



Inherited Long QT Syndrome: Recent Advances

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Outline

- What is Long QT (LQT) Syndrome
- Genetics of LQT
- Investigation and Management
- Some novel insights

Background

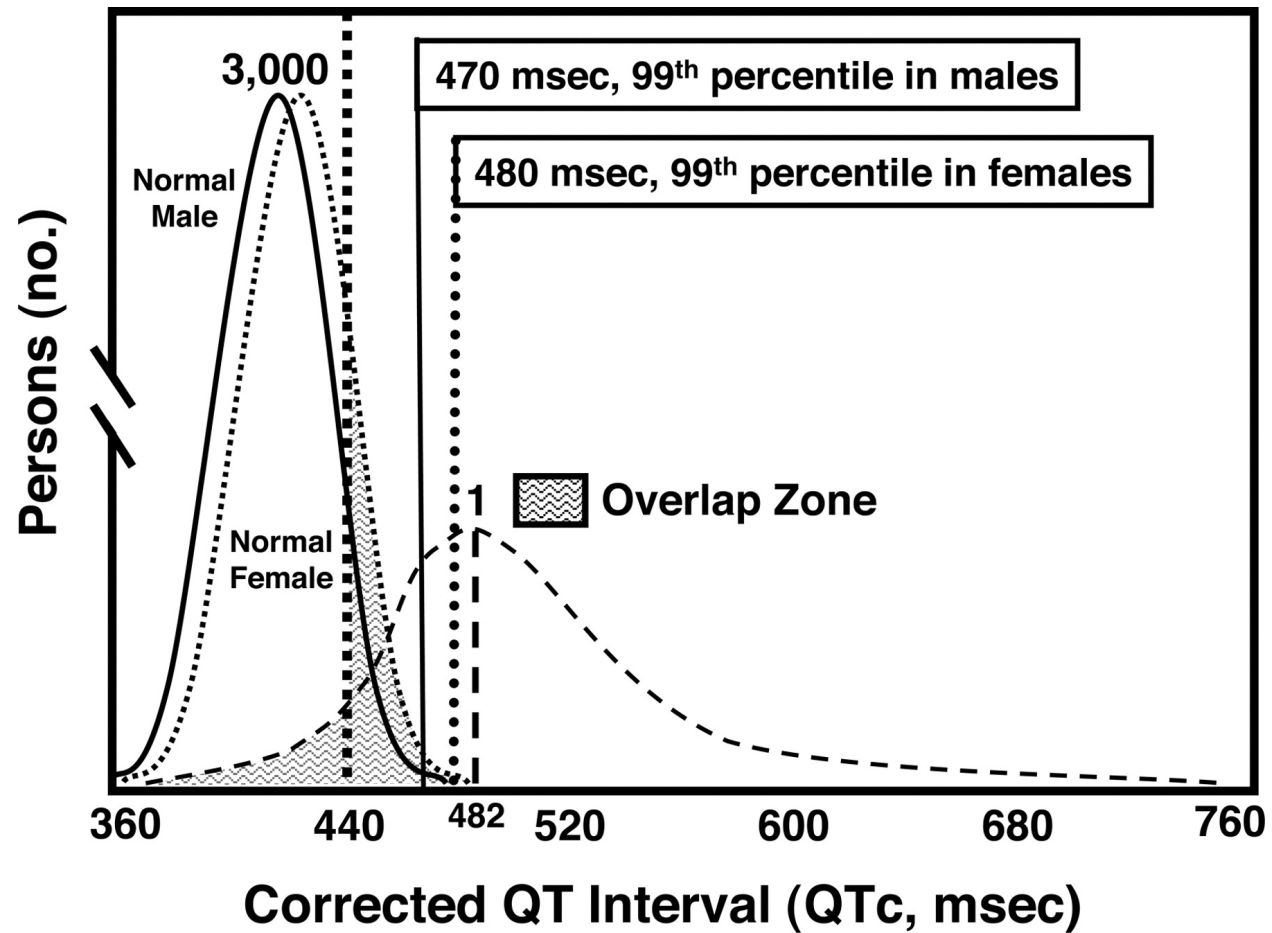
*ervell A, Lange-Nielsen F.
Congenital deaf-mutism, functional heart disease
with prolongation of the Q-T interval, and sudden
death. Am Heart J 1957;54:59-68*

*Romano C, Gemme G, Pongiglione R.
Aritmiocardiache rare dell'eta pediatrica, II:
Accessi sincopali per fibrillazione ventricolare
parossistica. Clin Pediatr. 1963;45:656–683.*

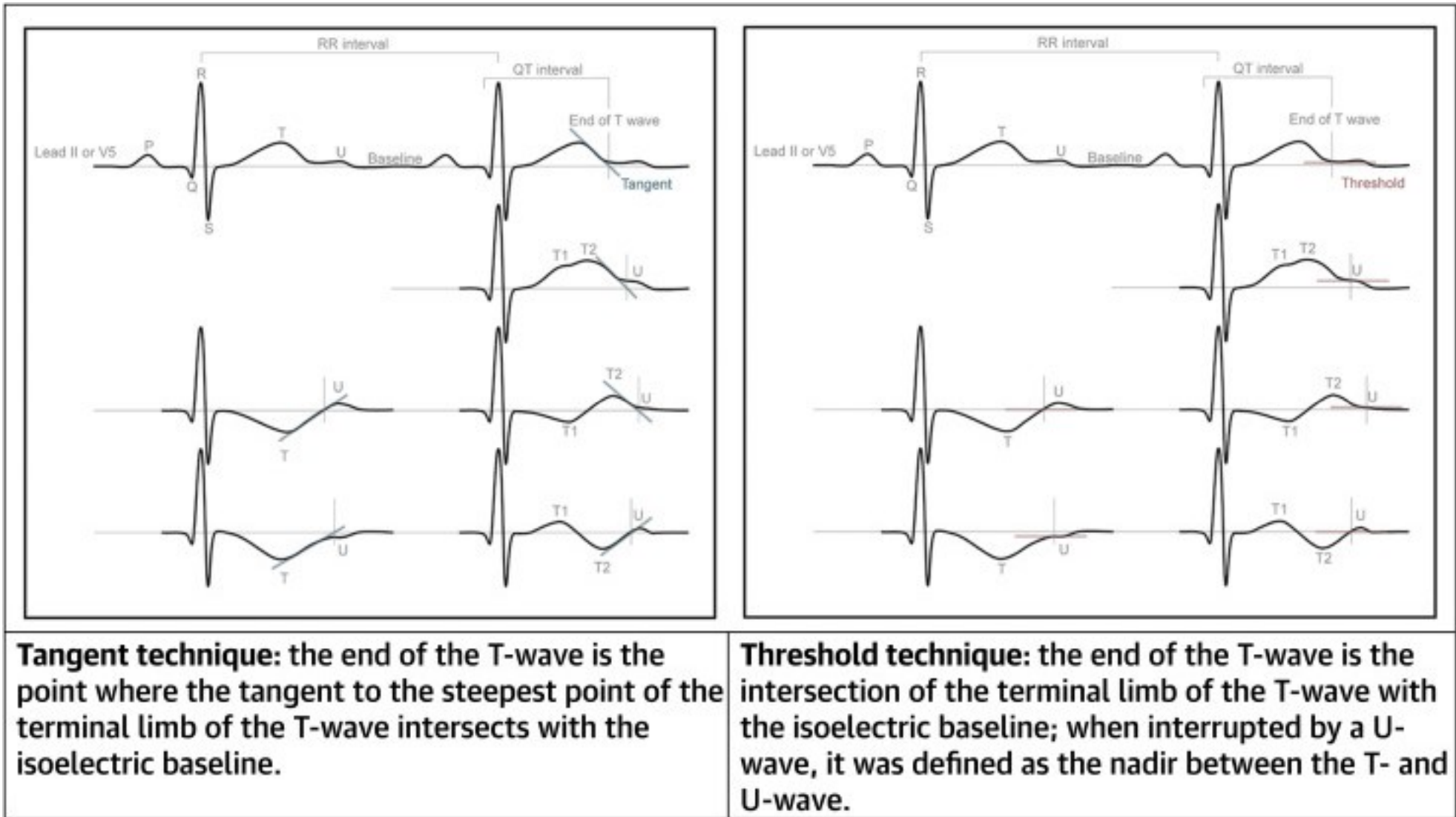
*Ward OC. A new familial cardiac syndrome in
children. J Ir Med Assoc. 1964;54:103–106.*

