Targeted next-generation sequencing helps to decipher the genetic and phenotypic heterogeneity of hypertrophic cardiomyopathy

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Abstract. Hypertrophic cardiomyopathy (HCM) is mainly associated with myosin, heavy chain 7 (*MYH7*) and myosin binding protein C, cardiac (*MYBPC3*) mutations. In order to better explain the clinical and genetic heterogeneity in HCM patients, in this study, we implemented a target-next generation sequencing (NGS) assay. An Ion AmpliSeq™ Custom Panel for the enrichment of 19 genes, of which 9 of these did not encode thick/intermediate and thin myofilament (TTm) proteins and, among them, 3 responsible of HCM phenocopy, was created. Ninety-two DNA samples were analyzed by the Ion Personal Genome Machine: 73 DNA samples (training set), previously genotyped in some of the genes by Sanger sequencing, were used to optimize the NGS strategy, whereas 19 DNA samples (discovery set) allowed the evaluation of NGS performance. In the training set, we identified 72 out of 73 expected mutations and 15 additional mutations: the molecular diagnosis was achieved in one patient with a previously wild-type status and the pre-excitation syndrome was explained in another. In the discovery set, we identified 20 mutations, 5 of which were in genes encoding non-TTm proteins, increasing the diagnostic yield by approximately 20%: a single mutation in genes encoding non-TTm proteins was identified in 2 out of 3 borderline HCM patients, whereas co-occuring mutations in genes encoding TTm and galactosidase alpha (GLA) altered proteins were characterized in a male with HCM and multiorgan dysfunction. Our combined targeted NGS-Sanger sequencing-based strategy allowed the molecular diagnosis of HCM with greater efficiency than using the conventional (Sanger) sequencing alone. Mutant alleles encoding non-TTm proteins may aid in the complete understanding of the genetic and phenotypic heterogeneity of HCM: co-occuring mutations of genes encoding TTm and non-TTm proteins could explain the wide variability of the HCM phenotype, whereas mutations in genes encoding only the non-TTm proteins are identifiable in patients with a milder HCM status.

Introduction

Hypertrophic cardiomyopathy (HCM), classically defined as the presence of idiopathic left ventricular hypertrophy, is the most common heritable cardiovascular disease (affecting at least 1 in 500 individuals); it is typically transmitted in an autosomal dominant pattern (1-3); however, sporadic cases associated with *de novo* mutations (1,4) and patients with maternally-inherited HCM (5,6) have also been reported. HCM is recognized as an important cause of sudden cardiac death (SCD), heart failure and embolic stroke secondary to atrial fibrillation (2).

At present, Online Mendelian Inherithance in Man (OMIM) classifies 25 different HCM phenotypes (http://omim.org/phenotypicSeries/PS192600) that are associated with as many different mutant genes, mostly encoding thick/intermediate and thin myofilament (TTm) proteins of the sarcomere. Disease-causing mutations in myosin, heavy chain 7 *(MYH7)* and myosin binding protein C, cardiac *(MYBPC3)* genes, encoding myofilament proteins, represent approximately 70% of >1,400 pathogenic alleles that have been characterized in HCM patients by using Sanger sequencing (2). Pathogenic alleles that do not encode for TTm proteins have also been identified in some HCM patients (7-12). Mutations in the genes, galactosidase alpha (*GLA*), lysosome-associated membrane protein 2 (*LAMP2*), and protein kinase AMP-activated non-catalytic

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subunit gamma 2 (*PRKAG2*), are responsible for distinct metabolic storage disorders with a clinical presentation and pattern of left-ventricular hypertrophy similar to HCM (1,3,13).

However, pathogenic alleles are not identified in 28-40% of HCM patients with a family history of HCM and 50-90% of sporadic HCM cases (13,14). On the other hand, 5-10% of HCM patients carry more than one mutation affecting one or more different genes (15); these complex genotypes are usually identified in patients with severe left ventricular hypertrophy (16), or with end-stage HCM (17) and in patients with severe manifestations of the disease, including advanced heart failure symptoms and sudden death (1,14).

In addition, the broad genetic and allelic heterogeneity can also be associated with a highly variable clinical phenotype, ranging from asymptomatic forms to sudden cardiac death (1,13), even within the same family and amongst family members that share the same pathogenic allele (18,19).

The conventional Sanger sequencing of single amplicons of sarcomeric genes is labor intensive, time consuming and expensive, showing in a large number of patients a negative test or a positive test, but associated with a low predictive clinical outcome. In consideration of these limitations, it is reasonable to adopt the massively parallel sequencing ability of the Next Generation Sequencing (NGS) technologies to decrease run times, lower the costs, use smaller amounts of genomic DNA (20) and, analyzing a larger number of genes, better decipher the relationship between genetic and phenotypic heterogeneity (21,22). In this context, the NGS methodology is replacing the conventional technology, in particular for the diagnosis of genetic disorders with high genetic heterogeneity that involve the screening of several genes or few genes with large coding region (23,24).

In this study, we used the NGS methodology, applied to the molecular characterization of HCM patients, to determine whether the screening of additional genes encoding non-TTm proteins may contribute to the better clarification of the relationship between the phenotypic and genotypic heterogeneity of HCM.

Patients and methods

Patients. All patients [n=92; mean age, 44.5 (±18.7) years; age range, 2-78 years] gave their informed consent to the study that was conducted according to the Declaration of Helsinki. The subjects were recruited between 2007 and 2015 from Italian Cardiology Units and addressed to our Human Genetics Laboratory for molecular diagnosis of HCM. The clinical diagnosis of primary HCM was based on medical history, a physical examination and on the echocardiographic demonstration of a hypertrophied left ventricle (LV) that could not be explained by another cardiac or systemic disease. In adults, a maximal LV wall thickness (LVWT) ≥15 mm, or the equivalent relative to the body surface area in children, was considered the determining criterion for HCM; the maximal LVWT between 10 and 14 mm, in conjunction with other features (i.e., family history, electrocardiogram abnormalities) prompted the diagnosis of borderline HCM (25,26).

