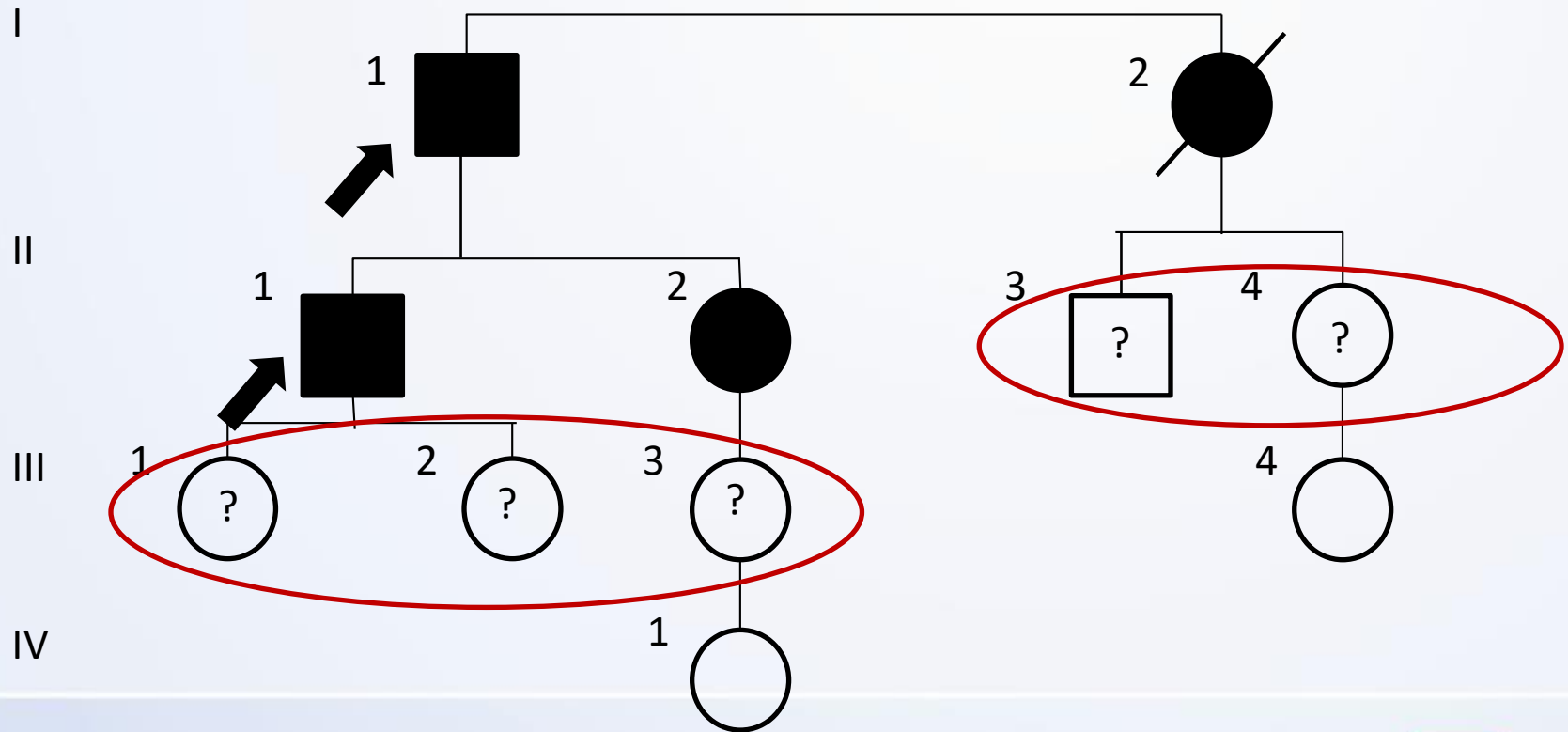


# **Dědičná progresivní AV blokáda s rozvojem dilatační kardiomyopatie**

**MUDr. A. Krebsová PhD.  
IKEM**



# Rodina: progresivní AV blokáda, rozvoj DCM, sVT



# NGS – sekvenování nové generace

## DNA Sequencing – Illumina TruSeq

### Target sequencig

- Panel kardiomyopatií
- Panel arytmiických syndromů aj.