- Estimated prevalence is 1 in 2,000
- Accurate measurement of QT interval is very important – usually lead II or V5
- Correction for heart rate: Bazett, Fridericia, linear regression models
- QTc measurements - resting, ambulatory and exercise
- What is 'abnormal' QTc?
 - >450ms (male), >460 ms (female)?

Tc values in normal population and patients with LQT



Measuring the QT interval

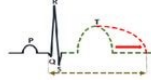

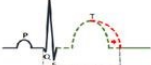
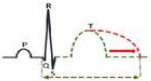


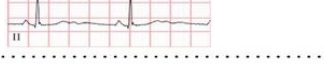



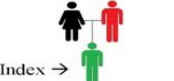



HRS/EHRA/APHRS expert consensus statement on the diagnosis and management of patients with inherited primary arrhythmia syndromes

Expert Consensus Recommendations on LQTS Diagnosis

1. LQTS is diagnosed:
 - a. In the presence of an LQTS risk score ≥ 3.5 in the absence of a secondary cause for QT prolongation *and/or*
 - b. In the presence of an unequivocally pathogenic mutation in one of the LQTS genes *or*
 - c. In the presence of a corrected QT interval for heart rate using Bazett's formula (QTc) ≥ 500 ms in repeated 12-lead electrocardiogram (ECG) and in the absence of a secondary cause for QT prolongation.
2. LQTS can be diagnosed in the presence of a QTc between 480 and 499 ms in repeated 12-lead ECGs in a patient with unexplained syncope in the absence of a secondary cause for QT prolongation and in the absence of a pathogenic mutation.

Schwartz Score

		Points	
Electrocardiographic findings <i>(in absence of acquired causes)</i>			
QTc duration <i>(calculated by Bazett formula)</i>	≥ 480 msec		3
	460-479 msec		2
	450-459 msec <i>(men)</i>		1
	≥ 480 msec		1
QTc 4th minute of recovery from exercise test			1
Torsades de Pointes* <i>(mutually exclusive)</i>			2
T-wave alternans			1
Notched T wave in 3 leads			1
Low resting heart rate	Below the 2 nd percentile for age		0.5
Clinical history			
Syncope* <i>(mutually exclusive)</i>	With stress		2
	Without stress		1
Congenital deafness			0.5
Family history <i>(the same family member cannot be counted twice for the rows below)</i>			
Family members with definite LQTS			1
Unexplained SCD <30 years among immediate family members			0.5

Definite LQTS is defined by an LQTS score ≥3.5 points

Intermediate probability of LQTS by an LQTS score of <3.5 and >1

Low probability of LQTS by ≤1 point. In the family history rows, the same family member cannot be counted in both categories.

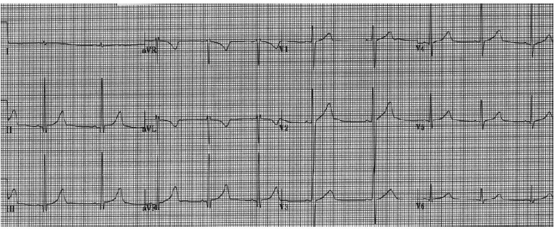
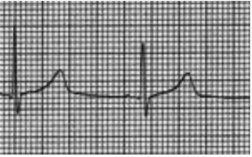
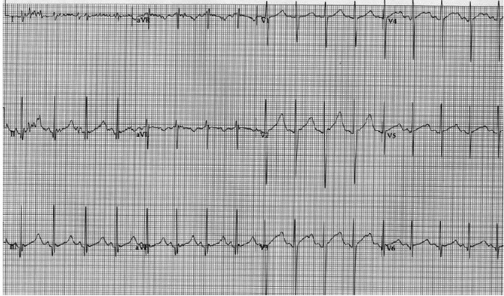
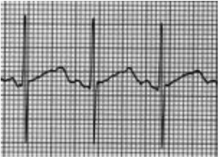

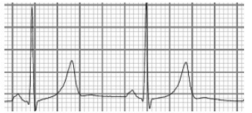


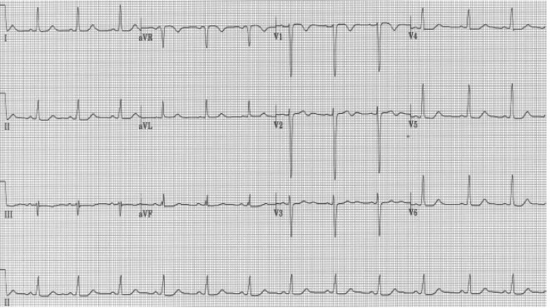
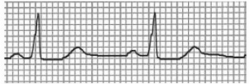
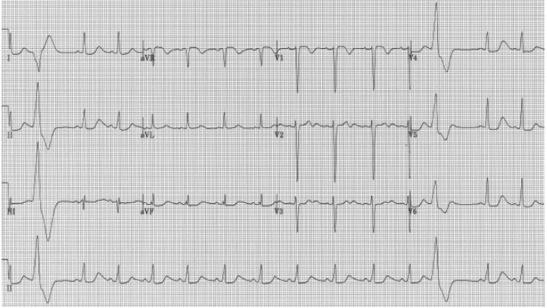
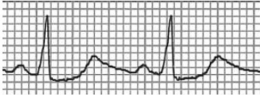
Wilde AA et al. Heart 2022;108:332-338

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Provocation Tests

	Baseline	Provocation
Stand-up Test	  <p>QT=440ms, RR=920ms QTc=459ms</p>	  <p>QT=420ms, RR=580ms QTc=551ms</p>
Exercise Test*	  <p>QT=450ms, RR=1020ms QTc=446ms</p>	  <p>QT=460ms, RR=680ms QTc=558ms</p>
Epinephrine Challenge	  <p>QT=420ms, RR=820ms QTc=464ms</p>	  <p>QT=450ms, RR=680ms QTc=546ms</p>

Clinical Genome Resource curated gene panels for LQT

Entity	Genetic evidence strong/moderate for causation		Genetic evidence weak/disputed for causation	
LQTS	<i>KCNQ1</i> (AD/AR)	(LQT1/JLNS)	<i>ANK2</i>	(LQT4)
	<i>KCNH2</i>	(LQT2)	<i>KCNE1*</i> (AD/AR)	(LQT5/JLNS)
	<i>SCN5A</i>	(LQT3)	<i>KCNE2</i>	(LQT6)
	<i>CALM1</i>		<i>CAV3</i>	(LQT9)
	<i>CALM2</i>		<i>SCN4B</i>	(LQT10)
	<i>CALM3</i>		<i>AKAP9</i>	(LQT11)
	<i>TRDN</i> (AR)		<i>SNTA1</i>	(LQT12)
	<i>KCNJ2</i>	(LQT7 Andersen-Tawil Syndrome)	<i>KCNJ5</i>	(LQT13)
<i>CACNA1C</i>	(LQT8 Timothy syndrome)			

