



De novo *CLTC* variants are associated with a variable phenotype from mild to severe intellectual disability, microcephaly, hypoplasia of the corpus callosum, and epilepsy

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Purpose: To delineate the genotype–phenotype correlation in individuals with likely pathogenic variants in the *CLTC* gene.

Methods: We describe 13 individuals with de novo *CLTC* variants. Causality of variants was determined by using the tolerance landscape of *CLTC* and computer-assisted molecular modeling where applicable. Phenotypic abnormalities observed in the individuals identified with missense and in-frame variants were compared with those with nonsense or frameshift variants in *CLTC*.

Results: All de novo variants were judged to be causal. Combining our data with that of 14 previously reported affected individuals ($n = 27$), all had intellectual disability (ID), ranging from mild to moderate/severe, with or without additional neurologic, behavioral, craniofacial, ophthalmologic, and gastrointestinal features. Microcephaly, hypoplasia of the corpus callosum, and epilepsy were more frequently observed in individuals with missense and in-frame

variants than in those with nonsense and frameshift variants. However, this difference was not significant.

Conclusions: The wide phenotypic variability associated with likely pathogenic *CLTC* variants seems to be associated with allelic heterogeneity. The detailed clinical characterization of a larger cohort of individuals with pathogenic *CLTC* variants is warranted to support the hypothesis that missense and in-frame variants exert a dominant-negative effect, whereas the nonsense and frameshift variants would result in haploinsufficiency.

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INTRODUCTION

The clinical consequences of pathogenic *CLTC* variants have been described in 14 individuals who presented with neurodevelopmental disability accompanied by variable phenotypic features.^{1–3} DeMari et al. identified a de novo frameshift variant in the *CLTC* gene in a 3-year-old girl with intellectual disability (ID) and dysmorphic features, postulating haploinsufficiency of *CLTC* as the pathogenetic mechanism.² More recently, 11 additional variants in *CLTC* were described in 13 individuals with ID, of whom five also had epilepsy.^{1,3,4} The effects of the DNA variants have neither been studied on the protein nor on the cellular level.

CLTC encodes clathrin heavy chain 1 (CHC1), a component of clathrin that consists of a polymer of three clathrin heavy chains and three clathrin light chains, which form a triskelion. This structure enables the formation of curved envelopes of hexagons and pentagons that cover the cytoplasmic face of clathrin-coated vesicles.⁵ These specialized organelles are involved in intracellular trafficking of receptors and endocytosis of a variety of macromolecules,⁶ as well as in the stabilization of kinetochore fibers in the mitotic spindle that aid congression of chromosomes to the metaphase plate.⁷ DeMari et al. noted that *CLTC* is highly expressed in the developing brain and probably plays a role in neuronal transmission by facilitating the recycling and/or release of

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vesicles at the presynaptic termini of neurons.² Experiments in *Drosophila melanogaster* showed that clathrin heavy chain (chc) is critical for synaptic vesicle recycling, further supporting a specific role for CHC1 in brain development.⁸

Here, we expand the phenotype of individuals with de novo *CLTC* variants, and delineate the genotype–phenotype correlation in individuals with likely pathogenic variants in the *CLTC* gene.

MATERIALS AND METHODS

We identified 11 previously unreported individuals with likely pathogenic variants in *CLTC*. Two were followed in the Department of Human Genetics at Radboud University Medical Center (Nijmegen, The Netherlands) and nine were ascertained through GeneMatcher.⁹ This study was approved by the institutional review board Commissie Mensgebonden Onderzoek Regio Arnhem-Nijmegen (2018–4733). Written informed consent was obtained for all individuals involved including permission to publish photographs. We characterized their phenotypes retrospectively. Additionally, we describe the clinical characteristics of two individuals whose *CLTC* variants, p.(Asp1207del) and p.(Gln1539*), were previously reported by Lelieveld *et al.*⁴ DNA extracted from peripheral blood was analyzed using diagnostic exome sequencing or ID gene panel sequencing including the *CLTC* gene, by standard procedures.^{4,10}

We used MetaDome¹¹ to generate a tolerance landscape, a regional genetic tolerance plot based on the ratio of observed missense and synonymous (d_N/d_S) variants from gnomAD r2.0¹² found in the protein-coding region of *CLTC*. The tolerance score is corrected for the sequence composition of the protein-coding region based on the total possible missense and synonymous variants and computed as a sliding window of 21 residues over the entirety of the protein. To investigate the effect of the variants on the structure and function of the clathrin coat complex, we used a combination of the fully determined N-terminal WD40 domain (PDB file 5ODS) and a C-alpha only structure of the full-length clathrin triskelion (PDB file 3IYV) for computer-assisted molecular modeling.¹³ We employed the Yet Another Scientific Artificial Reality Application (YASARA)/WHAT IF Twinset for structural alignments and subsequent analysis of the structures.¹⁴

Fisher's exact test, using a two-sided *p* value, was carried out to compare proportions of clinical features between groups of individuals with missense variants and in-frame deletions with nonsense and frameshift *CLTC* variants. If a specific variant, i.e., p.(Pro890Leu) and p.(Asp1207del), was found in multiple individuals, these were viewed as replicates and counted as one data point for the statistical analysis. After conducting Bonferroni correction for multiple testing, a *p* value of <0.0125 was considered significant.

