

Markéta Adamová on behalf of WG
of Cardiogenetics in Czech Genetic
Society (SLG-ČSL JEP)

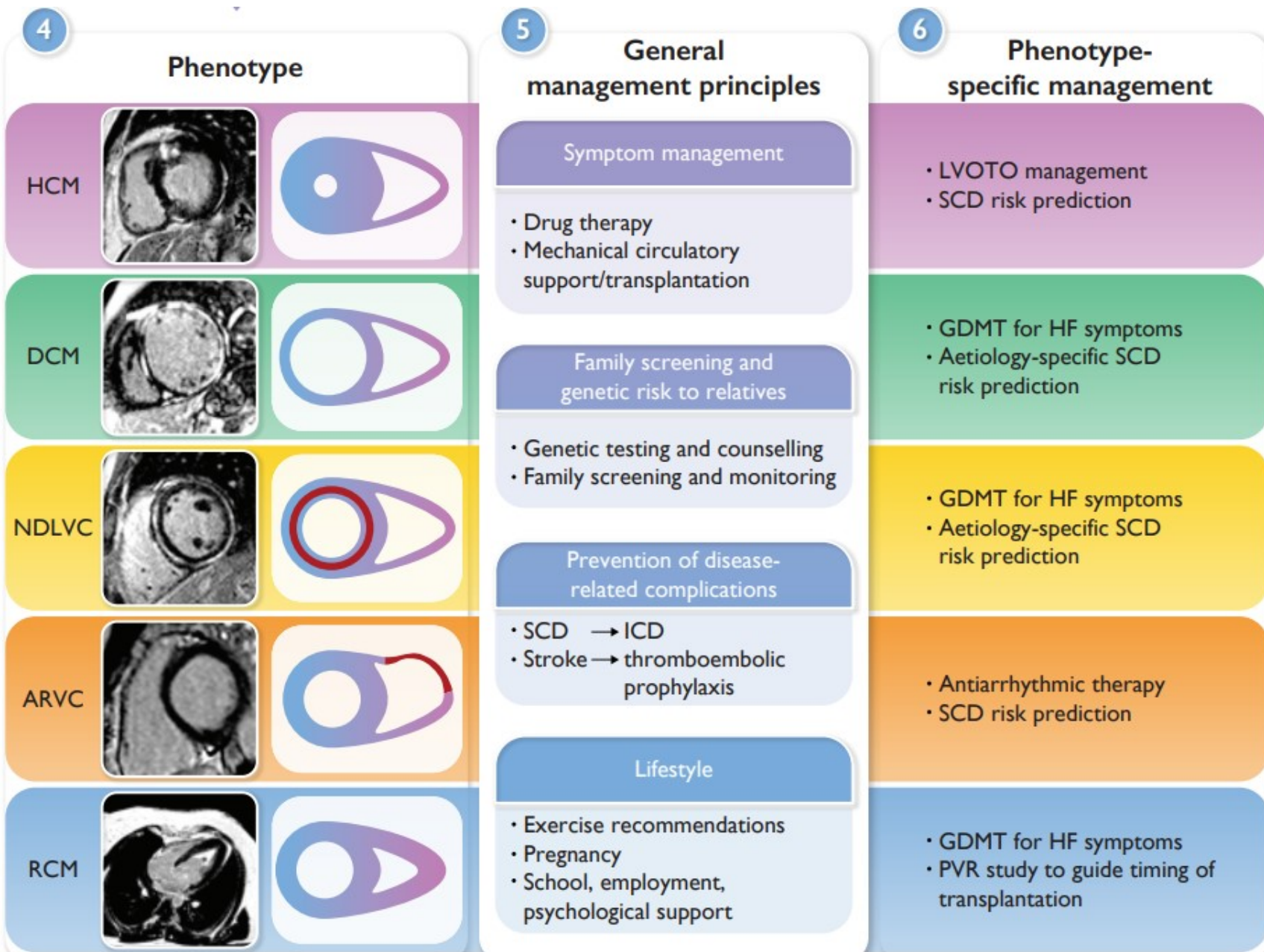


