Supplemental Table 1. The average total weights of vital organs and normalized average weight of vital organs[a]

Normalized Organ weight	SUNDS (N=148)	Control (N=444)	*P* value
TW (g)	5262.6± 604.3	5108.6± 808.8	.04
Brain	0.280±0.033	0.284±0.040	.39
Left lung	0.116±0.017	0.119±0.031	.26
Right lung	0.132±0.020	0.135±0.033	.43
Heart	0.067±0.008	0.065±0.010	.04
Liver	0.292±0.032	0.286±0.042	.12
Spleen	0.033±0.012	0.033±0.016	.80
Left kidney	0.029±0.006	0.028±0.005	.12
Right kidney	0.028±0.005	0.027±0.006	.43
Pancreas	0.023±0.005	0.023±0.006	.57

[a]TW = total weights (of vital organs including brain, lungs, heart, liver, spleen, kidneys, and pancreas).

Supplemental Table 2. The prevalence of non-significant microscopic findings[a]

Morphological changes	SUNDS (N=148) n (%)	Control (N=444) n (%)	*P* value	OR (95% CI)	comments
Myocardium: few lymphocytic infiltration	10 (6.76)	27 (6.08)	.77	1.12 (0.53, 2.37)	Not sufficient for viral myocarditis
Myocardium: few fatty infiltration	17(11.50)	29 (6.53)	.05	1.86 (0.99, 3.49)	Not sufficient for cardiomyopathy
Coronary artery: atherosclerosis	3 (2.03)	14 (3.15)	.67	0.64 (0.18, 2.24)	The stenosis of coronary artery <20%
CCS: few lymphocytic infiltration	3 (2.03)	4 (0.90)	.51	2.28 (0.50, 1.03)	Not sufficient for viral myocarditis
CCS: few fatty infiltration	12 (8.11)	15 (3.38)	.02	2.52 (1.15, 5.52)	Not sufficient for cardiomyopathy
CCS: slight stenosisof artery	5 (3.38)	4 (0.90)	.08	3.85 (1.02, 14.52)	The stenosis of artery <20%
Brain: neuronic amyloidosis	3 (2.03)	5 (1.13)	.68	1.82 (0.43, 7.70)	
Lung: adhesion between lobes of lung	18 (12.16)	59 (13.29)	.72	0.90 (0.51, 1.59)	
Liver: fatty degeneration of hepatocytes	42 (28.38)	94 (21.17)	.07	1.48 (0.97, 2.25)	Slight degeneration
Kidney: sporadic glomerulosclerosis	10 (6.76)	31 (6.98)	.93	0.97 (0.46, 2.02)	1-3 glomerulosclerosisper kidney slice
Spleen: hyalinosis of central artery	12 (8.11)	17 (3.83)	.04	2.22 (1.03, 4.76)	
Pancreas: hemorrhage without necrosis	3 (2.03)	8 (1.80)	1.0	1.13 (0.30, 4.31)	No inflammatory cell infiltration
Thymus: remain unwithered	73 (49.32)	81 (18.24)	<.001	4.36 (2.92, 6.52)	>40% area not be replaced with fat

[a]CCS = cardiac conduction system including the area of sinus node, atrio-ventricular node, and His bundle.

Supplemental Table 3. The age, height, heart structure, and the genetic findings in 44 SUNDS cases[a]

Group	n	Age (years)	Height (cm)	Heart weight (g)	LV Thickness (cm)	RV thickness (cm)	Tricuspid valve (cm)	Pulmonary valve (cm)	Mitral valve (cm)	Aortic valve (cm)
SUNDS	44	30.23± 8.00	169.05±6.61	364.78±67.15	1.22±0.18	0.32±0.07	11.80±0.96	7.87±0.83	9.42±1.07	6.99±0.79
A (+)	12	31.83±8.83	168.90±6.08	358.00±65.63	1.22±0.20	0.30±0.08	11.92±0.80	8.12±0.82	9.73±0.73	7.18±0.44
A (-)	32	29.63±7.74	169.11±6.90	367.30±68.77	1.21±0.17	0.33±0.06	11.76±1.02	7.77±0.83	9.31±1.16	6.92±0.88
P value		.42	.93	.71	.94	.24	.66	.26	.29	.38
C (+)	14	26.21±8.58	168.25±6.69	342.75±62.05	1.23±0.19	0.34±0.08	11.56±0.89	7.28±0.84	9.05±1.09	6.46±0.86
C (-)	30	32.10±7.12	169.44±6.67	375.36±68.12	1.21±0.18	0.31±0.06	11.92±0.99	8.15±0.67	9.60±1.03	7.25±0.61
P value		.02	.62	.17	.84	.21	.29	.002	.15	.003
A(+)/C(+)	22	28.77±8.76	168.05±6.62	349.11±67.61	1.21±0.20	0.32±0.08	11.67±0.90	7.73±0.96	9.27±1.00	6.79±0.84
A(-)C(-)	22	31.68±7.08	170.11±6.61	381.33±64.38	1.22±0.16	0.33±0.06	11.94±1.03	8.01±0.65	9.58±1.15	7.21±0.69
P value		.23	.35	.15	.85	.60	.39	.31	.38	.11

[a]A(+/-), C(+/-) refer to SUNDS cases with (+) /without (-) rare variants in primary arrhythmia (A) or caridomyopathy (C) associated genes;

A(+)/C(+) = A(+) or C(+); A(-) C(-) = neither A(+) nor C(+); LV = left ventricle; RV = right ventricle.

Online-Only Text

Methods

Some of the molecular/functional lines of evidence for pathogenicity that were assessed included whether the variant: (1) was a null variant (nonsense, frame-shift, canonical splice sites) in a gene where loss-of-function is a known mechanism of disease, (2) involved the same amino acid change as a previously established pathogenic variant regardless of nucleotide change, (3) was associated with a well-established in vitro or in vivo functional studies supportive of a damaging effect on the gene or gene product, (4) was located in a mutational hot spot and/or critical and well-established functional domain without benign variation, (5) was a novel missense change at an amino acid residue where a different missense change determined to be pathogenic has been seen before, and (6) had multiple lines of computational evidence supporting a deleterious effect on the gene or gene product.

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