

Genomics in Myocardial and Structural Heart Disease: From Generic to a Personalized Cardiovascular Approach

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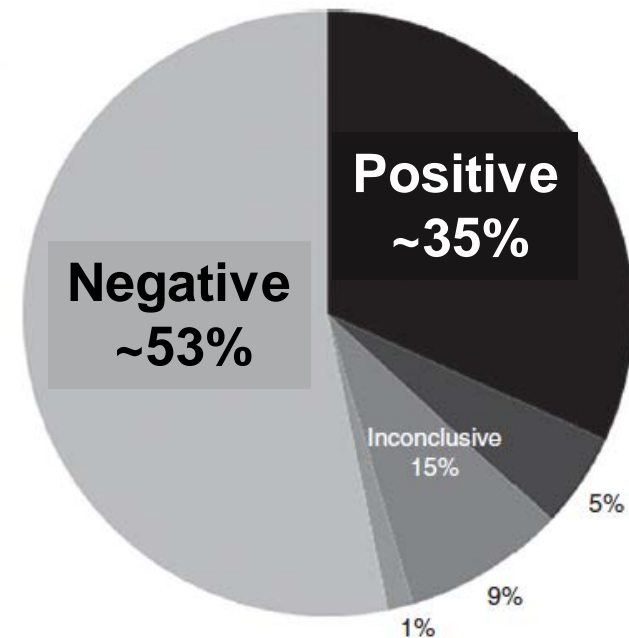
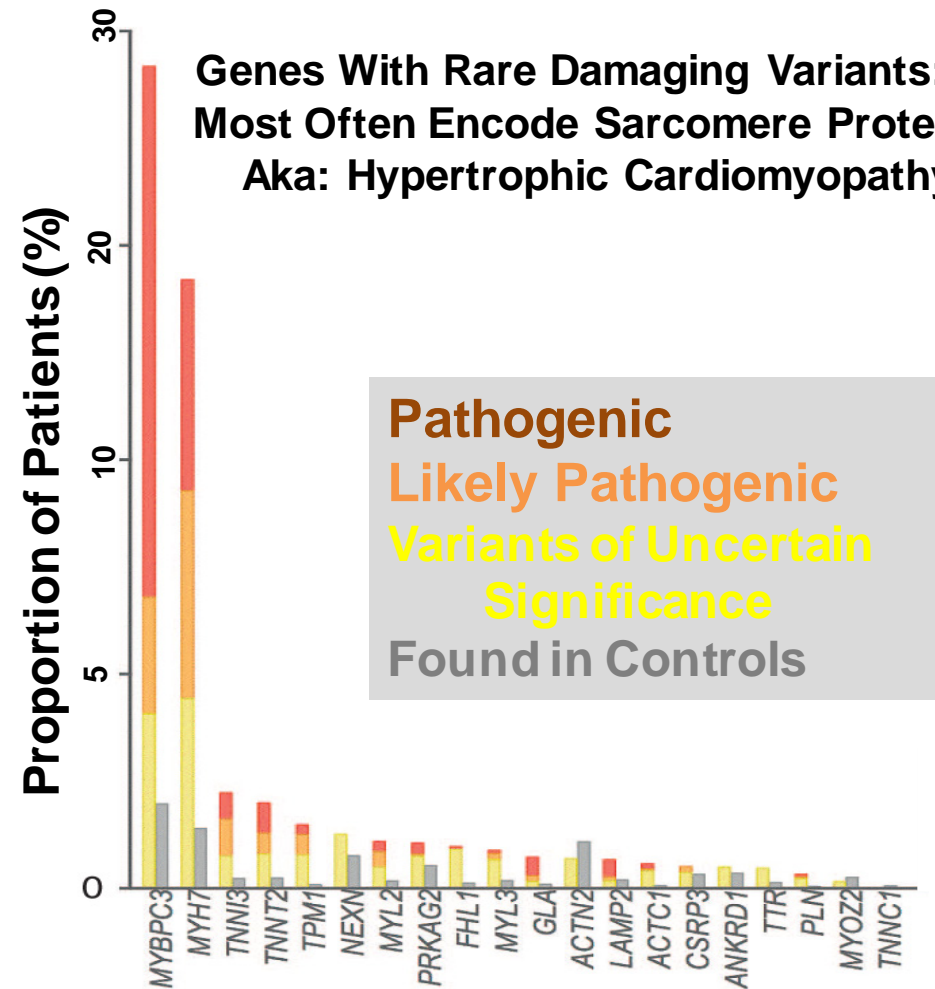
**Disclosure: CES is a founder and owns shares in Myokardia Inc.,
a startup company that develops therapeutics targeting the sarcomere**



Clinical Genetic Analyses of 7855 Cases Compared to 60,000 ExAC Controls

**Genes With Rare Damaging Variants:
Most Often Encode Sarcomere Proteins
Aka: Hypertrophic Cardiomyopathy**

**Variants Characteristics:
Rare, Found in $\leq 1:10,000$ Controls
Protein Damaging: Loss of Function
Deleterious Missense**