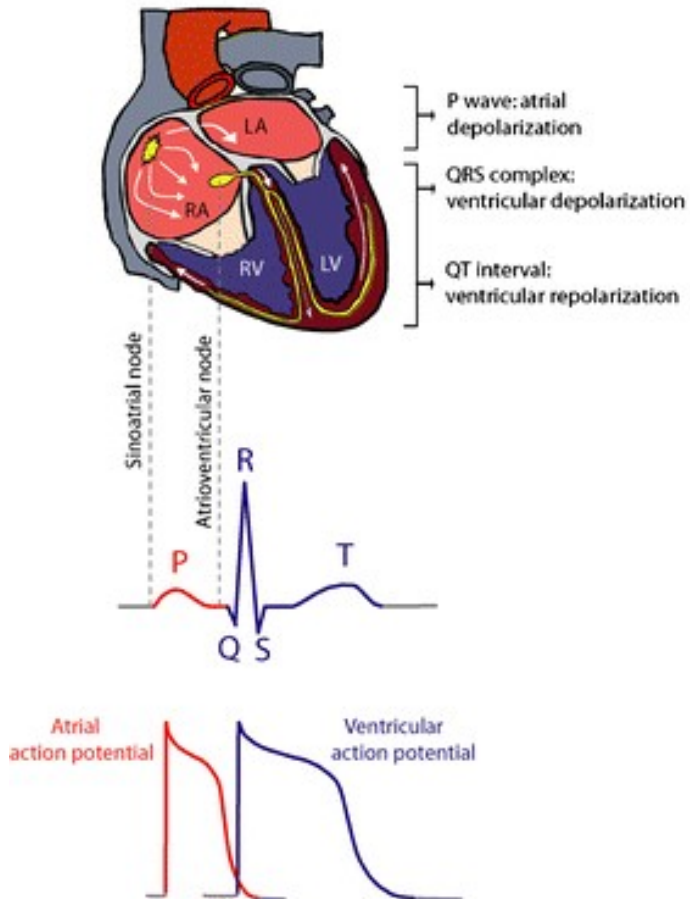
Interpretation of Genetic Variants

Pathogenic
Likely pathogenic
Variant of uncertain significance (VUS)
Likely benign
Benign

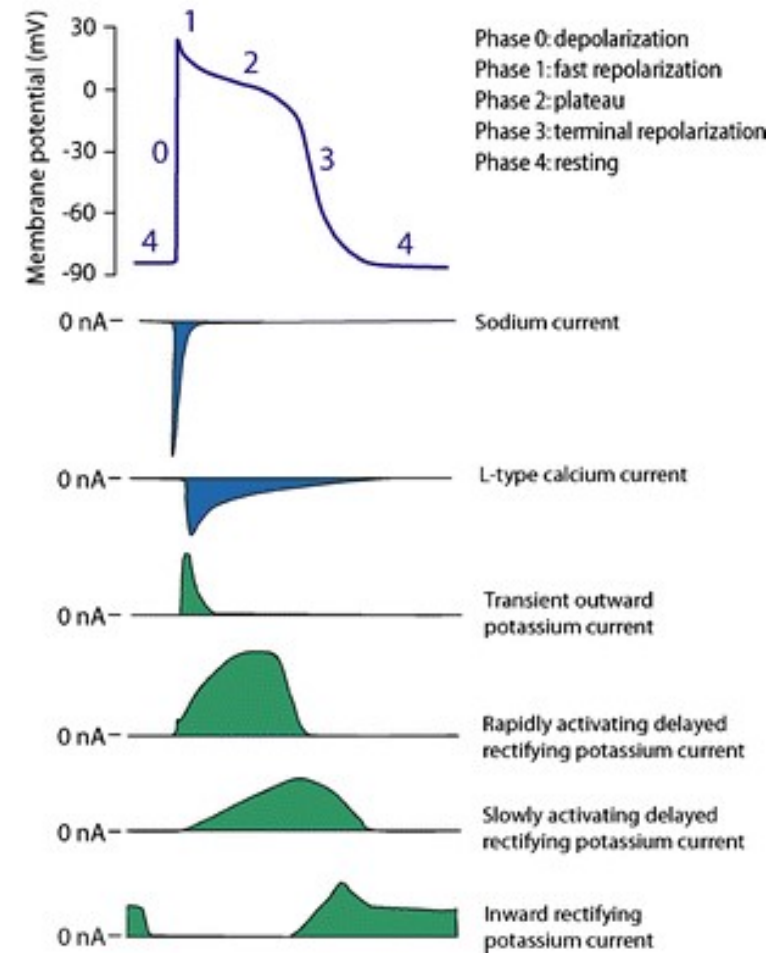
	Benign			Pathogenic		
	Strong	Supporting	Supporting	Moderate	Strong	Very strong
Population data	MAF is too high for disorder BA1/BS1 OR observation in controls inconsistent with disease penetrance BS2			Absent in population databases PM2	Prevalence in affecteds statistically increased over controls PS4	
Computational and predictive data		Multiple lines of computational evidence suggest no impact on gene /gene product BP4 Missense in gene where only truncating cause disease BP1 Silent variant with non predicted splice impact BP7 In-frame indels in repeat w/out known function BP3	Multiple lines of computational evidence support a deleterious effect on the gene /gene product PP3	Novel missense change at an amino acid residue where a different pathogenic missense change has been seen before PM5 Protein length changing variant PM4	Same amino acid change as an established pathogenic variant PS1	Predicted null variant in a gene where LOF is a known mechanism of disease PVS1
Functional data	Well-established functional studies show no deleterious effect BS3		Missense in gene with low rate of benign missense variants and path. missenses common PP2	Mutational hot spot or well-studied functional domain without benign variation PM1	Well-established functional studies show a deleterious effect PS3	
Segregation data	Nonsegregation with disease BS4		Cosegregation with disease in multiple affected family members PP1	Increased segregation data →		
De novo data				De novo (without paternity & maternity confirmed) PM6	De novo (paternity and maternity confirmed) PS2	
Allelic data		Observed in <i>trans</i> with a dominant variant BP2 Observed in <i>cis</i> with a pathogenic variant BP2		For recessive disorders, detected in <i>trans</i> with a pathogenic variant PM3		
Other database		Reputable source w/out shared data = benign BP6	Reputable source = pathogenic PP5			
Other data		Found in case with an alternate cause BP5	Patient's phenotype or FH highly specific for gene PP4			

Action Potential and Ion Currents

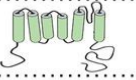
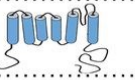
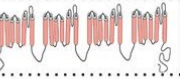




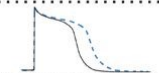
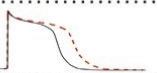



















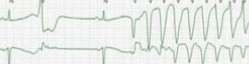
A Electrocardiogram (ECG)