The phenocopy of HCM was suspected in the presence of multiorgan involvement. In these cases, a multidisciplinary clinical approach was adopted for the final diagnosis (27).

The genomic DNA of each patient was extracted from peripheral leukocytes, using QIAsymphony S (Qiagen, Hilden, Germany) according to the manufacturer's instructions. Among the 92 DNA samples, 73 were used as a training set to optimize the performance of NGS technology; these DNA samples were already genotyped by the Sanger sequencing of 6 genes encoding TTm proteins [*MYH7*, *MYBPC3*, troponin T2, cardiac type (*TNNT2*), actin, alpha, cardiac muscle 1 (*ACTC1*), tropomyosin 1 (alpha) (*TPM1*) and troponin I3, cardiac type (*TNNI3*)] (1,3) and, where appropriate, another 2 genes encoding myofilament proteins [myosin light chain (*MYL)2* and *MYL3*] (1,3), or 3 genes (*GLA*, *LAMP2* and *PRKAG2*) responsible for rare metabolic disorders (1,3,13), were analyzed. This series has 63 DNA samples with mutant genotypes and 10 DNA samples with no previously identified mutations.

Another group of 19 DNA samples was adopted as the discovery set to evaluate the performance of NGS methodology in clinical routine HCM testing.

The clinical parameters (age at onset of HCM, LVWT, automatic implantable cardioverter defibrillator, family history of HCM/sudden cardiac death, left ventricular ejection fraction and other medical issues) were carefully reviewed for patients belonging at the discovery set and for those of the training set that, after NGS analysis, showed additional mutations in genes originally not analyzed by Sanger sequencing. Among these patients, of which 14 were males and 12 were female, the mean age at onset was 33.6 (±19.0) years, with an age range of 1-72 years; the mean LVWT was 18.7 (±6.6) mm and ranged from 10 to 34 mm; the mean LVEF (%) was 59.8 (±10.4).

Gene panel design. To implement the diagnostic genetic testing for HCM patients using NGS technology, in addition to the 11 genes previously screened, after analyzing the literature, we included additional 8 genes deemed most plausibly involved in the HCM phenotype. Among these, 2 genes encode myofilament proteins [thin: troponin C1, slows skeletal and cardiac type (*TNNC1*); and thick: myosin, heavy chain 6 (*MYH6*)]; one encodes a protein located in the M-band [myomesin 1 (*MYOM 1*)] (7); two encode Z-disk constituents [myozenin 2 (*MYOZ2)* and ankyrin repeat domain 1 (*ANKRD1*)] (8,9); vinculin (*VCL*) encodes the main costameric protein (10), calreticulin 3 (*CALR3*) encodes a Ca^{2+} sensitive/handling protein (11) and caveolin 3 (*CAV3*) encodes the major membrane protein of caveolae (12).

An Ion AmpliSeq™ Custom Panel (IACP) for the mutation screening of these 19 genes was designed using the Ion AmpliSeq Designer (IAD) software v.2.0.3. The design included all the coding exons with additional 10 bp of adjacent intronic regions. Overall, it represented approximately 42 kb of the target DNA sequence, i.e., 284 exons and 452 amplicons divided into 2 pools of primers for multiplex PCR.

Library preparation and NGS. DNA libraries were prepared using the Ion Ampliseq™ Library kit 2.0 (Thermo Fisher Scientific, Carlsbad, CA, USA) following the manufacturer's instructions.

Briefly, following quantification with a NanoDrop spectrophotometer (Thermo Fisher Scientific), 10 ng of genomic DNA was used in the multiplex PCR amplification of each of the 2 primer pools. For each sample, the 2 sets of multiplexed

amplicons were subjected to following steps: partial digestion of the primers and amplicon phosphorylation with FuPa reagent (Thermo Fisher Scientific), ligation of the barcode adapters and purification by Agencourt® AMPure® XP Reagent (Beckman Coulter, Brea, CA, USA).

All the DNA libraries were quantified by the Agilent High Sensitivity DNA kit on a 2100 Bioanalyzer (Agilent Technologies, Milan, Italy) and a Qubit® 2.0 Fluorometer using the dsDNA High Sensitivity assay kit (Thermo Fisher Scientific) before being diluted to a final concentration of 100 pmol/l in low TE; subsequently, 3 μl of each sample were pooled to a final concentration of 100 pmol/l. The final pool was further diluted to a concentration of 12 pmol/l in water and subjected to emulsion PCR and enrichment of Ion Sphere Particles (ISPs) using the Ion Torrent OneTouch™ 2 system (Thermo Fisher Scientific) according to the manufacturer's instructions; confirmation of template-positive ISPs and validation of enrichment were performed on Qubit® 2.0 Fluorometer using Ion sphere quality control kit (Thermo Fisher Scientific), according to the manufacturer's protocol. Enriched ISPs were loaded on Ion 314 or 316 chips and sequenced on the Ion Torrent Personal Genome Machine (PGM) (both from Thermo Fisher Scientific); the sequencing was performed using the PGM 200 Sequencing kit (Thermo Fisher Scientific).

Bioinformatics analysis. Raw data from PGM sequencing runs were processed using 2 software pipelines, Ion Reporter 4.0 (Thermo Fisher Scientific) and the CLC Genomics Workbench software version 6.5 (CLC Bio, Aarhus, Denmark). Sequencing reads were filtered for low-quality reads, trimmed for adapter sequences and tagged as belonging to the specific patient according to the barcode.