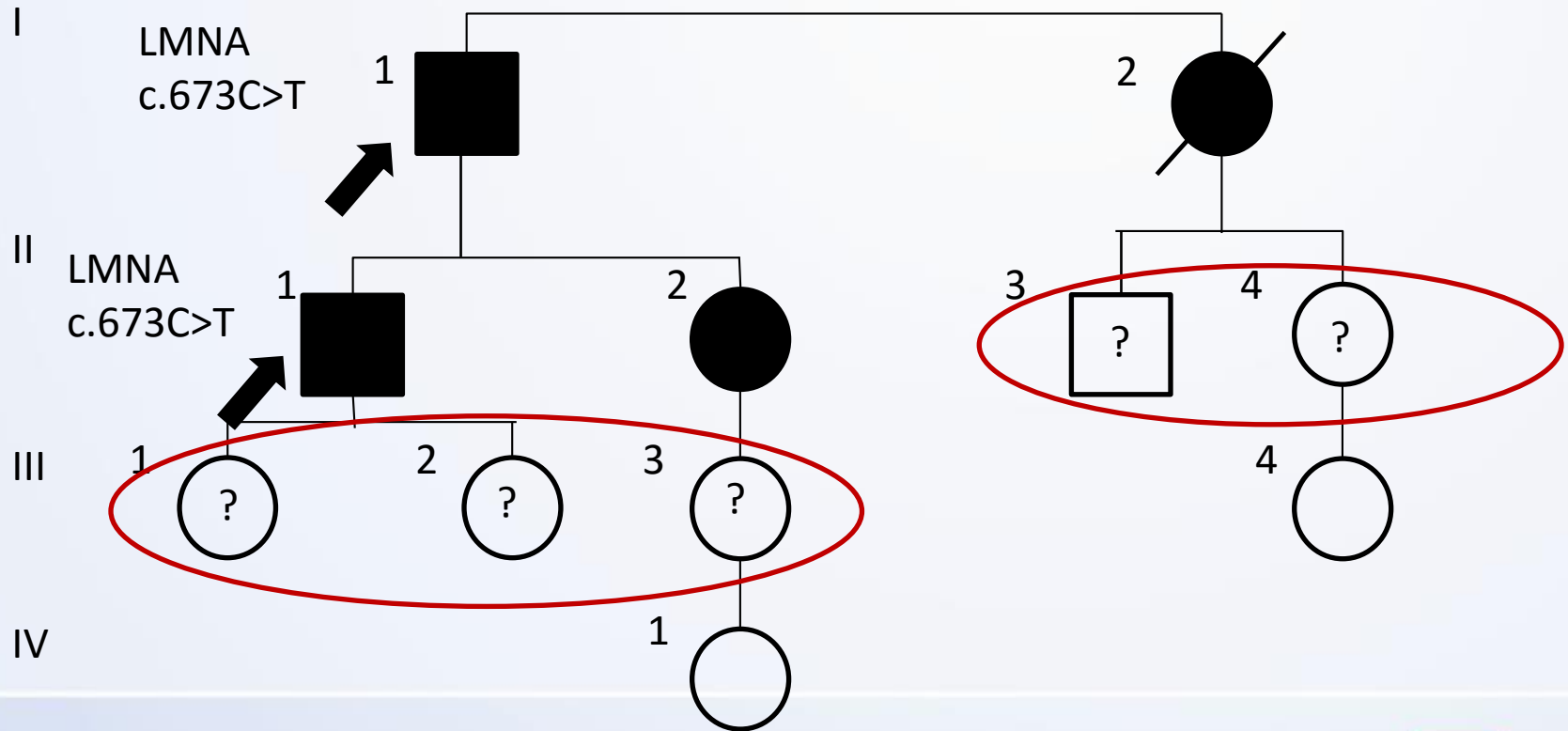
### Whole exome sequencig (WES)

