHD1	TNXB
AGT	CFHR5	FAT1	ITGA3	NEK8	PLCE1	TRAF3IP1
AGTR1	CFI	FGA	ITGA8	NOTCH2	PMM2	TRAP1
AGXT	CHD7	FN1	JAG1	NPHP1	PTPRO	TRPC6
ALG1	CLCN5	FOXC2	KANK1	NPHP3	REN	TTC21B
AMN	COL4A3	FRAS1	KANK2	NPHP4	RMND1	UMOD
ANKS6	COL4A4	FREM1	KANK4	NPHS1	ROBO2	VIPAS39
APOA1	COL4A5	FREM2	KIAA0556	NPHS2	RPGRIP1L	VPS33B
APOL1	COQ2	GATA3	KIAA0586	NUP107	RPM2B	WDR19
ARHGDI2	COQ6	GLA	LAMB2	NUP205	SALL1	WT1
ATXN10	CRB2	GLIS2	LMNA	NUP93	SCARB2	XPNPEP3
B2M	CTNS	GRHPR	LMX1B	NXF5	SDCCAG8	ZMPSTE24
BBIP1	CUBN	GRIP1	LRIG2	OCRL	SGPL1	ZNF423
BCS1L	CYP11B1	GSN	LYZ	OFD1	SIX5	
C3	CYP11B2	HNF1B	MAFB	OSGEP	SLC41A1	
CD151	DACT1	HOGA1	MAGI2	PAX2	SLC4A1	
CD2AP	DCDC2	HPSE2	MAP7D3	PBX1	SLC7A7	
CD46	DGKE	IFT27	MAPKBP1	PDSS1	SMARCAL1	
CEP164	DSTYK	IFT81	MUC1	PDSS2	SOX17	

Figure 2 Overview of the 141 genes that are analysed in the exome sequencing based Chronic Kidney Disease in young patients (CKD-Y) panel V.18 at University Medical Center Utrecht.

panel that do not overlap with the CKD-Y panel will not be included in the primary analyses. Patients with older versions of the CKD-Y and hereditary kidney disease panels can be included. We will record which version of the CKD-Y and/or hereditary kidney disease panel was used. The procedures for ES and variant filtering have been described before.²⁴ Copy number variation (CNV) detection was performed using an in-house adapted,

256 genes in Chronic Kidney Disease in Young patients (CKD-Y) panel v21						
ACE	BICC1	CUBN	HYLS1	MOCOS	PLCE1	TMEM138
ACTG2	BMPR2	CUL3	IFT27	MTR	PMM2	TMEM216
ACTN4	C3	CYP11B1	IFT74	MTRR	POC1B	TMEM231
ADAMTS9	C8ORF37	CYP11B2	IFT81	MTX2	PODXL	TMEM237
AGT	CACNA1D	CYP17A1	ILIRAP	MUC1	PTPRO	TMEM67
AGTR1	CACNA1H	DAAM2	INF2	MYH11	REN	TMEM72
AGXT	CC2D2A	DACT1	INPP5E	MYH9	RMND1	TNS2
AH1	CD151	DCDC2	INVS	MYO1E	ROBO2	TNXB
ALG1	CD2AP	DGKE	IQCB1	NEK8	RPGRIP1L	TOGARAM1
ALMS1	CD46	DLC1	ITGA3	NOS1AP	RRM2B	TP53RK
AMN	CDK20	DNAJB11	ITGA8	NOTCH2	SALL1	TPRKB
ANKS6	CEP104	DSTYK	ITGB4	NPHP1	SARS2	TRAF3IP1
ANLN	CEP164	E2F3	ITSN1	NPHP3	SCARB2	TRAP1
APOA1	CEP290	EMP2	ITSN2	NPHP4	SCNN1A	TRIM32
APOE	CEP41	EYA1	JAG1	NPHS1	SCNN1B	TRIM8
APOL1	CEP83	FAM149B1	KANK1	NPHS2	SCNN1G	TRPC6
APRT	CFB	FAN1	KANK2	NR3C1	SDCCAG8	TTC21B
ARHGAP24	CFH	FAT1	KANK4	NR3C2	SEC61A1	TTC8
ARHGDI2	CFHR1	FGA	KATNP	NUP107	SGPL1	UMOD
ARL13B	CFHR2	FN1	KCNJ5	NUP130	SIX1	VIPAS39
ARL6	CFHR3	FOXC2	KIAA0586	NUP160	SIX5	VPS33B
ARMC9	CFHR4	FRAS1	KIF3B	NUP205	SLC22A12	WDPCP
ATXN10	CFHR5	FREM1	KIRREL1	NUP85	SLC2A9	WDR19
AVIL	CFI	FREM2	KLHL3	NUP93	SLC3A1	WDR35
B2M	CHD7	GANAB	LAMB2	NXF5	SLC41A1	WDR60
B9D1	CLCN2	GAPVD1	LMNA	OCRL	SLC4A1	WDR73
B9D2	CLCN5	GATA3	LMX1B	OFD1	SLC7A7	WNK1
BBIP1	COL4A3	GATM	LRIG2	OSGEP	SLC7A9	WNK4
BBS1	COL4A4	GLA	LYZ	PAX2	SMARCAL1	WT1
BBS10	COL4A5	GLIS2	LZTF1	PBX1	SOX17	XDH
BBS12	COQ2	GRHPR	MAFB	PCM1	STX16	XPNPEP3
BBS2	COQ6	GRIP1	MAGI2	PDSS1	TBC1D8B	YRDC
BBS4	COQ8B	GSN	MAP7D3	PDSS2	TBX18	ZMPSTE24
BBS5	CPLANE1	HNF1B	MAPKBP1	PIBF1	TCTN1	ZNF423
BBS7	CRB2	HOGA1	MKKS	PKD1	TCTN2	
BBS9	CSPPI	HPSE2	MKS1	PKD2	TCTN3	
BCS1L	CTNS	HSD11B2	MMACHC	PKHD1	TMEM107	