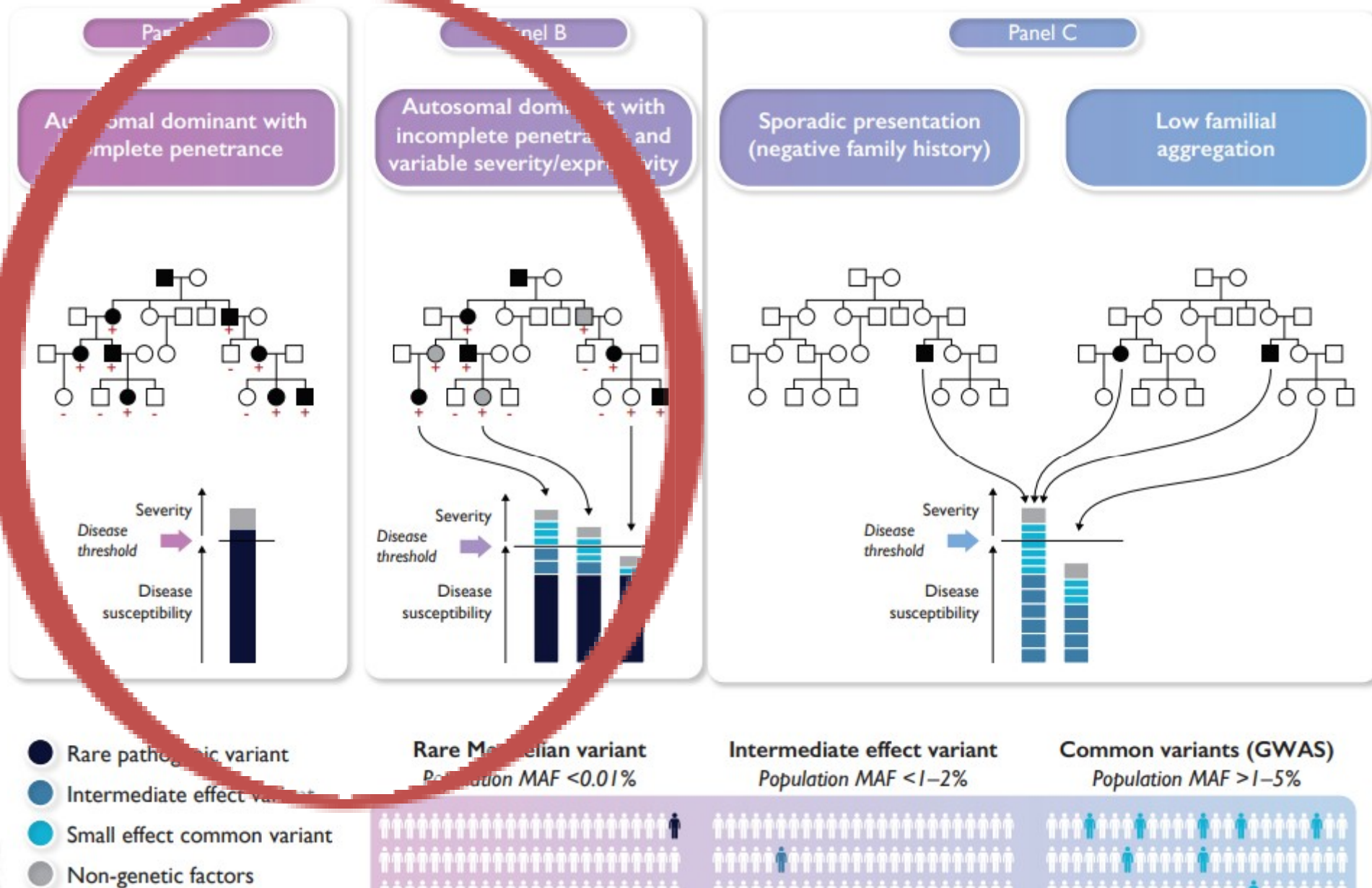
 **European
Reference
Network**
for rare or low prevalence
complex diseases

