A targeted sequencing panel identifies rare damaging variants in multiple genes in the cranial neural tube defect, anencephaly

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INTRODUCTION

Neural tube defects (NTDs) affecting the brain (anencephaly) are lethal before or at birth, whereas lower spinal defects (spina bifida) may lead to lifelong neurological handicap. Collectively, NTDs rank among the most common birth defects worldwide. This study focuses on anencephaly, which despite having a similar frequency to spina bifida and being the most common type of NTD observed in mouse models, has had more limited inclusion in genetic studies. A genetic influence is strongly implicated in determining risk of NTDs and a molecular diagnosis is of fundamental importance to families both in terms of understanding the origin of the condition and for managing future pregnancies. Here we used a custom panel of 191 NTD candidate genes to screen 90 patients with cranial NTDs (n = 85 anencephaly and n = 5 craniorachischisis) with a targeted exome sequencing platform. After filtering and comparing to our in-house control exome database (N = 509), we identified 397 rare variants (minor allele frequency, MAF < 1%), 21 of which were previously unreported and predicted damaging. This included 1 frameshift (PDGFRA), 2 stop-gained (MAT1A; NOS2) and 18 missense variations. Together with evidence for oligogenic inheritance, this study provides new information on the possible genetic causation of anencephaly.

KEYWORDS
anencephaly, craniorachischisis, molecular diagnosis, neural tube defects, targeted exome sequencing
heritability estimate of up to 70%. Despite this, the molecular basis in humans has proven difficult to resolve. This may be attributed to the high degree of heterogeneity between unrelated sporadic cases, incomplete penetrance and the general paucity of large individual families displaying Mendelian inheritance. The complex molecular requirements for normal neural tube closure are well illustrated by the occurrence of NTDs in more than 200 different mouse genetic models. It has been estimated that up to 70% of potential NTD cases are preventable by the mother taking periconceptional supplements of folic acid. However, evidence for causal mutations in genes regulating folate metabolism remain tenuous. In humans, planar cell polarity (PCP) gene variants have been reported in heterozygous form throughout the NTD phenotypic spectrum. When tested, these variants are mostly found in an unaffected parent, prompting speculation regarding incomplete penetrance effects, which may be explained by co-inheritance of additional variants in other closely related or interacting genes that remain undetected using the methodologies employed. This genetic interaction is evident in NTD mouse models doubly heterozygous for PCP genes, suggesting that a comprehensive study of PCP genes in humans would be a valuable exercise.

The patient cohorts in most candidate gene studies contain mixed primary and secondary neurulation phenotypes, typically including only a small number of craniorachischisis or anencephalic cases. There is therefore a relative lack of information concerning the genetic basis of anencephaly in humans. In contrast, exencephaly, the developmental forerunner of anencephaly, is present in more than 90% of mouse mutants that transmit NTDs in a Mendelian fashion. It is also striking that the primary folate-sensitive NTD in mouse models is exencephaly, with less supporting evidence for primary prevention of mouse spina bifida by folic acid supplementation. Even so, it is clear that both anencephaly and spina bifida can be prevented by folic acid in humans. In addition, there is a marked excess in females in anencephaly and craniorachischisis compared to spina bifida. Collectively, these data might suggest that genetic factors implicated in anencephaly and craniorachischisis could be different from those implicated in spina bifida cases.

In this study, we have carried out a comprehensive, targeted exome sequencing of fetuses with anencephaly using a panel of 191 genes with biological relevance to NTDs. Unlike the traditional gene-by-gene search method, this allowed us to test the hypothesis that multiple hits in different, but closely related genes may combine to provide an oligogenic explanation for NTD risk.