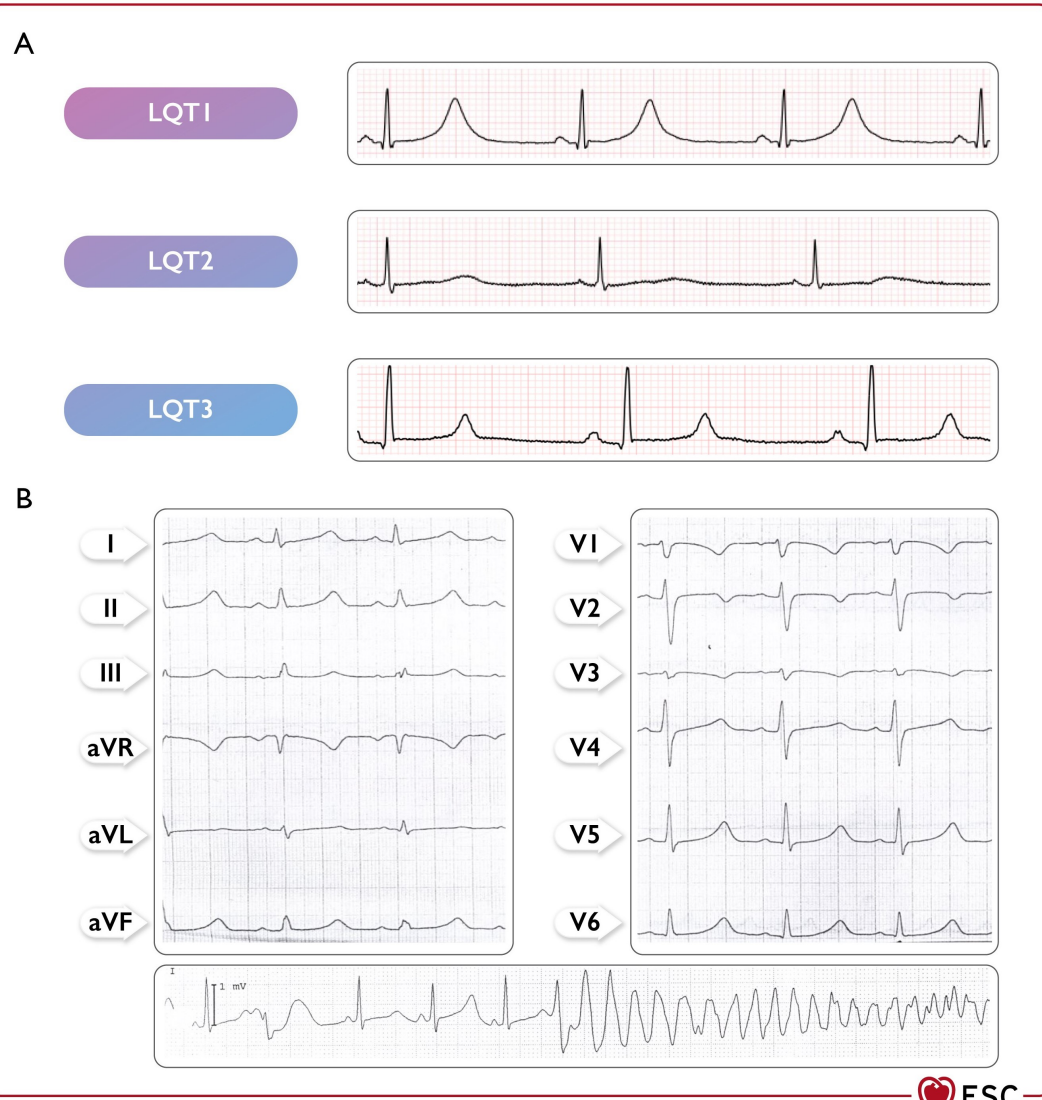
B Ventricular myocyte action potential



Genotype–phenotype relationship for the three most important subtypes

	Type 1	Type 2	Type 3
Gene	<i>KCNQ1</i>	<i>KCNH2</i>	<i>SCN5a</i>
Protein	K _v 7.1 	K _v 11.1 	Na _v 1.5 
Effect on current	I _{Ks} ↓ 	I _{Kr} ↓ 	I _{Na,L} ↑ 
Effect on action potential			
Frequency among LQTS	± 35% 	± 30% 	≤ 10% 
Penetrance	± 65% 	± 80% 	± 90% 
Typical resting ECG (V_s)			
QT change with exercise	Failure to shorten	Normal	Supranormal
Main trigger of events	Exercise (swimming) 	Arousal 	Rest 
Age of onset arrhythmias	Childhood 	Puberty 	Puberty 
Gender most at risk	♂ 	♀ 	♀ 
Onset of arrhythmias	 <i>Not pause-dependent</i>	 <i>Pause-dependent</i>	At lower heart rates
Therapy	Beta-blockers (+++) Left stellotomy	Beta-blockers (++) Left stellotomy Potassium supplementation	Beta-blockers (++) Sodium channel blocker Pacemaker

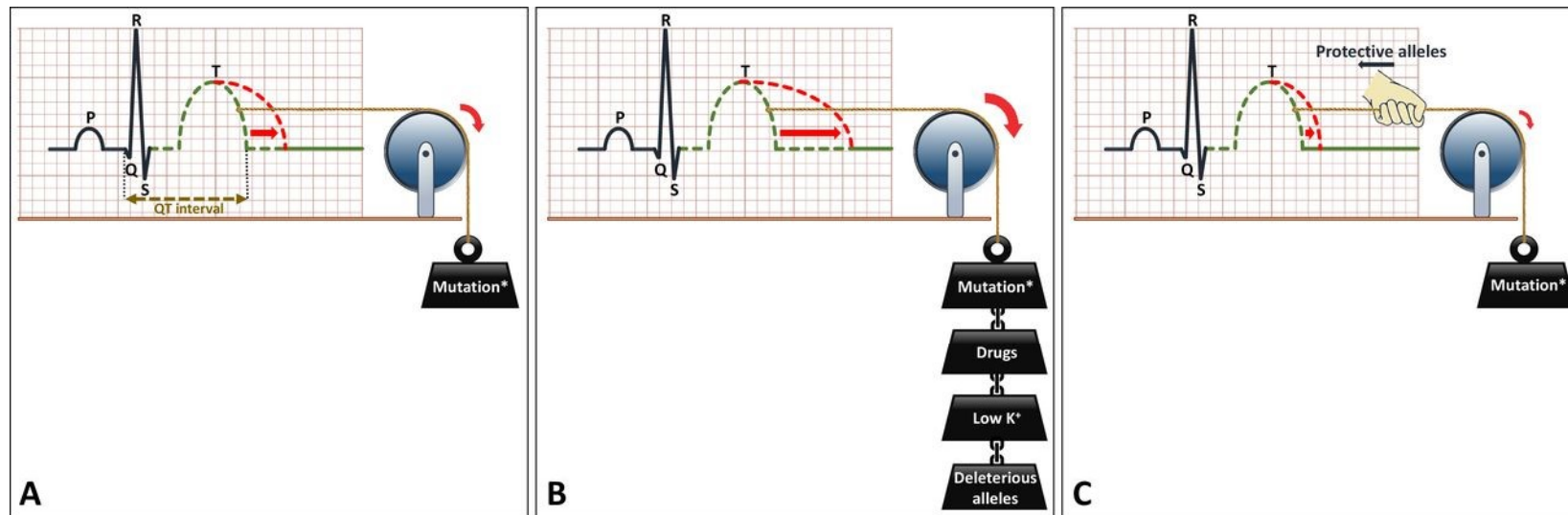
Gene-specific Long QT syndrome electrocardiograms and torsade-de-pointes



(A) ECG characteristics in the three major LQTS phenotypes.

(B) Example of Torsade-de-pointes in a male patient with a *SCN5A* (c.1238C>A, p.A413E) mutation.

Schematic representation of the effects of genetic and environmental factors in LQTS



- (A) LQTS-associated mutation causes prolongation of the QT interval on the ECG.
(B) Environmental factors such as certain drugs (which decrease repolarisation reserve) or hypokalaemia, or genetic factors (ie, deleterious alleles) act in a conjoint manner with the LQTS-associated mutation to further prolong the QT interval.
(C) Protective alleles counteract the effects of the mutation and may reduce the QT prolongation.