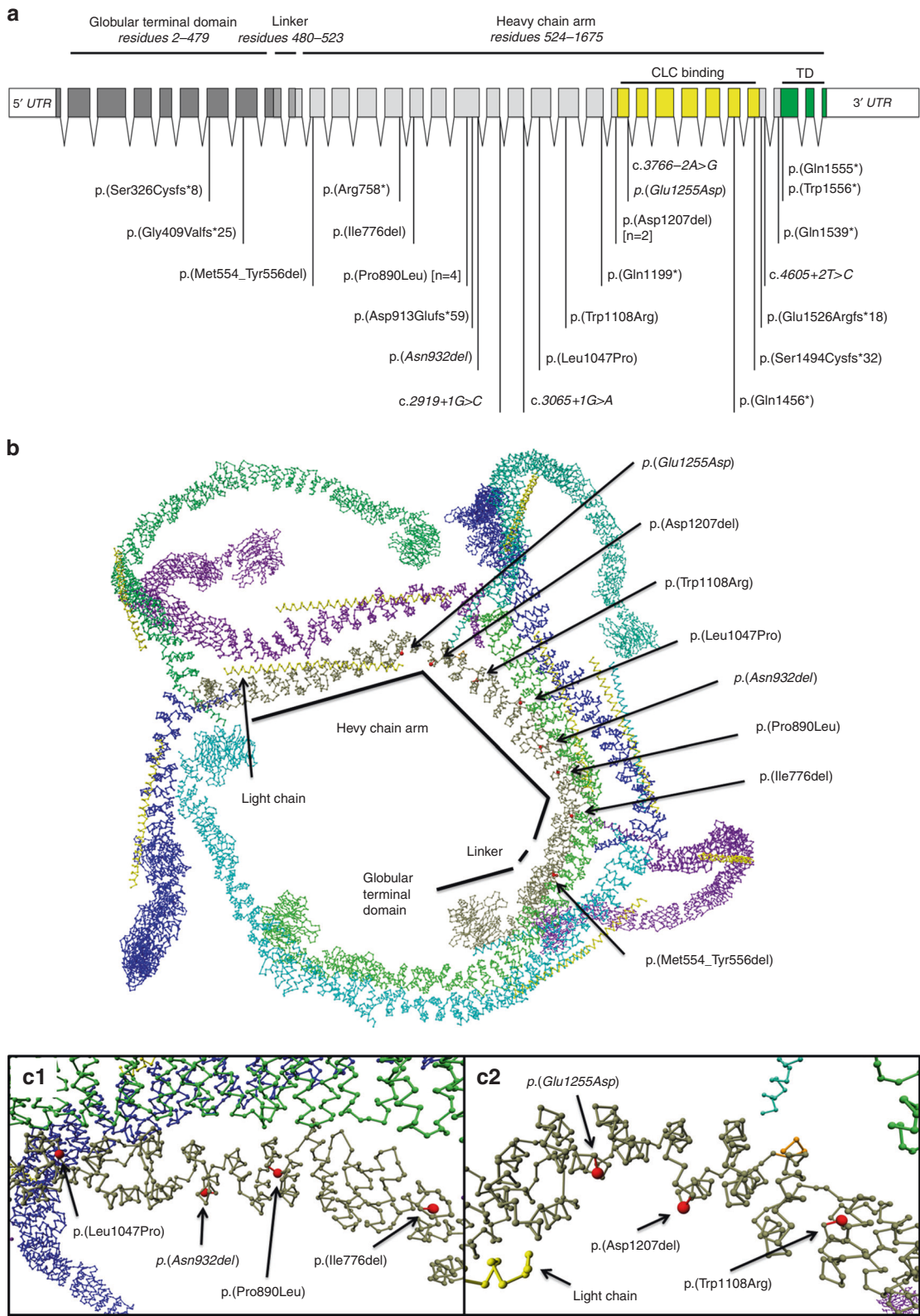
RESULTS

Three nonsense, two frameshift, two missense, and three splice site variants and three in-frame deletions were identified in *CLTC* (Fig. 1a; Table S1) in seven males and