- 4500 genů a přilehlých oblastí

### Whole genome sequencig (WGS)

- Kompletní geny, regulující sekvence

# Rodina: progresivní AV blokáda, rozvoj DCM, sVT



# Posouzení patogenicity mutace

NCBI dbSNP Short Genetic Variations

dbVar ClinVar GaP PubMed Nucleotide Protein

Search small variations in dbSNP or large structural variations in dbVar

Search Entrez dbSNP for  Go

Reference SNP (refSNP) Cluster Report: rs60682848 **\*\* With Pathogenic allele \*\***

RefSNP	Allele
Organism: human ( <a href="#">Homo sapiens</a> )	<b>Variation Class:</b> SNV: single nucleotide variation
Molecule Type: Genomic	<b>RefSNP Alleles:</b> C/T (FWD)
Created/Updated in build: 137/147	<b>Allele Origin:</b> C:germline T:germline
Map to Genome Build: <a href="#">107/Weight 1</a>	<b>Ancestral Allele:</b> C
<b>Validation Status:</b>	<b>Variation Viewer:</b> VarView
	<b>Clinical Significance:</b> With Pathogenic allele [ <a href="#">ClinVar</a> ]
	NA

Have a question about dbSNP? Try searching the SNP FAQ Archive!

Go

GENERAL

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Organism Data

dbSNP Homepage

NCBI Variation Resources

# Posouzení patogenicity mutace

## GeneView

GeneView via analysis of contig annotation: [LMNA](#) lamin A/C

View more variation on this gene (click to hide).

Clinical Source:  in gene region  cSNP  has frequency  double hit

### Primary Assembly Mapping

Assembly	SNP to Chr	Chr	Chr position
GRCh38.p2	Fwd	1	156134838

### RefSeqGene Mapping

RefSeqGene	Gene (ID)	SNP to R
<a href="#">NG_008692.2</a>	<a href="#">LMNA (4000)</a>	F

### Gene Model(s)

Function	mRNA			
	SNP to mRNA	Accession	Position	Allele change
STOP-GAIN	Fwd	<a href="#">NM_001257374.2</a>	<a href="#">424</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_001282624.1</a>	<a href="#">604</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_001282625.1</a>	<a href="#">1346</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_001282626.1</a>	<a href="#">922</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_005572.3</a>	<a href="#">922</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_170707.2</a>	<a href="#">922</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_170707.3</a>	<a href="#">922</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_170708.2</a>	<a href="#">922</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">NM_170708.3</a>	<a href="#">922</a>	CGA ⇒ TGA
STOP-GAIN	Fwd	<a href="#">XM_011509533.1</a>	<a href="#">419</a>	CGA ⇒ TGA
<b>cds-synon</b>	Fwd	<a href="#">XM_011509534.1</a>	<a href="#">317</a>	CCC ⇒ CCT
ncRNA	Fwd	<a href="#">XR_921781.1</a>	<a href="#">922</a>	NA ⇒ NA