International Consensus Standards for ECG Interpretation in Athletes

Abnormal ECG findings are unrelated to regular training or expected physiologic adaptation to exercise, may suggest the presence of pathologic cardiovascular disease, and require further diagnostic investigation

Prolonged QT interval

- $QTc \geq 470$ ms (male)
- $QTc \geq 480$ ms (female)
- $QTc \geq 500$ ms (marked QT prolongation)

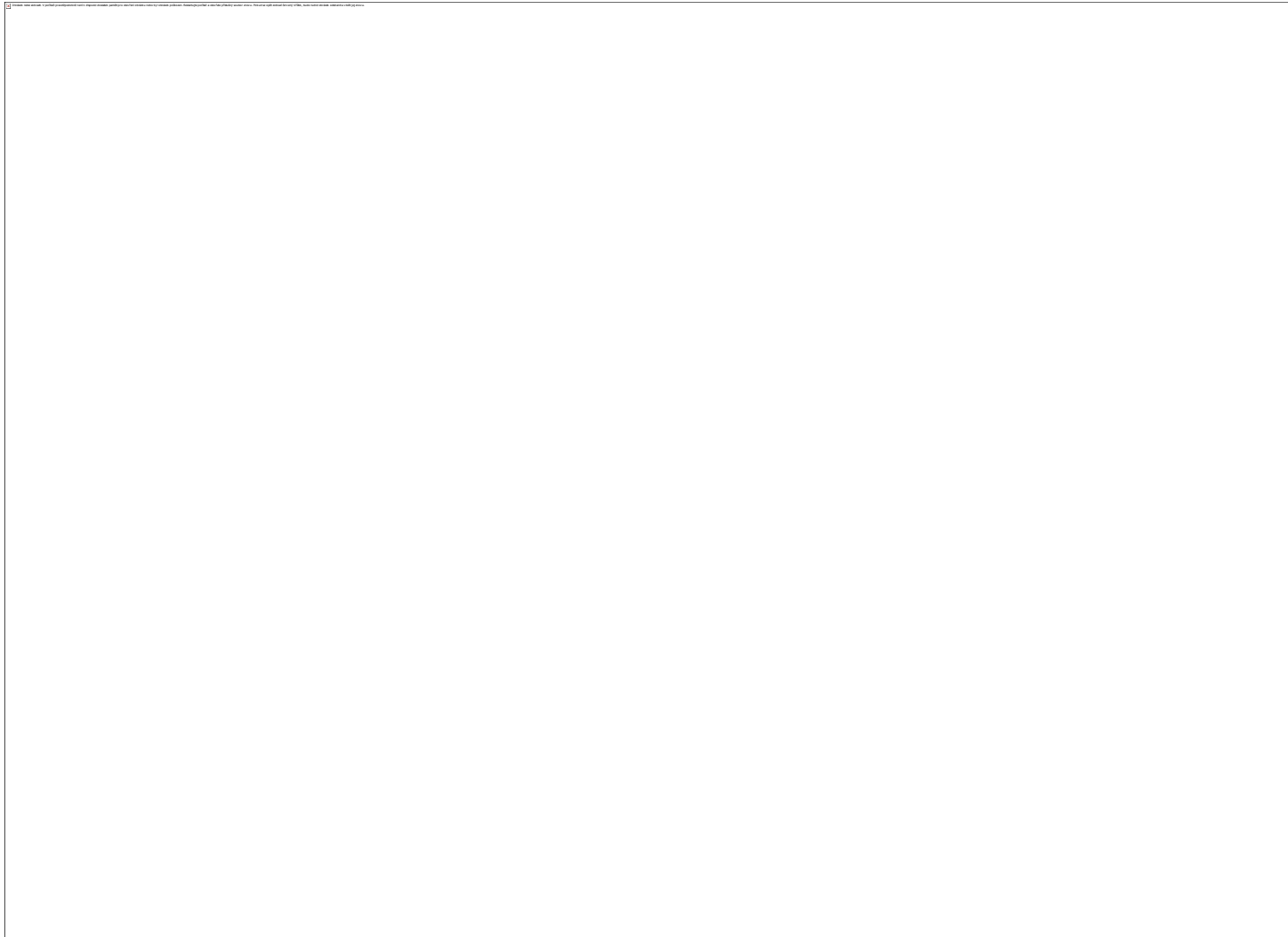
Management Options

- *Avoid electrolyte issues, such as hypokalaemia*

Management Options

- *Avoid electrolyte issues, such as hypokalaemia*
- Advice about participation in sports, although guidelines now less restrictive

Vigorous Exercise (>6 METS for >60hr / year) Study



N=1,413

Management Options

- *Advice about participation in sports*
- Avoidance of certain medications
- <https://crediblemeds.org/login>



Management Options

- *Advice about participation in sports*
- *Avoidance of certain medications*

- Medication
 - beta-blockers (ideally, nadolol / propranolol)
 - Mexiletine (LQT3 and some evidence for LQT2)
- Devices
 - Pacemaker
 - ICD
- Left cardiac sympathetic denervation

5-year risk models

Mazzanti

vs

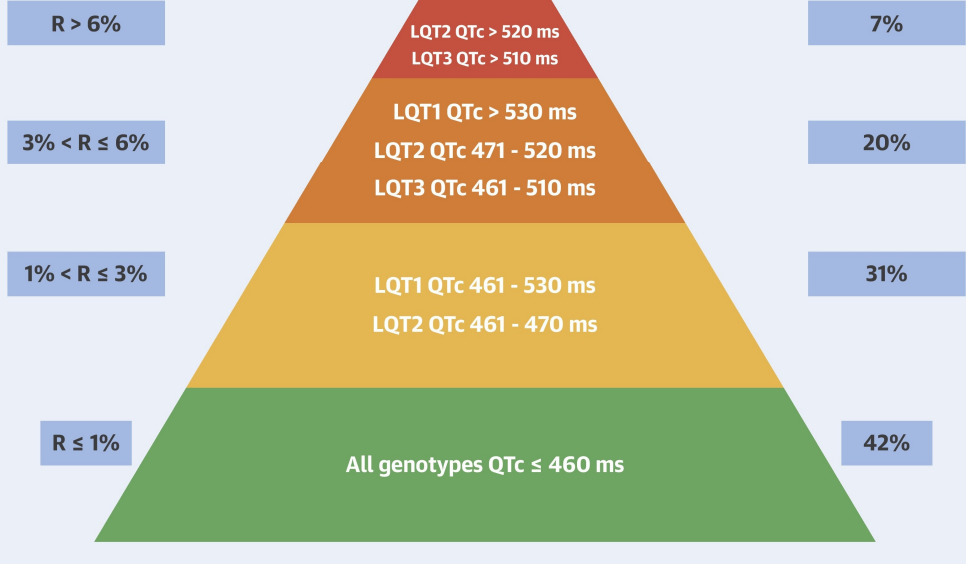
Rochester

CENTRAL ILLUSTRATION: 5-Year Risk of LAEs by Genotype and QTc Interval Before Therapy and Effect of BBs

Nadolol: HR 0.38; Other BB: HR 0.76

5-year risk of LAE off therapy (R)

Percentage (%) of patients



Mazzanti, A. et al. J Am Coll Cardiol. 2018;71(15):1663-71.

