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Pleuntje van der Sluijs, Marieke Joosten, Caroline Alby, Tania Attié-Bitach, Kelly Gilmore, Christele Dubourg, Mélanie Fradin, Tianyun Wang, Evangeline Kurtz-Nelson, Kaitlyn Ahlers, et al.

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ABSTRACT

Purpose: Genome-wide sequencing is increasingly being performed during pregnancy to identify the genetic cause of congenital anomalies. The interpretation of prenatally identified variants can be challenging and is hampered by our often limited knowledge of prenatal phenotypes. To better delineate the prenatal phenotype of Coffin-Siris syndrome (CSS), we collected clinical data from patients with a prenatal phenotype and a pathogenic variant in one of the CSS-associated genes.

Methods: Clinical data was collected through an extensive web-based survey.

Results: We included 44 patients with a variant in a CSS-associated gene and a prenatal phenotype; 9 of these patients have been reported before. Prenatal anomalies that were frequently observed in our cohort include hydrocephalus, agenesis of the corpus callosum, hypoplastic left heart syndrome, persistent left vena cava, diaphragmatic hernia, renal agenesis, and intrauterine growth restriction. Anal anomalies were frequently identified after birth in patients with *ARIDIA* variants (6/14, 43%). Interestingly, pathogenic *ARIDIA* variants were much more frequently identified in the current prenatal cohort (16/44, 36%) than in postnatal CSS cohorts (5%-9%).

Conclusion: Our data shed new light on the prenatal phenotype of patients with pathogenic variants in CSS genes.

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Introduction

Coffin-Siris syndrome (CSS) (OMIM 135900 and others) is characterized by neurodevelopmental delay and may be accompanied by hypoplasia of the fifth digit and/or nail, distinct facial features, hypertrichosis, and a varying degree of congenital anomalies.¹⁻⁶ In the current literature, most patients present with no prenatal ultrasound (US) anomalies. Congenital diaphragmatic hernia,⁷ hypoplastic left heart syndrome (HLHS),⁸ and intrauterine growth restriction (IUGR)⁹ have been occasionally described, whereas agenesis of the corpus callosum (ACC)¹⁰ is observed more frequently.

Application of prenatal genome-wide sequencing is rapidly becoming standard care.¹¹⁻¹⁵ The interpretation of prenatally identified variants can be challenging because of the limited knowledge of prenatal phenotypes, because most genome-wide sequencing in diagnostics and research has focused on postnatal phenotypes. CSS is no exception to this rule. For example, we recently detected a novel de novo missense variant in *SMARCA4* (OMIM 614609) in a fetus with HLHS. HLHS had been described in 1 patient with *ARIDIA*-CSS⁸ before. With this little information, it was difficult to be certain about the pathogenicity of the variant, showing a typical difficulty encountered in current genetic practice.

M.C. Haak and G.W.E. Santen are co-last authors.

*Correspondence and requests for materials should be addressed to Gijs W.E. Santen, Department of Clinical Genetics, Leiden University Medical Center, Postbus 9600, 2300 RC Leiden. E-mail address: santen@lumc.nl

A full list of authors and affiliations appears at the end of the paper.

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This study aimed to increase knowledge of the prenatal phenotype of CSS by presenting a detailed description of the prenatal features in a cohort of patients with 1 or more prenatal US anomalies and a pathogenic variant in one of the CSS-related genes.

Materials and Methods

Patient collection

Patients were collected through our outpatient CSS expertise center in the Leiden University Medical Center, Leiden, the Netherlands. Additional patients were included through international contacts, from physicians contacting us for second opinions, through contacts with the Baylor Genetics Laboratory, and through laboratories who reported pathogenic variants in LOVD¹⁶ and ClinVar.¹⁷ We also included patients who were presented at conferences and via the fetal sequencing consortium, which consists of an international group of medical professionals who discuss results of prenatal diagnostics in a biweekly case meeting.