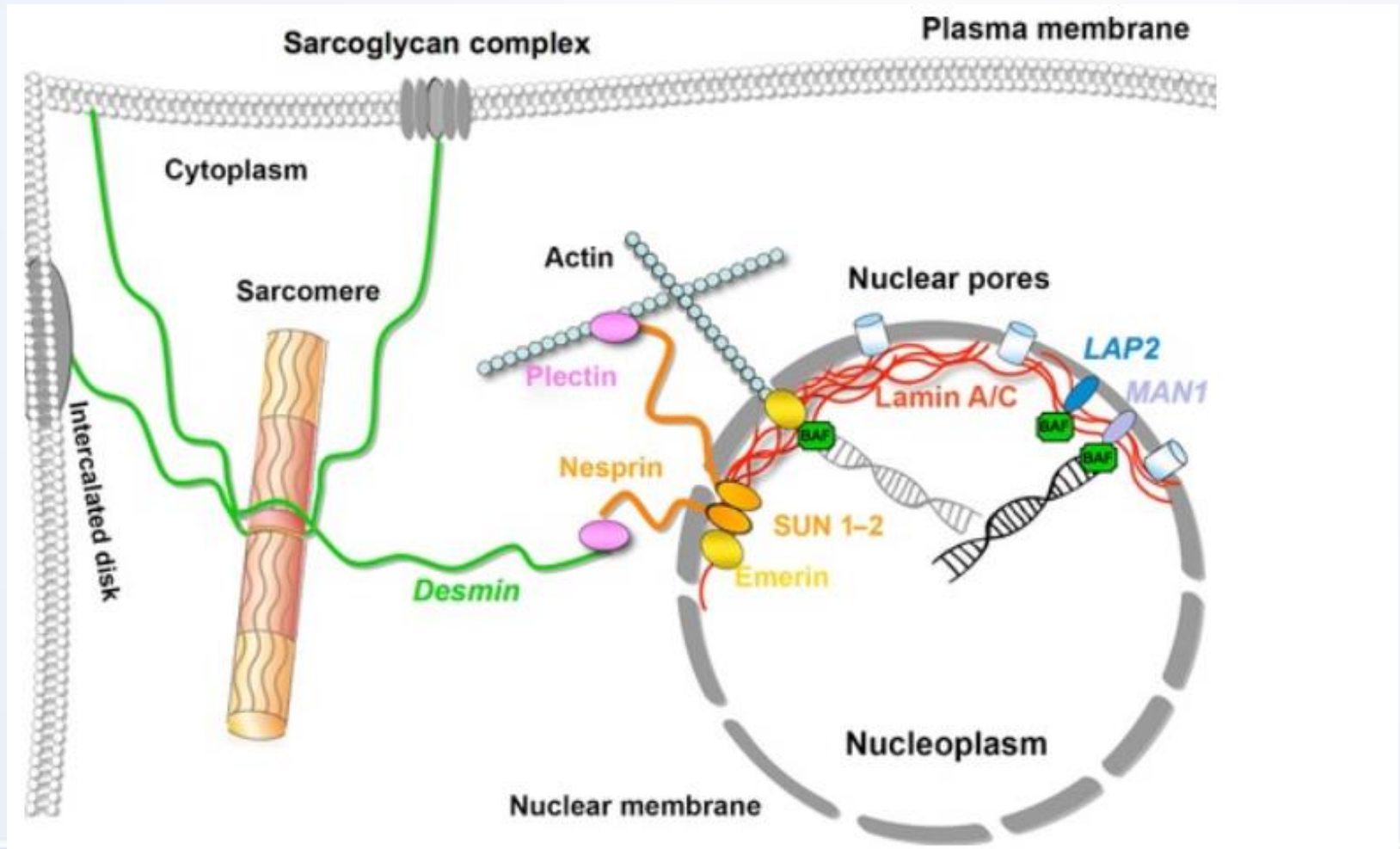
# The Genetic Code

How do 64 different codons produce 20 different amino acids?

		Second Letter					
		U	C	A	G		
1st letter	U	UUU   Phe UUC   UUA   Leu UUG	UCU   UCC   Ser UCA   UCG	UAU   Tyr UAC   UAA   Stop UAG   Stop	UGU   Cys UGC   UGA   Stop UGG   Trp	U C A G	
	C	CUU   CUC   Leu CUA   CUG	CCU   CCC   Pro CCA   CCG	CAU   His CAC   CAA   Gln CAG	CGU   CGC   Arg CGA   CGG	U C A G	
	A	AUU   AUC   Ile AUA   AUG   Met	ACU   ACC   Thr ACA   ACG	AAU   Asn AAC   AAA   Lys AAG	AGU   Ser AGC   AGA   Arg AGG	U C A G	
	G	GUU   GUC   Val GUA   GUG	GCU   GCC   Ala GCA   GCG	GAU   Asp GAC   GAA   Glu GAG	GGU   GGC   Gly GGA   GGG	U C A G	