Using the spectrum of the expected mutations in the training set, the parameters for variant calling were established to minimize the number of false-positive results and guarantee the characterization of all the true-positive calls; the following filter thresholds were considered: minimum allele frequency for single-nucleotide polymorphism (SNP) and indel (SNP% ≥20), phred-like quality score of the called variant (Qcall ≥20) and depth of coverage (Depth ≥20).

Coverage assessment was carried out by the Ion Coverage Analysis plug-in v4.0-r77897 and CLC Bio Coverage statistics module. Moreover, alignments were visually inspected with Integrative Genome Viewer (28) to know the depth of analysis of each single nucleotide of the target region and the information concerning the read of the fragments with forward or reverse primer only.

We considered correctly covered, and hence suitable for mutations analysis, only exons (and their adjacent boundary sequences) with a read depth >20 reads (20X) for each targeted nucleotide; in detail, this parameter of coverage was requested for i) the 99% of the target region with respect to 11 genes previously screened in routine molecular diagnosis by Sanger sequencing; ii) the 95% of the target region for the remaining 8 genes.

Filtering approach and putative mutations assignment. To distinguish potential disease-causing mutations from common variants with a minor allele frequency (MAF) ≥1%, the nucleotide alterations were initially filtered against the variations reported in dbSNP138 (http://www.ncbi.nlm.nih.gov/SNP/), the HapMap v3.3, the Exome Variant Server (EVS; http://evs.gs.washington.edu/EVS/), the 1000 Genomes Project (www.1000genomes.org) hg19 (patch9) and the Exome Aggregation Consortium (ExAC; exac.broadinstitute.org).

Nonsense, frameshift, canonical splice site (±2 bp) mutations, together with missense mutations already unequivocally described as associated with the HCM phenotype (or with other forms of cardiomyopathies), and reported in the Human Genome Mutation Database (29) (HGMD, http://www.hgmd.org/; release 2015.4) as disease-causing mutations (DM), were considered as 'pathogenic variants'.

To evaluate the effect on protein function of the missense mutations not described in the literature or annotated in HGMD as DM? (DM of questionable pathological relevance), the *in silico* prediction of pathogenicity was established by Polyphen2 (http://genetics.bwh.harvard.edu/pph2/), Mutation Taster (http://www.mutationtaster.org/) and SIFT human protein (http://sift.jcvi.org/) algorithms. Afterward, we classified these missense mutations either as 'pathogenic variants' when the pathogenic impact was predicted by all algorithms or as 'likely pathogenic variants' when the pathogenic impact was predicted by 2 out of 3 algorithms.

Taking into account the stringent above-mentioned criteria, we evaluated that, in the training set, 67 out of 73 expected mutations were classifiable as 'pathogenic variants', while the remaining 6 were predicted as 'likely pathogenic variants'; of these, 52 mutations were annotated in HGMD.

Sanger sequencing of uncovered regions and validations of putative variants. Using Sanger sequencing, we analyzed the exons classified as uncovered in order to reach the percentage of target region correctly covered; moreover, the new non-synonymous nucleotide variants identified were also confirmed by Sanger sequencing.

In brief, exons containing the nucleotide variants were amplified using Taq Platinum (Invitrogen, Carlsbad, CA, USA) with specific flanking primers and sequenced using Big Dye v3.1 (Thermo Fisher Scientific); fragments of PCR and products of sequencing were purified by Agencourt AMPure XP and CleanSEQ, respectively, on automated station Biomek FX (Beckman Coulter). Sequencing was carried out on 3130 and 3730 xl automated sequencers (Thermo Fisher Scientific). Data analysis was performed using SeqScape v2.5 software (Thermo Fisher Scientific).

The history of atrial fibrillation between the different groups of patients was compared using Fisher's exact test. A p-value <0.05 was considered to indicate a statistically significant difference.

Results

IACP performance. To verify the theoretical coverage of the 19 genes, all 284 coding exons were analyzed with IAD software: 259 (91.2%) were ascribed to theoretical covered exons. The NGS analysis of the 73 samples (the training set) showed a coverage >20X for each target nucleotide into 253 exons (97.7%) (Table I). The remaining exons were classifiable with unsuitable coverage and therefore were screened by conventional (Sanger) sequencing.

Table I. List of HCM genes included in the NGS panel and percentage of investigated exons that are correctly profiled.

Gene	Total	*MYH7*	*MYBPC3*	*TNNT2*	*ACTC1*	*TPM1*	*TNNI3*	*MYL2*	*MYL3*	*GLA*	*LAMP2*	*PRKAG2*	*MYH6*	*TNNC1*	*ANKRD1*	*MYOM1*	*MYOZ2*	*CAV3*	*CALR3*	*VCL*
No. of exons submitted into 'Ion AmpliSeq Designer' (IAD)	284	38	34	16	6	10	8	7	6	7	9	16	37	6	9	37	5	2	9	22
No. of theoretical exons correctly covered by IAD	259	37	31	16	6	9	8	7	5	7	9	11	29	5	9	36	5	2	7	20
Total theoretical exons correctly covered by IAD/ total exons submitted into IAD										259/284 (91.2%)										
No. of exons successfully sequenced with coverage >20X for each targeted nucleotide	253	35	29	15	6	8	7	7	5	7	9	10	27	6	9	36	5	2	9	21
Total exons successfully sequenced/total exons correctly covered by IAD										253/259 (97.7%)										

NGS. next generation sequencing; HCM, hypertrophic cardiomyopathy; IAD, Ion AmpliSeq Designer.