Figure 3 Overview of the 256 genes that are analysed in the exome sequencing based Chronic Kidney Disease in young patients (CKD-Y) panel V.21 at University Medical Center Utrecht. Bold genes are also on the CKD-Y panel V.18.

Table 1 Classification of variants according to ACMG guidelines²⁶

Class	Description
1	Clearly not pathogenic, common polymorphism
2	Unlikely to be pathogenic, diagnosis not confirmed molecularly
3	Unknown significance/pathogenicity, does not exclude or confirm diagnosis
4	Likely to be pathogenic, consistent with the diagnosis
5	Clearly pathogenic, result confirms the diagnosis

ACMG, American College of Medical Genetics.

diagnostically validated, version of the ExomeDepth CNV detection tool.²⁵

Primary and secondary analyses

The primary analysis will address the diagnostic yield of the CKD-Y panel, defined as the percentage of positive test results (ie, pathogenic variant(s) explaining the cause of the disease), in the overall cohort of patients with unexplained CKD and an eGFR <60 mL/min/1.73 m² before the age of 50 years. We will perform a sensitivity analysis in patients with onset eGFR <60 mL/min/1.73 m² between the age of 18 and 50 years. The pathogenicity of variants will be determined according to the standards and guidelines from the American College of Medical Genetics and Genomics.²⁶ With this standard, variants are classified into five categories using several lines of evidence, such as available literature, patient databases and in silico prediction programmes. Class one variants are clearly not pathogenic; class five variants are clearly pathogenic. Class three are variants of uncertain significance/pathogenicity (VUS), these variants do not confirm or exclude the diagnosis (table 1).²⁶ For the determination of the diagnostic yield, only class 4 and class 5 variants will be considered as a 'positive test result' to determine the diagnostic yield. In cases with two class 4/5 variants in an autosomal recessive gene, these will only be considered a 'positive test result' if testing in parents has confirmed the variants are positioned in trans.

Secondary analyses include subgroup analyses according to age and eGFR at first presentation, family history and the presence of extrarenal symptoms. A positive family history for CKD is recorded if the participant either has a first (parent or child), second (siblings, grandparents, grandchildren), third (aunts, uncles, nephews, nieces) or fourth (cousins) degree relative with CKD. Family history will be obtained from combining information present in the EHR with information obtained from the questionnaire. Other secondary analysis aims to define the percentage of genetic tests with a clinical consequence. A genetic diagnosis is considered to have a clinical consequence if it: (1) negated the need for kidney biopsy, (2) triggered or negated the need for immunosuppressive

therapy, (3) provides prognostic information, that is, the risk of post-transplantation anti-glomerular basement membrane (GBM) nephritis, (4) led to, or should lead to, referral to other specialties (eg, ophthalmologist), (5) led to targeted work-up for associated symptoms or extra-renal manifestations, (6) affected surveillance frequency, (7) led to, or should lead to, genetic testing in potential living related kidney donors, (8) enabled more precise (preconception) genetic counselling for the patient or family members or (9) led to more precise or extensive follow-up of potentially affected family members.

