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# Charcot-Marie-Tooth Neuropathy Type 4H – RETIRED CHAPTER, FOR HISTORICAL REFERENCE ONLY

Synonyms: Charcot-Marie-Tooth Disease Type 4H, CMT4H

Valérie Delague, PhD<sup>1</sup> Created: August 8, 2013.

# Summary

NOTE: THIS PUBLICATION HAS BEEN RETIRED. THIS ARCHIVAL VERSION IS FOR HISTORICAL REFERENCE ONLY, AND THE INFORMATION MAY BE OUT OF DATE.

# **Clinical characteristics**

Charcot-Marie-Tooth neuropathy type 4H (CMT4H) is a demyelinating form of CMT that is characterized by early onset (usually before age 3 years; range: birth to age 10 years) and slow progression. The degree of distal muscle weakness and amyotrophy varies between affected individuals as does the presence or absence and severity of foot deformities, scoliosis, and sensory involvement. Neuropathic pain has not been reported. To date, findings in18 individuals with molecularly confirmed CMT4H from 13 families have been reported.

## **Diagnosis/testing**

CMT4H is suspected in individuals with typical findings of CMT (distal amyotrophy, foot deformities), early onset, and slow progression. Motor nerve conduction velocities (MNCVs) and sensory nerve conduction velocities (SNCVs) are abnormal. The diagnosis is established by the presence of biallelic *FGD4* pathogenic variants.

## Management

*Treatment of manifestations:* Often management is by a multidisciplinary team that includes neurologists, physiatrists, orthopedic surgeons, and physical and occupational therapists. Treatment is symptomatic and may include: ankle/foot orthoses (AFOs); physiotherapy (daily heel cord stretching exercises and physical activity to prevent contractures and help preserve flexibility); surgery to correct severe pes cavus deformity and/or spine deformities; and forearm crutches, canes, and/or wheelchairs for mobility. Musculoskeletal pain may be treated with acetaminophen or nonsteroidal anti-inflammatory drugs (NSAIDs).

Surveillance: Regular (annual) evaluation to determine neurologic status and functional disability.

**Author Affiliation:** 1 Inserm/Aix-Marseille Université, UMR S910, Génétique Médicale et Génomique Fonctionnelle, Faculté de Médecine de la Timone, Marseille, France; Email: valerie.delague@univ-amu.fr.

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*Agents/circumstances to avoid:* Obesity because it makes walking more difficult; medications that are toxic or potentially toxic to persons with CMT.

### **Genetic counseling**

CMT4H is inherited in an autosomal recessive manner. At conception, each sib of an affected individual has a 25% chance of being affected, a 50% chance of being an asymptomatic carrier, and a 25% chance of being unaffected and not a carrier. Carrier testing for at-risk family members and prenatal diagnosis for pregnancies at increased risk are possible if the pathogenic variants in the family have been identified.

# Diagnosis

## **Clinical Diagnosis**

Formal diagnostic guidelines for Charcot-Marie-Tooth type 4H (CMT4H) do not exist.

Note: Although the CMT Neuropathy Score (CMTNS) and CMTNS version 2 (CMTNS2) are widely used in the diagnosis of CMT [Shy et al 2005, Murphy et al 2011], their limited ability to measure disability and severity of the disease in children under age ten years [Haberlová & Seeman 2010, Pagliano et al 2011] makes their use in the diagnosis of early childhood-onset disease like CMT4H problematic.

**The diagnosis of Charcot-Marie-Tooth neuropathy type 4H (CMT4H) is suspected** in individuals with findings typically observed in CMT (distal amyotrophy, foot deformities) and the following (see also Table 1):

- Early onset. The imprecise retrospective data available indicate that symptoms typically appear before age three years, with a range presumed to be birth to ten years.
- Slow progression. Despite early onset, the disease is stable with only very slow progression.
- Scoliosis; onset before age ten years (observed in some, but not all, affected individuals)
- Abnormal motor nerve conduction velocities (MNCVs) and sensory nerve conduction velocities (SNCVs). In the lower limbs, MNCVs were non-recordable in 8/9 individuals tested and severely reduced in one; SNCVs were non-recordable in 8/8 individuals tested. In the upper limbs, MNCVs were non-recordable in 3/16 and severely reduced in 13/16; SNCVs were non-recordable in 8/9 and reduced in one (for details see Table 2 [pdf]).
- Family history consistent with autosomal recessive inheritance. Parental consanguinity is common; parents are not affected unless multigenerational consanguinity exists. Note: Disease severity and disability vary even within the same family (i.e., among individuals with the same pathogenic variants).