- **The start codon is AUG.** Methionine is the only amino acid specified by just one codon, AUG.
- **The stop codons are UAA, UAG, and UGA.** They encode no amino acid. The ribosome pauses and falls off the mRNA. The stretch of codons between AUG and a stop codon is called an **open reading frame (ORF)**. Computer analysis of DNA sequence can predict the existence of genes based on ORFs.
- **Other amino acids** are specified by more than one codon--usually differing at **only the third position**.

# Lamin A/C

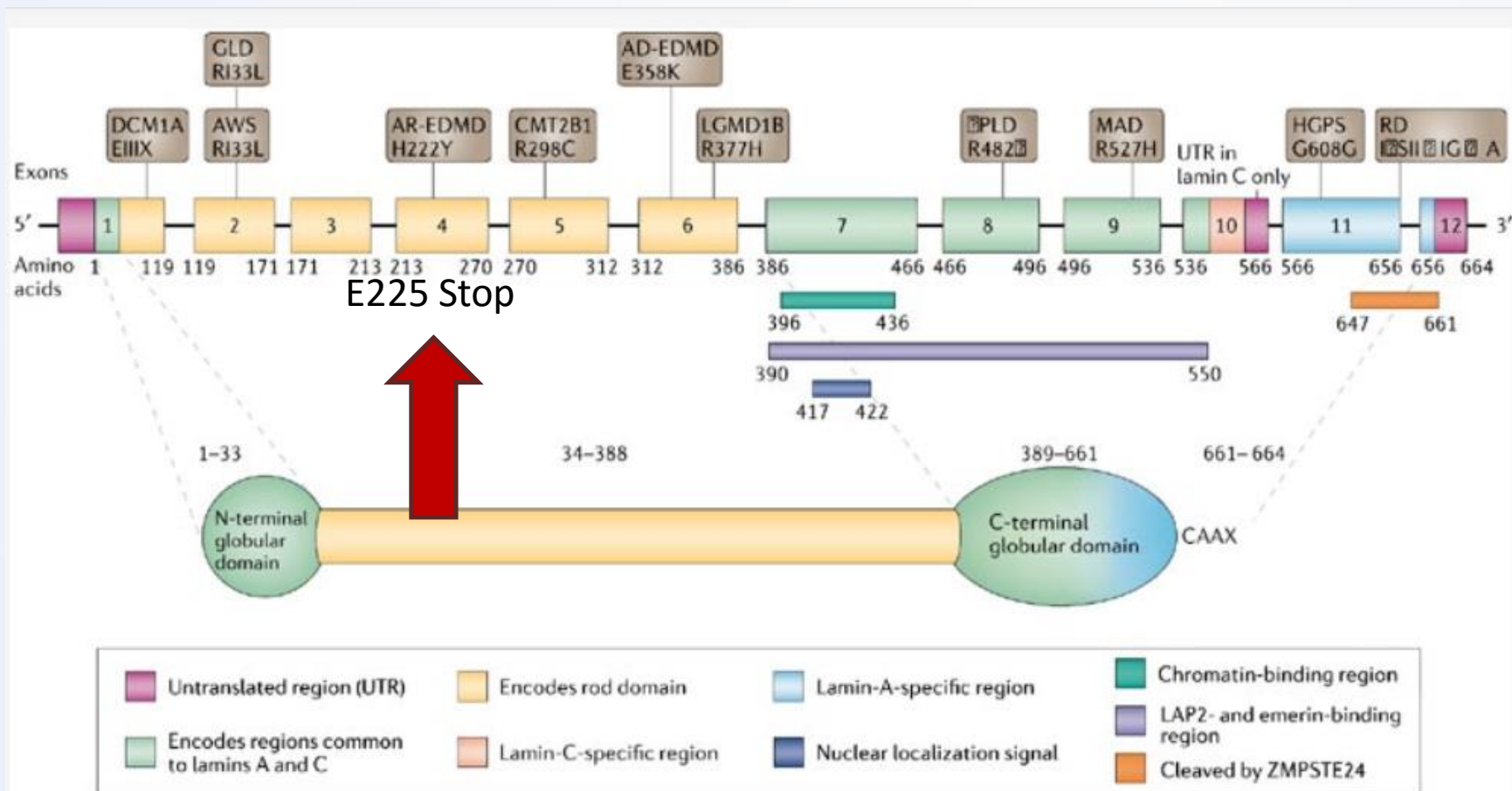