Tertiary outcomes will be the percentage of participants in which a VUS was identified and the number of incidental/secondary findings (results unrelated to the initial indication for genetic testing). In addition, if a molecular diagnosis is identified and a kidney biopsy from the native kidney is present, we will assess if the biopsy findings match the molecular diagnosis. Finally, we will perform health economic analyses to determine if MPS in patients with unexplained CKD is cost-effective.

We will report the number of participants who withdraw from participating in the VARIETY study after initial inclusion and the number of participants who have initially been included, but on further analysis by the study team did not match the inclusion criteria. Participants without results from genetic testing will be excluded from all analyses. If information is missing from the EHR, we will ask the general practitioner to deliver the missing data within participants' consent. If the data cannot be retrieved, it will be regarded as 'unknown'. In case eGFR at CKD onset is missing, the first available eGFR or serum creatinine measurement since the diagnosis of CKD will be used.

Statistical analysis

Statistical analysis will be performed with IBM SPSS statistics for Windows, V.23 (IBM). An overall significance level of 0.05 will be handled.

Continuous variables that are normally distributed will be presented as mean and standard deviation. Non-normally distributed variables will be expressed as median and interquartile range. Frequencies and percentages will be used to describe categorical variables such as gender, family history, renal replacement therapy, extrarenal manifestations, and diagnostic yield. The χ^2 or Fisher's exact test will be used to compare differences in categorical variables between the different subgroups of the secondary analysis. Logistic regression will be performed to identify characteristics associated with a genetic diagnosis.

Sample size calculation

The minimal sample size was calculated using the following formula,²⁷ based on the study's primary endpoint:

$$n = \frac{Z^2 * P(1-P)}{d^2}$$

Based on the literature, the expected percentage of positive test results is 17%.¹⁴ Assuming a level of confidence (z) of 1.96 and precision (d) of 0.05,²⁷ a minimum of 217 participants are required for a reliable assessment of the primary outcome. In order to be clinically and politically significant, we aim to increase the sample size of this prospective cohort study beyond the largest currently available retrospective study, that is, to include at least 282 patients in the current study.^{20 27}

Data management

Study data will be recorded digitally using the secure REDCap (Research Electronic Data Capture) web application (REDCap, Nashville, Tennessee, USA) hosted at the UMCG.^{28 29} Data collection and entry is performed by trained investigators from the UMCG. To minimise differences and errors in data entry, investigators from the UMCG will travel to other participating centres for data collection and entry in REDCap. Data validation in REDCap will be performed according to a data validation plan, which has been made in collaboration with the UMCG Research Data Support and approved by the Institutional Review Board. Data analysis will take place on validated and anonymised data. On study closure, data will be extracted from REDCap and exported to SPSS for analysis.

Patient and public involvement

Patients and/or the public were not involved in the design of this study.

ETHICS AND DISSEMINATION

Ethical approval for the study has been obtained from the institutional review board of the UMCG (METc 2019/106). The study is conducted in accordance with the WMA Declaration of Helsinki. The results of the study will be presented at (inter)national congresses and submitted for open access publication in peer-reviewed journals. In addition to the primary results, related to the main research questions as defined above, case reports/series may be submitted for publication in case of unique or interesting findings and these will also be submitted for publication in peer-reviewed journals. In accordance with the information sheet for participants, the main results and any publications from the VARIETY study will also be made available on the study website. After completion of the study and publication of the main results, request for re-use of the data can be submitted to the corresponding author.