**The diagnosis of CMT4H is established** in individuals with biallelic *FGD4* pathogenic variants [De Sandre-Giovannoli et al 2005, Delague et al 2007, Reddy et al 2008] (Table 1).

Gene <sup>1</sup>	Method	Pathogenic Variants Detected <sup>2</sup>	Variant Detection Frequency by Method <sup>3</sup>
FGD4	Sequence analysis <sup>4</sup>	Sequence variants <sup>5</sup>	13/13 6

1. See Table A. Genes and Databases for chromosome locus and protein.

2. See Molecular Genetics for information on allelic variants.

3. The ability of the test method used to detect a variant that is present in the indicated gene

4. Sequence analysis detects variants that are benign, likely benign, of uncertain significance, likely pathogenic, or pathogenic.

Pathogenic variants may include small intragenic deletions/insertions and missense, nonsense, and splice site variants; typically, exon or whole-gene deletions/duplications are not detected. For issues to consider in interpretation of sequence analysis results, click here. 5. The test method does not allow detection or large genomic rearrangements within *FGD4*. However, except for deletions/duplications in CMT1A, large genomic rearrangements are not known as frequent molecular defects in CMT disease.

6. Individuals with CMT4H or autosomal recessive demyelinating CMT with clinical signs consistent with CMT4H [Delague et al 2007, Stendel et al 2007, Fabrizi et al 2009, Houlden et al 2009, Hayashi et al 2013]. Almost all pathogenic variants described to date were homozygous and in individuals born to consanguineous parents.

Note: When molecular genetic testing is not available, sural nerve biopsy can be considered; however, histologic findings are not specific to CMT4H, and thus not confirmatory.

**Histologic findings consistent with the diagnosis of CMT4H.** Moderate to severe loss of myelinated fibers, mainly affecting large caliber fibers, probably secondary to a demyelination-remyelination process is observed in all individuals with CMT4H undergoing nerve biopsy reported to date (see Table 2 [pdf]). The remaining fibers usually have features of congenital hypomyelination (e.g., myelin thickening) and other signs of altered myelination (e.g., onion bulbs and myelin outfoldings). Although myelin outfoldings are not specific to CMT4H, they are observed in only a few CMT subtypes (CMT4B1, CMTB2, and CMT4F), and thus could support molecular genetic testing of *FGD4*.

# **Clinical Characteristics**

## **Clinical Description**

Charcot-Marie-Tooth neuropathy type 4H (CMT4H), an autosomal recessive demyelinating form of CMT, is characterized by early onset and slow progression. The most common findings observed in published reports of 18 affected individuals from 13 families with molecularly confirmed CMT4H are summarized in Table 3 (see Table 2 [pdf] for a comprehensive summary).

The degree of distal muscle weakness and amyotrophy varies between affected individuals as does the presence or absence and severity of foot deformities, scoliosis, and sensory involvement.

Although individuals with CMT do experience neuropathic pain that is usually moderate, preferentially located in the extremities, and symmetric [Ribiere et al 2012], neuropathic pain has not been documented in CMT4H.