# **Jaká doplňující vyšetření by jste indikovali v případě podezření na laminopatii ?**

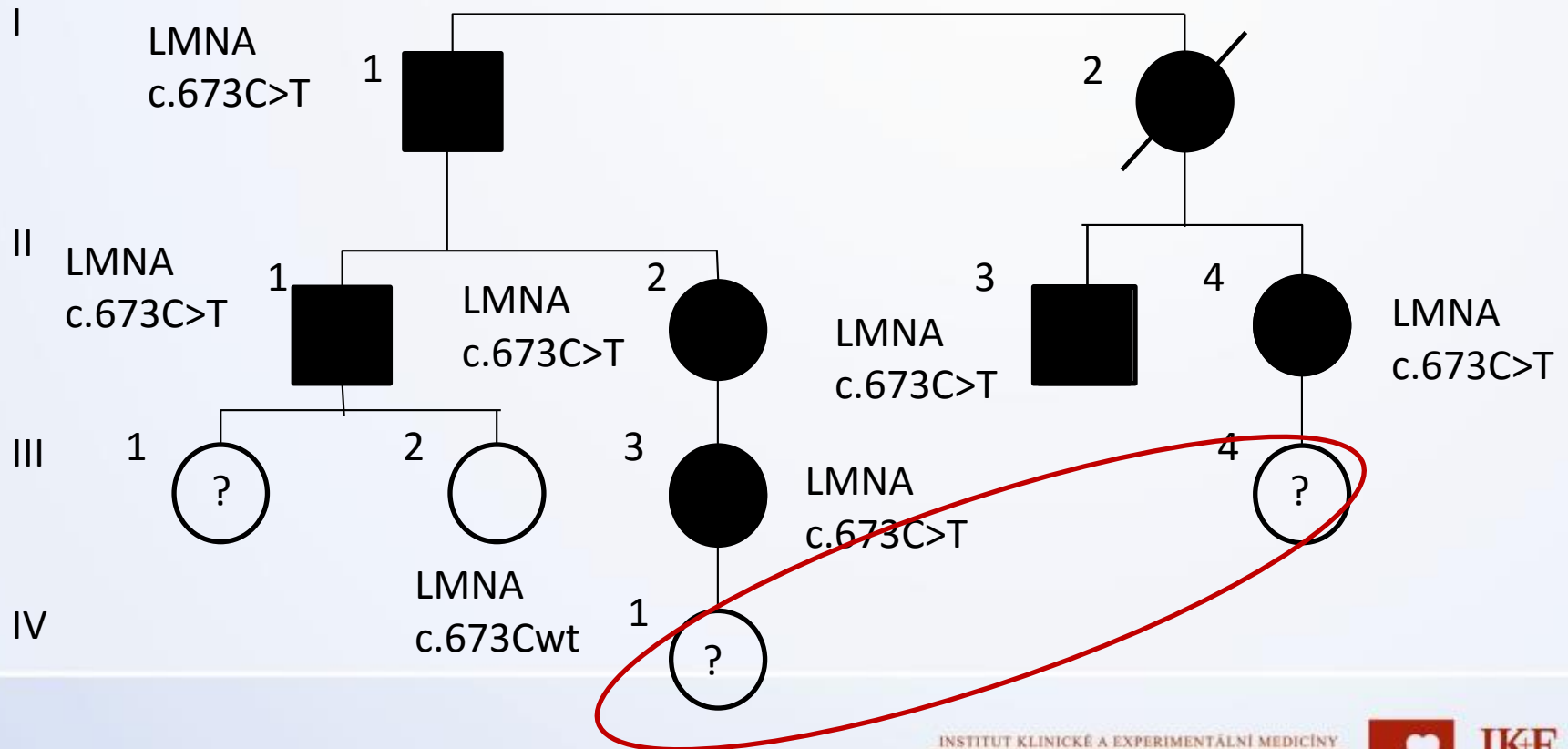
1. **Vyšetření MR s cílem nalézt specifický obraz časného/pozdního syčení myokardu**
2. **Scintigrafické vyšetření srdečního svalu (Tc 99 – DPD)?**
3. **Neurologické vyšetření?**
4. **Laboratorní vyšetření kreatinkinázy?**
5. **Laboratorní vyšetření Fe, ferritinu a transferinu?**
6. **Podrobné oční vyšetření oftalmogenetické ambulanci?**
7. **Podrobné kožní vyšetření (cutis laxa, striae, angiokeratomy aj.)?**
8. **Podrobné vyšetření ORL (hypakuse)?**