six females (median age: 14 years; range: 8 months to 41 years). Variants were confirmed to be de novo, except for p.(Ser1494Cysfs*32) identified in individual 12. This variant was not detected in the healthy mother or sister, and could not be studied in the father, who was not available for further investigation. None of the variants were present in gnomAD.¹² All missense variants had a Combined Annotation Dependent Depletion (CADD) score above 25.¹⁵ Furthermore, *CLTC* is depleted from truncating and missense variants in healthy individuals (probability of loss of function in tolerance [pLi] = 1.00 and missense *z*-score = 8.09, respectively)¹² suggestive for such variants being under strong purifying selection. As the pLi and missense *z*-score provide an indication over the entire gene, we generated a tolerance landscape with MetaDome that displays regional tolerance or intolerance to missense and synonymous variation. The *CLTC* missense variants and in-frame deletions are all located at positions that are intolerant to variation (Fig. S1). Altogether, these data support the pathogenicity of the *CLTC* variants.

The de novo *CLTC* variants are scattered throughout the gene. The missense variants and in-frame deletions of one to three amino acid residues are found in the part of the protein that contains the CHCR repeats, which is a long area that comprises seven repeats spanning amino acid residues 537–1566. The 3D structure of the CHC1 protein showed that the de novo missense *CLTC* variants do not cluster in three-dimensional proximity (Fig. 1b). However, these variants may affect the interaction with other clathrin heavy and light chains as CHC1 interacts with three light chains to form clathrin, ultimately changing the structure of the clathrin-coated vesicle (Fig. 1c).¹⁶ The nonsense and frameshift variants are all expected to result in nonsense-mediated messenger RNA (mRNA) decay.

All individuals presented with motor and/or speech delay (*n* = 13). All had ID that varied from mild to severe (Tables S2, S3). Neuropsychiatric features, noted in the majority of individuals (9/12), included attention deficit–hyperactivity disorder (ADHD) (4/9) and autism (3/10). Epilepsy (for the specific type, see Table S2) occurred in less than half of the individuals (5/13); had onset in the neonatal period, early infancy, or adulthood; and was fully controlled with antiepileptic drugs. Additional neurologic problems were observed, such as hypotonia (7/10), ataxia (2/8), and spastic gait (1/10). The majority of individuals had structural brain abnormalities (8/10) (Fig. 2a–f), which consisted of hypoplasia of the corpus callosum (a thin, small corpus callosum, but with all segments present), dilated Virchow–Robin spaces, asymmetric or dilated ventricles, frontal atrophy, pontocerebellar atrophy, and abnormal myelination. Hypoplasia of the corpus callosum occurred in five of these eight individuals (Fig. 2c–f). Microcephaly was observed in three of 13 individuals, all of whom had hypoplasia of the corpus callosum. Subtle craniofacial abnormalities were observed in all individuals (Fig. 2g–n). Facial dysmorphisms included a long face with a high, narrow forehead; wide nasal bridge; wide-set and long palpebral fissures; dysplastic ears that were large, protruding,



and/or low-set; a deep philtrum consisting of prominent philtral ridges giving rise to an exaggerated groove in the midline; a wide mouth with thick lower vermillion; and large upper central incisors. Rarely, mild facial asymmetry was noticed. Ophthalmologic abnormalities were common (8/12),

including strabismus (4/8) and abnormalities of refraction (4/8). Finally, gastrointestinal abnormalities were also diagnosed in more than 50% of individuals (7/13).

We hypothesized that the nonsense and frameshift variants have a different mode of action than the missense and