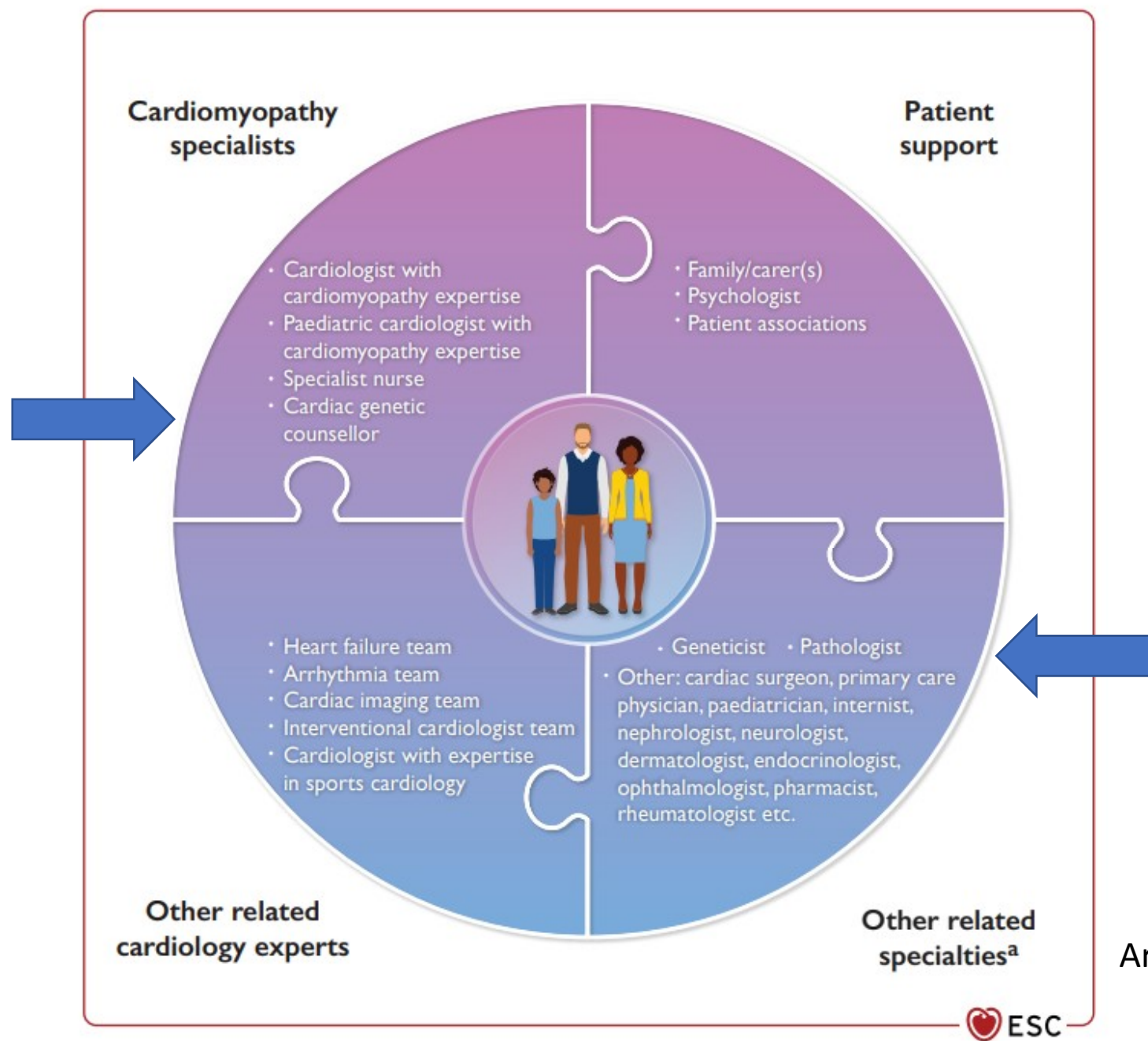
 **Network**
Heart Diseases
(ERN GUARD-HEART)

 **Member**
Institut klinické a experimentální
medicíny – Klinika kardiologie
Centrum vysoce specializované péče
o pacienty s dědičným kardiovaskulárním
onemocněním