2 | MATERIALS AND METHODS

2.1 | NTD and healthy control human DNA samples

The sample group for this study comprised 85 fetuses with anencephaly and 4 with craniorachischisis that underwent pregnancy termination following prenatal diagnosis by ultrasound in the north east of England between 1992 and 2011. Although folic acid supplements were recommended from 1991 onwards there was no mandatory folate fortification of food for this population and folic acid supplement use, typically 400 μg/day, has been estimated to have an uptake of up to around 30%. Fibroblast samples were collected by the Northern Genetics Service following signed consent and approved for research under The Newcastle Upon Tyne Hospitals NHS Trust Ethical Committee. DNA was extracted from fetal fibroblasts using the DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany) following the manufacturer’s protocol. One further craniorachischisis sample obtained from Hammersmith Hospital, London, UK was also included, making a total of 90 NTD samples. No parental samples were available for the NTD cases. Control DNA samples were extracted from whole blood obtained from 6 healthy white Europeans (2 trios) in the Moore cohort. The samples were collected under the guidelines of the Hammersmith and Queen Charlotte’s and Chelsea Hospitals’ NHS Trusts Research Ethics Committee (registration no. 2001/6029).

2.2 | Selection of NTD candidate genes

The targeted gene panel for NTDs included 191 genes that were selected by one of several criteria. These included genes that encode enzymes of folate one-carbon metabolism or components of the PCP or related cell polarity pathways that are implicated in normal neurulation in animal models. Additional members of these pathways were added even where a role in neurulation has not yet been directly indicated and also multiple gene family members, for example, CELSR1, CELSR2 and CELSR3, irrespective of whether there was a prior established link with NTDs. The panel design also included a number of prominent genes underlying NTDs in well-studied mouse models (eg, PAX3 and ZIC3; see gene panel list in Table S1 in Appendix S3, Supporting information).

2.3 | Target enrichment library preparation and sequencing

Custom capture libraries were generated from 3 μg gDNA using the SureSelectXT Reagent kit (Agilent Technologies, Santa Clara, California). RNA baits (Table S1 in Appendix S3) were designed using Sure-Design (Agilent Technologies), with an estimated average coverage of 98.2% of targeted regions. Samples were sequenced with MiSeq Reagent kit v3 (150 cycle; 2 × 75 bp) on the MiSeq Sequencing System (Illumina, San Diego, California).

2.4 | Sequence alignment, variant annotation and filtering

An in-house pipeline was used for the sequence alignment, variant calling and annotation. FASTQ files were trimmed with Cutadapt and the sequencing reads were aligned to the human reference genome (hg19) using the Burrows-Wheeler Aligner (v0.6.1-r104). SAMtools (v0.1.18) was used to generate mpileup files for variant calling with VarScan2 (v2.3.6) to generate VCF files. Only variants with >30 read depths, >0.2 variant frequency, and average quality score of >20 were called. Candidate variants were manually checked on the integrative genomics viewer. Principal component
analysis was used to assess sample relatedness (Methods in Appendix S2).

2.5 | Variant filtering and prioritization

Variants were annotated with Ensembl Variant Effect Predictor (v73: http://www.ensembl.org/info/docs/tools/vep/index.html). Provean,19 SIFT,20 PolyPhen2,21 Condel,22 REVEL23 and MutationTaster24 were used for predicting the effects of variants. REVEL score >0.5 were used as threshold for classifying pathogenic variants. Intronic, synonymous, 3' and 5' UTR, up- and downstream variants were removed. Rare variants were defined as minor allele frequency (MAF) <1% in the Exome Aggregation Consortium (ExAC) Database.25 Variants that were specific to NTD patients and not present in the capture control (N = 6), in-house exome controls (N = 509) and in the dbSNP,26 1000 Genomes Project,27 ExAC, and the Genome Aggregation Database (gnomAD)25 were labeled "Novel," and were verified by Sanger sequencing (Methods in Appendix S2).