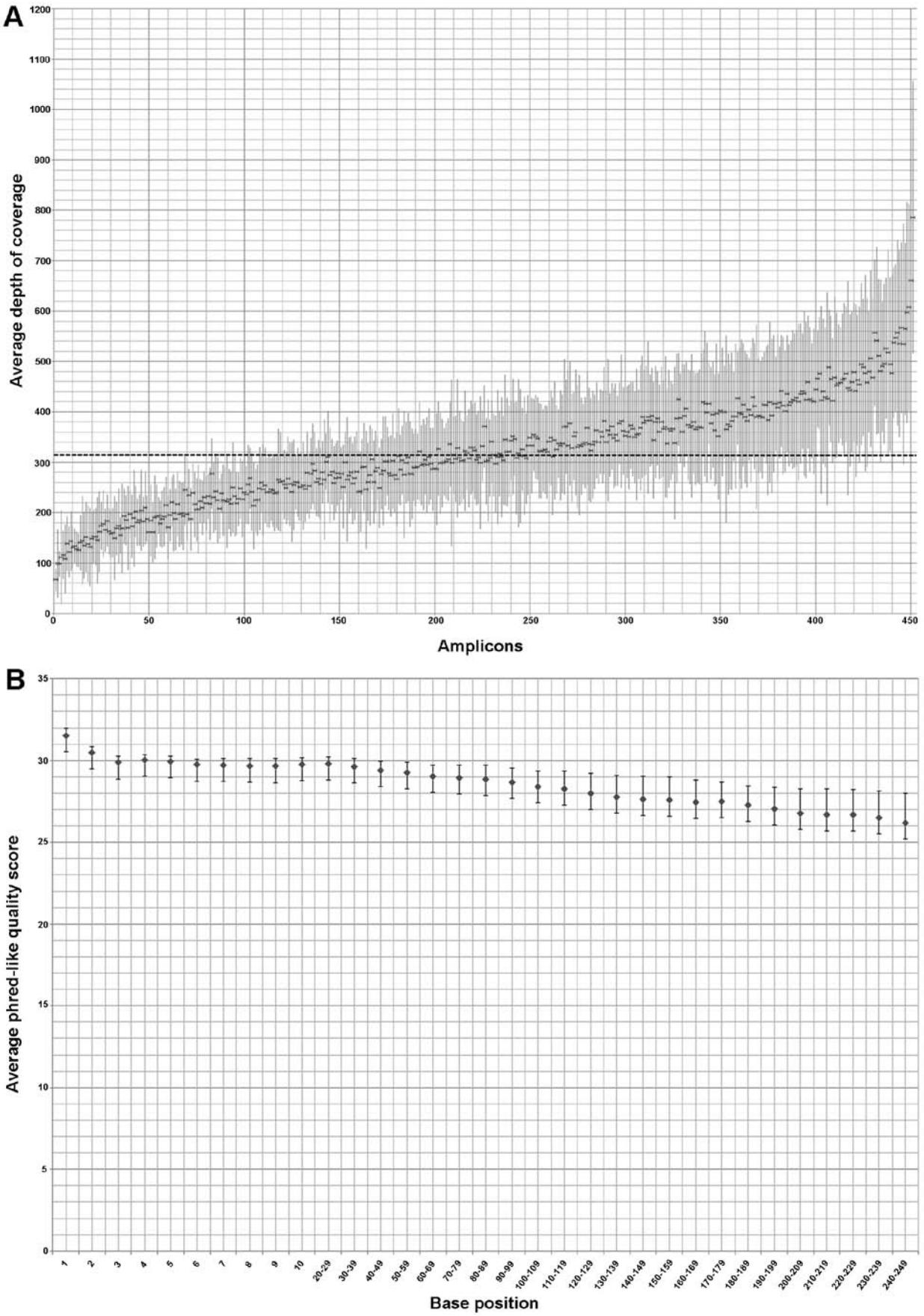

Figure 1. Depth of coverage and phred-like quality score of 73 samples belonging to training set; the dots and the bars represent the mean values and standard deviation, respectively. (A) Distribution of the average depth of coverage of all 452 amplicons (ordered according to the mean coverage, from the least to the most represented in the mean depth of coverage per-amplicon); the dashed line indicates the mean coverage (318X) concerning the 452 enriched amplicons of all patients. (B) Distribution of the average phred-like quality score related to each base of every amplicon that composes the alignment: the values are included between 26,2 and 31,5.

The mean depth of coverage per amplicon in the 73 samples of the training set was 318X and only 21 (4.6%) out of 452 amplicons showed a mean depth <150 reads (Fig. 1A). Six out of the 73 samples had an average read depth <150X and, among these, only 2 samples had an average read depth <100X.

The average phred-like quality score respect at each base position of the training set ranged between 26.2 and 31.5, with the minimum and maximum value of the standard deviation equal to 0.41 and 1.79, respectively (Fig. 1B).

The training set: 'PGM™ Runs' evaluation in covered regions shows expected and additional mutations. The IACP sequencing of the training set confirmed the presence of 72 out of 73 expected mutations (detection rate of approximately 99%) with the known allelic status (Table II). In one sample we missed the deletion of the nucleotide at the position 2610 into *MYBPC3* that is located within a homopolymer of 6 cytosines; in addition, in all samples, we observed the false-positive call *MYH7*:c.136T>C.

Furthermore, following 'PGM Runs' evaluation of the genes not previously investigated by Sanger sequencing, we identified 15 additional mutations (Table II) of which 10 were in genes encoding proteins different from (TTms) (4 were in genes encoding a protein located in the M-band, 2 were in encoding Z-disk constituents genes, 2 were in metabolic genes and 2 were in the *CAV3* gene). Taking into account the stringent criteria established in the 'Patients and methods' section, 10 out of 15 additional mutations could be ascribed to the category 'pathogenic variants', while the remaining 5 were classified as 'likely pathogenic variants' (Table II).