Patient selection

Inclusion criteria were (1) the presence of any anomaly that was mentioned in US reports, excluding so called soft-markers (eg, echogenic focus in the left ventricle) and (2) a pathogenic or likely pathogenic genetic variant in a CSS-associated gene (*ARID1A*, *ARID1B*, *ARID2*, *BICRA*, *DPF2*, *SMARCA2* duplication, *SMARCA4*, *SMARCB1*, *SMARCC2*, *SMARCD1*, *SMARCE1*, *SOX11*, *SOX4*). The exclusion criterium was the ACC as the sole prenatal US anomaly in combination with a pathogenic *ARID1B* variant, because the association between the ACC and pathogenic *ARID1B* variants is well established.^{10,18}

Timing of the identification of the genetic variant could be prenatal, postnatal, or postmortem.

Data collection

Data were collected through an online questionnaire. If required, genetic data were completed using Alamut version 2.11.

A patient was considered to have IUGR if it was reported as such by the contributing clinician.

Results

Genetic variants

In total, 44 patients with variants in *ARID1A* ($n = 16$, 36%), *ARID1B* ($n = 19$, 43%), *SMARCA4* ($n = 3$, 7%), and *SMARCB1* ($n = 6$, 14%) and a prenatal phenotype detected

by US were identified (Supplemental Table 1). Variants were classified using the American College of Medical Genetics and Genomics/Association for Molecular Pathology criteria.

Phenotype

The clinical features are summarized in Tables 1 and 2. The median time in weeks of gestation at which the first US anomalies were detected tends to be lowest among patients with *ARID1A* variants (14+5 weeks), followed by *ARID1B* (20+0 weeks), *SMARCA4* (20+0 weeks), and *SMARCB1* (24+0 weeks) (Supplemental Figure 1). Unless stated otherwise, frequencies in the text refer to anomalies that were detected prenatally. The total prevalence of features (detected prenatally or by postnatal assessment) in this cohort is shown in Table 1.

Genotype-phenotype correlation

ARID1A

Of the 16 *ARID1A* pregnancies, 11 (69%) were terminated on request of the parents because the anomalies diagnosed by US carried a poor prognosis. One pregnancy led to an intrauterine fetal death, and one resulted in a child who died shortly after birth. Brain anomalies were most frequently present (10/15, 73%), especially hydrocephalus ($n = 7$) and ACC ($n = 5$). Cardiac anomalies were reported in 60% (9/15). HLHS was detected in 2 fetuses and hypoplastic right heart in 1 fetus. Persistent left vena cava ($n = 3$) and double outlet right ventricle ($n = 3$) were cardiovascular anomalies reported in a subset of fetuses. In one case, the ventricular septal defect and patent ductus arteriosus spontaneously resolved at 4 months of age. Renal anomalies were observed in 27% (4/15) of cases, including 1 case with unilateral renal agenesis who received a peritoneal dialysis catheter at the age of 1 year and a renal transplant 6 years later. Diaphragmatic hernia was detected in 13% (2/15) of fetuses, and in 3 cases, a diaphragmatic hernia was identified during postnatal investigation (34%, 5/15). Postnatal investigation also revealed supernumerary ribs in 2 patients and anal anomalies in 43% (6/14); 4 patients had anal atresia and 2 patients had an anteriorly placed anus.

ARID1B

Despite excluding isolated ACC cases for *ARID1B*, brain anomalies were detected in 76% (13/17) of *ARID1B* cases, but only in a subset during pregnancy (29.4%, 5/17). Most often, ACC was not detected prenatally. Cardiac anomalies were present in 19% (3/16), including 1 fetus with HLHS. Fetus 18 with a complex cardiac defect also had a 22q11 deletion. This patient died during her first day of life because of respiratory insufficiency. Another fetus had unilateral renal agenesis.

SMARCA4

Of the 3 fetuses with a *SMARCA4* variant, 2 had a severe cardiac anomaly (ie, HLHS). One of these patients died