2.6 | Mutation burden analysis

The burden of carrying multiple rare/novel variants within the 191 candidate genes was compared between the NTD and the ExAC cohorts. To allow an unbiased gene-level comparison, the sequencing coverage of the targeted regions was analyzed between the 2 cohorts. The exon coordinates for the canonical transcripts of all 191 genes were extracted as a Browser Extensible Data (BED) file from the University of California Santa Cruz (UCSC) database, which was used as the reference sequence for target regions. The percentage coverage of the targeted bases at ≥30 read depths was calculated using Picard (http://broadinstitute.github.io/picard/) for the NTD samples, and the coverage information for the ExAC data was downloaded from the ExAC database. The gene-level coverage between the cohorts was compared using Student's t test (2-tailed). Because the sample-level information is not available at the ExAC database, the number of each variant was compared in the burden analysis for consistency as described in D’Alessandro et al.28 Only rare/novel variants predicted to be damaging were used for further analysis. Fisher's exact test (2-tailed) was used to assess the enrichment of rare/novel variants on the genes showing comparable sequence coverage. Bonferroni correction was performed by multiplying the each P-value with the number of genes used in the test (n = 13).

3 | RESULTS

On average, 97.5% of bases were covered at ≥30 read depth across 191 genes, indicating a high targeting efficiency. A mean target coverage depth of x110 was achieved with more than 96% of reads having Phred quality score greater than Q30 (corresponds to 99.9% base call accuracy). A total of 1380 variants, which passed quality control, were identified of which 1359 were single nucleotide variants (SNVs) and 21 were insertions/deletions (Indels) (Figure 1).

3.1 | Relatedness analysis

Principal component analysis identified 3 samples (52F03, 00F133 and 389F07) with higher variation than the rest of the samples which might be suggestive of different ethnic background (Figure S1 in Appendix S1). Apart from the healthy control trios (child-mother-father) included in the capture sequencing, kinship analysis did not indicate relatedness between any of the samples (Figure S2 in Appendix S1), including 2 NTD cases which carried an identical extremely rare variant in the CELSR1 gene (described below).
3.2 Previously reported pathogenic mutations associated with NTDs

One craniorachischisis/exomphalos sample (01F29A) was found to carry a pathogenic missense variant (c.676G>A; p.Ala226Thr; rs104894043) in the Sonic Hedgehog (SHH) gene, which was previously identified in an autosomal-dominant holoprosencephaly 3 (HPE3) patient (OMIM: 142945). HPE3 is characterized by midline brain and craniofacial abnormalities, and it is possible that this variant either contributes to the NTD, whilst other characteristics of HPE are masked by the severity of the midline craniorachischisis/exomphalos phenotype in this individual. One fetus with anencephaly (735F97) carried a rare missense mutation (c.2852C>T; p.Ser951Tyr; rs147472391) in glycine decarboxylase (GDC), which was previously reported as one of the causative mutated alleles in a compound heterozygous patient with the autosomal recessive disorder, non-ketotic hyperglycinemia (NKH, OMIM: 605899). GLDC encodes a component of the glycine cleavage system (GCS) in mitochondrial folate one-carbon metabolism, which has previously been implicated in both mouse and human NTDs. Another individual with anencephaly (706F07) was heterozygous for a missense variant (c.200C>T; p.Thr67Ile; rs28941785) in the cystathionine gamma-lyase (CYP) gene, which causes cystathioninuria in a recessive form.

3.3 Unreported and rare variants

After filtering out intron, 3' and 5' UTR and synonymous variants, a total of 397 rare (MAF < 1%, including novel) variants were identified in 89/90 NTD cases from 110/191 of the panel of NTD candidate genes. Of these, 209 variants were predicted to be damaging by at least one of the mutation effect predictors described in Methods (summarized in Table S2 in Appendix S3). Following an additional filter to include our in-house exomes (n = 509) and publically available data (1000Genome, dbSNP, ExAC and gnomAD), there remained 21 novel variants that were predicted to be damaging (1 frameshift, 2 stop-gained and 18 missense; Table 1).