The training set: the additional mutations are identified in HCM subjects with arrhythmias or with pre-excitation syndrome. The 15 additional mutations belong to 11 out of 73 patients (15%) (Table III). In 2 patients, we identified only mutations of genes encoding TTm proteins, while in the remaining 9 patients, we characterized co-occurring mutations of genes encoding TTm/non-TTm proteins. Three out of 9 subjects with mutations of genes encoding TTm and non-TTm proteins had a personal history characterized by atrial fibrillation and non-sustained ventricular tachycardia episodes. Additionally, the NGS re-analysis permitted the identification of: i) two mutations in the *MYL2* gene in one teenager affected by hypertrophic obstructive cardiomyopathy that initially, following Sanger analysis, was classified as wild-type; ii) the missense mutation *LAMP2*:p.(Val310Ile), already described as causative of Danon disease, in a young female affected by HCM and with the typical Wolff-Parkinson-White (WPW) electrocardiographic pattern (shortened PR interval and delta wave).

The discovery set: PGM™ Runs evaluation for 19 HCM-related genes in 19 patients. The IACP sequencing of 19 DNA samples, and the following PGM Runs evaluation for all genes of the panel, allowed the identification of 20 mutations in 7 genes (Table IV).

Thirteen mutations were identified in 2 major sarcomeric genes, *MYBPC3* and *MYH7*; all 13 mutations were classified as 'pathogenic variants'.

The remaining 7 mutations were identified in the following genes: i) *MYH6* (2 mutations in thick filament); ii) *MYOM1* (2 mutations in M-band protein); iii) *MYOZ2* (one mutation in Z-disk constituent); iv) *GLA* and *LAMP2* (one mutation each in metabolic genes). Four mutations were classified as 'pathogenic variants' and the remaining 3 were considered as 'likely pathogenic variants'. No false-positive result was identified in our discovery set.

The discovery set: mutations in genes encoding non-TTm proteins are identified in borderline HCM status and in an HCM subject with an extremely complex phenotype. The 20 mutations were identified in 15 out of 19 patients (Table V). A single mutant allele in genes encoding non-TTm proteins was identified in 3 patients without a family history of HCM; by contrast, the 5 patients that had a family history of HCM carried a single mutant allele in genes encoding TTm proteins. Two out of 3 patients with only a single mutant allele in genes (*LAMP2* for female patient, *MYOM1*) encoding non-TTm proteins had a diagnosis of borderline HCM, while the male patient with co-occuring mutations in genes encoding TTm proteins (*MYBPC3* and *MYH6*) and in the *GLA* gene showed the diagnostic parameter of HCM (LVWT, 19 mm) together with a history of atrial fibrillation and multiorgan involvement (skin, eyes, ears and thyroid), typical of Fabry disease of male patients.

Discussion

Hereditary HCM is historically known as an autosomal dominant disease and is associated mainly with mutations in the *MYBPC3* and *MYH7* genes. Over the past years, it has become increasingly evident that the same pathogenic mutation, even within the same family, shows a highly variable presentation and clinical course in different individuals (18,19). Contextually, it has been shown that hereditary HCM can also be associated with mutations of genes that do not encode TTm proteins (7-12) and, in some patients, more than one pathogenic mutation has been identified (22). In consideration of this complexity, as well as the possibility of shedding new light on the relationship between the genetic and the phenotypic heterogeneity, in this study, we designed a target NGS panel, using the Ion Torrent PGM system, in order to simultaneously analyze a total of 19 genes encoding not only TTm proteins, but also other sarcomeric proteins and some non-sarcomeric proteins that cause HCM phenocopies (1,3,13).

Our training set allowed us to calibrate the NGS methodology (enrichment, library preparation and bioinformatics analysis parameters). With respect to all 284 coding exons, the coverage at >20X depth for each target nucleotide (see Patients and methods) includes 253 out of 259 exons correctly profiled by IAD. This not uniform coverage of our design, as previously reported, could be linked to aspects concerning the target gene enrichment strategy and at the efficiencies of PCR amplification during library preparation (30). It has been reported that regions with high a GC content are more difficult to amplify and, also, the PGM system has showed a poor coverage within AT-rich exonic segments of *P. falciparum* (31). Additionally, in our NGS gene panel, specific genomic regions, such as those with a high homology of the *MYH6* and *MYH7* genes, contribute greatly to this inadequate coverage.

With respect to the target NGS study by Gómez *et al* (32), our diagnostic HCM workflow provides the analysis of a larger

Table II. Pathogenic or likely pathogenic variants identified by Ion AmpliSeq™ Custom Panel (IACP) sequencing into the training set following Runs evaluation for expected and additional mutations of 73 HCM patients.