Alfares et al Genet Med, 2015

Walsh et al Genet Med, 2016

Histopathologic Impact of LVH Genes

Force

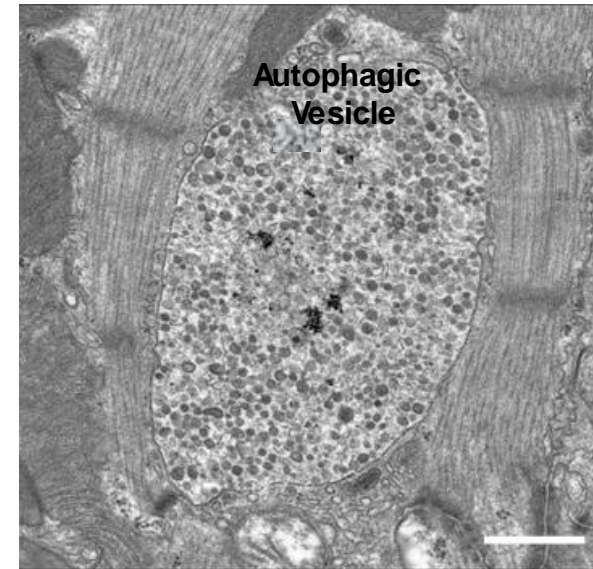
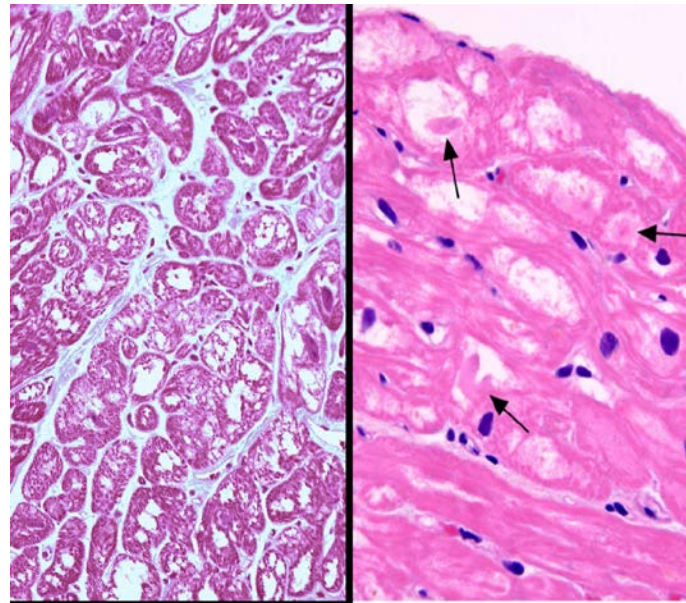
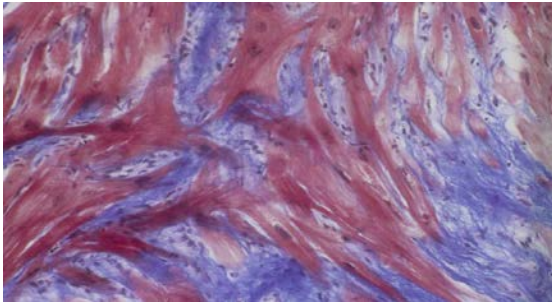
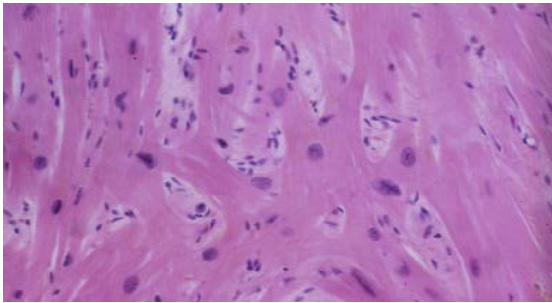
MYH7, MYBPC3
TNNT2, TNNI3
MYL3, MYL2
TPMI, ACTC
ACTN, MYOZ2