Table 1 Clinical characteristics of included patients

Clinical Features	ARID1A					ARID1B					SMARCA4					SMARCB1				
	(n = 16 ^a)	Detected by US ^b	Detected by Postnatal Investigation	Total Affected	% Total	(n = 19)	Detected by US ^b	Detected by Postnatal Investigation	Total Affected	% Total	(n = 3)	Detected by US ^b	Detected by Postnatal Investigation	Total Affected	% Total	(n = 6)	Detected by US ^b	Detected by Postnatal Investigation	Total Affected	% Total
Sex, female	15	—	—	9	60%	19	—	—	5	26%	3	—	—	2	67%	6	—	—	4	67%
First US anomaly, time of AD in days, n (min-max, median)	12	—	—	(84-224, 103)		14	—	—	(60-259, 140)		3	—	—	(82-145, 140)		6	—	—	(140-231, 168)	
Anomalies																				
Placenta anomaly	15	1	—	1	7%	19	—	—	—	—	3	—	—	—	—	6	—	—	—	—
Single umbilical artery	15	7	—	7	47%	19	3	1	4	21%	3	—	—	—	—	6	—	—	—	—
Oligohydramnios	15	3	—	3	20%	19	3	—	3	16%	3	—	—	—	—	6	—	—	—	—
Polyhydramnios	15	—	—	—	—	19	3	—	3	16%	3	—	—	—	—	6	1	—	1	17%
IUGR	15	2	—	2	13%	19	4	—	4	21%	3	—	—	—	—	6	3	—	3	50%
Short femur	15	2	—	2	13%	19	—	—	—	—	3	—	—	—	—	6	—	—	—	—
Brain anomaly	15	1-	1	11	73%	17	5	8	13	76%	3	—	—	—	—	6	3	1	4	67%
Hydrocephalus	15	7	—	7	47%	17	1	—	1	6%	3	—	—	—	—	6	—	—	—	—
ACC	14	5	1	6	43%	17	—	7	7	41%	3	—	—	—	—	5	2	—	2	40%
Ventriculomegaly	14	4	—	4	29%	17	2	—	2	12%	3	—	—	—	—	5	1	1	2	40%
Dandy Walker malformation	14	1	2	3	21%	17	—	—	—	—	3	—	—	—	—	5	—	—	—	—
intracranial cysts	14	2	2	4	29%	17	1	—	1	6%	3	—	—	—	—	5	1	—	—	—
Enlarged cisterna magna	14	—	1	1	7%	17	2	—	2	12%	3	—	—	—	—	5	1	1	2	40%
Cerebellar vermian atrophy or hypoplasia	14	2	3	5	36%	17	1	1	2	12%	3	—	—	—	—	5	—	1	1	20%
Increased NT	15	7	—	7	47%	19	3	—	3	16%	3	1	—	1	33%	6	—	—	—	—
Cardiovascular anomaly	15	9	3	12	80%	16	3	3	6	38%	3	2	—	2	67%	6	1	1	2	33%
Vascular anomaly	15	—	—	8	53%	15	2	2	4	27%	3	1	—	1	33%	6	1	—	1	17%
Aortic arch anomaly	15	2	1	3	20%	14	2	—	2	14%	3	1	—	1	33%	6	1	—	1	17%
Involving the vena cava	15	3	1	4	27%	14	—	—	—	—	3	—	—	—	—	6	—	—	—	—
Patent ductus arteriosus ^c	15	n.a.	1	1	7%	14	1	—	1	7%	3	n.a.	—	—	—	6	n.a.	—	—	—
Cardiac anomaly	15	9	1	10	67%	15	3	—	3	20%	3	2	—	2	67%	6	1	1	2	33%
Hypoplastic left heart	15	2	—	2	13%	16	1	—	1	6%	3	2	—	2	67%	6	—	—	—	—
Hypoplastic right heart	15	1	—	1	7%	16	—	—	—	—	3	—	—	—	—	6	—	—	—	—
Atrioventricular canal	15	1	1	2	13%	14	—	—	—	—	3	—	—	—	—	6	—	—	—	—
DORV	15	3	—	3	20%	14	—	—	—	—	3	—	—	—	—	6	—	—	—	—
Septal defect (isolated or in combination with other structural cardiac anomalies)	15	4	5	9	60%	14	—	2	2	14%	3	1	—	1	33%	6	—	1	1	17%
Valve defect	15	—	—	3	20%	14	—	—	—	—	3	2	—	2	67%	6	—	—	—	—
Cardiac position/Dextrocardia	15	1	—	1	7%	14	—	—	—	—	3	—	—	—	—	6	1	—	1	17%
Cardiovascular intervention	4	—	—	—	—	14	—	—	1	7%	3	—	—	1	33%	6	—	—	—	—
Diaphragmatic hernia	15	2	3	5	33%	16	1	—	1	6%	3	2	—	2	67%	6	—	—	—	—
Anal anomaly	14	n.a.	6	6	43%	15	n.a.	—	—	—	3	n.a.	—	—	—	6	n.a.	—	—	—
Renal anomaly	15	4	3	7	47%	16	1	1	2	13%	3	1	—	1	33%	6	3	—	1	17%
Renal dysplasia	14	—	3	3	21%	15	—	1	1	7%	3	—	—	—	—	6	—	—	—	—
Renal agenesis	14	3	—	2-3	13-20%	15	—	—	—	—	3	—	—	—	—	6	—	—	—	—
Hydronephrosis ^c	4	—	—	—	—	15	1	—	1	7%	3	—	—	—	—	6	2	—	1	17%
Genitourinary anomaly	12	—	5	5	42%	15	—	8	8	53%	3	—	—	—	—	6	—	3	3	50%
Urinary anomaly	14	—	2	2	14%	15	—	3	3	20%	3	—	—	—	—	6	—	1	1	17%
Genital anomaly	14	—	2	2	14%	15	—	3	3	20%	3	—	—	—	—	6	—	2	2	67%
Cryptorchidism ^c	6	n.a.	—	—	—	14	n.a.	10	10	71%	1	n.a.	n.a.	n.a.	—	2	n.a.	2	2	100%
Hypospadias	6	n.a.	1	1	17%	14	—	—	—	—	1	n.a.	n.a.	n.a.	—	2	n.a.	1	1	50%
Digit anomaly	14	n.a.	10	10	71%	11	—	4	4	36%	2	—	2	100%	4	—	3	3	75%	
Nail anomaly	11	n.a.	6	6	55%	11	n.a.	5	5	45%	2	n.a.	2	2	100%	2	n.a.	1	1	50%
TOP	11 ¹	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Mean time AD, days	10	—	—	(101-161, 132.1)	67%	1	—	—	(144)	5%	—	—	—	—	—	1	—	—	(159)	17%
IUFD	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
Mean time AD, days	1	1	—	(126-126, 126)	7%	19	—	—	—	—	3	—	—	—	—	6	—	—	—	—
Died	17	—	—	13	87%	19	—	—	2	11%	3	—	—	1	33%	6	—	—	1	17%