We identified 3 novel loss-of-function (LoF) variants. These included a frameshift variant c.3029_3030delAG which introduces a premature stop codon (p.Arg1011ThrfsTer4) in the platelet derived growth factor receptor alpha (PDGFRα) gene (Figure 2A). In ExAC, 3 unique LoF variants are reported in PDGFRα with a pLI = 1, indicating extreme intolerance for LoF. Pdgfra-null mice are embryonic lethal with severe NTDs and PDGFRα promoter haplotypes have been associated with NTD susceptibility in humans. A stop-gain variant c.360C>G (p.Cys120Ter) was detected in the methionine adenosyltransferase 1A (MAT1A) gene (Figure 2B). In ExAC, 2 unique stop-gain LoF variants are reported in MAT1A with a pLI = 0.75. MAT1A encodes methionine adenosyltransferase (MAT) which catalyzes the conversion of methionine to 5'-adenosylmethionine (SAM), the universal methyl donor. Mutations in the MAT1A gene are reported to cause MAT I/III deficiency, a condition characterized by persistent hypermethioninemia not accompanied by elevated homocysteine or tyrosine. Disturbance in the methionine cycle has been found to cause NTDs in experimental models in the mouse. However, clinical manifestations of MAT deficiency are variable, including no neurological abnormalities. Also, a stop-gain variant c.1893C>A (p.Tyr631Ter) was detected in the nitric oxide synthase 2 (NOS2) gene (Figure 2C). In ExAC, 20 LoF variants are reported in NOS2 with a pLI = 0, suggesting tolerance of LoF and low confidence of causal effect. However, NOS2 has been previously associated with a cranial NTD phenotype where A/G genotype of the rs4795067 SNP within NOS2 was shown to be associated specifically with increased cranial NTD risk.

One individual (283F06) was heterozygous for a novel missense variant in the catalytic N-terminal domain of the methylenetetrahydrofolate reductase (MTHFR) gene (c.601C>T; p.His201Tyr) (Figure 2D), which was predicted to be damaging by all 6 mutation predictors tested (Table 1). This individual was also heterozygous for the common MTHFR c.677C>T variant, and also carries a rare glycine decarboxylase (GLDC) c.2203G>T missense variant, possibly indicating a compromised FOCM in this patient. Interestingly, 2 unrelated patients harbor an identical extremely rare (gnomAD frequency 1/276 358) missense variant (c.7549G>A; p.Val2517Met) within the transmembrane receptor domain of the cadherin, EGF LAG seven-pass G-type receptor 1 (CELSR1) gene, which encodes a core protein of the PCP pathway (Figure 2E, Table S2 in Appendix S3). Heterozygous missense mutations in CELSR1 gene have previously been reported in a number of NTD patients.

Two novel and 3 rare SCRIB missense variants were identified in 5 anencephaly cases (Table 1 and Table S2 in Appendix S3). SCRIB mutations have previously been implicated in human craniorachischisis. Three samples carried more than 1 variant within the same gene: sample 01F292 had 2 rare FAT4 variants (c.739C>T; c.6607C>T), f11-278 had 1 novel (c.8335C>G) and 1 rare (c.5587C>T) variants in CELSR3 and 693F06 had 2 rare missense variants (c.3109G>C; c.824G>A) in NOS2.