GENETIC BASIS FOR CARDIOMYOPATHY IN A REPRESENTATIVE COHORT IN THE CZECH REPUBLIC



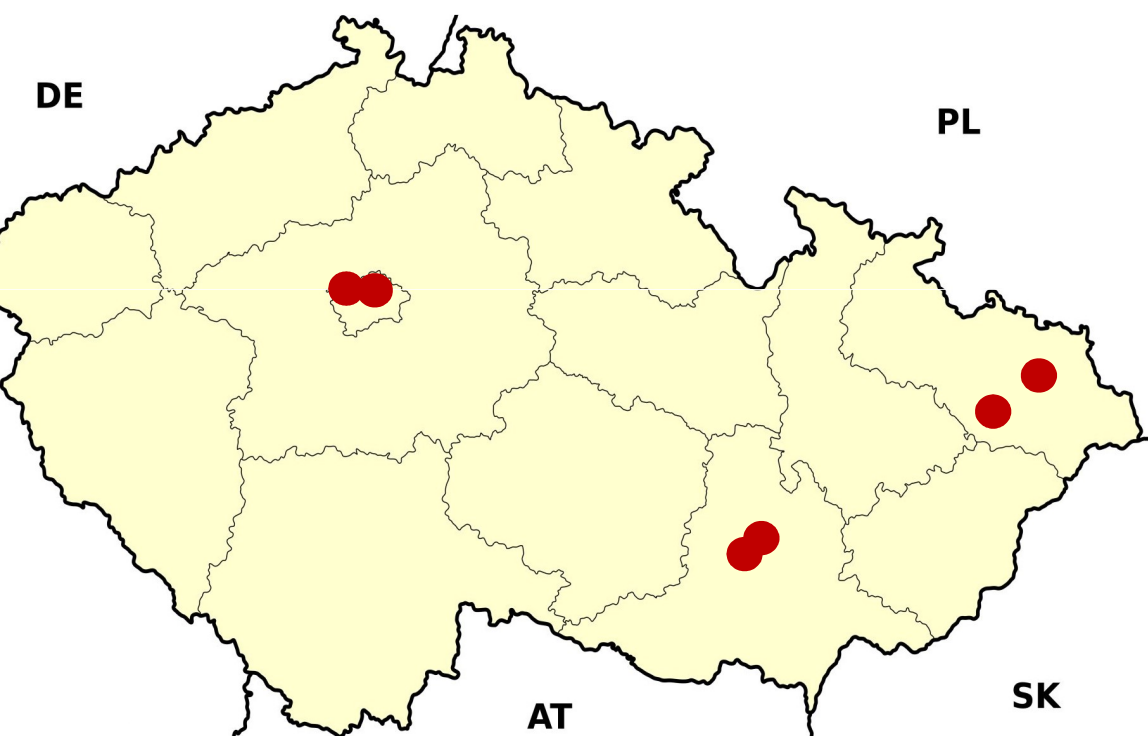




Arbelo et al. (2023)

Figure 5 Multidisciplinary care of cardiomyopathies. ^aThe list presented is not exhaustive and represents examples of specialties that often interact in the care of cardiomyopathy patients.

Working group of cardiogenetics within Czech Genetic Society (SLG-ČSL JEP)



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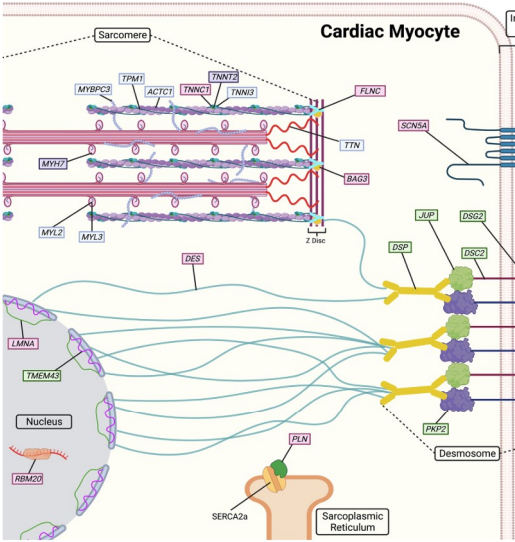
Agel – Nový Jičín
FN Brno
Cytogenetic Laboratory - Brno
FN Motol
FN Ostrava
VFN Prague



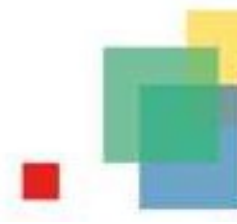
Genes with definite association with CMPs

(according to ESC and ESHG guidelines)