Metabolism

PRKAG2: Glycogen
GAA (Pompe):
Glycogen
GLA (Fabry):
Glycosphingolipids

Clearance

LAMP2: Cellular
Debris
DES: Misfolded
Protein
TTR: Amyloid

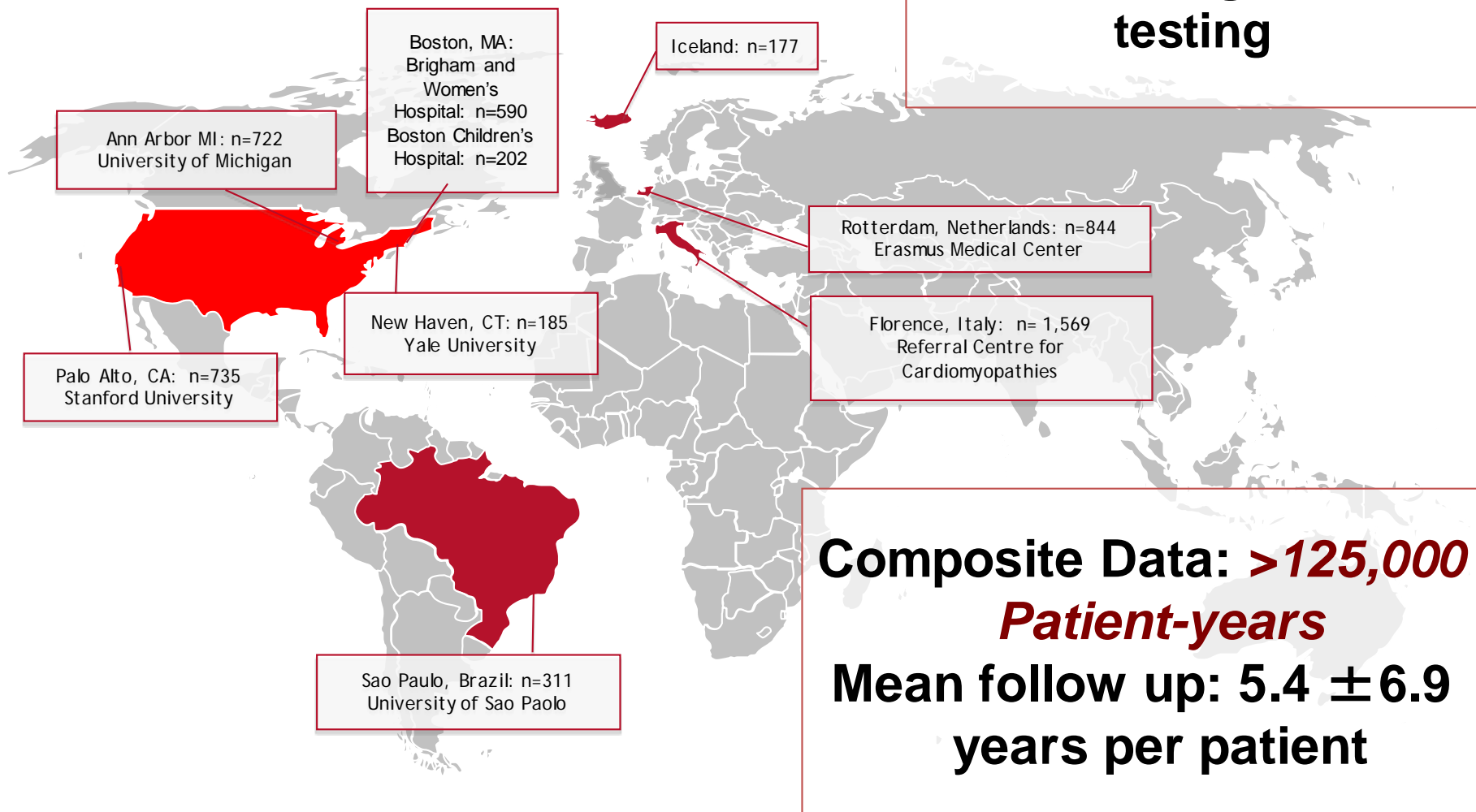


Clinical Impact of LVH Genes

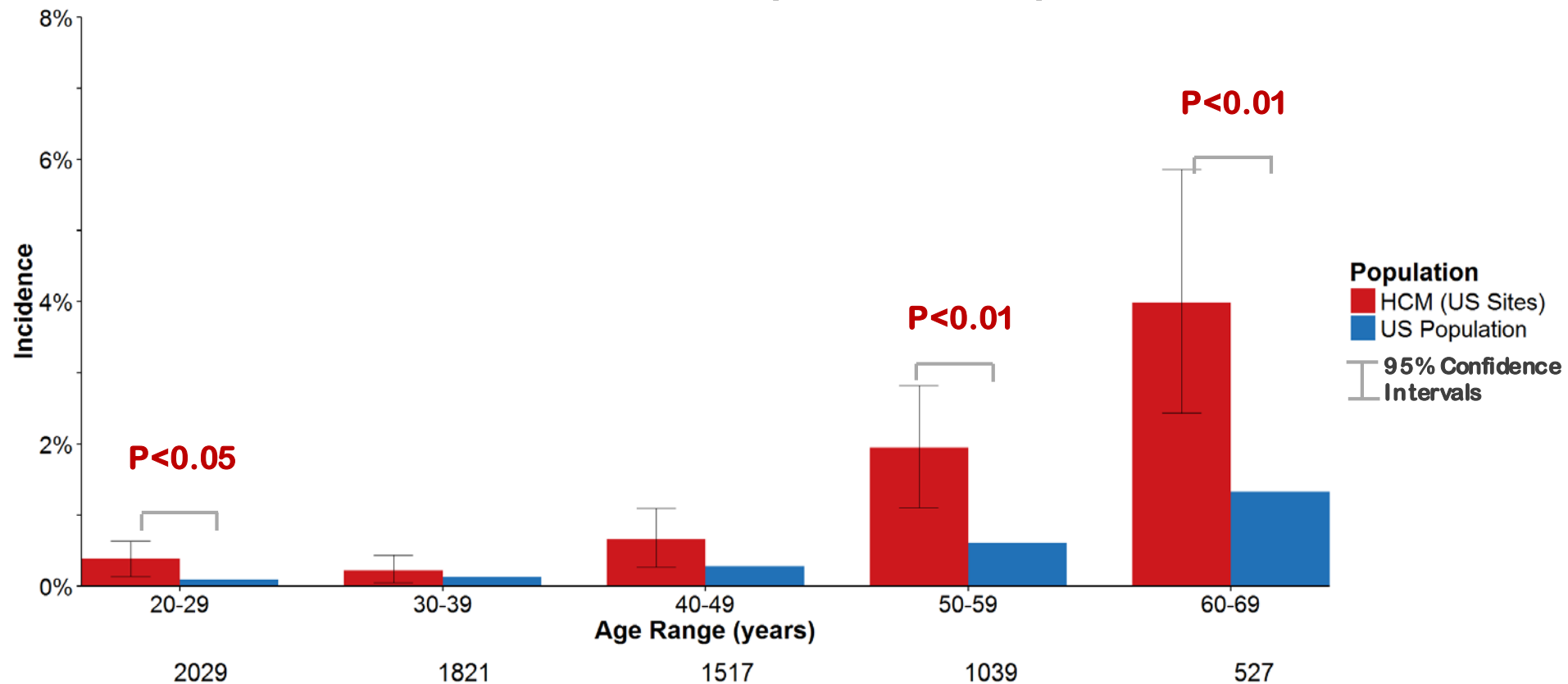
Gene	Inheritance	Outcomes
Sarcomere Proteins	Dominant	Adolescent or Later Onset Atrial Fibrillation in ~25% Low SCD & HF Risk
PRKAG2 Disease	Dominant	Adolescent Onset Progressive Conduction Highest Pacemaker Rates
LAMP2	X-linked	Childhood Onset, Massive LVH, Systemic Disease, VT, VF, Early Death
GLA	X-linked	Mid-Life Onset; Renal Disease, Progresses to HF (50 yrs) Therapeutic Enzyme

A GLOBAL INITIATIVE

More Than **6000**
HCM Patient Records
55% with genetic
testing



Age-Matched Mortality: 4108 HCM Patients vs US Population (1999-2014) *Ho, C. et al, in review*

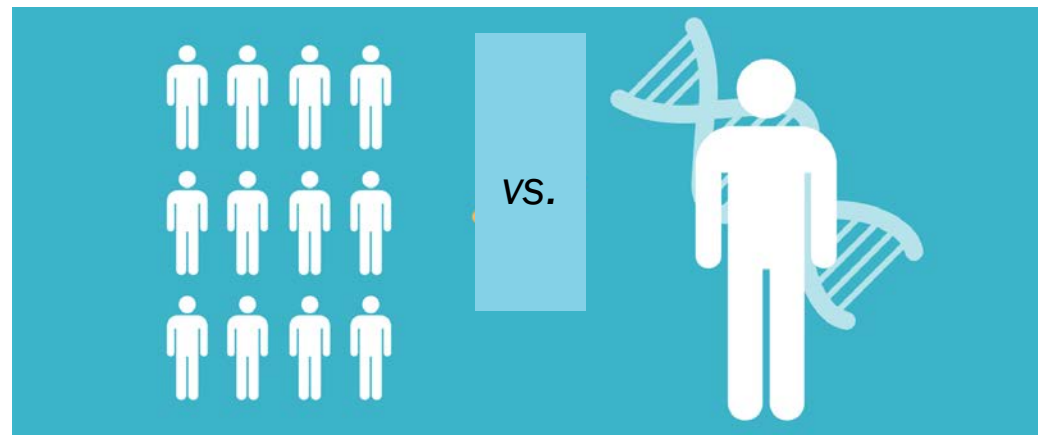


Age group	Incidence in US general population (%)	Incidence in HCM patients (%) (US sites)	P-value for difference in risk
20-29	0.09	0.39	< 0.05
30-39	0.13	0.22	0.44
40-49	0.28	0.66	0.09
50-59	0.61	1.95	< 0.01
60-69	1.33	3.99	< 0.01