3.4 Genes harboring multiple novel and rare variants

In 51/191 genes we identified more than 1 novel and/or rare variants predicted to be damaging (Table S2 in Appendix S3). To assess for potential enrichment of rare/novel damaging variants in the NTD cohort (N = 90) compared to the ExAC controls (N = 60 706), a mutation burden analysis was carried out. To eliminate the possibility of identifying significant enrichment differences due to sequencing coverage variation between the cohorts, percentage coverage of the targeted regions at ≥30 read depth for all 191 genes were compared between the NTD cases and the ExAC controls. As expected, on average NTD cases showed higher percentage coverage, due to the nature of the targeted capture sequencing design. Therefore, further analysis was limited to genes showing percentage differences not greater than 3.5% between the cohorts. This resulted in 13 genes that were comparable to each other (97.5% in NTD cases vs 95.7% in controls; t-test P-value = 0.13, 2-tailed), and 8 of these genes (COBL, FAT4, MTRR, PDGFRα, PRICKLE2, SALL4, TCN2 and TXN2) had at least 1 rare/novel variant predicted to be damaging which could be used for further analysis. Using Fisher’s exact test, we identified 4 genes (COBL, FAT4, PDGFRα and TXN2) that showed significant enrichment in the NTD cases (Table 2). Of these, COBL and FAT4 stayed statistically significant after the multiple test correction (Table S4 in Appendix S3).
| ID    | Position | Gene   | cDNA     | Protein   | Type       | Provean | SIFT     | PolyPhen | Condel   | REVEL | Mutation Taster | 88F97* |
|-------|----------|--------|----------|-----------|------------|---------|----------|----------|----------|-------|-----------------|--------|
| 283F06| chr1:11856442 | G     | A        | MTHFR     | c.601C>T   | p.His201Tyr | Missense | Neutral | Neutral   | Neutral | Deleterious     | 0.932  |
| 436F98| chr1:13268208923 | T    | C        | NID1      | c.577A>G   | p.Ile193Val | Neutral  | Neutral | Neutral   | Neutral | Tolerated       | 0.217  |
| 01F576| chr3:125828823 | T    | G        | ALDH1L1   | c.2341A>C  | p.Thr761Pro | Missense | Deleterious | Deleterious | Benign   | Neutral                  | 0.36   |
| 451F999| chr3:48680471 | G    | A        | CELS3     | c.1047T>C  | p.Cys349Gly | Missense | Deleterious | Deleterious | Nonsynonymous | Benign                  | NA     |
| 465F06| chr4:126372318 | G    | A        | FAT4      | c.10147T>A | p.Gly3383Ser | Missense | Probably damaging | Disease causing | Neutral   | NA              | 0.435  |
| 229F08| chr4:126384816 | C    | T        | FAT4      | c.11893T>C | p.Pro3965Ser | Missense | Tolerated | Tolerated | Neutral   | Deleterious       | 0.642  |
| 00F191| chr4:55156627 | C    | A        | PDGFRA    | c.3029_3030delAG | p.Arg1011ThrfsTer4 | Frameshift | NA         | NA         | NA       | Disease causing | 0.418  |
| 439F03| chr10:82040481 | G    | T        | NOS2      | c.1893C>A  | p.Tyr631Ter | Stop-gained | NA         | NA         | NA       | Disease causing | 0.495  |
| 485F06| chr11:34477676 | T    | G        | TP53      | c.850A>T   | p.Thr284Ser | Missense | Neutral   | Tolerated | Possibly damaging | Disease causing | 0.776  |
| 556F05| chr12:6670718 | C    | G        | ERCC2     | c.345C>A   | p.E115G      | Missense | Nonsynonymous | Deleterious | Deleterious | Disease causing | 0.129  |
| 97F91 | chr17:26096144 | A    | T        | SHROOM4   | c.311T>C   | p.Cys104Ser | Missense | Neutral   | Neutral   | Possibly damaging | Disease causing | 0.171  |

Abbreviations: A, altered base; NA, not applicable; R, reference base. Higher REVEL score indicate increased likelihood that the variant is disease-causing. 88F97* had more than 1 novel damaging variants.
FIGURE 2 DNA sequence electropherograms, protein conservations and position of the genetic variants in relation to the protein domains. Protein domain figures were created with MutationMapper (http://www.cbioportal.org/mutation_mapper.jsp, v1.0.1). (A) PDGFRA frameshift deletion mutation. I-set, immunoglobulin I-set domain; Pkinase_Tyr, protein tyrosine kinase. (B) MAT1A stop-gained mutation. S-AdoMet_synth_N, S-adenosylmethionine synthetase, N-terminal domain. S-AdoMet_synth_M, S-adenosylmethionine synthetase, central domain; S-AdoMet_synth_C, S-adenosylmethionine synthetase, C-terminal domain. (C) NOS2 stop-gained mutation. NO_synthase, nitric oxide synthase, oxygenase domain; Flavodoxin_1, flavodoxin. FAD_binding_1, FAD binding domain; NAD_binding_1, oxidoreductase NAD-binding domain. (D) CELSR1 missense mutation. Lam, Laminin G domain; GAIN, GPCR-autoproteolysis inducing (GAIN) domain; 7tm_2, 7 transmembrane receptors. (E) MTHFR missense mutation. MTHFR, methylenetetrahydrofolate reductase.
3.5 | Multiple damaging variants by samples