Condition	Genes
HCM	<i>ACTC1, MYBPC3, MYH7, TNNT2, MYL2, MYL3, TNNI3, TPM1</i>
HCM Phenocopy	<i>GLA, FHL1, FLNC, LAMP2, PLN, PTPN11, RAF1, RIT1, TTR</i>
DCM	<i>DES, TTN, TNNT2, RBM20, MYH7, LMNA, FLNC, DSP, BAG3, PLN, SCN5A, TNNC1, TNNT2, JPH2, ACTC1, ACTN2,NEXN, TNNI3, TPM1, VCL, DMD</i>
ARVC	<i>PKP2, DSG2, DSC2, DSP, JUP, TMEM43, PLN, DES, FLNC</i>
RCM	<i>TNNI3, TNNT2, DES</i>

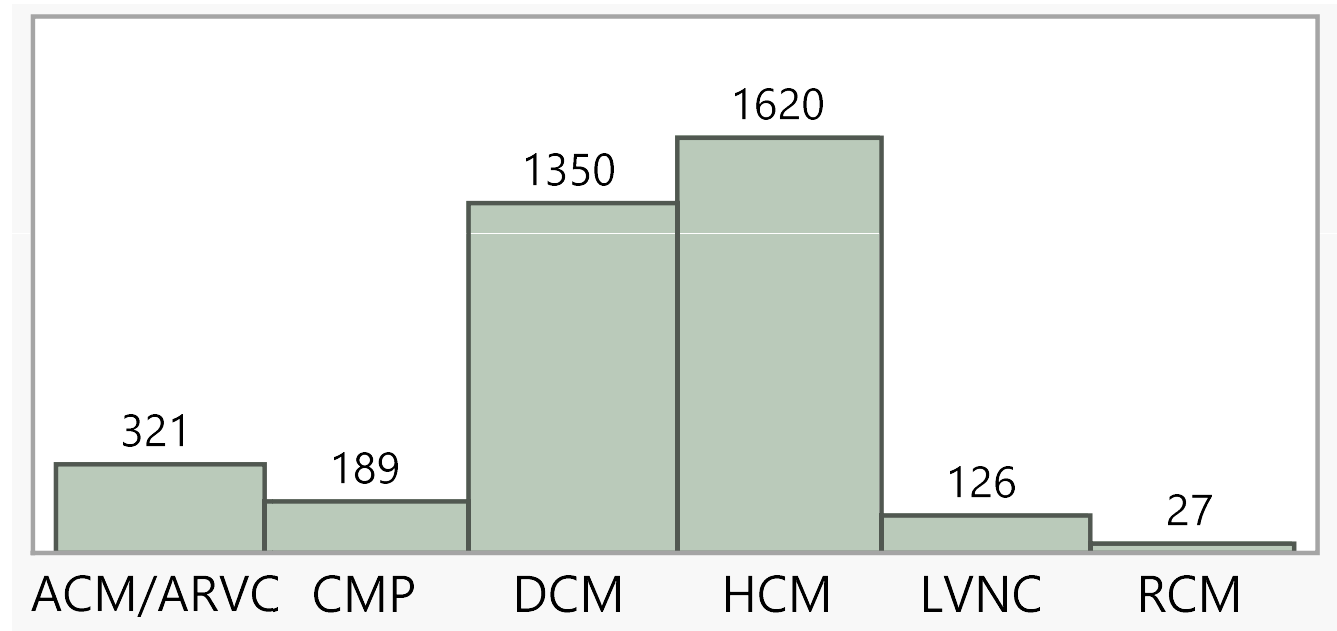


Hespe S. et al.



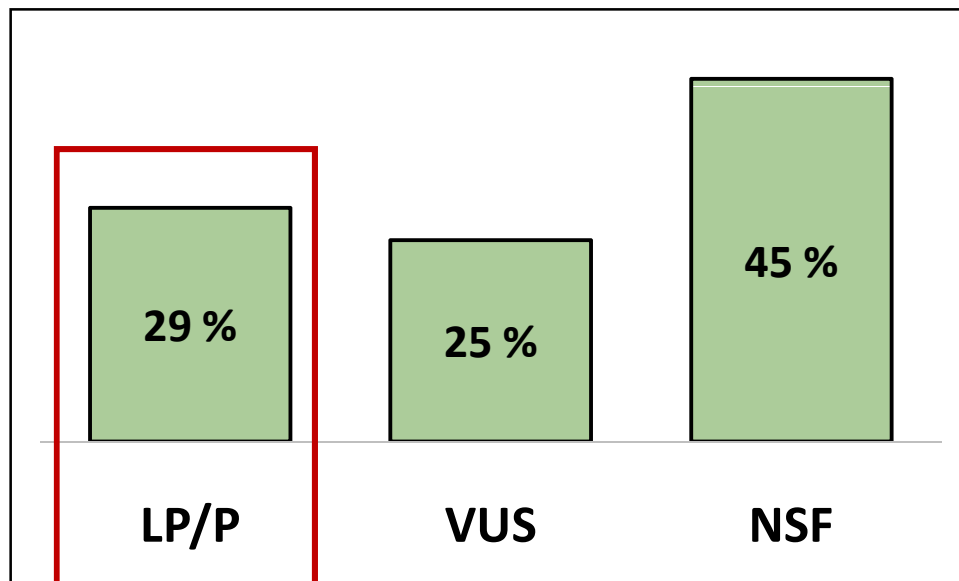
Czech patients in total 3633 with any CMPs