CONCLUSION AND STUDY STATUS

Genetic testing shows promising results as a diagnostic tool in adults with CKD and it has the potential to resolve CKD cases with an unknown aetiology. However, further research is needed in a clinical setting to define the position of MPS-based diagnostics in clinical practice



and to determine which subpopulations will have the highest diagnostic yield. Here, we outlined the design for a prospective cohort study that will determine the diagnostic yield of MPS-based renal gene panel testing in patients with unexplained CKD. The fact that unexplained CKD has not been uniformly defined by international (guideline) committees or institutions may slightly impact external validity of our findings. However, results from this study are likely a step forward in informing physicians and policymakers involved in implementation of genetic testing in patients with unexplained CKD. Inclusion started on 31 July 2019. As of September 2021, 248 patients have been included.

Author affiliations

¹Department of Internal Medicine, Division of Nephrology, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands

²Department of Internal Medicine, Section Nephrology, Amsterdam University Medical Center, University of Amsterdam, Amsterdam, The Netherlands

³Department of Genetics, University Medical Center Utrecht, Utrecht University, Utrecht, The Netherlands

⁴Department of Genetics, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands

Acknowledgements Several authors of this publication (AMvE, NVAMK and MHdB) are members of the European Reference Network for Rare Kidney Diseases (ERKNet) - Project ID no. 739 532.

Contributors AdH and MHdB wrote the first draft of the manuscript. ME, LV, BvdZ, AMvE and NVAMK gave feedback and contributed to manuscript revision. All authors read and approved the submitted version.

Funding This collaboration project is cofinanced by Sanofi Genzyme and the Dutch Ministry of Economic Affairs and Climate Policy by means of the PPP Allowance made available by the Top Sector Life Sciences & Health to stimulate public-private partnerships (grant numbers RVO/6320 and IMAGEN/LSHM20009).

Competing interests MHdB and LV have received research support and lecture fees (all to institution) from Sanofi Genzyme related to the current study. NVAMK has received reimbursement of travel expenses for lectures related to the current study from Sanofi Genzyme.

Patient and public involvement Patients and/or the public were not involved in the design, or conduct, or reporting, or dissemination plans of this research.

Patient consent for publication Not applicable.

Provenance and peer review Not commissioned; externally peer reviewed.

Supplemental material This content has been supplied by the author(s). It has not been vetted by BMJ Publishing Group Limited (BMJ) and may not have been peer-reviewed. Any opinions or recommendations discussed are solely those of the author(s) and are not endorsed by BMJ. BMJ disclaims all liability and responsibility arising from any reliance placed on the content. Where the content includes any translated material, BMJ does not warrant the accuracy and reliability of the translations (including but not limited to local regulations, clinical guidelines, terminology, drug names and drug dosages), and is not responsible for any error and/or omissions arising from translation and adaptation or otherwise.

Open access This is an open access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited, appropriate credit is given, any changes made indicated, and the use is non-commercial. See: <http://creativecommons.org/licenses/by-nc/4.0/>.