Gene	Nucleotide change	Effect on protein	Annotation[b] (HGMD or NCBI)	Predicted impact on protein	Variant frequency	Coverage	Q score
ACTC1	c.707C>T	p.(Ser236Phe)	KU324679 (present study)	Pathogenic[d]	0.48	348	31.81
ACTC1	c.992T>A	p.(Ile331Asn)	KU324680 (present study)	Pathogenic[d]	0.48	41	29.5
GLA	c.514T>C	p.(Cys172Arg)	CM003746 [DM]	Pathogenic[c]	0.5	1116	31.87
GLA	c.1146C>A	p.(Cys382*)	KU508439 (present study)	Pathogenic[c]	0.32	671	25.31
LAMP2	c.239G>T	p.(Gly80Val)	KU508440 (present study)	Likely pathogenic[d]	0.49	271	28.6
LAMP2	c.741+1G>T	Mis-splicing	KU557502 (present study)	Pathogenic[c]	0.5	177	29.23
MYBPC3	c.223G>A	p.(Asp75Asn)	HM090070 [DM]	Pathogenic[c]	0.46	173	30.15
MYBPC3	c.506-2A>C	Mis-splicing	CS109051 [DM]	Pathogenic[c]	0.43	191	28.22
MYBPC3	c.557C>T	p.(Pro186Leu)	CM106110 [DM]	Pathogenic[c]	0.42	45	29.47
MYBPC3	c.649A>G	p.(Ser217Gly)	CM109108 [DM?]	Pathogenic[d]	0.48	295	26.67
MYBPC3	c.772G>A	p.(Glu258Lys)	CM981322 [DM]	Pathogenic[c]	0.5	526	30.12
MYBPC3	c.913_914delTT	p.(Phe305ProfsX27)	CD086092 [DM]	Pathogenic[c]	0.45	410	27.48
MYBPC3	c.977G>A	p.(Arg326Gln)	CM020155 [DM?]	Likely pathogenic[d]	0.45	451	27.1
MYBPC3	c.1003C>T	p.(Arg335Cys)	KU508441 (present study)	Pathogenic[d]	0.5	288	31.23
MYBPC3	c.1090G>A	p.(Ala364Thr)	CM152770 [DM]	Pathogenic[c]	0.53	232	27.45
MYBPC3	c.1112C>G	p.(Pro371Arg)	CM102043 [DM]	Pathogenic[c]	0.47	355	28.62
MYBPC3	c.1174delG	p.(Ala392Leufs*14)	CD086093 [DM]	Pathogenic[c]	0.51	183	26.15
MYBPC3	c.1458-1G>A	Mis-splicing	rs397515903 (dbSNP)	Pathogenic[c]	0.61	241	29.65
MYBPC3	c.1505G>A	p.(Arg502Gln)	CM981325 [DM]	Pathogenic[c]	0.43	521	30
MYBPC3	c.1564G>A	p.(Ala522Thr)	CM057197 [DM]	Pathogenic[c]	0.55	182	29.82
MYBPC3	c.1591G>C	p.(Gly531Arg)	CM068013 [DM]	Pathogenic[c]	0.57	142	26.98
MYBPC3	c.1615A>G	p.(Ile539Val)	CM1412245 [DM]	Pathogenic[c]	0.51	215	29.22
MYBPC3	c.1624G>C	p.(Glu542Gln)	CM971007 [DM]	Pathogenic[c]	0.5	176	32.78
MYBPC3	c.1670dup	p.(Ala558Argfs*10)	KU508442 (present study)	Pathogenic[c]	0.54	396	29.51
MYBPC3	c.1696T>A	p.(Cys566Ser)	KU508443 (present study)	Pathogenic[d]	0.35	440	28.53
MYBPC3	c.1790G>A	p.(Arg597Gln)	CM122972 [DM]	Pathogenic[c]	0.51	635	31.83
MYBPC3	c.2198G>A	p.(Arg733His)	CM092564 [DM]	Pathogenic[c]	0.44	159	29.97
MYBPC3	c.2258dupT	p.(Lys754Glufs*79)	CI063699 [DM]	Pathogenic[c]	0.56	167	29.6
MYBPC3	c.2309-2A>G	Mis-splicing	CS043648 [DM]	Pathogenic[c]	0.48	126	29.91
MYBPC3	c.2311G>A	p.(Val771Met)	CM056362 [DM]	Pathogenic[c]	0.52	246	31.59
MYBPC3	c.2429G>A	p.(Arg810His)	CM034546 [DM]	Pathogenic[c]	0.26	528	31.23
MYBPC3	c.2449C>G	p.(Arg817Gly)	KU508444 (present study)	Pathogenic[d]	0.42	105	22.86
MYBPC3	c.2610delC[a]	p.(Ser871Alafs*8)	CD0910615 [DM]	Pathogenic[c]	-	-	-
MYBPC3	c.2618C>T	p.(Pro873Leu)	CM116747 [DM]	Pathogenic[c]	0.75	106	24
MYBPC3	c.2864_2865 delCT	p.(Pro955Argfs*95)	CD982813 [DM]	Pathogenic[c]	0.5	599	28.31
MYBPC3	c.2906-2A>G	Mis-splicing	KU508445 (present study)	Pathogenic[c]	0.46	233	22.6
MYBPC3	c.2992C>G	p.(Gln998Glu)	CM043548 [DM]	Pathogenic[c]	0.48	120	28.12
MYBPC3	c.3065G>C	p.(Arg1022Pro)	CM058261 [DM?]	Pathogenic[d]	0.42	223	27.13
MYBPC3	c.3103G>A	p.(Ala1035Thr)	rs552505566 (present study)	Likely pathogenic[d]	0.39	46	31
MYBPC3	c.3192dupC	p.(Lys1065Glnfs*12)	CI068119 [DM]	Pathogenic[c]	0.51	95	28.26
MYBPC3	c.3331-1G>A	Mis-splicing	KU508446 (present study)	Pathogenic[c]	0.45	78	30.25
MYBPC3	c.3364A>T	p.(Thr1122Ser)	KU508447 (present study)	Pathogenic[d]	0.6	102	30.52
MYBPC3	c.3370T>C	p.(Cys1124Arg)	CM119645 [DM]	Pathogenic[c]	0.55	137	28.65
MYBPC3	c.3551C>A	p.(Thr1184Asn)	CM086857 [DM]	Pathogenic[c]	0.51	184	29.78
MYBPC3	c.3560T>G	p.(Leu1187Arg)	CM086863 [DM]	Pathogenic[c]	0.48	198	29.1
MYBPC3	c.3697C>T	p.(Gln1233*)	CM014069 [DM]	Pathogenic[c]	0.48	422	30.3
MYBPC3	c.3775C>T	p.(Gln1259*)	KU508448 (present study)	Pathogenic[c]	0.5	263	23.1

Table II. Continued.