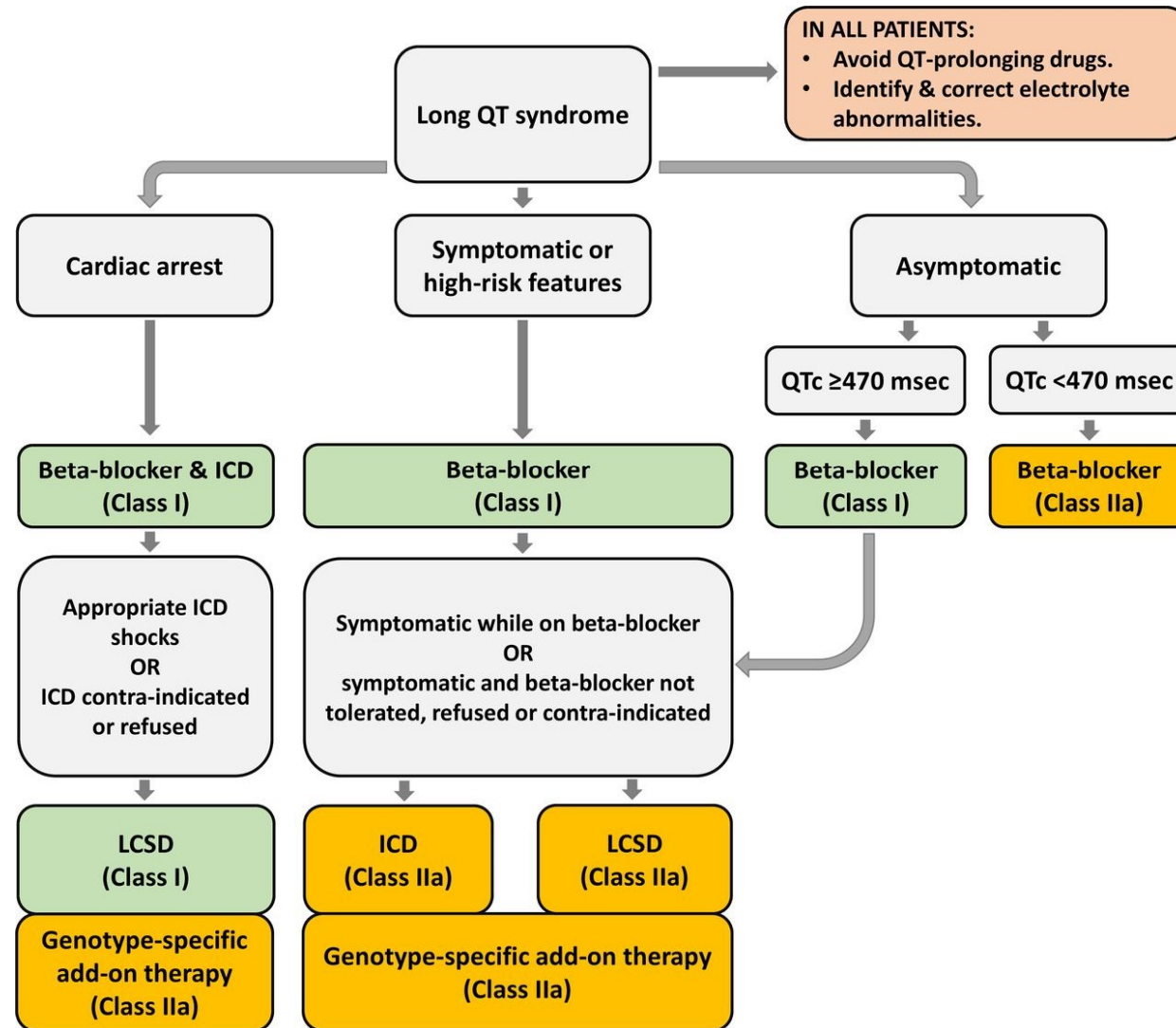


LAE – life-threatening arrhythmic events; n=1,710

	Women						Age	Men						
	On BB			Off BB				On BB			Off BB			
LQT1	440	0.1	0.2	0.5	0.1	0.3	0.9	≤8 years	0.5	1.1	3.1	1.0	2.3	6.3
	470	0.1	0.2	0.5	0.2	0.4	1.0		0.5	1.2	3.3	1.1	2.5	6.7
	500	0.1	0.2	0.5	0.2	0.4	1.1		0.5	1.3	3.5	1.1	2.7	7.2
	550	0.1	0.2	0.6	0.2	0.4	1.2		0.6	1.5	3.9	1.3	3.0	8.0
LQT1	440	0.5	1.1	3.0	1.0	2.3	6.1	13 - < 20 years	0.3	0.6	1.7	0.5	1.3	3.5
	470	0.5	1.2	3.2	1.0	2.4	6.6		0.3	0.7	1.8	0.6	1.4	3.7
	500	0.5	1.3	3.4	1.1	2.6	7.0		0.3	0.7	1.9	0.6	1.5	4.0
	550	0.6	1.4	3.9	1.2	2.9	7.9		0.3	0.8	2.2	0.7	1.7	4.5
LQT1	440	0.2	0.5	1.4	0.4	1.0	2.8	≥20 years	0.1	0.3	0.8	0.2	0.6	1.6
	470	0.2	0.5	1.5	0.5	1.1	3.0		0.1	0.3	0.8	0.3	0.6	1.7
	500	0.2	0.6	1.6	0.5	1.2	3.2		0.1	0.3	0.9	0.3	0.7	1.8
	550	0.3	0.6	1.8	0.6	1.3	3.6		0.2	0.4	1.0	0.3	0.7	2.0
LQT2	440	0.1	0.2	0.7	0.2	0.5	1.4	≤8 years	0.7	1.6	4.4	1.4	3.3	8.9
	470	0.1	0.3	0.7	0.2	0.5	1.5		0.7	1.7	4.7	1.5	3.6	9.5
	500	0.1	0.3	0.8	0.2	0.6	1.6		0.8	1.9	5.0	1.6	3.8	10.1
	550	0.1	0.3	0.8	0.3	0.6	1.7		0.9	2.1	5.6	1.8	4.3	11.3
LQT2	440	0.7	1.6	4.3	1.4	3.3	8.7	13 - < 20 years	0.4	0.9	2.4	0.8	1.8	5.0
	470	0.7	1.7	4.6	1.5	3.5	9.3		0.4	0.9	2.6	0.8	2.0	5.3
	500	0.8	1.8	4.9	1.6	3.7	9.9		0.4	1.0	2.8	0.9	2.1	5.7
	550	0.9	2.0	5.5	1.8	4.2	11.1		0.5	1.1	3.1	1.0	2.4	6.4
LQT2	440	0.3	0.7	1.9	0.6	1.5	4.0	≥20 years	0.2	0.4	1.1	0.3	0.8	2.3
	470	0.3	0.8	2.1	0.7	1.6	4.3		0.2	0.4	1.2	0.4	0.9	2.4
	500	0.3	0.8	2.2	0.7	1.7	4.6		0.2	0.5	1.3	0.4	1.0	2.6
	550	0.4	0.9	2.5	0.8	1.9	5.1		0.2	0.5	1.4	0.5	1.1	2.9
LQT3	440	0.3	0.6	1.7	0.5	1.3	3.5	≤8 years	1.8	4.2	11.0	3.6	8.4	21.5
	470	0.3	0.7	1.8	0.6	1.4	3.7		1.9	4.5	11.7	3.9	9.0	22.9
	500	0.3	0.7	1.9	0.6	1.5	4.0		2.0	4.8	12.5	4.2	9.7	24.3
	550	0.3	0.8	2.2	0.7	1.7	4.5		2.3	5.3	14.0	4.7	10.8	26.9
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	470	1.9	4.4	11.5	3.8	8.9	22.5		1.0	2.5	6.6	2.2	5.1	13.3
	500	2.0	4.7	12.3	4.1	9.5	23.9		1.1	2.6	7.1	2.3	5.4	14.2
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	470	0.8	2.0	5.3	1.7	4.1	10.8		0.5	1.1	3.0	1.0	2.3	6.2
	500	0.9	2.1	5.7	1.9	4.4	11.5		0.5	1.2	3.2	1.0	2.5	6.6
	550	1.0	2.4	6.4	2.1	4.9	12.9		0.6	1.3	3.6	1.2	2.8	7.4

