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Liège | Théâtre de Liège | Belgium

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70th ESCVS
International congress of the European Society
for Cardiovascular and Endovascular Surgery



7th IMAD meeting

Curating genes and variants for heritable thoracic aortic disease A dynamic process!

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Gene curation: rationale

More genes:

😊 Higher detection rate

😞 More VUSs



Gene curation: what?



qualitatively define gene-disease validity using a classification scheme based on the strength of evidence supporting the relationship



standardized semi-quantitative approach to evaluate available evidence and arrive at such a classification

Gene curation: how?

Figure 10: Clinical Validity Summary Matrix

GENE/DISEASE PAIR:				
Assertion criteria	Genetic Evidence (0-12 points)	Experimental Evidence (0-6 points)	Total Points (0-18)	Replication Over Time (Y/N)
Description	Case-level, family segregation, or case-control data that support the gene-disease association	Gene-level experimental evidence that support the gene-disease association	Sum of Genetic & Experimental Evidence	> 2 pubs w/ convincing evidence over time (>3 yrs.)
Assigned Points	A	B	C	D
CALCULATED CLASSIFICATION		LIMITED	0.1-6	
		MODERATE	7-11	
		STRONG	12-18	
		DEFINITIVE	12-18 & Replicated Over Time	
Valid contradictory evidence (Y/N)*	List PMIDs and describe evidence: E			
CURATOR CLASSIFICATION			F	
FINAL CLASSIFICATION			G	

Process

One-on-one teams

(ClinGen) Curator

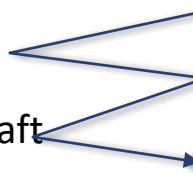
Clinical Domain Expert

(familiar with curation framework)



(familiar with disease and genes)

literature search
enter data and create draft
classification



Search terms
Select relevant publications
Advise as needed (e.g. experimental data)

Expert group review + approval



Definitive

Role has been repeatedly demonstrated in research & clinical diagnostic settings • Upheld over time (in general, at least 3 years) • No valid contradictory evidence

Strong

Excess of pathogenic variants in cases vs. controls OR • Multiple pathogenic variants in unrelated probands • Several different types of supporting experimental data • ≥ 2 independent studies • No valid contradictory evidence

Moderate

≥ 3 unrelated probands with pathogenic variants • Some supporting experimental data • No valid contradictory evidence

Limited

< 3 unrelated probands with pathogenic variants OR • Multiple variants reported in unrelated probands but *without* sufficient evidence for pathogenicity per 2014 ACMG criteria

No Evidence Reported

No evidence reported for a causal role in disease (candidate genes, etc.).

Disputed

Valid evidence *refuting* a role for this gene in this disease is equivalent to or stronger than existing evidence *supporting* this role.

Evidence Against

Evidence refuting the role of the gene in the specified disease has been reported and significantly outweighs any evidence supporting the role.

How might one use “clinical validity”?