		Age in Yrs at First Symptoms / Last Exam	Age in	Distal Muscles				Distal		
Patient <sup>1</sup>	Origin		Mos at Walking	Weakness <sup>2</sup>	Muscle Atrophy <sup>3</sup>	Foot Deformity <sup>4</sup>	Scoliosis <sup>5</sup>	Sensory Loss <sup>6</sup>	Functional Impairment	Reference
Ia <sup>7</sup>	Lebanon	1-2 / 15	Delayed, 15-36	+++	++	++	+++	++	Moderate to severe: unsteady gait, walking w/out aid	Delague et al
Ib <sup>7</sup>	Lebanon	1-2 / 18	Delayed, 15-36	+++	++	++	-	++	Mild: unsteady gait, walking w/out aid	[2007]
Ic <sup>7</sup>	Lebanon	4 / 13	12	+++	++	+	++	++	Unknown	Stendel et al [2007]
II	Algeria	2 / unknown	Unknown	++	++	+	+	Unknown	Moderate: walking w/out aid, waddling gait	Delague et al [2007]
III	Turkey	<1/30	Delayed	+++	++	+	-	+	Unknown	
IV	Turkey	2 / unknown	Delayed, 26	++	+	-	-	-	Unknown	Stendel et al [2007]
V	Tamil	9 / unknown	16	+	+	-	-	-	Unknown	
VIa	Northern Ireland	Childhood <sup>8</sup> / 58	Unknown	+	+	+	-	++	Moderate: walking w/out aid at 58 yrs	Houlden
VIb	Northern Ireland	Childhood <sup>9</sup> / 50	Unknown	++	Unknown	+	-	++	Severe: at 50, walking w/2 crutches or wheelchair	et al [2009]
VII	Italy	<1 / 20	17	+	+	+	+	+	Moderate: unsteady gait w/ steppage	Fabrizi et al [2009]
VIII	Lebanon	5 / 21	14	+	+	+	-		Moderate: walking w/out aid	Baudot et al [2012]
IX	Algeria	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown	

Table 3. Clinical Characteristics of CMT4H in 18 Individuals from 13 Families

Patient <sup>1</sup> Origi		Age in Yrs at	Age in	Distal Musc	les		Scoliosis <sup>5</sup>	Distal		Reference	
	Origin	Symptoms / Last Exam	Mos at Walking	Weakness <sup>2</sup>	Muscle Atrophy <sup>3</sup>	Deformity <sup>4</sup>		Sensory Loss <sup>6</sup>	Impairment		
Xa	Tunisia	3/6	16	+++	++	+	+	-	Walking on tiptoes		
Xb	Tunisia	3 / 18	Normal	+++	++	+	++	+		Boubaker et al [2013]	
Xc	Tunisia	3 / 22	Normal	+++	++	+	+++	+	Spine surgery at age 16		
XI	Japan	Childhood / unknown	Unknown	Unknown	Unknown	+	Unknown	Unknown	Walked w/out assistance until 65 years; severe gait disturbance from 68 yrs	Havashi	
XII	Japan	Birth / unknown	11	Unknown	Unknown	+	Unknown	Unknown	Abnormal gait from 3 yrs	et al [2013]	
XIII	Japan	4 / unknown	14	Unknown	Unknown	Unknown	Unknown	Unknown	Frequent falls from age 4 years; walked w/ limp from 6 yrs		

Table 3. continued from previous page.

For further information see Table 2 (pdf).

1. Roman numerals = family; letters = sibs

2. - = not affected; + = mild in the lower extremities; ++ = marked in the lower extremities; ++ = also affected the hands and forearms

3. - = affected; + = mild; ++ = severe

4. - = no deformities; + = pes cavus and hammer toes; ++ = pes equinus and toes retraction

5. - = none; + = mild; ++ = severe; +++ = surgery required

6. - = no deficit; + = decreased sensibility; +++ = no sensibility

7. Patients Ia, Ib, and Ic are from three different branches of the same Lebanese family. See also Table 5.

8. Difficulty running and poor balance

9. Clumsiness

### **Genotype-Phenotype Correlations**

No genotype-phenotype correlations can be established in the 18 affected individuals from 13 families with molecularly confirmed CMT4H; remarkably, individuals homozygous for nonsense or frameshift variants do not have more severe manifestations than individuals with missense variants (summarized in detail in Table 2 [pdf]).

### Prevalence

CMT4H is rare and it is difficult to estimate its prevalence. Only 13 families with molecularly confirmed CMT4H have been published to date.

Table 4 summarizes the proportion of individuals with CMT4H in published studies of CMT4. These studies have shown that *FGD4* pathogenic variants are most commonly homozygous variants identified in consanguineous families.

Table 4. Proportion of Individuals with CMT4H in Published Studies

# of Individuals w/CMT4H / Total # of Individuals w/CMT4	# of Individuals w/CMT4H / # of Individuals in the Study w/an Identified Pathogenic Variant	References
3/103 (~3%)	3/7 (43%)	Hayashi et al [2013]
2/45 (~4.5%) 1	2/28 (7%)	Baets et al [2011]
4/63 (~6.3%) <sup>2</sup>	Unknown	Stendel et al [2007]
1/12 (~8.3%)	Unknown	Houlden et al [2009]
5/108 (~4.6%)	Unknown	Delague et al [2007]; Delague, personal communication

1. The proportion of CMT4H is probably higher than indicated, as a number of individuals in this series have autosomal dominant inheritance.