Predicted 5-year risk of life-threatening arrhythmic events (ACA, SCD, or appropriate shocks) for patients with a single mutation in LQT1, LQT2, or LQT3. Blue colour indicates a predicted 5-year risk of <4%, yellow colour 4% to < 6%, and red colour ≥ 6%. Numbers in this figure are percentage. Wang et al. Front CV Med 2022

Schematic flow chart for the therapeutic choices in LQTS



Wilde AA et al. Heart 2022;108:332-338

Long QT Syndrome: importance of reassessing arrhythmic risk after treatment initiation

Key Question

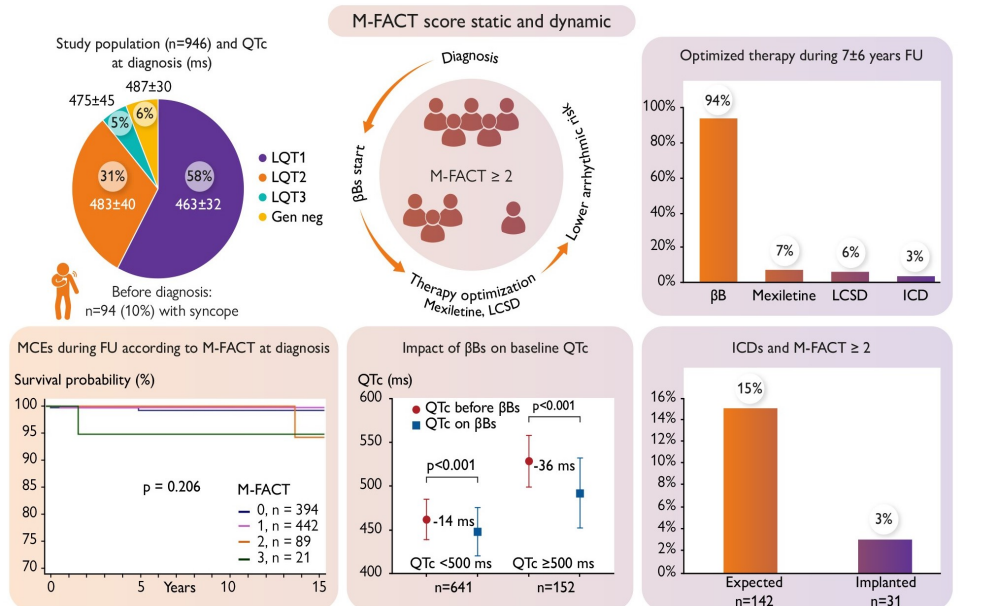
Does an M-FACT score ≥ 2 in long QT syndrome (LQTS), previously proposed as a cut-off for the implant of the implantable cardioverter defibrillator (ICD), effectively identify high-risk patients? Can therapy modify parameters critical for risk assessment, thus reducing the predicted arrhythmic risk? Does dynamic risk reassessment outperform a single assessment at first visit?

Key Finding

In 946 patients with LQTS, none died during 7 \pm 6 year follow-up. Beta-blockers, often accompanied by mexiletine and left cardiac sympathetic denervation, shortened QTc, a parameter pivotal for risk stratification, thus voiding its predictive value. Dynamic risk assessment with timely therapeutic optimization significantly decreased the number of ICDs which would have been implanted based on baseline M-FACT score without enhancing risk of life-threatening events.

Take Home Message

In LQTS patients a single risk prediction made at diagnosis, prior to therapeutic optimization, is likely to overestimate risk and to result in unnecessary ICD implantations, with a negative impact on quality of life.



M-FACT Risk Score for evaluating risk of appropriate ICD therapy

	- 1 Point	0 Points	1 Point	2 Points
Event free on therapy for >10 y	Yes	—	—	—
QTc (ms)	—	≤500	>501–≤550	≥551
Prior SCA	—	No	Yes	—
Events on therapy	—	No	Yes	—
Age at implantation (y)	—	>20	≤20	—

Adapted from Schwartz PJ, Spazzolini C, Priori SG, et al. Who are the long-QT syndrome patients who receive an implantable cardioverter-defibrillator and what happens to them?: data from the European Long-QT Syndrome Implantable Cardioverter-Defibrillator (LQTS ICD) Registry. Circulation 2010;122:1278; with permission.

M (minus 1 point), F (500, 550 ms), A (age), C (cardiac arrest), T (events on therapy)

N=946, no history of aborted cardiac arrest before diagnosis or cardiac events below age 1 yr

M-FACT score ≥ 2

LQT 1,2,3 and genotype-negative patients included

Inherited Cardiac Diseases Clinic

- Multi-disciplinary
 - Cardiologists (adult and paediatric), specialist nurses, geneticists
 - Liaison with forensic staff, genetics counsellors, psychologists
- Detailed personal and family history
- Previous cardiac investigations
- Protocols for investigation
- Genetic testing, where appropriate, which may facilitate cascade screening
- Provision of information (verbal and written)

Novel Insights

KCNQ1 suppression-replacement gene therapy in transgenic rabbits with type 1 long QT syndrome

Key Question

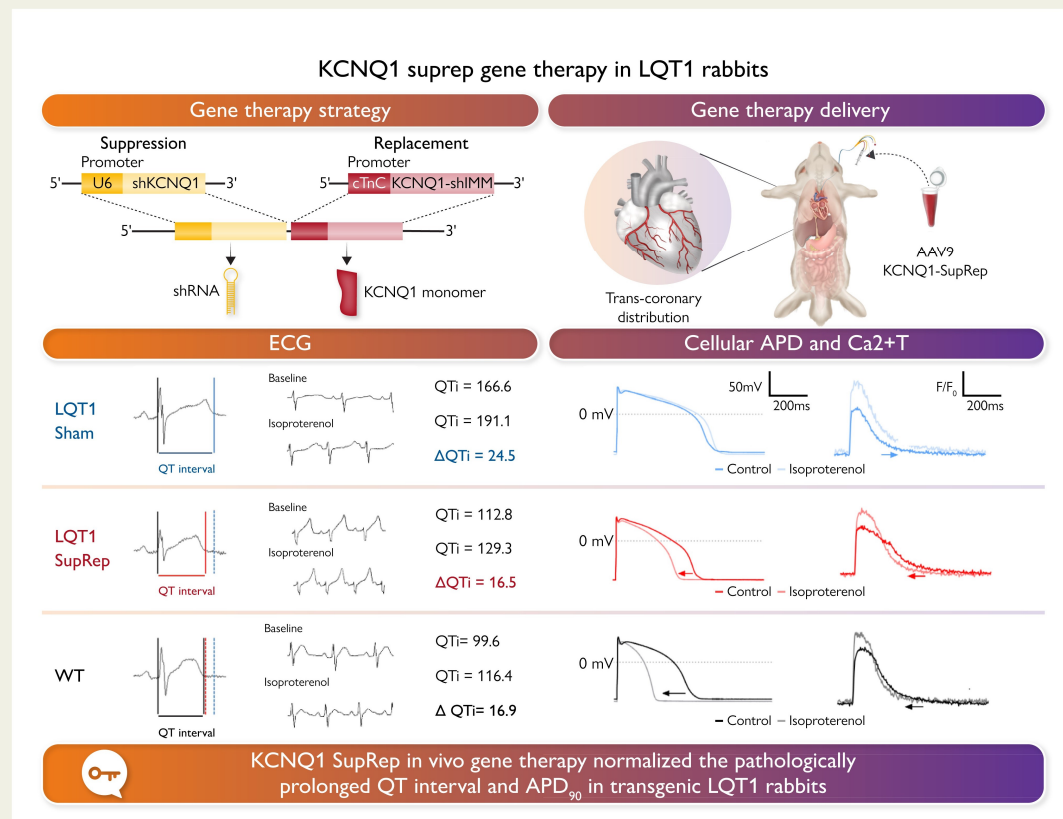
Can AAV9-mediated KCNQ1 suppression-replacement (SupRep) gene therapy restore physiological KCNQ1 function and rescue the diseased phenotype in transgenic LQT1 rabbits?