Finally, we investigated the possible effects of multiple gene interaction within the same samples. On average, each NTD patient sample carried 9 rare/novel variants, with approximately 3 of these variants predicted to be damaging. In the NTD capture controls ($n = 4$ unrelated), each carried 2 novel/rare variants on average, with approximately 1.5 of these predicted to be damaging (Table S3 in Appendix S3). Out of 90 NTD cases, 75 carried more than 1 novel/rare damaging variant involving 98 candidate genes (Table S2 in Appendix S3). As can be seen from the diversity of the genes affected, there was no clear recurring pattern in which the same set of genes was affected throughout the samples; rather, each case exhibited an individually unique set of variants. However, some of the patients showed multiple hits within PCP-associated genes. Five anencephaly cases carried rare or novel CELSR1 missense variants, three of whom carried additional rare potentially damaging PCP variants: 01F377 (CELSR1 c.6362G>A and PRICKLE4 c.730C>G), 2F07 (CELSR1 c.8807C>T and DVL3 c.1622C>T), 618F05 (CELSR1 c.8282C>T and SCRIB c.3979G>A). One patient (I93-80) had a novel PTK7 missense variant (c.655A>G) with a rare CELSR2 missense variant (c.1192C>T). Three patients carried missense variants both in FZD and other PCP-associated genes: 01F552 (FZD6 c.1531C>T and CELSR2 c.3800A>G), 335F07 (FZD6 c.544G>A and 2 FAT4 missense variants c.5792A>G; c.10384A>G), and 465F99 (rare FZD1 missense variant c.211C>T and a novel FAT4 missense variant c.10147G>A).

4.1 | PDGFRA

A novel PDGFRA frameshift variant c.3029_3030delAG leading to premature stop codon (p.Arg1011ThrfsTer4) was identified in an anencephalic patient. PDGFRA is a cell-surface tyrosine kinase receptor, which has an essential role in embryonic development and cell proliferation.41 Homozygous Pdgfra mutant mice are embryonic lethal presenting with a wavy neural tube and cranial region closure failure.34 In humans, the PDGFRA-promoter haplotype H1 was found to confer low transcriptional activity and has been associated with increased NTD risk.35 Therefore, it is possible that the reduced abundance of PDGFRA caused by the LoF variant could have led to the anencephaly phenotype in our patient. In addition, 2 other cases (99F590 and 735F97) carried a rare missense variant c.236G>A (p.Gly79Asp) in PDGFRA. Overall, these findings resulted in a nominal significant enrichment of PDGFRA variants in NTD cases compared to the healthy controls in the burden analysis.

4.2 | Folate one-carbon metabolism

Despite the well-documented benefits of folic acid in NTD prevention, the actual mechanism of folate action is still unknown. Genes involved in folate one-carbon metabolism (FOCM) have been studied extensively as NTD candidates. Early reports described an association between NTDs and a common variant c.677C>T within the MTHFR gene in Dutch and Irish populations, although a subsequent meta-analysis concluded that the increased NTD risk for this variant was only present within the Irish population (reviewed in Reference 42). Subsequently many genes encoding folate pathway enzymes, transporters and receptors have been studied with mostly inconsistent findings.7 More recently, several candidate variants were identified in AMT and GLDC, 2 of the genes constituting the mitochondrial GC.5,32 In the present study, we identified a novel missense variant affecting the catalytic domain of the MTHFR gene. This patient additionally carried the c.677C>T variant, and a rare missense variant (c.2203G>T) in the GLDC gene. It is possible that this combination of genotypes caused sub-optimal folate metabolism, leading to anencephaly. In addition, we have identified 4 more patients (1 craniorachischisis and 3 anencephaly) carrying rare GLDC variants predicted to be damaging. One patient (735F97) was heterozygous for the missense variant c.2852C>A (p.Ser951Tyr) previously reported in a patient with NKH.30 While Mthfr-null mice do not display a NTD
phenotype. Gldc deficient mice variably display NTDs and/or features of NKH. We did not identify variants in other GCS genes, AMT or GCSH, after filtering for frequency (<1% MAF) and mutation prediction in our cohort.