ACC, agenesis of the corpus callosum; AD, amenorrhea duration; DORV, double outlet right ventricle; IUFD, intrauterine fetal death; IUGR, intrauterine growth restriction; n.a., not applicable, NT, nuchal translucency; TOP, termination of pregnancy; US, ultrasound.

^aOne fetal case/TOP no additional information available.

^bSeparately reported as US anomaly.

^cOnly data of non-TOP and IUFD cases.

Table 2 Distribution of genetic variants per gene within our cohort and within published CSS cohorts

Gene	Total	%	CSS cohort		CSS cohort		CSS cohort		Cumulative		P-value Fisher's exact
			Santen et al ^{a,b}	Wieczorek et al ^{a,b}	Tsurusaki/ Sekiguchi et al ^{a,b}	Frequency of CSS Cohorts Combined ^{a,b}	Frequency of CSS Cohorts Combined ^{a,b}				
<i>ARID1A</i>	16/44	36.4%	4/45	8.9%	1/21	4.8%	6/78	7.7%	11/144	7.6%	<.01
<i>ARID1B</i>	19/44	43.2%	28/45	62.2%	14/21	76.2%	48/78	61.5%	90/144	62.5%	.04
<i>SMARCA4</i>	3/44	6.8%	4/45	8.9%	0/21	0.0%	7/78	9.0%	11/144	7.6%	1.00
<i>SMARCB1</i>	6/44	13.6%	4/45	8.9%	1/21	4.8%	8/78	10.3%	13/144	9.0%	.40

CSS, Coffin-Siris syndrome.

^aOnly patients with pathogenic variants in a CSS-associated gene were taken into account.

^bNumbers may not add up to 100%, because pathogenic variants in other CSS-associated genes were detected.

postnatally as a result of her congenital anomalies. The fetus without a severe cardiac anomaly had hydrops, diaphragmatic hernia, double renal collecting system, and abnormal feet position. Parents decided to continue this pregnancy after they received the genetic results at 19+4 weeks of gestation.

