CMT2 WITH PYRAMIDAL TRACT INVOLVEMENT DUE TO ARG329HIS MUTATION IN ALANYL-TRNA SYNTHETASE (AARS)

(1) Callegari I, (2) Cortese A, (2) Rossor AM, (3) Houlden H, (2) Reilly MM.

(1) Neuroscience Consortium, University of Pavia, Monza Policlinico and Pavia Mondino, Italy; (2) MRC Centre for Neuromuscular Diseases, National Hospital for Neurology and Neurosurgery, UCL Institute of Neurology, Queen Square, London, UK; (3) Department of Molecular Neuroscience, UCL Institute of Neurology, London, UK; National Hospital for Neurology and Neurosurgery, Queen Square, London, UK.

Introduction	Objectives							
Mutations in amynoacyl tRNA synthetases (ARSs), enzymes that catalyse the covalent attachment of amino acids to their cognate tRNA, are responsible for autosomal dominant CMT2, Intermediate CMT (CMT-I) and dHMN.	To report a case of <i>AARS</i> Arg329His mutation in a patient with CMT2 and pyramidal signs, a feature not previously reported within patients carrying Arg329His mutation. To review current knowledge clinical features and genetic findings of CMT relate ARSs mutations.							
Case report								
Disease onset	Neurologic examination							
37y, Male Development: bilateral clonus at 3 months of age, persisting till adolescence <u>chief complain</u> : ankle instability progressive walking difficulties and distal sensory loss from the third decade <u>Clinical course</u> : slowly progressive with moderate disability <u>PMH</u> : uneventful	<u>Cranial nerves</u> : normal <u>Atrophy</u> : moderate UL, marked LL <u>Weakness:</u> UL: proximal: normal; distal: mild (ABP 5-/4+) LL: proximal: normal strength, distal: severe <u>Sensation:</u> Light touch and pinprick: reduced to ankles							

CMTES: 18

Paraclinical investigations

Brain and spinal cord MRI: normal.

		Mot	or	Sensory			
	CMAP (mV)	MCV (m/s)	DML (ms)	F wave latenc y (ms)		SAP (uV)	SCV (m/s)
ref	>2	>40.6	<5.8		ref	>6	>42
Peroneus	0,0	34,9	21,1	Not elicita ble	Suralis	0,67/0,17	39,2/24,4
ref	>5	>41	<5.5				
Tibialis	0,7/0,3	32,8/19,3	9,9/11,7	NE			
ref	>5	>46.8	<4		ref	>8	>46.8
Median	5,9/5,3	36,4/39,1	10,75	45,35	Median	4,9/4,8	38,3/37,7



Vibratory: I MCP reduced; hallux: absent; knee: reduced <u>Reflexes</u>: **UL: brisk**; reduced at knees, absent at ankles **Bilateral Babinski**

<u>Steppage gait</u>

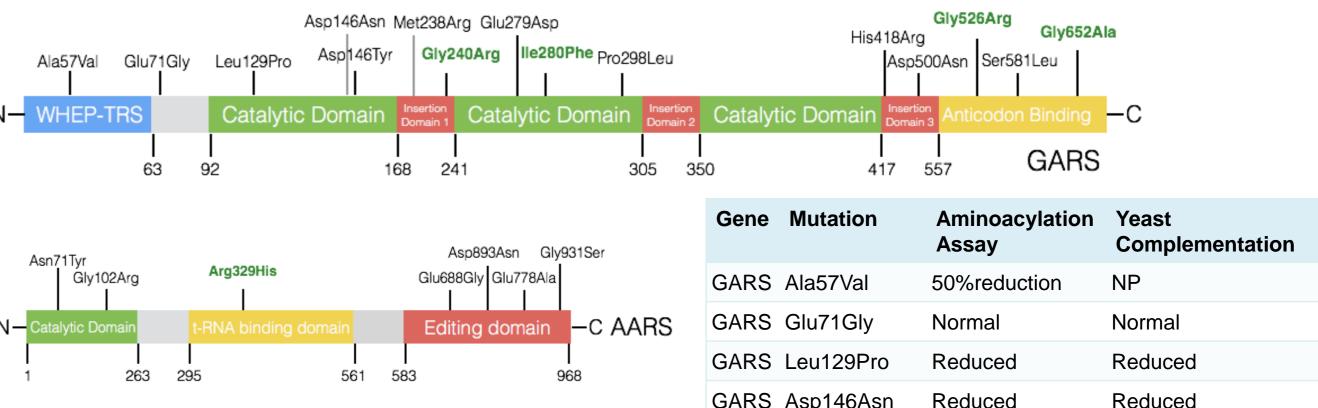
Workout

Sanger sequencing of *PMP22*, *GJB1*, *MPZ*, *GDAP* and *MFN2*: negative.

<u>SureSelect Focused Exome sequencing</u> (Agilent Technologies, Santa Clara CA, USA): c.986G>A, p.Arg329His mutation in AARS.