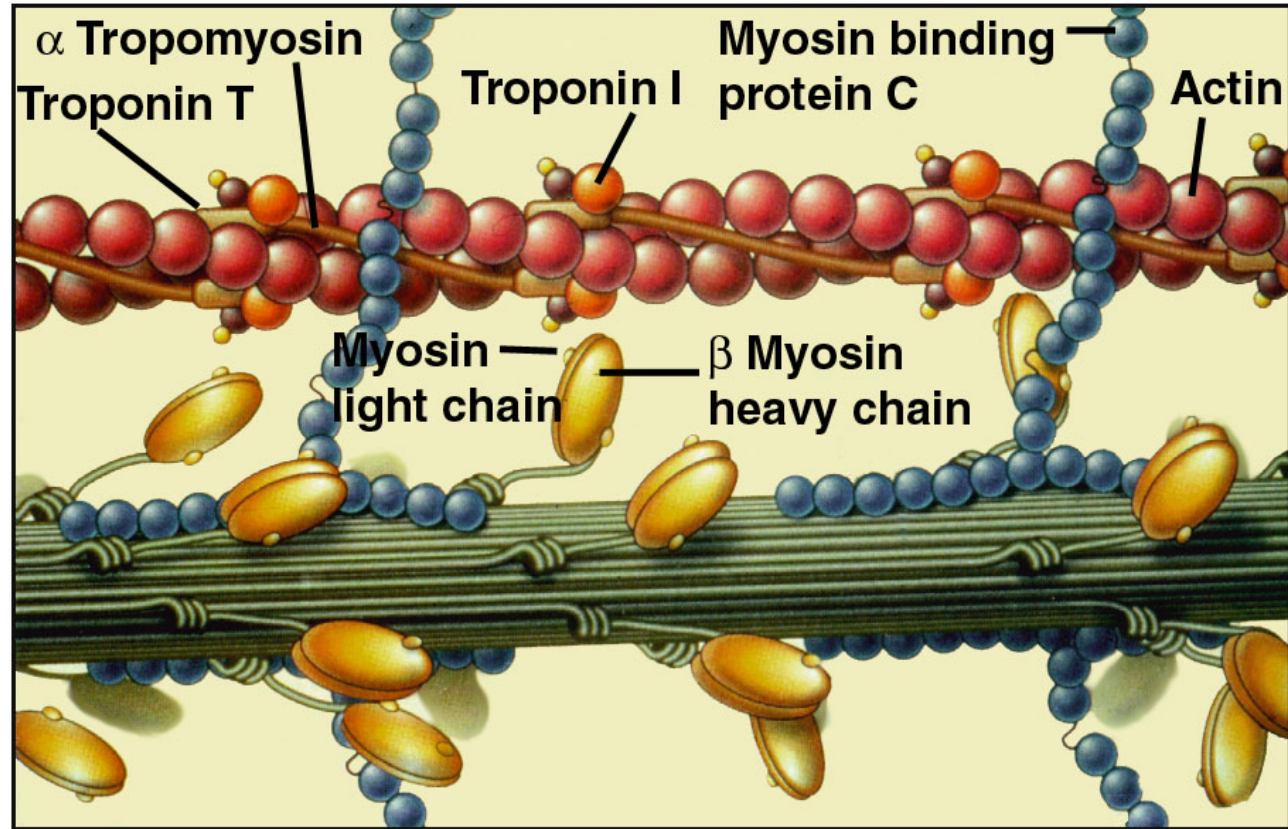
Identify individual differences and specific subgroups from broader populations

GENETICS: BRINGING MORE PRECISION TO MEDICINE



Improve traditional one-size-fits-all to individualized approach
Best for the **average** patient → Best for **this** patient

How Do Sarcomere Gene Mutations Cause Disease?

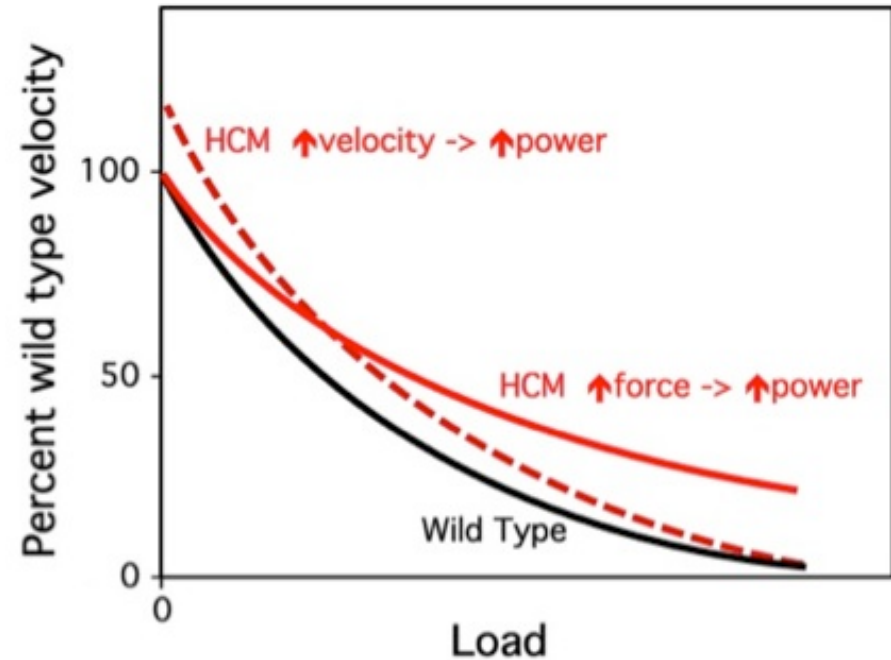
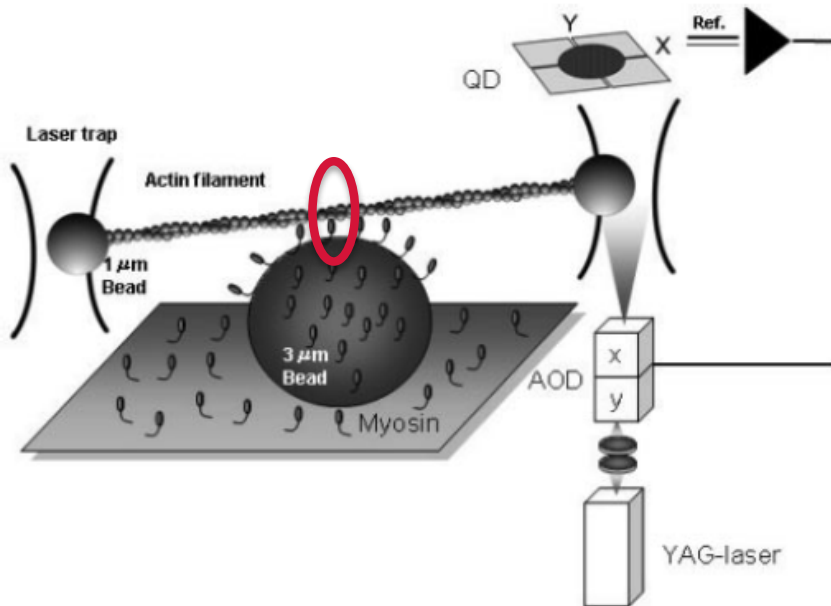
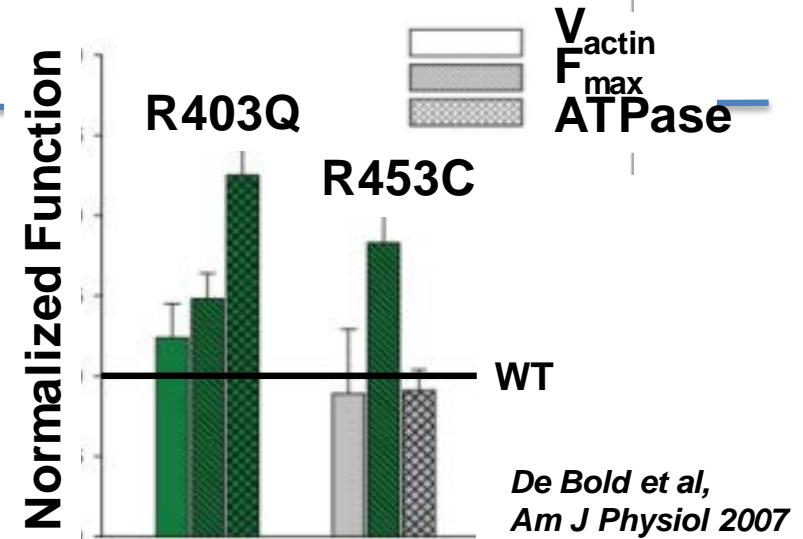
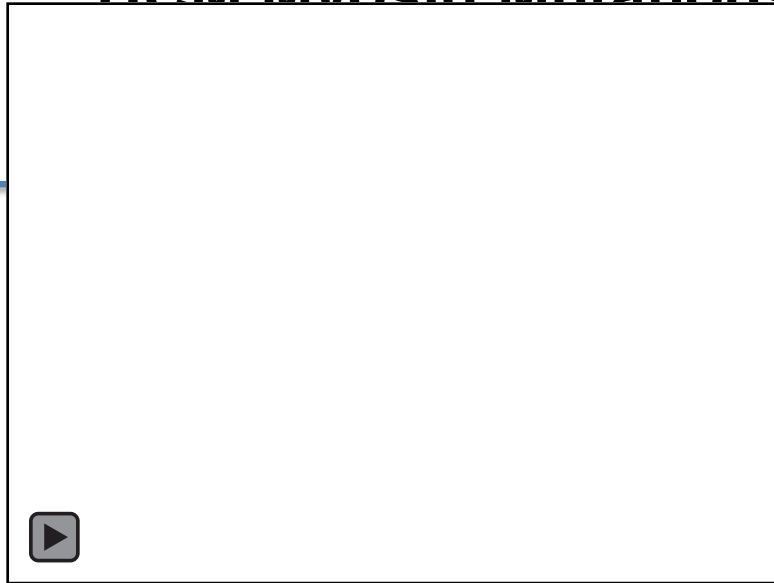