2. All affected individuals had (1) demyelinating sensorimotor neuropathy with onset in the first decade and (2) at least one of the following: (a) parental consanguinity or at least one other affected sib; (b) severely slowed NCVs (<15 m/s for the motor median nerve); (c) prominent scoliosis; and (d) myelin outfoldings on nerve biopsy. No parents of affected individuals had clinical or neurophysiologic findings of CMT.

# **Genetically Related (Allelic) Disorders**

No phenotypes other than those discussed in this *GeneReview* are known to be associated with pathogenic variants in *FGD4*.

# **Differential Diagnosis**

See Charcot-Marie-Tooth Neuropathy.

## Management

### **Evaluations Following Initial Diagnosis**

To establish the extent of disease and needs in an individual diagnosed with Charcot-Marie-Tooth neuropathy type 4H (CMT4H), the following evaluations are recommended:

• Physical examination to determine extent of weakness and atrophy, pes cavus, gait stability, sensory loss, and skeletal deformities. In children with CMT, one should use the CMTPedS score defined by Burns et al [2012], a reliable, well-tolerated, valid, and sensitive global measure of disability for children with CMT from the age of 3 years [Burns et al 2012].

Although the CMT Neuropathy Score (CMTNS) and CMTNS version 2 (CMTNS2) are widely used in the diagnosis of CMT [Shy et al 2005, Murphy et al 2011], they have shown limited potential in measuring disability and disease severity in children younger than age ten years [Haberlová & Seeman 2010, Pagliano et al 2011].

The transition from the CMTPedS in childhood to the CMTNS2 in adulthood has been evaluated [Burns et al 2013]; together, the two measures provide a continuum for lifelong measurement of disability in patients with CMT.

- Orthopedic consultation to evaluate skeletal deformities such as foot deformities (pes cavus) and scoliosis and to determine the need for a surgery and/or ankle/foot orthoses
- Clinical genetics consultation and/or pediatric neurology consultation

#### **Treatment of Manifestations**

Individuals with CMT4H are often evaluated and managed by a multidisciplinary team that includes neurologists, physiatrists, orthopedic surgeons, and physical and occupational therapists [Carter et al 1995, Grandis & Shy 2005].

Treatment is symptomatic and may include the following:

- Ankle/foot orthoses (AFOs) to correct foot drop and aid walking [Carter et al 1995]
- Physiotherapy with daily heel cord stretching exercises to help prevent Achilles' tendon shortening and physical activity adapted to the abilities of each individual to prevent contractures and help preserve flexibility
- Orthopedic surgery to correct severe pes cavus deformity [Guyton & Mann 2000, Ward et al 2008]
- Surgery to correct spine deformities
- Forearm crutches or canes for gait stability
- Wheelchairs as needed because of gait instability
- Treatment of musculoskeletal pain with acetaminophen or nonsteroidal anti-inflammatory drugs (NSAIDs) [Carter et al 1998]

#### **Surveillance**

Appropriate surveillance includes annual evaluation by a team comprising physiatrists, neurologists, and physical and occupational therapists to determine neurologic status and functional disability.

### **Agents/Circumstances to Avoid**

Obesity is to be avoided because it makes walking more difficult.

Medications that are toxic or potentially toxic to persons with CMT comprise a spectrum of risk ranging from definite high risk to negligible risk. See the Charcot-Marie-Tooth Association website (pdf) for an up-to-date list.

### **Evaluation of Relatives at Risk**

See Genetic Counseling for issues related to testing of at-risk relatives for genetic counseling purposes.

### **Therapies Under Investigation**

Search ClinicalTrials.gov in the US and EU Clinical Trials Register in Europe for access to information on clinical studies for a wide range of diseases and conditions. Note: There may not be clinical trials for this disorder.

## **Genetic Counseling**

Genetic counseling is the process of providing individuals and families with information on the nature, mode(s) of inheritance, and implications of genetic disorders to help them make informed medical and personal decisions. The following section deals with genetic risk assessment and the use of family history and genetic testing to clarify genetic status for family members; it is not meant to address all personal, cultural, or ethical issues that may arise or to substitute for consultation with a genetics professional. —ED.