SMARCB1

IUGR was reported for 50% (3/6) of fetuses with a *SMARCB1* variant. Brain anomalies were reported for 2 fetuses. One fetus had an abnormal cardiac position (ie, ventricular axis and apex to the right of the midline) with biventricular hypertrophy and a minor size discrepancy of the great arteries, and 1 fetus had a cardiac septal defect that was detected postnatally. Two fetuses had hydronephrosis on prenatal US, of which 1 case resolved postnatally. During postnatal assessment, it appeared that both males with *SMARCB1* variants had cryptorchidism.

Discussion

Genotype

In total, we identified 44 CSS cases with prenatal US anomalies, making this the largest case series to date. *ARID1A* ($n = 16$) or *ARID1B* ($n = 19$) variants were most frequent in this prenatal cohort. The frequency of *ARID1A* variants in particular was remarkable. *ARID1A* variants were overrepresented among the cases that did not survive into the neonatal period (76.5%, $n = 13$ for *ARID1A* vs 23.5%, $n = 4$ for the non-*ARID1A* group, $P < .001$). Furthermore, the median gestational age at which the anomalies were detected was earlier (14+5 weeks for *ARID1A* vs 20+0 weeks for the non-*ARID1A* group) (Supplemental Figure 1), although the difference was not significant ($P = .17$). This may fit with our previous finding that *ARID1A* variants in postnatal cases are frequently present in a mosaic state,¹ which suggests that nonmosaic pathogenic *ARID1A* variants may lead to an embryonically severe or lethal phenotype. The likely explanation for the relative lack of postnatal *ARID1A* variants (Table 2) is that most fetuses with full

pathogenic variants display severe congenital anomalies, leading to a large proportion of pregnancy terminations as well as fetal and neonatal demise. Thus far, such cases were less likely to undergo extensive diagnostic sequencing. Contrary to our previous findings where all 4 patients with *ARID1A* variants appeared mosaic in lymphocytes,¹ all patients in this cohort appear to have the pathogenic variant in 50% of sequence reads.

Phenotype

Frequent findings in fetal cases with pathogenic *ARID1A* variants, such as hydrocephalus, hypoplastic left or right heart syndrome, renal agenesis, diaphragmatic hernia, and postnatally detected anal anomalies, have not been previously recognized as part of the CSS phenotypic spectrum. Sporadically, patients have been reported with one of these anomalies and a pathogenic variant in a CSS-associated gene.^{6,7,18-20} Unilateral renal agenesis was reported among patients with clinically diagnosed CSS in the era before identification of CSS genes.^{21,22}

Pregnancies were terminated in 68.8% (11/16) of the *ARID1A* cases, which makes it impossible to assess severity of developmental delay or treatment response postnatally. Compared with reported congenital and/or structural anomalies among *ARID1A* patients,^{1-4,23} the severity of the congenital anomalies in our *ARID1A* cases appears to be more severe (Table 1).

The postnatal *ARID1B* phenotype has been extensively reported on by our group and others.^{10,18,24,25} Although we excluded patients with ACC as the sole prenatal presenting feature, 29.4% (5/17) had 1 or more brain anomalies. IUGR was detected more frequently in our cohort compared with previously reported frequencies in patients¹⁸ (Fisher's exact, $P = .04$), which might indicate that it is more common in the subset of patients with congenital anomalies. The frequency of cardiac anomalies in the fetal series does not differ significantly from previously reported frequencies in patients¹⁸ (Fisher's exact, $P = 1.00$).

It is remarkable that all *SMARCA4* fetuses had severe congenital anomalies, which have not previously been reported among patients with *SMARCA4* variants. Li et al⁹ do

report other prenatal findings in 6 of 13 patients with *SMARCA4* variants (ie, IUGR [$n = 4$], cardiac anomaly [$n = 2$], and ACC [$n = 1$]).