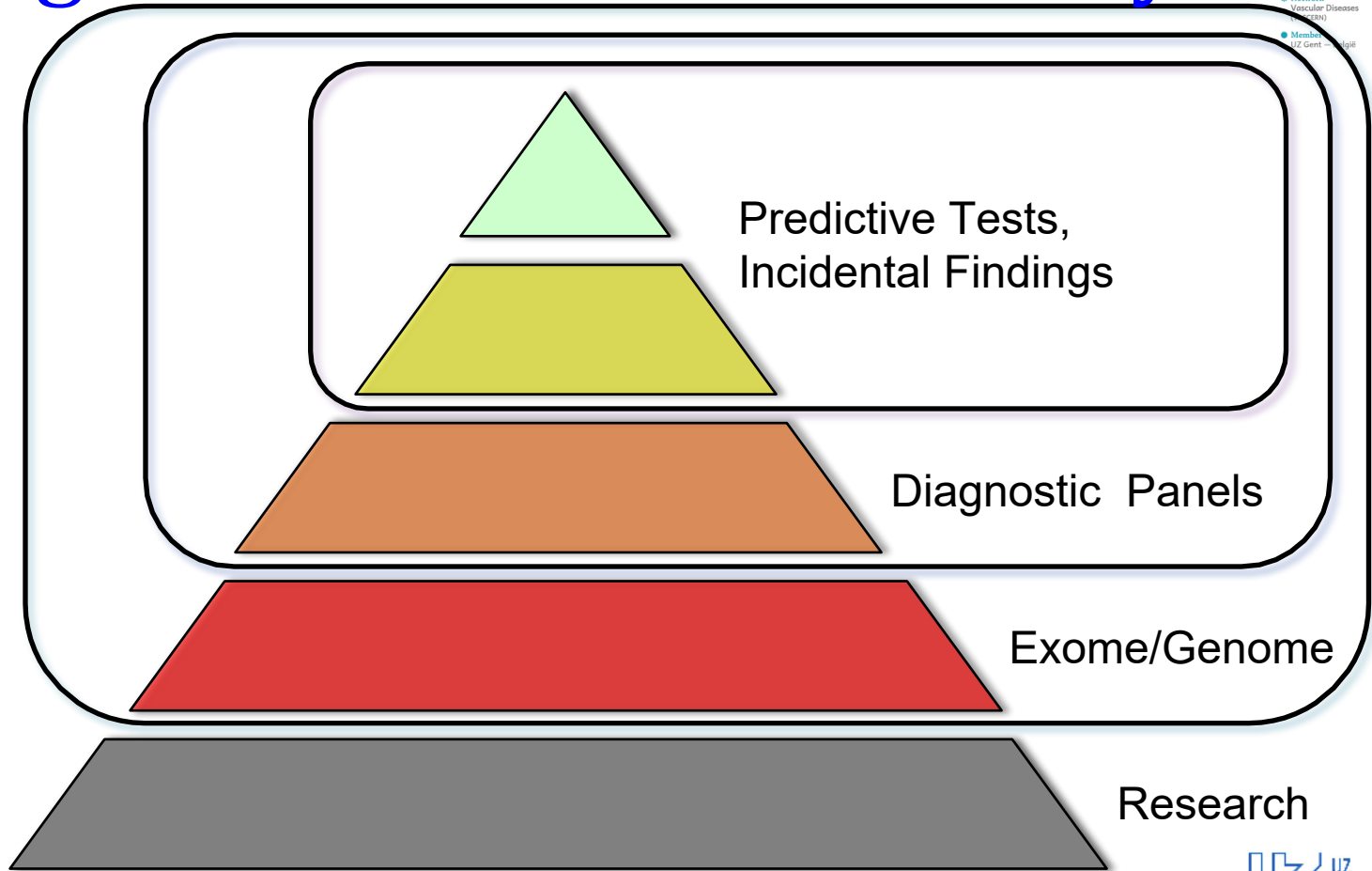
Definitive evidence

Strong evidence

Moderate evidence

Limited evidence

Disputed / no evidence



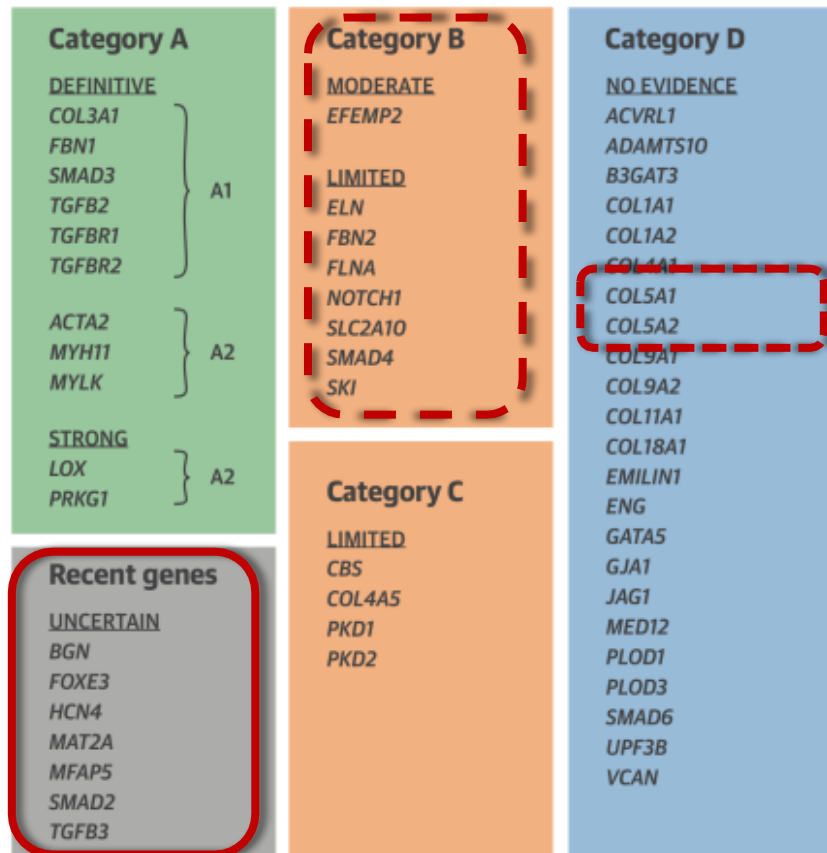
CENTRAL ILLUSTRATION Evaluation of the Clinical Validity of Genes for Heritable Thoracic Aortic Aneurysms and Dissections (HTAAD)

HTAAD Gene Curation 2016-2018

Category A	Category B	Category D
DEFINITIVE	MODERATE	NO EVIDENCE
COL3A1	EFEMP2	ACVRL1
FBN1		ADAMTS10
SMAD3	LIMITED	B3GAT3
TGFB2	ELN	COL1A1
TGFBR1	FBN2	COL1A2
TGFBR2	FLNA	COL4A1
	NOTCH1	COL5A1
ACTA2	SLC2A10	COL5A2
MYH11	SMAD4	COL9A1
MYLK	SKI	COL9A2
		COL11A1
STRONG		COL18A1
LOX		EMILIN1
PRKG1		ENG
	Category C	GATA5
	LIMITED	GJA1
	CBS	JAG1
	COL4A5	MED12
	PKD1	PLOD1
	PKD2	PLOD3
		SMAD6
		UPF3B
		VCAN
Recent genes		
UNCERTAIN		
BGN		
FOXE3		
HCN4		
MAT2A		
MFAP5		
SMAD2		
TGFB3		

Renard, M. et al. J Am Coll Cardiol. 2018;72(6):605-15.

CENTRAL ILLUSTRATION Evaluation of the Clinical Validity of Genes for Heritable Thoracic Aortic Aneurysms and Dissections (HTAAD)



Update Needed

+ “New” genes

THSD4

LTBP3

ARIH1

IPO8

Publications!



**Gene panel quality:
validity – NOT number**



Curated lists:

ID patients/families at
risk for thoracic aortic
disease

↓ burden of
uninformative diagnostic
testing results by ↓ nr of
screened genes



**The list is Dynamic and
needs update!!**

Thank you!

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