### **Mode of Inheritance**

Charcot-Marie-Tooth neuropathy type 4H (CMT4H) is inherited in an autosomal recessive manner.

### **Risk to Family Members**

#### Parents of a proband

- The parents of an affected individual are obligate heterozygotes (i.e., carriers of one mutant allele).
- Heterozygotes (carriers) are asymptomatic.

#### Sibs of a proband

- At conception, each sib of an affected individual has a 25% chance of being affected, a 50% chance of being an asymptomatic carrier, and a 25% chance of being unaffected and not a carrier.
- Once an at-risk sib is known to be unaffected, the risk of his/her being a carrier is 2/3.
- Heterozygotes (carriers) are asymptomatic.

**Offspring of a proband.** The offspring of an individual with CMT4H are obligate heterozygotes (carriers) for a pathogenic variant in *FGD4*.

Other family members. Each sib of the proband's parents is at a 50% risk of being a carrier.

## **Carrier (Heterozygote) Detection**

Carrier testing for at-risk family members is possible if the pathogenic variants in the family have been identified.

## **Related Genetic Counseling Issues**

#### Family planning

- The optimal time for determination of genetic risk, clarification of carrier status, and discussion of the availability of prenatal testing is before pregnancy.
- It is appropriate to offer genetic counseling (including discussion of potential risks to offspring and reproductive options) to young adults who are affected, are carriers, or are at risk of being carriers.

**DNA banking** is the storage of DNA (typically extracted from white blood cells) for possible future use. Because it is likely that testing methodology and our understanding of genes, allelic variants, and diseases will improve in the future, consideration should be given to banking DNA of affected individuals.

## **Prenatal Testing and Preimplantation Genetic Testing**

Once the pathogenic variants have been identified in an affected family member, prenatal testing for a pregnancy at increased risk and preimplantation genetic testing for CMT4H are possible.

Differences in perspective may exist among medical professionals and within families regarding the use of prenatal testing, particularly if the testing is being considered for the purpose of pregnancy termination rather than early diagnosis. While decisions regarding prenatal testing are the choice of the parents, discussion of these issues is appropriate.

#### Resources

GeneReviews staff has selected the following disease-specific and/or umbrella support organizations and/or registries for the benefit of individuals with this disorder and their families. GeneReviews is not responsible for the information provided by other organizations. For information on selection criteria, click here.

#### • Association CMT France

France Phone: 820 077 540; 2 47 27 96 41 www.cmt-france.org

#### Charcot-Marie-Tooth Association (CMTA)

PO Box 105 Glenolden PA 19036 Phone: 800-606-2682 (toll-free); 610-499-9264 Fax: 610-499-9267 Email: info@cmtausa.org www.cmtausa.org

#### European Charcot-Marie-Tooth Consortium

Department of Molecular Genetics University of Antwerp Antwerp Antwerpen B-2610 Belgium Fax: 03 2651002 Email: gisele.smeyers@ua.ac.be

#### • Hereditary Neuropathy Foundation, Inc.

432 Park Avenue South 4th Floor New York NY 10016 Phone: 855-435-7268 (toll-free); 212-722-8396 Fax: 917-591-2758 Email: info@hnf-cure.org www.hnf-cure.org

- My46 Trait Profile Charcot Marie Tooth disease
- National Library of Medicine Genetics Home Reference Charcot-Marie-Tooth disease
- NCBI Genes and Disease
  Charcot-Marie-Tooth syndrome

#### • TREAT-NMD

Institute of Genetic Medicine University of Newcastle upon Tyne International Centre for Life Newcastle upon Tyne NE1 3BZ United Kingdom Phone: 44 (0)191 241 8617 Fax: 44 (0)191 241 8770 Email: info@treat-nmd.eu Charcot-Marie-Tooth Disease

#### • Association Francaise contre les Myopathies (AFM)

1 Rue de l'International BP59 Evry cedex 91002 France **Phone:** +33 01 69 47 28 28 **Email:** dmc@afm.genethon.fr www.afm-telethon.fr