ORCID iD

Amber de Haan <http://orcid.org/0000-0003-4228-6927>

REFERENCES

- Hill NR, Fatoba ST, Oke JL, *et al.* Global prevalence of chronic kidney disease - A systematic review and meta-analysis. *PLoS One* 2016;11:e0158765.
- JC L, Zhang LX. Prevalence and Disease Burden of Chronic Kidney Disease. In: *Advances in experimental medicine and biology*, 2019.
- Jha V, Garcia-Garcia G, Iseki K, *et al.* Chronic kidney disease: global dimension and perspectives. *Lancet* 2013;382:260–72.
- Go AS, Chertow GM, Fan D, *et al.* Chronic kidney disease and the risks of death, cardiovascular events, and hospitalization. *N Engl J Med* 2004;351:1296–305.
- Gansevoort RT, Correa-Rotter R, Hemmelgarn BR, *et al.* Chronic kidney disease and cardiovascular risk: epidemiology, mechanisms, and prevention. *Lancet* 2013;382:339–52.
- Luciano RL, Moeckel GW. Update on the native kidney biopsy: core curriculum 2019. *Am J Kidney Dis* 2019;73:404–15.
- Scheckner B, Peyser A, Rube J, *et al.* Diagnostic yield of renal biopsies: a retrospective single center review. *BMC Nephrol* 2009;10:11.
- Titze S, Schmid M, Köttgen A, *et al.* Disease burden and risk profile in referred patients with moderate chronic kidney disease: composition of the German chronic kidney disease (GCKD) cohort. *Nephrol Dial Transplant* 2015;30:441–51.
- Neild GH. Primary renal disease in young adults with renal failure. *Nephrol Dial Transplant* 2010;25:1025–32.
- Kramer A, Pippias M, Noordzij M, *et al.* The European renal association - European Dialysis and Transplant Association (ERA-EDTA) registry annual report 2016: a summary. *Clin Kidney J* 2019;12:702–20.
- Connaughton DM, Bukhari S, Conlon P, *et al.* The Irish kidney gene project--prevalence of family history in patients with kidney disease in Ireland. *Nephron* 2015;130:293–301.
- Skrunes R, Svarstad E, Reisæter AV, *et al.* Familial clustering of ESRD in the Norwegian population. *Clin J Am Soc Nephrol* 2014;9:1692–700.
- Mallett A, Patel C, Salisbury A, *et al.* The prevalence and epidemiology of genetic renal disease amongst adults with chronic kidney disease in Australia. *Orphanet J Rare Dis* 2014;9:98.
- Groopman EE, Marasa M, Cameron-Christie S, *et al.* Diagnostic utility of exome sequencing for kidney disease. *N Engl J Med* 2019;380:142–51.
- Jarvik GP, Evans JP. Mastering genomic terminology. *Genet Med* 2017;19:491–2.
- Snoek R, van Jaarsveld RH, Nguyen TQ, *et al.* Genetics-first approach improves diagnostics of ESKD patients <50 years old. *Nephrol Dial Transplant* 2022;37:349–57.
- Lata S, Marasa M, Li Y, *et al.* Whole-exome sequencing in adults with chronic kidney disease: a pilot study. *Ann Intern Med* 2018;168:100–9.
- Ottlewski I, Münch J, Wagner T, *et al.* Value of renal gene panel diagnostics in adults waiting for kidney transplantation due to undetermined end-stage renal disease. *Kidney Int* 2019;96:222–30.
- Connaughton DM, Kennedy C, Shril S, *et al.* Monogenic causes of chronic kidney disease in adults. *Kidney Int* 2019;95:914–28.
- de Haan A, Eijgelsheim M, Vogt L, *et al.* Diagnostic yield of next-generation sequencing in patients with chronic kidney disease of unknown etiology. *Front Genet* 2019;10:1264.
- Knoers N, Antignac C, Bergmann C, *et al.* Genetic testing in the diagnosis of chronic kidney disease: recommendations for clinical practice. *Nephrol Dial Transplant* 2022;37:239–54.
- Carriazo S, Vanessa Perez-Gomez M, Ortiz A. Hypertensive nephropathy: a major roadblock hindering the advance of precision nephrology. *Clin Kidney J* 2020;13:504–9.
- van Eerde A, Rookmaker M, Snoek R. Handreiking Erfelijke Nieraandoeningen en Urinewegafwijkingen en Nefrologische Verwijsindicaties Klinische Genetica, 2018. Available: <https://www.nefro.nl/sites/www.nefro.nl/files/richlijnen/Handreiking%20genetische%20diagnostiek%20bij%20nierziekten%2C%202018.pdf>
- Dubail J, Huber C, Chantepie S, *et al.* Slc10A7 mutations cause a skeletal dysplasia with amelogenesis imperfecta mediated by Gag biosynthesis defects. *Nat Commun* 2018;9:3087.
- Plagnol V, Curtis J, Epstein M, *et al.* A robust model for read count data in exome sequencing experiments and implications for copy number variant calling. *Bioinformatics* 2012;28:2747–54.
- Richards S, Aziz N, Bale S, *et al.* Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of medical genetics and genomics and the association for molecular pathology. *Genet Med* 2015;17:405–24.

- 27 Pourhoseingholi MA, Vahedi M, Rahimzadeh M. Sample size calculation in medical studies. *Gastroenterol Hepatol Bed Bench* 2013;6:14–17.
- 28 Harris PA, Taylor R, Thielke R, *et al.* Research electronic data capture (REDCap)--a metadata-driven methodology and workflow process for providing translational research informatics support. *J Biomed Inform* 2009;42:377–81.
- 29 Harris PA, Taylor R, Minor BL, *et al.* The REDCap Consortium: building an international community of software platform partners. *J Biomed Inform* 2019;95:103208.