Key Finding

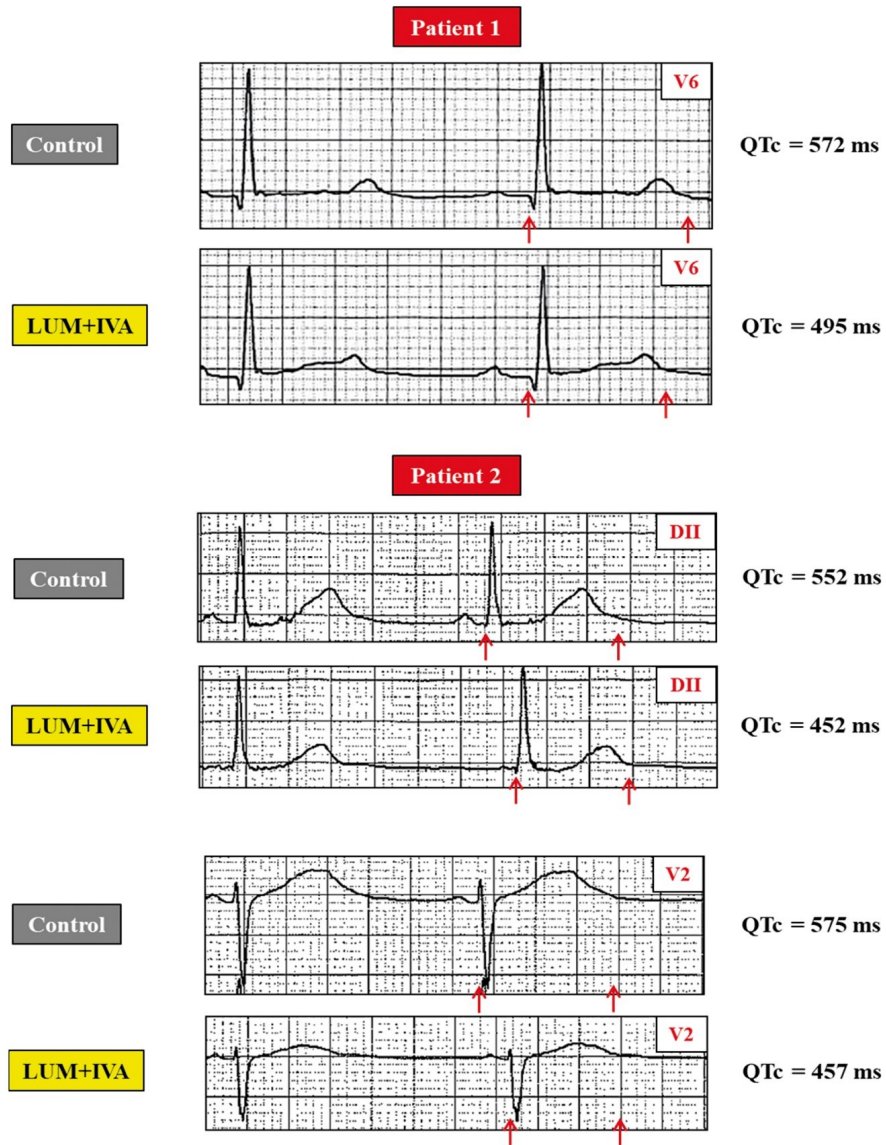
Treatment of LQT1 rabbits with AAV9-KCNQ1-SupRep gene therapy, delivered via targeted intra-aortic root injections, resulted in significant shortening of the pathologically prolonged QT_i and cellular APD₉₀ towards those observed in wild type (WT) rabbits. SupRep treated LQT1 rabbits demonstrated a physiological behavior under β-adrenergic stimulation.

Take Home Message

In vivo KCNQ1-SupRep gene therapy rescues the physiological QT_i and APD₉₀ to those observed in WT rabbits both at baseline and after provocation with isoproterenol. This translational study might impact future LQT1 treatment.



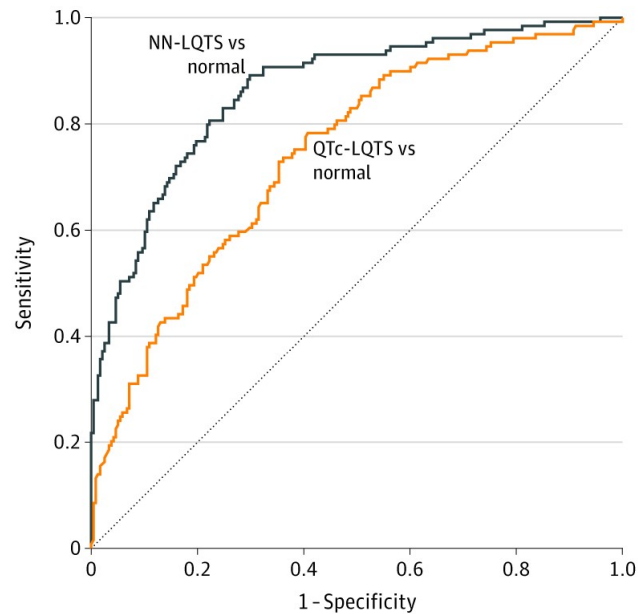
From patient-specific induced pluripotent stem cells to clinical translation - lumacaftor



Schwartz P et al. Eur Heart J 2019;40:1832-1836

From: Use of Artificial Intelligence and Deep Neural Networks in Evaluation of Patients With Electrocardiographically Concealed Long QT Syndrome From the Surface 12-Lead Electrocardiogram

JAMA Cardiol. 2021;6(5):532-538. doi:10.1001/jamacardio.2020.7422



QTc-LQTS vs normal

	Estimated negative	Estimated positive
Real negative	154	84
Real positive	35	94

NN-LQTS vs normal

	Estimated negative	Estimated positive
Real negative	185	53
Real positive	25	104

Performance of Convolutional Neural Network (CNN) in Concealed Long QT Syndrome (LQTS) Detection Receiver operating characteristics curve and confusion matrix showing performance of the CNN to distinguish patients with concealed LQTS (corrected QT [QTc] ≤ 450 milliseconds) from those dismissed normal. NN indicates neural network.

Summary

- LQT affects ~1 in 2,000 of the population
- Multi-disciplinary team approach essential
- Accurate measurement of QTc interval and calculation of Schwartz score
- Genetics offer diagnostic and, on occasions, prognostic and therapeutic options; cascade screening available when genotype identified
- Risk stratification important – dynamic process
- Increasing patient expectations about personalised medicine. Shared decision making very important. Optimisation of therapeutic options of clear benefit.