4.3 | Gene-gene interactions and the PCP pathway

Both gene-environment and gene-gene interactions are believed to play an important role in NTD etiology. In humans, NTD cases are mostly sporadic and putative mutations reported to date are predominantly heterozygous, sometimes with incomplete penetrance. Therefore, it has been suggested that human NTDs exhibit a polygenic or oligogenic pattern of inheritance involving multiple heterozygous gene mutations. Such genetic interactions are evident from the many doubly heterozygous NTD mouse models that have been described.

In the present study, the majority of cases (75/90) carried more than 1 rare damaging variant, without revealing an obvious pattern of co-inheritance. This might be partly attributed to the fact that the analysis was conducted using a MAF <1% and damaging predictions, which might have excluded a possible contribution of more common alleles. Despite this, we identified 3 anencephalic fetuses that were double heterozygotes, carrying missense variants in CELSR1 gene and a variant in other PCP-related genes SCRIB, PRICKLE4, and DVL3. In addition, 2 unrelated anencephalic patients carried the same, extremely rare CELSR1 missense variant (c.7549G>A; 1/276 358 genomeAD). Rare variants in CELSR1 have previously been reported in both open and closed NTD types. Two previous NTD cases have been reported to be doubly heterozygous either for CELSR1 or DVL2. Celsr1 homozygous mutant (Celsr1Crsh/Crsh) mice show craniorachischisis,

suggesting that the CELSR1 gene is likely to be implicated in both human and mouse NTD etiology.

4.4 | Burden analysis

To maximize the number of the cases to be analyzed, only a small number of controls were included in the sequencing platform. Therefore, to perform burden analysis, the public database (ExAC) was used. However, because of the lack of similarity in the sequence coverage in many of the genes between the NTD and control cohorts, we were only able to assess 13/191 genes. COBL encodes an actin regulator protein, and the Vangl2/CobL101/C102 mutant mice show exencephaly, indicating an interaction between these genes. FAT4 encodes a protocadherin family protein that is associated with the PCP pathway. A study of Fat4-null mice described impaired convergent extension with faulty ureteric tubule elongation. However, in humans, mutations in this gene are implicated in both Van Maldergem Syndrome 2 [OMIM: 615546], characterized by intellectual disability with typical craniofacial features, and Hennekam Lymphangiectasia-Lymphphedema Syndrome 2 [OMIM: 616006], which causes lymphatic dysplasia.

5 | CONCLUSION AND FUTURE STUDIES

We have identified novel and rare variants within genes with known biological association with NTDs, specifically focusing on folate metabolism and PCP pathways. This study highlights the potential involvement of PCP genes including CELSR1 in association with anencephaly phenotypes, and also PDGFRα as strong NTD candidates in humans. Further identification and functional testing of genetic factors will lead to improved understanding of molecular mechanisms of NTD, and ultimately may help to create a targeted and cost-effective method of screening genes for the clinical management of families with a history of NTD-affected pregnancy.

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Conflict of interest

The authors declare that they have no conflict of interest.

Author contributions

M.I. performed laboratory experiments, analyzed data, and drafted the manuscript. T.C. helped with the experimental design and data
analysis. C.B. created the in-house pipeline used for the sequencing alignment and variant annotations. C.J. analyzed and provided in-house exome sequencing data. C.E. coordinated sample collection and experimental design. J.D. assisted with experimental procedures. G.E.M., N.D.E.G., A.J.C., N.L. and P.S. provided intellectual contributions for study design and data interpretation. All authors critically revised the manuscript and approved the final version.

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