HCM Pathogenic Variants Predominate in:

Myosin Binding Protein C: Loss of Function

β Myosin Heavy Chain: Missense

HCM Myosin Mutations Increase Sarcomere Power



Diastolic Dysfunction Drives Symptoms in HCM

↑ Pulmonary Pressure > Dyspnea

↑ Atrial Pressure > Atrial Stretch

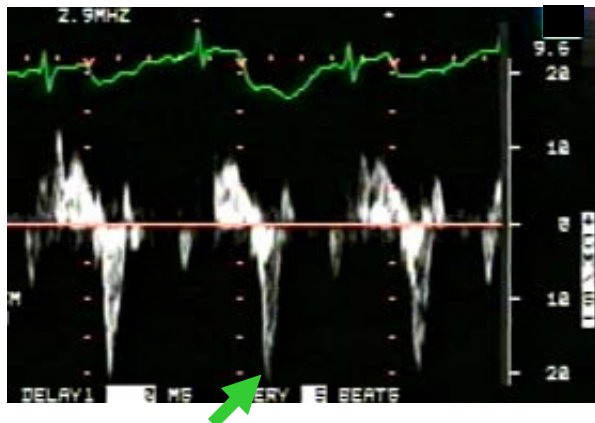
>> Atrial Fibrillation

>> Atrial Thrombus

>> Stroke

↑ Myocardial Ischemia

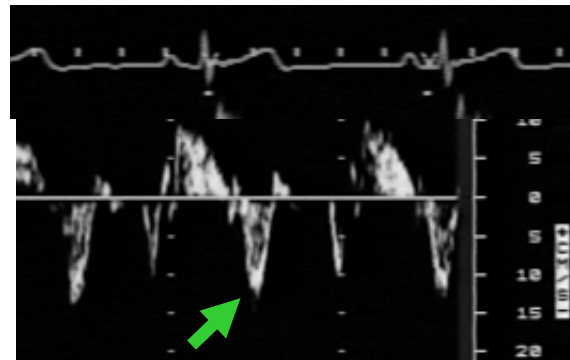
>> Heart Failure



Normal

Age 23 years

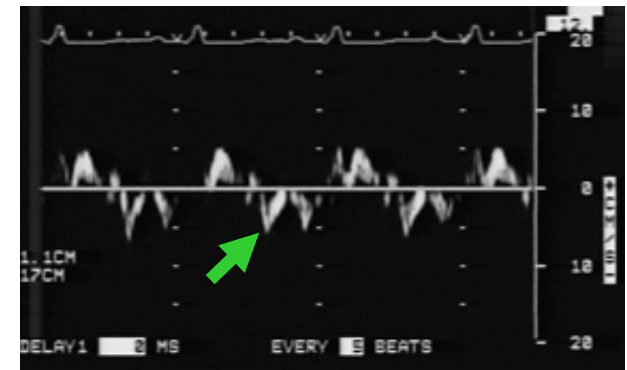
E' velocity: 20.1 cm/sec



Preclinical: Mutation+ No LVH

Age 24 years

E' velocity: 10.5 cm/sec



Overt HCM

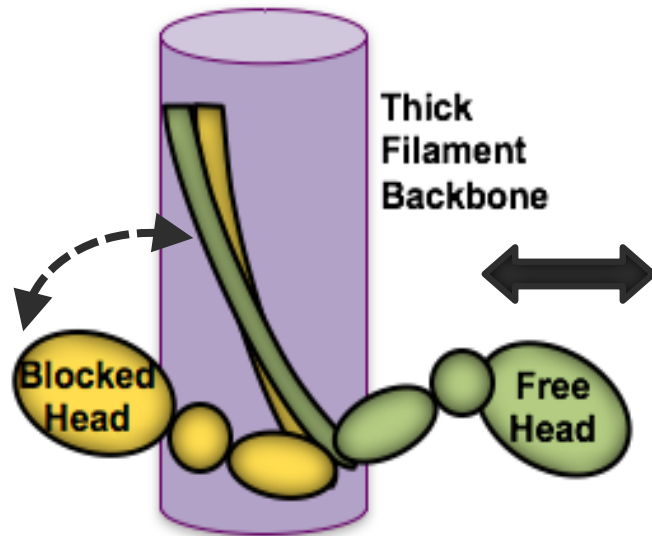
Age 35 years

E' velocity: 5.2 cm/sec

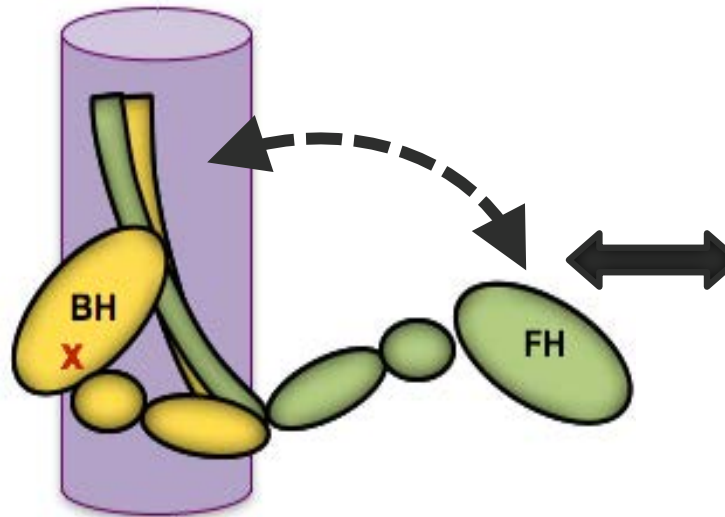


Cardiac Cycle: Contraction & Two Phases of Relaxation

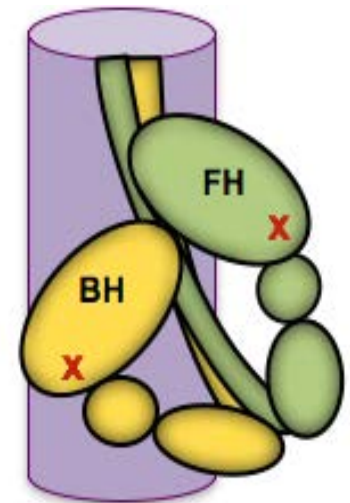
Contraction



Disordered Relaxation (DRX)