The most frequent US anomaly in *SMARCB1* variants was IUGR, which is a frequent, nonspecific prenatal US finding. Where the postnatal *SMARCB1* patient group usually presents with a phenotype considered at the severe end of the CSS spectrum,^{1,6,25} there does not appear to be a more severe prenatal presentation for this gene compared with patients with *ARID1A*, *ARID1B*, or *SMARCA4* variants. However, we show here that growth delay,^{1,4} which is a prevalent feature among reported patients with CSS and is often more extreme in *SMARCB1* patients, is detected prenatally as IUGR in several patients.

We did not identify patients with a prenatal presentation and a pathogenic variant in the other CSS-related genes (*ARID2*, *BICRA*, *DPF2*, *SMARCA2* duplication, *SMARCC2*, *SMARCD1*, *SMARCE1*, *SOX11*, *SOX4*) during this study. It is possible that prenatal US anomalies are less prevalent among these patients. The number of patients known with pathogenic variants in these genes is, however, still relatively small, so a prenatal phenotype may be identified in the future.

Not all cases in this cohort underwent a similar US examination, which is reflected by the fact that not all anomalies were detected prenatally. Table 1, however, gives an overview of the potential for prenatal detection if every fetus would have been examined on the level of a tertiary referral center. Because not every case underwent extensive US examination, this may be an underestimation.

Conclusion

This study highlights the prenatal phenotypic spectrum of CSS in a prenatal cohort with a molecularly confirmed pathogenic variant in a CSS-associated gene. Pathogenic variants in *ARID1A* were identified much more frequently in this group than in cohorts of postnatal patients with CSS. Frequently observed prenatal anomalies include hydrocephalus, ACC, HLHS, double outlet right ventricle, persistent left vena cava, congenital diaphragmatic hernia, renal agenesis, and IUGR, indicating that the prenatal phenotype of CSS significantly differs from the postnatal phenotype. This difference may be explained by an increased rate of pregnancy termination for fetuses at the severe end of the spectrum and in increased chance of fetal or postnatal demise. Genome-wide sequencing has been less frequently applied in such cases until now, leaving this part of the CSS spectrum undiscovered.

Data Availability

De-identified patient data will be made available on request to the corresponding author.

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Author Information

Conceptualization: P.J.v.d.S., G.W.E.S.; Data Curation: P.J.v.d.S., G.W.E.S.; Formal Analysis: P.J.v.d.S., G.W.E.S.; Funding Acquisition: M.O., E.E.E., N.L.V., G.W.E.S.; Investigation: P.J.v.d.S., G.W.E.S.; Methodology: P.J.v.d.S., G.W.E.S.; Project Administration: P.J.v.d.S.; Resources: P.J.v.d.S., M.J., C.A., T.A.-B., K.G., C.D., M.F., T.W., E.C.K.-N., K.P.A., P.A., C.P.B., M.A., A.Ba., M.v.d.B., S.B., T.B., A.By., M.C., C.C., K.C., A.M.C.-G., J.C.D., K.E.M.D., D.D., S.F., E.H.G., S.G., L.C.P.G., P.A.G., S.E.H., M.L., F.M., J.M., H.N., M.O., K.P., S.P., B.P., F.S.-S., C.S., C.T. E.T., A.T.V.-v.S., F.R.Z., H.S., R.K.E., E.E.E., N.L.V., Y.W., J.L.G., R.J.W., J.R., G.W.E.S.; Supervision: M.C.H., G.W.E.S.; Validation: P.J.v.d.S., G.W.E.S.; Visualization: P.J.v.d.S., G.W.E.S.; Writing-original draft: P.J.v.d.S., M.C.H., G.W.E.S.; Writing-review and editing: P.J.v.d.S., M.J., C.A., T.A.-B., K.G., C.D., M.F., T.W., E.C.K.-N., K.P.A., P.A., C.P.B., M.A., A.Ba., M.v.d.B., S.B., T.B., A.By., M.C., C.C., K.C., A.M.C.-G., J.C.D., K.E.M.D., D.D., S.F., E.H.G., S.G., L.C.P.G., P.A.G., S.E.H., M.L., F.M., J.M., H.N., M.O., K.P., S.P., B.P., F.S.-S., C.S., C.T. E.T., A.T.V.-v.S., F.R.Z., H.S., R.K.E., E.E.E., N.L.V., Y.W., J.L.G., R.J.W., J.R., M.C.H., G.W.E.S.