Fig. 1 De novo CLTC variants. (a) Distribution of de novo variants in the *CLTC* gene in a schematic representation of the structure of the *CLTC* gene (NM_004859.3. 2; NP_004850.1; Uniprot: <https://www.uniprot.org/uniprot/Q00610>). Indicated are the globular terminal domain (TD) (residues 2–479), the flexible linker (residues 480–523), and the heavy chain arm (residues 524–1675) with clathrin heavy chain repeats (CHCR), which is involved in binding a clathrin light chain (CLC binding; residues 1213–1522) and contains the trimerization domain (TD; residues 1550–1675). Variants identified in this study are indicated in bold and variants located in a splice site are indicated in italics. (b) 3D structure of the clathrin coat complex (PDB file 3iyv) showing one centrally located CLTC protein (in gray) with the abovementioned domains and with the position of de novo in-frame *CLTC* variants in the protein (red points). Eight additional clathrin heavy chains, interacting with the centrally located CLTC protein, are shown in different colors (blue, green, and purple). Note the interaction of the C-terminal helix (trimerization domain) with two other heavy chains (blue/green). Smaller clathrin light chains, which are located close to the proximal domain of the heavy chain, are shown in yellow. (c) 3D structure close-ups of the clathrin complex displayed in (b), showing specific domains of the centrally located protein encoded by the *CLTC* gene (in gray) with de novo in-frame *CLTC* variants (in red), surrounded by clathrin heavy chains (in blue, green, and purple) and clathrin light chains (in yellow). (c1) Close-up of the distal segment of the heavy chain arm, showing that in-frame variants occur in an area that is in close interaction with the other heavy chains. An abnormal or loss of interaction with other heavy chains is predicted to affect the local structure of the clathrin coat complex. (c2) Close-up of the proximal segment of the heavy chain arm, showing that variants occur nearby a clathrin light chain and/or the KR-loop residues 1161–1165 (shown in orange), which is considered relevant for the regulation of the interactions with the light chain (Wilbur *et al.*¹⁶ Dev Cell 2010;18(5):841–848), likely resulting in an abnormal or loss of interactions with both heavy and light chains. Panels (c1) and (c2) were made using PDB file 3iyv.

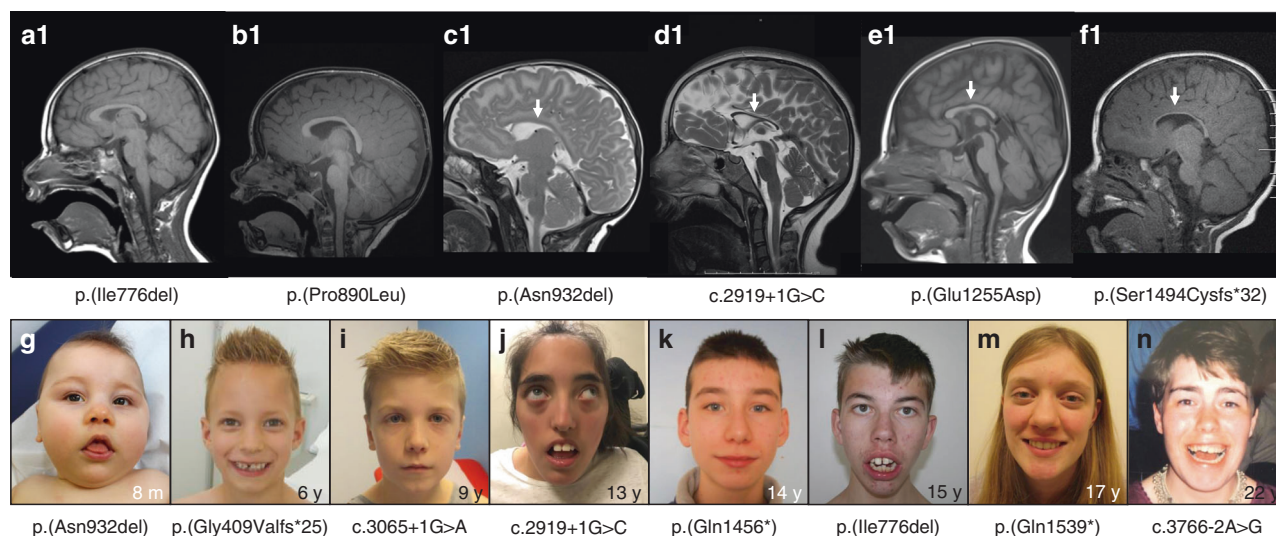


Fig. 2 Individuals with likely pathogenic de novo *CLTC* variants. (a–f) Brain magnetic resonance imaging (MRI). The structure of the corpus callosum was normal in (a) individual 3 at 5 years (T1) and (b) individual 4 at 23 months, while hypoplasia of the corpus callosum (white arrows) was observed in (c) individual 5 at 2 months (T2), (d) individual 6 at 11 years (T2), (e) individual 9 at 4 years (T1), and (f) individual 12 at 2.5 years. (g–n) Craniofacial dysmorphism, such as long face with high forehead, large ears, long palpebral fissures, midface hypoplasia, bulbous tip of the nose, deep philtrum, wide mouth, and large upper central incisors (individuals are ordered by increasing age at clinical photograph).