# Lamin A/C – DCM, EDMD, HGPS



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Nature Reviews | Genetics

# Rodina: segregace mutace LMNA/C – odhad rizika





## 2015 ESC Guidelines for the management of patients with ventricular arrhythmias and the prevention of sudden cardiac death

The Task Force for the Management of Patients with Ventricular Arrhythmias and the Prevention of Sudden Cardiac Death of the European Society of Cardiology (ESC)

re-entry ventricular tachycardia refractory to medical therapy.			346
An ICD should be considered in patients with DCM and a confirmed disease-causing <i>LMNA</i> mutation and clinical risk factors. <sup>d</sup>	IIa	B	
Amiodarone should be considered in			

ACE = angiotensin-converting enzyme; CAD = coronary artery disease; DCM = dilated cardiomyopathy; EPS = electrophysiological study; HF = heart failure; ICD = implantable cardioverter defibrillator; *LMNA* = lamin A/C; LVEF = left ventricular ejection fraction; MRA = mineralocorticoid receptor antagonists; NSVT = non-sustained ventricular tachycardia; NYHA = New York Heart Association; PVS = programmed ventricular stimulation; SCD = sudden cardiac death; VA = ventricular arrhythmia; VT = ventricular tachycardia.

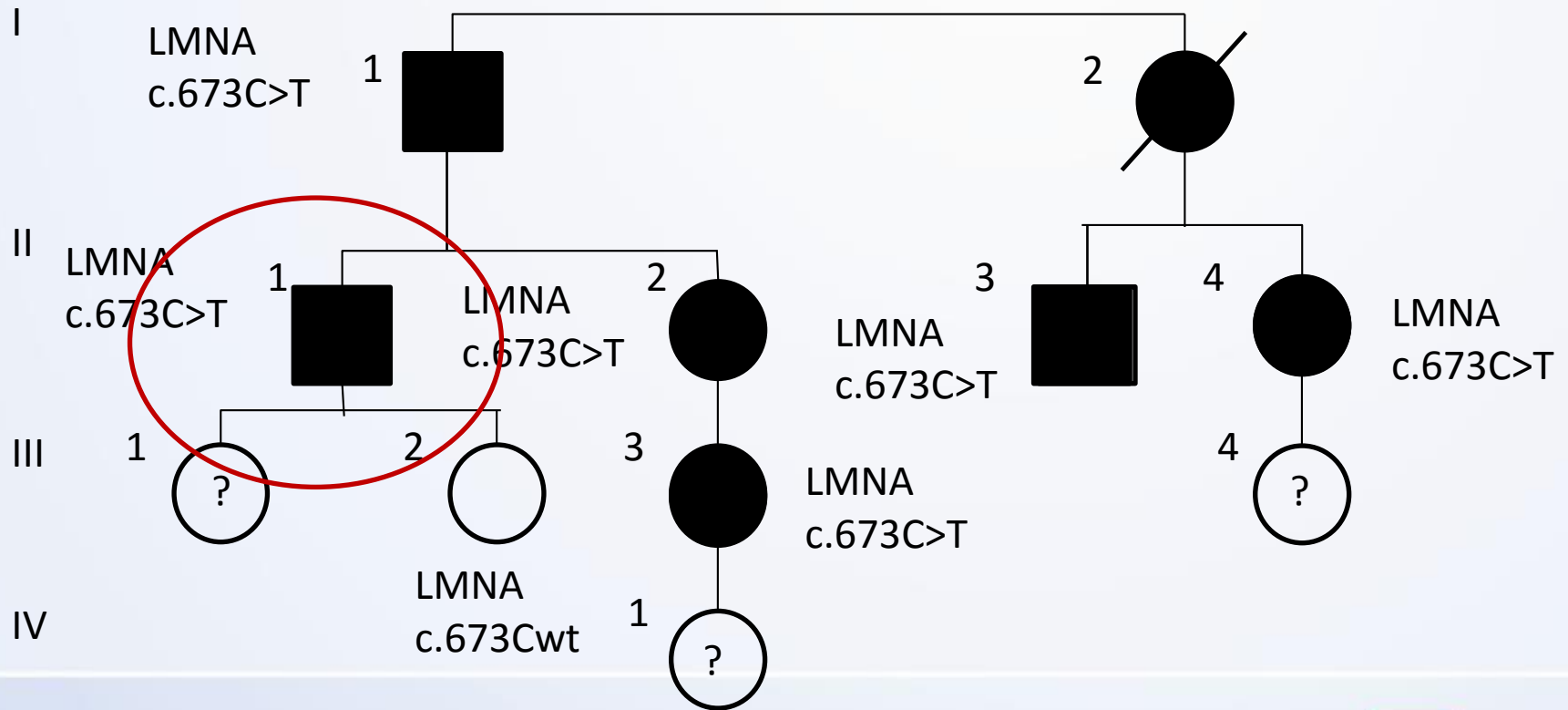
<sup>a</sup>Class of recommendation.

<sup>b</sup>Level of evidence.

<sup>c</sup>Reference(s) supporting recommendations.

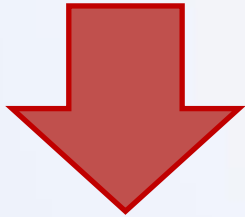
<sup>d</sup>Risk factors in patients with a confirmed *LMNA* mutation: NSVT during ambulatory electrocardiogram monitoring, LVEF <45% at first evaluation, male sex and non-missense mutations (insertion, deletion, truncations or mutations affecting splicing).

# Rodina: segregace mutace LMNA/C – odhad rizika

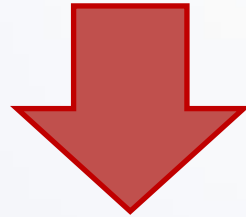


# Výstupy kardiogenetiky

*„genetická stratifikace onemocnění“*



•Hodnocení rizika u  
rodinných příslušníků



•Individualizovaná  
(presympt. terapie)



•Preimplantační  
diagnostika

# Grantové prostředky

- 00064203, CZ.2.16/3.1.00/24022,
- NF-CZ11-PDP-3-003-2014
- LD14073
- MZ 15-27682A

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Doc. M. Macek Sr.





**Děkuji za pozornost!**  
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