Super Relaxation (SRX)



X= ATPase Inhibited

Energy Consumption

*Vibert & Craig, J Cell Biol; 1985,
Woodhead et al, Nature 2005
Alamo et al eLife 2017*



Do HCM Variants Alter SRX and DRX Interacting Residues?

(Alamo et al eLife. 2017)

Variant Analyses in 6112 HCM and 1315 DCM Patients and 33,370 Controls

Analyses in 6112 HCM Patient Analyses:

Myosin:

Pathogenic Variants: 78% alter Interacting Residues ($p=5.25e-13$)

Likely Path Variants: 44% alter Interacting Residues ($p=7.04e-06$)

ELC and RLC:

Pathogenic Variants: All alter Interacting Residues

71% HCM Mutations alter Charge of Normal Residue

Analyses in Other Cohorts:

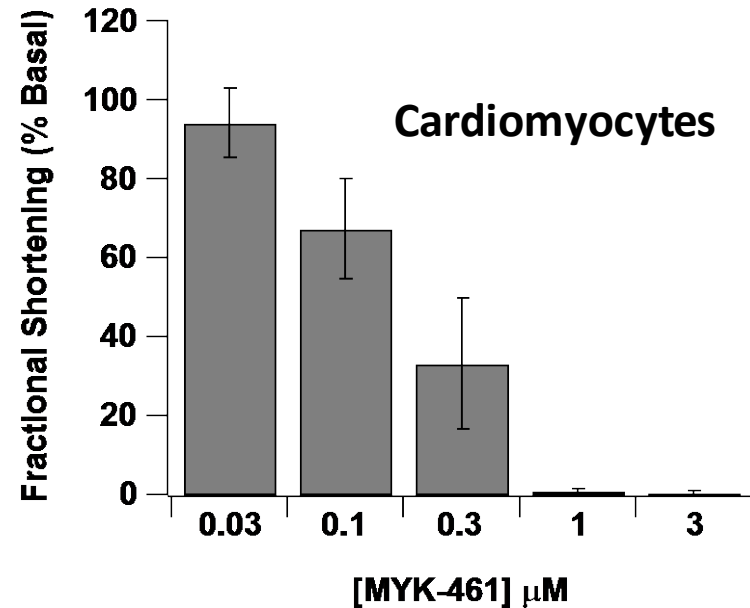
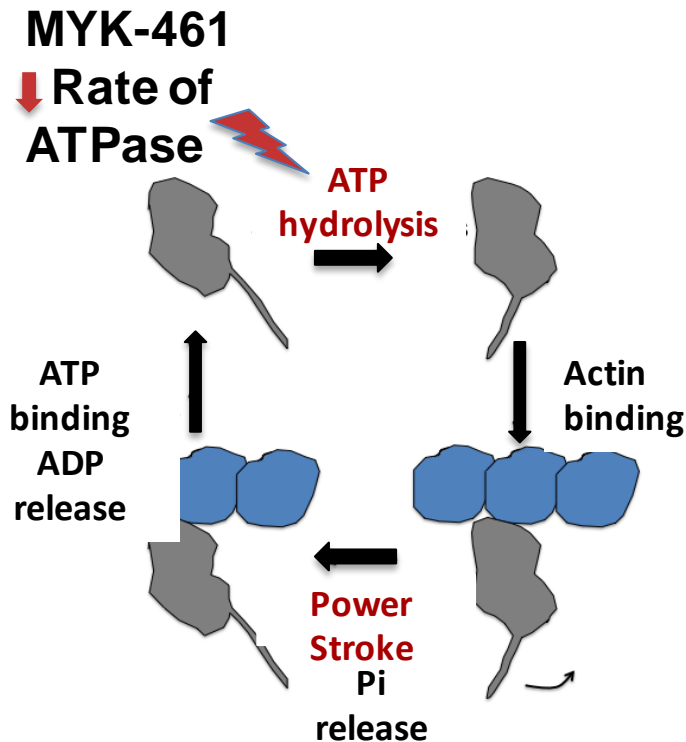
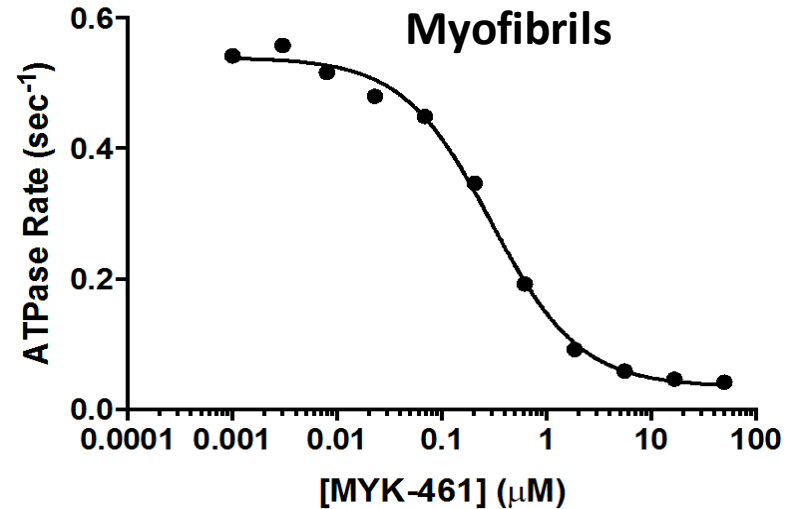
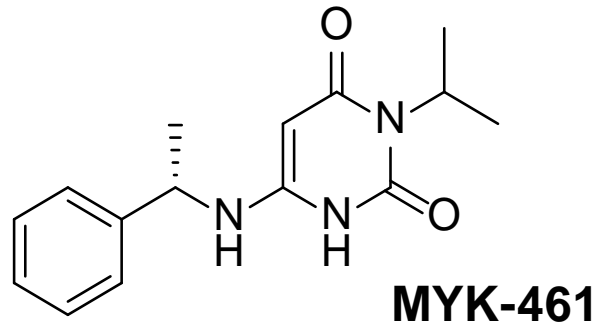
1315 DCM Patients: No enrichment in Interacting Residues ($p=0.66$)