Gene	Nucleotide change	Effect on protein	Annotation[b] (HGMD or NCBI)	Predicted impact on protein	Variant frequency	Coverage	Q score
MYH7	c.676G>A	p.(Ala226Thr)	KU319883 (present study)	Likely pathogenic[d]	0.54	120	26.77
MYH7	c.1208G>A	p.(Arg403Gln)	CM900168 [DM]	Pathogenic[c]	0.5	418	31.68
MYH7	c.1549C>A	p.(Leu517Met)	CM034554 [DM]	Pathogenic[c]	0.49	201	26.95
MYH7	c.1988G>A	p.(Arg663His)	CM993620 [DM]	Pathogenic[c]	0.49	247	28.56
MYH7	c.2102G>A	p.(Gly701Asp)	KU508453 (present study)	Pathogenic[d]	0.51	431	32.93
MYH7	c.2804A>T	p.(Glu935Val)	KU508449 (present study)	Pathogenic[d]	0.62	174	32.51
MYH7	c.2890G>C	p.(Val964Leu)	CM087588 [DM?]	Pathogenic[d]	0.42	179	27.32
MYH7	c.3113T>C	p.(Leu1038Pro)	CM095777 [DM]	Pathogenic[c]	0.5	194	28.45
MYH7	c.3133C>T	p.(Arg1045Cys)	CM086874 [DM]	Pathogenic[c]	0.48	159	27.57
MYH7	c.3236G>A	p.(Arg1079Gln)	CM102044 [DM]	Pathogenic[c]	0.51	129	31.65
MYH7	c.4040A>G	p.(Tyr1347Cys)	KU508450 (present study)	Pathogenic[d]	0.5	202	29.54
MYH7	c.4348G>A	p.(Asp1450Asn)	CM122821 [DM]	Pathogenic[c]	0.41	51	27.85
MYH7	c.4472C>G	p.(Ser1491Cys)	CM050712 [DM?]	Likely pathogenic[d]	0.52	522	28.63
MYH7	c.4690G>A	p.(Glu1564Lys)	KU508451 (present study)	Likely pathogenic[d]	0.25	522	28.46
MYH7	c.5287G>A	p.(Ala1763Thr)	CM1411014 [DM]	Pathogenic[c]	0.49	348	30.56
PRKAG2	c.905G>A	p.(Arg302Gln)	CM011949 [DM]	Pathogenic[c]	0.51	438	22.13
TNNI3	c.220C>G	p.(Arg74Gly)	KU508452 (present study)	Pathogenic[d]	0.22	362	26.83
TNNI3	c.439G>C	p.(Val147Leu)	CM1411021 [DM]	Pathogenic[c]	0.99	538	26.04
TNNI3	c.485G>A	p.(Arg162Gln)	CM034575 [DM]	Pathogenic[c]	0.57	234	28.55
TNNI3	c.581A>G	p.(Asn194Ser)	CM1414551 [DM]	Pathogenic[c]	0.56	178	27.41
TNNT2	c.83C>T	p.(Ala28Val)	CM063210 [DM]	pathogenic[c]	0.52	174	26.89
TNNT2	c.247G>A	p.(Glu83Lys)	CM034581 [DM]	Pathogenic[c]	0.46	307	32.69
TNNT2	c.275G>A	p.(Arg92Gln)	CM951218 [DM]	Pathogenic[c]	0.46	897	25.98
TNNT2	c.536C>T	p.(Ser179Phe)	CM002871 [DM]	Pathogenic[c]	0.5	699	26.38
TNNT2	c.832C>T	p.(Arg278Cys)	CM951222 [DM]	Pathogenic[c]	0.6	126	29.11
TPM1	c.644C>T	p.(Ser215Leu)	CM087722 [DM]	Pathogenic[c]	0.46	669	26.13
MYOM1	**c.139A>G**	p.(Ser47Gly)	rs202145133 (dbSNP)	Likely pathogenic[d]	0.37	50	25.25
MYOM1	**c.1514A>C**	p.(Glu505Ala)	KU508437 (present study)	Likely pathogenic[d]	0.58	68	27.97
MYOM1	**c.2087G>A**	p.(Arg696His)	KU508438 (present study)	Pathogenic[d]	0.51	662	31.44
MYOM1	**c.2110G>A**	p.(Glu704Lys)	rs149528866 (dbSNP)	Likely pathogenic[d]	0.47	258	27.57
MYH6	**c.3883G>C**	p.(Glu1295Gln)	rs34935550 (dbSNP)	Pathogenic[d]	0.46	74	28.3
MYH6	**5476_5477delGGinsAA**	p.(Gly1826Asn)	CX103031 [DM]	Pathogenic[c]	0.3	361	23.38
MYH6	**c.5797-2A>G**	Mis-splicing	KU508454 (present study)	Pathogenic[c]	0.49	424	19.97
MYOZ2	**c.36A>C**	p.(Lys12Asn)	KU508455 (present study)	Pathogenic[d]	0.5	350	30.44
LAMP2	**c.928G>A**	p.(Val310Ile)	CM057189 [DM]	Pathogenic[c]	0.49	103	31.68
CAV3	**c.216C>G**	p.(Cys72Trp)	CM980306 [DM]	Pathogenic[c]	0.31	393	27.2
CAV3	**c.233C>T**	p.(Thr78Met)	CM065052 [DM]	Pathogenic[c]	0.49	712	31.89
ANKRD1	**c.827C>T**	p.(Ala276Val)	CM095438 [DM?]	Likely pathogenic[d]	0.51	330	30
MYL2	**c.206T>C**	p.(Met69Thr)	KU319885 (present study)	Pathogenic[d]	0.46	315	31.78
MYL2	**c.401A>C**	p.(Glu134Ala)	CM086879 [DM]	Pathogenic[c]	0.51	438	22.13
GLA	**c.937G>T**	p.(Asp313Tyr)	CM930335 [DM?]	Likely pathogenic[d]	1	517	25.61