in-frame variants. This might result in phenotypic differences. Therefore, we compared the proportion of severe ID, epilepsy, microcephaly, and hypoplasia of the corpus callosum in six individuals with unambiguous missense variants or in-frame deletions in *CLTC* with the proportions in ten individuals with proven de novo nonsense or frameshift variants. Of note, in-frame variants possibly affecting splicing were excluded from this analysis. Although differences did not reach significance, severe ID, epilepsy, microcephaly, and hypoplasia of the corpus callosum were more frequent in the group of individuals with in-frame variants than in individuals with nonsense and frameshift variants (3/6 vs. 0/10, 4/6 vs. 1/9, 2/6 vs. 0/9, 2/6 vs. 0/9, respectively; Fisher's exact *p* values > 0.05; Tables S1 and S4). Of note, while the clinical triad epilepsy, microcephaly, and hypoplasia of the corpus callosum occurred in two of six individuals with likely pathogenic

in-frame *CLTC* variants, it was not observed in any of the ten individuals with a frameshift variant (Fisher's exact *p* value = 0.125).

DISCUSSION

We describe the clinical manifestations observed in 13 individuals with 11 novel and 2 recurrent de novo variants in *CLTC*. Considering these 13 and the 14 previously reported individuals,^{1,2} a variable phenotype was observed, ranging from ID and subtle, but consistent, dysmorphic facial features to ID associated with microcephaly, brain abnormalities, and epilepsy. Notably, hypoplasia of the corpus callosum was the most common structural cerebral anomaly identified. Cerebral palsy (ataxic, hypotonic, or spastic) affecting gait was also recurrently seen. Neuropsychiatric features, including ADHD and/or autistic behavior, were observed in more than half of

the individuals. Although recognizable, facial features are rather nonspecific. While previously rarely reported, vision abnormalities were common in our cohort.

The phenotypic variability observed in individuals with de novo *CLTC* variants is associated with allelic heterogeneity. A more severe phenotype, comprising severe ID, microcephaly, hypoplasia of the corpus callosum, and epilepsy was more frequently reported in individuals with missense and in-frame *CLTC* variants than with nonsense and frameshift variants. In particular, the triad microcephaly, callosal hypoplasia, and epilepsy occurred in two individuals with a missense variant or an in-frame deletion. Although the difference was not significant, this suggests that different types of pathogenic variants in *CLTC* may lead to different mechanisms of action. We proposed that truncating variants lead to a loss-of-function effect resulting in milder clinical manifestations, while missense and in-frame variants may contribute to a dominant-negative effect resulting in more severe clinical features. The suggestion of Hamdan *et al.*¹ that “truncating de novo variants affecting the C terminus of *CLTC* tended to be associated with hypotonia, global developmental delay, and ID” falls within our more comprehensive hypothesis. Other additional genetic and nongenetic factors may eventually further explain the variability in the severity of the phenotype observed in these two groups of individuals. For instance, the four individuals with the de novo p.(Pro890Leu) variant presented with ID without epilepsy or callosal hypoplasia. Another example is given by the individual with the p.(Asp1207del) variant. Besides severe ID and callosal hypoplasia, he also had cerebral visual impairment, which may be associated with a likely pathogenic variant in the candidate *UHMK1* gene.¹⁷ Since almost all *CLTC* variants described to date are private, we envision that the detailed clinical characterization of a larger cohort of individuals with pathogenic *CLTC* variants will be needed to further prove our hypothesis.

The variable expressivity associated with allelic heterogeneity in *CLTC* poses challenges to genetic counseling and warrants a comprehensive clinical evaluation and long-term multidisciplinary follow-up of these individuals, involving pediatricians, neurologists, psychiatrists, ophthalmologists, and medical geneticists, among others. While more severely affected individuals manifest moderate/severe ID associated with the clinical triad microcephaly, hypoplasia of the corpus callosum, and epilepsy, the less severely affected individuals may manifest mild ID/learning disability without epilepsy or brain abnormalities. Although not confirmed so far, the existence of individuals with inherited variants cannot be excluded, due to the mild phenotype associated with some likely pathogenic *CLTC* variants.

In summary, the clinical implications of pathogenic *CLTC* variants constitute a phenotypic spectrum, varying from mild ID to severe ID, microcephaly, hypoplasia of the corpus callosum, and epilepsy. An individual's phenotype seems to be more severe when associated with pathogenic missense and

in-frame variants, likely leading to a dominant-negative effect, and less severe when associated with variants resulting in nonsense-mediated mRNA decay. Taken together, our findings suggest that there is a genotype–phenotype correlation in *CLTC*-related ID and neurologic/neuroradiologic abnormalities and corroborate the importance of precise clinical characterization of additional individuals to firmly establish this association.

SUPPLEMENTARY INFORMATION

The online version of this article (<https://doi.org/10.1038/s41436-019-0703-y>) contains supplementary material, which is available to authorized users.

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DISCLOSURE

The authors declare no conflicts of interest.

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