33,370 Control Subjects: No enrichment in IHM Residues ($p=0.23$)

*HCM Variants Increase Sarcomere Power and Impair Relaxation
That Together Increase Energy Demands*

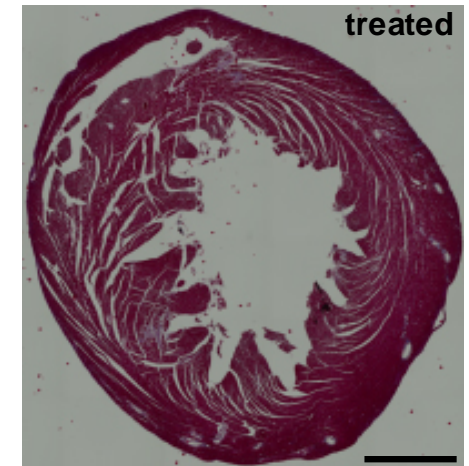
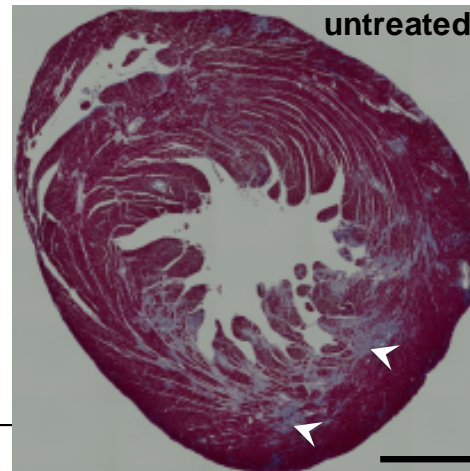
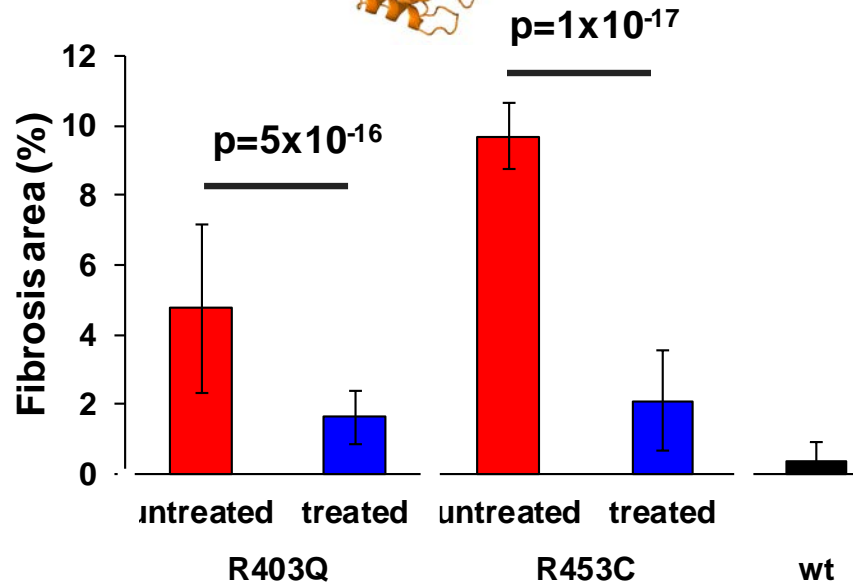
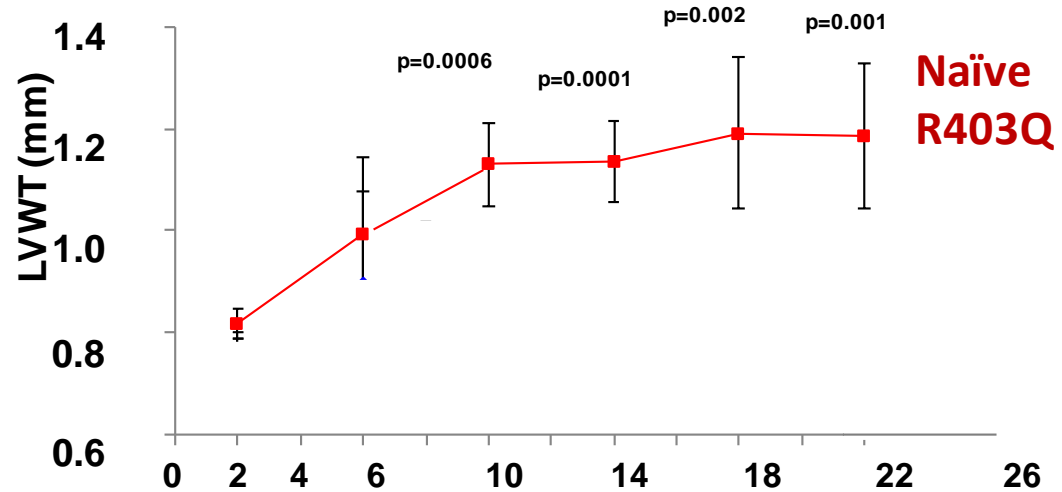
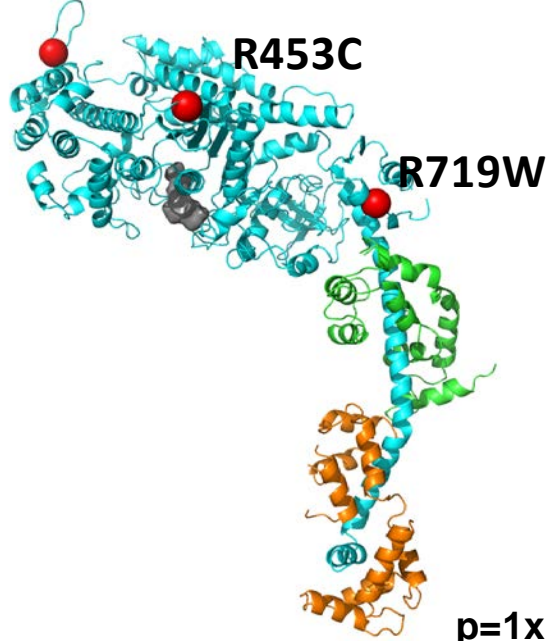
MYK-461 (Mavacamten): Inhibits Myosin ATPase Improves HCM Biophysical and Clinical Finding