#### • European Neuromuscular Centre (ENMC)

Lt Gen van Heutszlaan 6 3743 JN Baarn Netherlands **Phone:** 31 35 5480481 **Fax:** 31 35 5480499 **Email:** enmc@enmc.org www.enmc.org

#### • Muscular Dystrophy Association - USA (MDA)

222 South Riverside Plaza Suite 1500 Chicago IL 60606 **Phone:** 800-572-1717 **Email:** mda@mdausa.org www.mda.org

 Muscular Dystrophy UK 61A Great Suffolk Street London SE1 0BU United Kingdom Phone: 0800 652 6352 (toll-free); 020 7803 4800 Email: info@musculardystrophyuk.org www.musculardystrophyuk.org

RDCRN Patient Contact Registry: Inherited Neuropathies Consortium
 Patient Contact Registry

## **Molecular Genetics**

*Information in the Molecular Genetics and OMIM tables may differ from that elsewhere in the GeneReview: tables may contain more recent information.* —ED.

Locus Name	Gene	Chromosome Locus	Protein	Locus-Specific Databases	HGMD	ClinVar
CMT4H	FGD4	12p11.21	FYVE, RhoGEF and PH domain- containing protein 4	IPN Mutations, FGD4 FGD4 homepage - Leiden Muscular Dystrophy pages	FGD4	FGD4

Table A. Charcot-Marie-Tooth Neuropathy Type 4H: Genes and Databases

Data are compiled from the following standard references: gene from HGNC; chromosome locus from OMIM; protein from UniProt. For a description of databases (Locus Specific, HGMD, ClinVar) to which links are provided, click here.

Table B. OMIM Entries for Charcot-Marie-Tooth Neuropathy Type 4H (View All in OMIM)

609311	CHARCOT-MARIE-TOOTH DISEASE, TYPE 4H; CMT4H
611104	FYVE, RhoGEF, AND PH DOMAIN-CONTAINING PROTEIN 4; FGD4

**Gene structure.** *FGD4* comprises 17 exons, of which 14 are coding exons. The gene covers a genomic region of about 14 kb. There are several isoforms, but the major transcript (NM\_139241.2) is 2931 bp long (2301 bp of coding sequence). For a detailed summary of gene and protein information, see Table A, **Gene**.

**Pathogenic variants.** 14 *FGD4* pathogenic variants have been described in 13 families. *FGD4* single-nucleotide variants have been described (occurring throughout the gene), including missense, nonsense, frameshift, splice site, and splicing variants.

See Table 5 for *FGD4* variants.

Table 5. FGD4 Variants Identified in the 13 Reported Families

Family	Origin	Consanguinity	DNA Nucleotide Change (Alias <sup>1</sup> )	Location in the Gene	Predicted Protein Change	Reference
Ia, Ib <sup>2</sup>	Lebanon	Yes	c.893T>G <sup>3</sup>	Exon 7	p.Met298ArgfsTer8 <sup>3</sup>	Delague et al [2007]
Ic <sup>2</sup>	Lebanon	Yes	c.893T>G <sup>3</sup>	Exon 7	p.Met298Arg <sup>3</sup>	Stendel et al [2007]
II	Algeria	Yes	c.893T>C	Exon 7	p.Met298Thr	Delague et al [2007]

Family	Origin	Consanguinity	DNA Nucleotide Change (Alias <sup>1</sup> )	Location in the Gene	Predicted Protein Change	Reference
III	Turkey	Yes	c.670C>T		p.Arg224Ter	
IV	Turkey	Yes	c.1628_1629delGA (1627_1628delGA or 1626_1627delAG)	Exon 13	p.Glu543GlyfsTer5	Stendel et al [2007]
V	Tamil	Sporadic	c.1756G>T	Exon 14	p.Gly586Ter	
VI	Northern Ireland	Yes	c.823C>T	Exon 6	p.Arg275Ter	Houlden et al [2009]
VII	Italy	Yes	c.1762-2A>G	Intron 14	p.Tyr587fsTer14	Fabrizi et al [2009]
VII	Lebanon	Yes	c.1698G>A	Exon 14	p.Met566Ile	Baudot et al
IX	Algeria	Yes	c.1325G>A	Exon 10	p.Arg442His	[2012]
X	Tunisia	Yes	c.514_515dupG (514_515insG)	Exon 4	p.Ala172GlyfsTer27	Boubaker et al [2013]
XI	Japan	Yes/no	c.1888_1892delAAAGG (1890_1894del)	Exon 15	p.Lys630AsnfsTer5	
XII	Japan	Yes/no	c.[837-2A>G + 1132+1G>A]	Intron 6/ intron 8	p.[Trp279fsTer + Tyr355fsTer2]	Hayashi et al [2013]
XIII	Japan	No/unknown	c.837-1G>A	Intron 6	p.Glu280LysfsTer23	

*Table 5. continued from previous page.* 

For further information see Table 2 (pdf).