Probands	Count
Total	3633
Female	1202/3633 (33 %)
Male	2431/3633 (67 %)
Mean age	53 ± 17

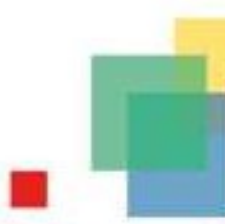


Genetic yield in all CMPs

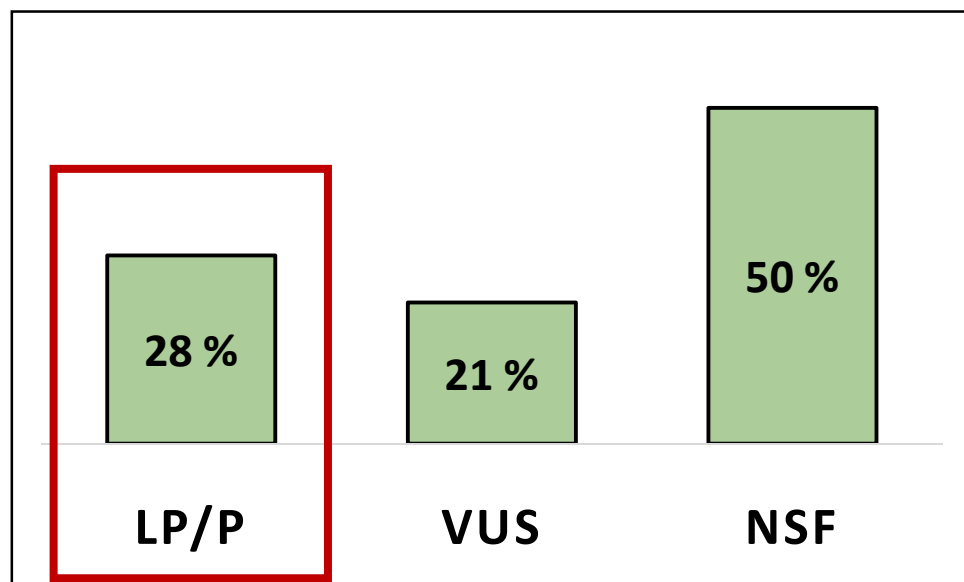
(3633 probands/patients)



Gene	Count	(%)
MYBPC3	262	24.8
TTN	248	23.5
MYH7	150	14.2
PKP2	56	5.3
LMNA	34	3.2
DSP	29	2.7
FLNC	29	2.7
TNNT2	28	2.6
TNNI3	26	2.4
RBM20	17	1.6
SCN5A	14	1.3
TPM1	14	1.3



Genetic yield in HCM (1620 probands)