Green et al, Science 2016



MYK-461 (Mavacamten): ↓ LVH & Fibrosis in HCM Models

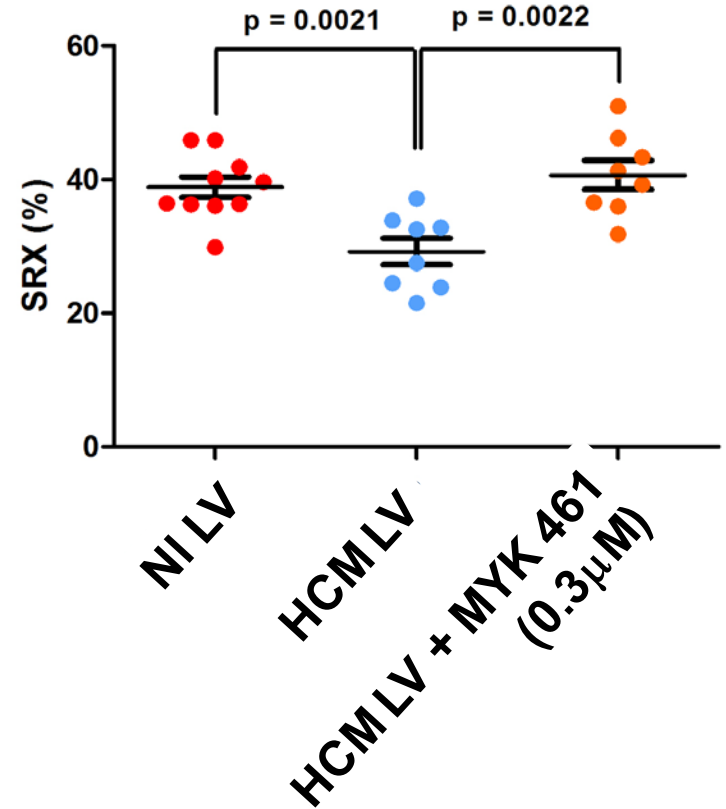
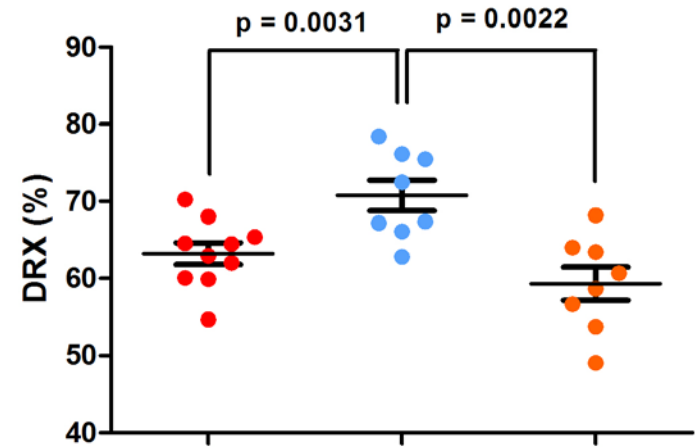
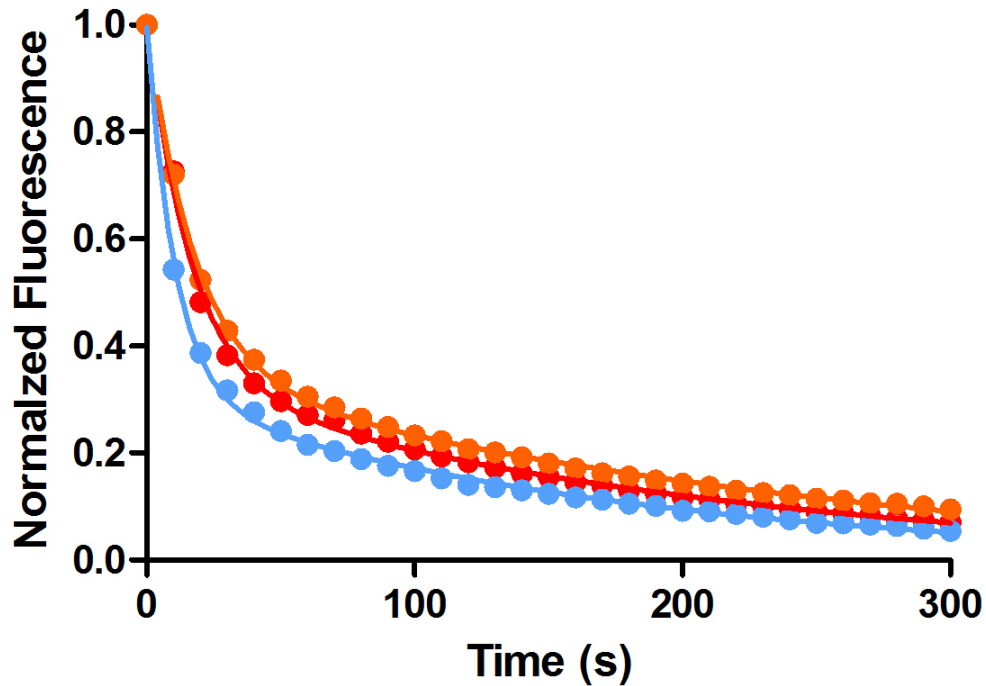
R403Q



Green et al, Science 2016

MYK-461 (Mavacamten): ↑ Relaxation in Human HCM LV

- NI LV
- HCM LV
- HCM LV + MYK 461 (0.3 μ M)



Translating Genetic Insights into Practice and Treatment

Opportunities

- Improves Risk Stratification
- Targets Healthcare Resources for Patients and Family Members
- Enables Mechanistic Discoveries from which New Therapeutic Targets Emerge



Challenges

- High Costs (but Falling Fast) & Inconsistent Insurance Coverage
- Variant Interpretation Remains Incomplete (VUS)
- Disease Modifiers (both Good and Bad) Remain Unknown
- Unexpected, Incidental Findings
- Knowledge Gaps among Physicians and Patients

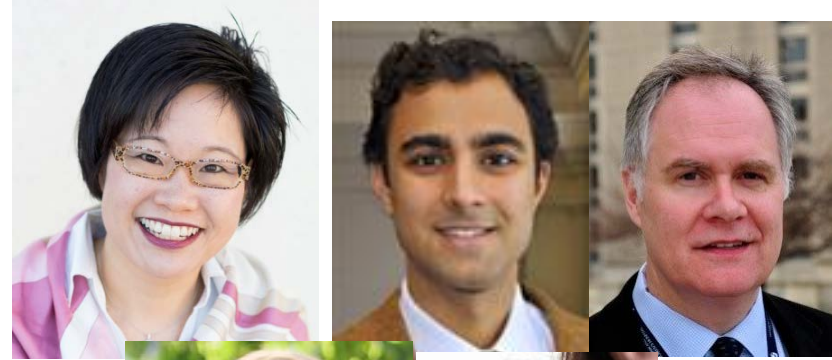
Hypertrophic Cardiomyopathy

- **Mutations Inform Biophysical Processes by which the Sarcomere Functions throughout Cardiac Cycle**
 - ↑ **Systolic Performance: Direct Motor Function Effects**
 - ↓ **Diastolic Performance**
 - ↓ **SRX:DRX Ratio**
 - ↑ **ATP Consumption**
- **Sarcomere = Direct Therapeutic Target**
 - Small Molecules (461) Normalize Biophysical Properties**
 - Potential to Treat Disorders Beyond HCM**
- **Still More to Do in HCM:**
 - Uncover Causes of Mutation-negative Disease**
 - Recruitment Ongoing:**
 - Seidman@Genetics.Med.Harvard.Edu**



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