Ethics Declaration

The Institutional Review Board of Leiden University Medical Center, Leiden, The Netherlands provided approval waivers for using de-identified data and publishing aggregated data (no: G18.098 and G21.129) without obtaining specific informed consent. Clinical data was de-identified by allocating patient numbers. Where possible, informed consent was obtained by the referring clinician.

Conflict of Interest

All authors declare no conflicts of interest.

Additional Information

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Authors

Pleuntje J. van der Sluijs¹ , Marieke Joosten², Caroline Alby^{3,4}, Tania Attié-Bitach^{3,4}, Kelly Gilmore⁵, Christele Dubourg⁶, Mélanie Fradin⁷, Tianyun Wang⁸, Evangeline C. Kurtz-Nelson⁹, Kaitlyn P. Ahlers⁹, Peer Arts¹⁰, Christopher P. Barnett^{11,12}, Myla Ashfaq¹³, Anwar Baban¹⁴, Myrthe van den Born², Sarah Borrie¹³, Tiffany Busa¹⁵, Alicia Byrne^{10,16}, Miriam Carriero¹⁷, Claudia Cesario¹⁸, Karen Chong^{19,20}, Anna Maria Cueto-González²¹, Jennifer C. Dempsey²², Karin E.M. Diderich², Dan Doherty^{22,23}, Stense Farholt²⁴, Erica H. Gerkes²⁵, Svetlana Gorokhova^{15,26}, Lutgarde C.P. Govaerts², Pernille A. Gregersen^{27,28}, Scott E. Hickey^{29,30}, Mathilde Lefebvre^{31,32}, Francesca Mari¹⁷, Jelena Martinovic^{3,33}, Hope Northrup¹³, Melanie O'Leary³⁴, Kareesma Parbhoo²⁹, Sophie Patrier³⁵, Bernt Popp³⁶, Fernando Santos-Simarro³⁷, Corinna Stoltenburg³⁸, Christel Thauvin-Robinet^{31,39}, Elisabeth Thompson^{11,12}, Anneke T. Vulto-van Silfhout⁴⁰, Farah R. Zahir⁴¹, Hamish S. Scott^{10,12,16,42}, Rachel K. Earl⁹, Evan E. Eichler^{8,43}, Neeta L. Vora⁵, Yael Wilnai⁴⁴, Jessica L. Giordano^{45,46}, Ronald J. Wapner^{45,46}, Jill A. Rosenfeld^{47,48}, Monique C. Haak⁴⁹, Gijs W.E. Santen^{1,*} 

Affiliations

¹Department of Clinical Genetics, Leiden University Medical Center, Leiden, The Netherlands; ²Department of Clinical Genetics, Erasmus MC, University Medical Center Rotterdam, The Netherlands; ³Department of Histo-Embryology and Cytogenetics, Necker-Enfants Malades Hospital, AP-HP, Paris, France; ⁴National Institute of Health and Medical Research (INSERM), University of Paris, Imagine Institute, Paris, France; ⁵Department of Obstetrics and Gynecology, Division of Maternal-Fetal Medicine, University of North Carolina School of Medicine, Chapel Hill, NC; ⁶Department of Molecular Genetics and Genomics, Rennes University Hospital Center (CHU), Rennes, France; ⁷Department of Clinical Genetics, Centre