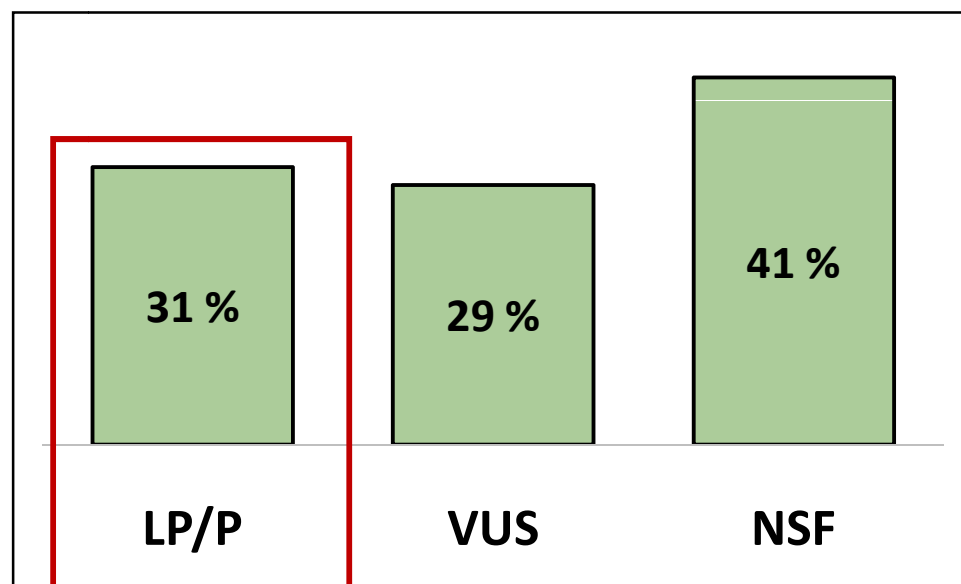


Gene	Count	(%)
MYBPC3	241	52.3
MYH7	112	24.3
TNNI3	16	3.4
TPM1	11	2.3
TNNT2	9	1.9
PTPN11	7	1.5
LAMP2	6	1.3
GLA	5	1.1
PRKAG2	5	1.1
TTN	5	1.1
MYL3	4	0.8
Total	461	



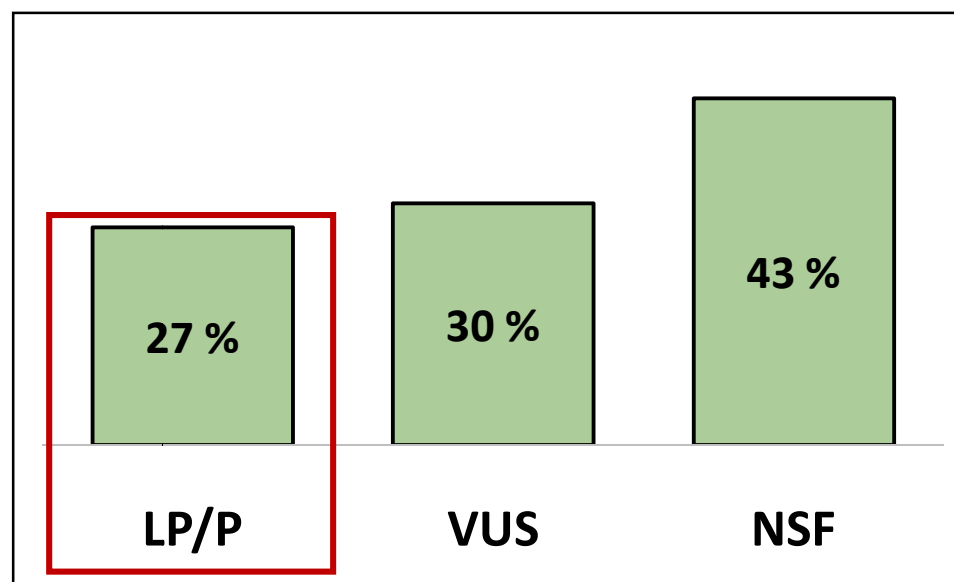
Genetic yield in DCM (1350 probands)

Gene	Count	(%)
<i>TTN</i>	214	51.9
<i>LMNA</i>	25	6.1
<i>FLNC</i>	19	4.6
<i>MYH7</i>	19	4.6
<i>DSP</i>	16	3.8
<i>TNNT2</i>	13	3.1
<i>RBM20</i>	12	2.9
<i>BAG3</i>	11	2.6
<i>MYBPC3</i>	11	2.6
<i>NEXN</i>	9	2.1
Total	412	



Genetic yield in ACM/ARVC (321 probands)

Gene	Count	(%)
<i>PKP2</i>	49	56.3
<i>DSP</i>	9	10.3
<i>FLNC</i>	4	4.5
<i>TTN</i>	4	4.5
<i>LMNA</i>	3	3.4
<i>SCN5A</i>	3	3.4
<i>DSC2</i>	2	2.3
<i>DSG2</i>	2	2.3
<i>MYBPC3</i>	2	2.3
<i>MYH7</i>	2	2.3
Total	87	