Reference sequences: NM\_139241.2 and NP\_640334.2

1. Variant designation that does not conform to current naming conventions

2. Two individuals from different branches of the same Lebanese family

3. Stendel et al [2007] described c.893T>G as a missense variant leading to p.Met298Arg substitution, but Delague et al [2007] simultaneously described the same pathogenic variant in two other branches from the same Lebanese family and demonstrated that it is, in fact, a splicing variant predicted to result in a truncated protein of 305 amino acids instead of the full-length 766 residues (p.298MetfsTer8), or in total absence of the protein.

**Normal gene product.** *FGD4* encodes FRABIN (FGD1-related F-actin binding protein), a 766-amino acid protein (NP\_640334.2) (105 kd), with five functional domains: a N-terminal F-actin binding domain, one DH (Dbl homology) domain, two PH (pleckstrin homology) domains, and one cysteine-rich FYVE domain [Delague et al 2007].

DH domains were first identified in the Dbl protein (and are present in many proteins where they play a key role in the catalysis of GDP to GTP exchange); while PH and FYVE domains are mainly involved in interactions with different forms of phosphoinositides.

FRABIN is a Rho GDP/GTP nucleotide exchange factor (RhoGEF), specific for Cdc42, a member of the Rho family of small GTP binding proteins (Rho GTPases) [Obaishi et al 1998, Umikawa et al 1999]. Rho GTPases play a key role in regulating signal transduction pathways in eukaryotes. In particular, they have a pivotal role in mediating actin cytoskeleton changes during cell migration, morphogenesis, polarization, and division [Etienne-Manneville & Hall 2002, Jaffe & Hall 2005].

The role of FRABIN in peripheral nerve is not well known; however, overexpression of Frabin in embryonic rat spinal motoneurons and rat RT4 schwannoma cells showed that Frabin colocalizes with F-actin in neurite tips and growth cones, and induces the formation of filopodia-like microspikes [Delague et al 2007, Stendel et al 2007].

Also, a recent study in a mouse model of CMT4H [Horn et al 2012] has shown that Frabin regulates the RhoGTPase Cdc42 and endocytosis in Schwann cells.

**Abnormal gene product.** Most *FGD4* pathogenic variants described to date are predicted to be loss-of-function variants. In particular, nonsense, frameshift, splice site and splicing variants are predicted to lead to either a truncated protein or to complete absence of FRABIN. No data describing the effect of the pathogenic variants at the protein level in individuals with CMT4H have been published to date.

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#### 42. PubMed PMID: 19047708.

# **Chapter Notes**

### **Author Notes**

#### Author's Team

My team leads translational research in the field of Inherited Peripheral Neuropathies (mostly Charcot-Marie-Tooth disease), a group of neuromuscular disorders affecting peripheral nerve. Our aim is to better understand the genetics and physiopathology of this group of diseases. We focus our research on autosomal recessive forms of these diseases, by studying large consanguineous families. By using traditional positional cloning strategies, combined to high-throughput Next Generation Sequencing strategies, we identify new defective genes in Inherited Peripheral Neuropathies. We further study the physiopathology of these diseases, by developing different models, in order to identify potential therapeutic strategies for these diseases. We study in particular two CMT subtypes: CMT4H, caused by pathogenic variants in *FGD4/FRABIN* and *AR-CMT2A*, caused by pathogenic variants in *LMNA*.

In close relationship with the Molecular Genetics Department of The Children's Hospital "La Timone," we develop innovative diagnosis strategies.

### **Revision History**

- 19 September 2019 (ma) Chapter retired: Covered in Charcot-Marie-Tooth Hereditary Neuropathy Overview
- 8 August 2013 (me) Review posted live
- 1 April 2013 (vd) Original submission

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