de Référence Maladies Rares Anomalies du Développement, CHU de Rennes, Rennes, France; ⁸Department of Genome Sciences, University of Washington School of Medicine, Seattle, WA; ⁹Department of Psychiatry and Behavioral Sciences, University of Washington, Seattle, WA; ¹⁰Department of Genetics and Molecular Pathology, Centre for Cancer Biology, An Alliance Between SA Pathology and the University of South Australia, Adelaide, South Australia, Australia; ¹¹Paediatric and Reproductive Genetics Unit, Women's and Children's Hospital, North Adelaide, South Australia, Australia; ¹²School of Medicine, University of Adelaide, Adelaide, South Australia, Australia; ¹³Department of Pediatrics, Division of Medical Genetics, McGovern Medical School, University of Texas Health Science Center at Houston, Houston, TX; ¹⁴Department of Pediatric Cardiology and Cardiac Surgery, Bambino Gesù Children's Hospital and Research Institute, Scientific Institute for Research, Hospitalization and Healthcare, Rome, Italy; ¹⁵Service de Génétique Médicale, Hôpital de la Timone, APHM, Marseille, France; Department of Medical Genetics, Timone Hospital, APHM, Marseille, France; ¹⁶Australian Genomics, Parkville, Victoria, Australia; ¹⁷Medical Genetics, University of Siena, Siena, Italy; ¹⁸Medical Genetics Lab, Bambino Gesù Children's Hospital and Research Institute, Scientific Institute for Research, Hospitalization and Healthcare, Rome, Italy; ¹⁹The Prenatal Diagnosis and Medical Genetics Program, Department of Obstetrics and Gynecology, Mount Sinai Hospital, University of Toronto, Toronto, Ontario, Canada; ²⁰Division of Clinical and Metabolic Genetics, Department of Pediatrics, The Hospital for Sick Children, University of Toronto, Toronto, Ontario, Canada; ²¹Department of Clinical and Molecular Genetics, Vall d'Hebron Barcelona Hospital Campus, Barcelona, Spain; ²²Department of Pediatrics, University of Washington, Seattle, WA; ²³Center for Integrative Brain Research, Seattle Children's Research Institute, Seattle, WA; ²⁴Department of Children and Adolescents, University Hospital Rigshospitalet, Copenhagen, Denmark; ²⁵Department of Genetics, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands; ²⁶Aix Marseille University, INSERM, Marseille Medical Genetics, U 1251, Marseille, France; ²⁷Department of Clinical Genetics, Aarhus University Hospital, Aarhus, Denmark; ²⁸Pediatrics and Adolescent Medicine, Centre for Rare Diseases, Aarhus University Hospital, Aarhus, Denmark; ²⁹Division of Genetic & Genomic Medicine, Nationwide Children's Hospital, Columbus, OH; ³⁰Department of Pediatrics, The Ohio State University College of Medicine, Columbus, OH; ³¹Inserm UMR 1231 GAD, Genetics of Developmental Anomalies, F21000 Dijon, France; ³²Functional Unit of Foetal Pathology, Pathological Anatomy Department, CHR Orleans, Orleans, France; ³³Unit of Fetal Pathology, Antoine Beclere Hospital, AP-HP, Clamart, France; ³⁴Broad Center for Mendelian

Genomics, Broad Institute of MIT and Harvard, Cambridge, MA; ³⁵Department of Pathology, CHU Charles Nicolle, Rouen, France; ³⁶Institute of Human Genetics, University Hospital Erlangen, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany; ³⁷Institute of Medical and Molecular Genetics, Hospital Universitario La Paz, Hospital La Paz Institute for Health Research, Centre for Biomedical Network Research on Rare Diseases, Instituto de Salud Carlos III, Madrid, Spain; ³⁸Department of Neuropaediatrics, Charité - Berlin University of Medicine, Berlin, Germany; ³⁹Reference Center for Rare Diseases, « Intellectual Disabilities from rare causes », CHU Dijon Bourgogne, F21000 Dijon, France; ⁴⁰Department of Human Genetics, Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center, Nijmegen, The Netherlands; ⁴¹Department of Medical Genetics, University of British Columbia, Children's and Women's Hospital, Vancouver, British Columbia, Canada; ⁴²ACRF Cancer Genomics Facility, Centre for Cancer Biology, An Alliance Between SA Pathology and the University of South Australia, Adelaide, South Australia, Australia; ⁴³Howard Hughes Medical Institute, University of Washington, Seattle, WA; ⁴⁴Genetic Institute, Tel Aviv Sourasky Medical Center, Tel Aviv, Israel; ⁴⁵Institute for Genomic Medicine, Columbia University Medical Center, New York, NY; ⁴⁶Division of Maternal-Fetal Medicine, Department of Obstetrics and Gynecology, Columbia University Vagelos Medical Center, New York, NY; ⁴⁷Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX; ⁴⁸Baylor Genetics Laboratories, Houston, TX; ⁴⁹Department of Obstetrics and Fetal Medicine, Leiden University Medical Center, Leiden, Netherlands

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