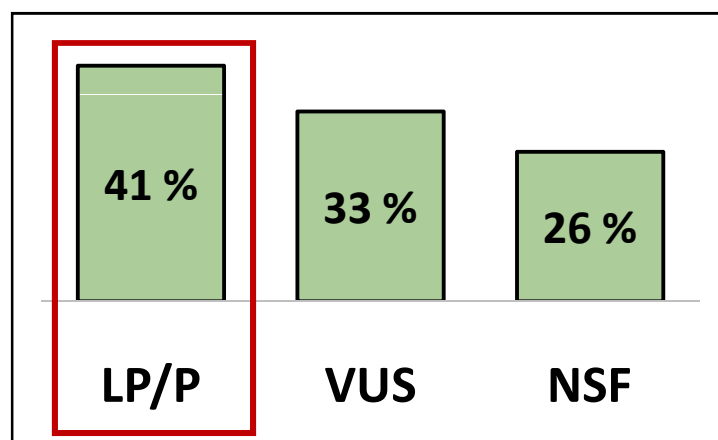


Genetic yield according to clinical diagnosis

RCM (27 probands), LVNC (126 probands)

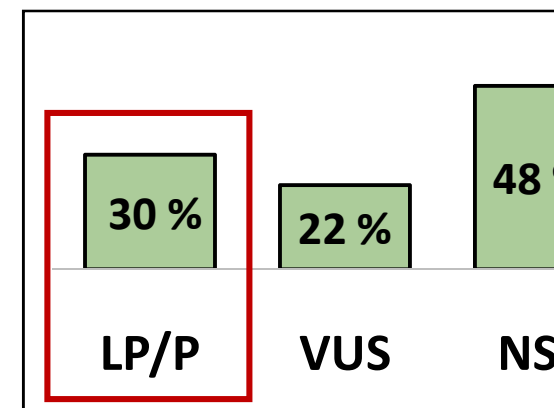
RCM

Gene	Count	(%)
<i>MYH7</i>	3	27.2
<i>TNNT2</i>	3	27.2
<i>FLNC</i>	1	9.1
<i>OBSCN</i>	1	9.1
<i>BPC3</i>	1	9.1
<i>ACTN1</i>	1	9.1
<i>ACTN2</i>	1	9.1
Total	11	



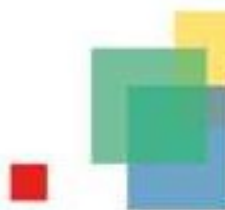
LVNC

Gene	Count	(%)
<i>MYH7</i>	13	34.2
<i>TTN</i>	10	26.3
<i>RBM20</i>	3	7.8
<i>OBSCN</i>	2	5.2
<i>RYR2</i>	2	5.2
<i>TNNT2</i>	2	5.2
<i>ACTC1</i>	1	2.6
<i>ACTN2</i>	1	2.6
<i>FLNC</i>	1	2.6
<i>GATA4</i>	1	2.6
Total	38	



MYBPC3: Frequent DNA variants in Czech population with regional distribution

Variant	Frequency
NM_000256.3(MYBPC3):c.3697C>T (p.Gln1233Ter)	80
NM_000256.3(MYBPC3):c.3697C>T (p.Gln1233Ter).....predominates in Moravian and Silesian regions	
NM_000256.3(MYBPC3):c.3190+5G>A	12
NM_000256.3(MYBPC3):c.977G>A (p.Arg326Gln)	11
NM_003476.5(CSRP3):c.208G>T (p.Gly70Trp)	11
NM_000256.3(MYBPC3):c.814C>T (p.Arg272Cys)	9
NM_000256.3(MYBPC3):c.1028delC (p.Thr343MetfsTer7)	9



Conclusions

- ❑ First Czech national, pseudoanonymized, representative cohort, studying the genetic architecture of heart failure (3633 patients).
- ❑ Interlaboratory cooperation is crucial for standardisation of variant analysis and the connection of family information among the molecular genetic laboratories.
- ❑ Genetic yield in CMPs is 29 %, most frequently mutated genes are *MYBPC3*, *TTN*, *MYH7* and *PKP2*.
- ❑ Genetic architecture reflects the special characteristic of our central European population, missing DNA variants in some genes (eg. *TMEM43*, *JUP*, *VCL*, *TNNC1*, *MYL3*).



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Thank you for your attention!



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