Literature revision

	GARS	AARS	HARS	KARS	MARS	YARS	WARS	Asp146Asn Met238Arg Glu279Asp	His418Ar	Gly526Arg g Gly652/	la
Mutations	17	6	5	1 comp het	2	3	1	Ala57Val Glu71Gly Leu129Pro Asp146Tyr Gly240Arg lle280Phe Pro298Leu		500Asn Ser581Leu	
Families	18 5	13	4	1	2	2	3				0
Sporadic cases, n (%)		0	I	-	-	I	0	N-WHEP-TRS Catalytic Domain Insertion Domain 1 Catalytic Domain 1 Domain 2			
Patients	43	42	23	1	4	3	7	63 92 168 241 305 3	50 417	557 GANS	1
Phenotype d-HMN-V	12	1					3		Gene Mutation	Aminoacylation	Yeast
CMT2D	8	5	-	-	- 2	-	-	Asp893Asn Gly931Ser		Assay	Complementatio
CMTI	-	5	1	1	-	3	-	Aspossash Giyashaer Giyaazag Giyaazag Giyaazag Giyaazag Giyashaer Giyashaer	GARS Ala57Val	50%reduction	NP
CMT1	_	1	-	-	-	-	-		GARS Glu71Gly	Normal	Normal
CMT2/d-HMN	3	-	2	-	-	-	-	N—Catalytic Domain t-RNA binding domain Editing domain —C AARS			
Atypical	_	1	-	-	-	-	-	1 263 295 561 583 968	GARS Leu129Pro	Reduced	Reduced
Age of Onset	0-35	0-55	22,05 ± 3,5	NA	45-67	I-VI dec	11,7 ± 0,6		GARS Asp146Asn	Reduced	Reduced
	16,6 ± 1,8	23,6 ± 2,8			44,4 ± 4,94			Pro134His	GARS Ser211Phe	Reduced	NP
Age at first visit	37,4 ± 3,5	42,8 ± 2,88	44,7 ± 3,8	NA	51,4 ± 4,87	NA	37,7 ± 6,7	Asp175Glu	GARS Pro244Leu	Reduced	Reduced
Site of onset								Thr132lle Arg137GIn Asp364Tyr	GARS Gly240Arg	Reduced	Normal
UL	57%	3%	5%	NA	25%	33%	100%	N- WHEP-TRS Catalytic Domain tRNA binding - C HARS	GARS Ile280Phe	Reduced	Normal
UL + LL	24% 16%	92% 5%	79% 16%	NA NA	50% 25%	- 67%	-	I I I 5 49 69 394 408 507	GARS His418Arg	Reduced	Reduced
Motor deficit at	1070	5%	1070	INA	2376	0770	-		GARS Asp500asn	Normal	NP
NE											
UL	23%	-	-	NA	-	-	-	Tyr173SerfsX7	GARS Gly526Arg	Reduced	Reduced
	-	54%%	25%	NA	-	-	-	Leu133His	GARS Ser581Leu	Normal	NP
UL + LL Siensory deficit	77%	46%	75%	NA	100%	100%	100%	N- Anticodon Binding Catalytic Domain -C KARS	GARS Gly598Ala	Reduced	Viable
at NE									AARS Asn71Tyr	Reduced	Reduced
LL	10%	58%	48%	NA	-	-	-	1 125 234 575 625	AARS Gly102Arg	Np	Reduced
UL + LL	19%	27%	35%	NA	100%	100%	-		AARS Arg329His	Reduced	Reduced
None UL	70% 40%	15% -	17%	NA -	-	-	100%		AARS Glu778Ala	Normal	Normal
predominance	4070	_	_	-	_	-		Arg618Cys Pro800Thr	HARS Thr132lle	Np	Reduced
Cranial nerves	3 cases	1 mutation	-	-	-	-	-	N- Glutathione S-transferase, C-terminal tRNA binding Domain WHEP-TRS - C MARS		-	
involvement	(7%)	(16%)							HARS Pro134His	Np	Reduced
Pyramidal signs	Babinski	Brisk DTR	Brisk DTR	-	-	-	-	1 92 180 266 658 845 897 900	HARS Arg137GIn	Np	Reduced
	18%	and	60%						HARS Asp175Glu	Np	Partially Reduced
	Brisk DTR 5%	Babinski 16%							HARS Asp364Tyr	Np	Reduced
Scoliosis	6 (14%)	-	-	-	-	_	-	Asp81lle	KARS Leu133His	Reduced	Normal
Other signs	Mild	1 case	-	Developmental	-	-	-	Gly41Arg Glu196Lys	KARS Tyr173serfsx7	Np	Reduced
	increase	mis-		delay, self-				N- Catalytic Domain Anticodon recognition C-terminal - C YARS	KARS Ile302Met	Normal	Normal
	CPK (5%)	diagnosed as CIDP		abusive behavior,				1 230 364 528	MARS Arg618Cys	Np	Reduced
		as CIDP		dimorphism,				1 230 304 320		-	
				vestibular					YARS Gly41Arg	Reduced	Dominant Neg
				Schwannoma				His257Arg	YARS Glu196Lys	Reduced	Dominant Neg
Median MNCV (m/s)	47,3 ± 1,2			39,5	52,5	29-50	55,2 ± 2,3	N – WHEP Catalytic Domain anti-codocn binding Catalytic domain – C WARS	YARS 153– 156delVKQV	Reduced	Np
% ≤ 45 m/s	41%	72%	66%	-	-	-	0%		, WAR His257Arg	Reduced	Reduced



Conclusions