[a]Undetected mutation after NGS analysis. [b]Reference nucleotide data: starting with CM/CX/CI/CD/CS/HM for variants annotated in HGMD; starting with KU/rs for variants annotated in NCBI (GenBank, accession no./dbSNP). [c]Mutations annotated in Human Genome Mutation Database (HGMD, http://www.hgmd.org/; release 2015.4) as DM (disease-causing mutations) and nonsense, frameshift, canonical splice site (±2 bp) mutations identified in this study (or annotated only in dbSNP) were classified as 'pathogenic'. [d]The missense mutations not annotated in HGMD and those described as 'DM of questionable pathological relevance' (DM?) were classified as i) 'pathogenic variants' if the pathogenic impact was predicted by all algorithms; ii) 'likely pathogenic variants' if the pathogenic impact was predicted by two out of three algorithms. Bold font indicates the additional mutations identified only by NGS analysis. NGS, next generation sequencing; HCM, hypertrophic cardiomyopathy.

Table III. HCM patients belonging at training set that, after NGS analysis, show pathogenic or likely pathogenic variants in genes originally not analyzed using Sanger sequencing.

No. of patient (gender)	Age at onset (years)	LVWT (mm)	AICD (yes, no)	Family history of HCM/SCD (yes, no/yes, no)	Other medical (recurrent or episodic) issues	LVEF (%)	Mutations
#94 (F)	30	24	No	No/no	None	65	*MYBPC3*: c.1174delG p.(Ala392fsX405) *MYH7*: c.161G>T p.(Arg54Leu)[a] *TNNT2*: c.832C>T p.(Arg278Cys) ***MYOM1*: c.2087G>A p.(Arg696His)**
#241 (F)	17	<15[b]	No	No/no	H-tx	44	*TNNT2*: c.83C>T p.(Ala28Val) *LAMP2*: c.741+1G>T ***MYOM1*: c.1514A>C p.(Glu505Ala)**
#314 (M)	48	21	No	Yes/no	History of hypertension	62	*MYBPC3*: c.1458-1G>A ***MYOM1*: c.139A>G p.(Ser47Gly)** ***MYOM1*: c.2110G>A p.(Glu704Lys)** ***MYH6*: c.3883G>C p.(Glu1295Gln)**
#656 (M)	56	15	No	No/no	AF, NSVT	65	*MYBPC3*: c.2610del p.(Ser871AlafsX8) ***GLA*: c.937G>T p.(Asp313Tyr)**
#692 (F)	65	22	No	Yes/no	History of hypertension	65	*MYBPC3*: c.1624G>C p.(Glu542Gln) ***MYOZ2*: c.36A>C p.(Lys12Asn)**
#748 (F)	16	17	Yes	Yes/yes	NSVT, AF, WPW syndrome	60	*MYH7*: c.5287G>A p.(Ala1763Thr) ***LAMP2*: c.928G>A p.(Val310Ile)**
#787 (M)	45	32	Yes	Yes/no	Dyslipidemia, nodular thyroid disease, NSVT, AF, AFL	60	*MYBPC3*: c.2429G>A p.(Arg810His) *MYBPC3*: c.3370T>C p.(Cys1124Arg) ***CAV3*: c.216C>G p.(Cys72Trp)**
#800 (F)	25	16	No	Yes/yes	None	50	*TNNT2*: c.536C>T p.(Ser179Phe) ***MYH6*: c.5797-2A>G** ***MYH6*: c.5476_5477delinsAA p.(Gly1826Asn)**
#834 (F)	14	24	Yes	Yes/yes	LGE at CMR imaging	68	*TNNT2*: c.275G>A p.(Arg92Gln) ***CAV3*: c.233C>T p.(Thr78Met)**
#854 (M)	46	19	No	Yes/no	None	60	*MYBPC3*: c.506-2A>C ***ANKRD1*: c.827C>T p.(Ala276Val)**
#865 (M)	14	28	Yes	Yes/no	HOCM, myocardial bridge on AIA, v-fib	60	***MYL2*: c.401A>C p.(Glu134Ala)** ***MYL2*: c.206T>C p.(Met69Thr)**

Bold font indicates additional mutations in *MYH6*, *MYL2* or in genes encoding non-TTm proteins identified only by NGS analysis. [a]Uncovered regions: mutation identified only by Sanger sequencing; [b]Original borderline diagnosis of HCM has been modified in dilated cardiomyopathy. WPW, Wolff-Parkinson-White; AICD, automatic implantable cardioverter defibrillator; H-tx, heart transplantation; LVWT, left ventricular wall thickness; AF, atrial fibrillation; NSVT, non-sustained ventricular tachycardia; AFL, atrial flutter; LGE, late gadolinium enhancement; AIA, anterior interventricular artery; CMR, cardiac magnetic risonance; v-fib, ventricular fibrillation; HOCM, hypertrophic obstructive cardiomyopathy; LVEF, left ventricular ejection fraction; SCD, sudden cardiac death; NGS, next generation sequencing; HCM, hypertrophic cardiomyopathy.

Table IV. Pathogenic or likely pathogenic variants identified by Ion AmpliSeq™ Custom Panel (IACP) sequencing into the discovery set consisting of 19 HCM DNA samples.

	Gene	Nucleotide change	Effect on protein	Annotation (HGMD or NCBI)	Predicted impact on protein	Variant frequency	Coverage	Q score
13 mutations	*MYBPC3*	c.506-2A>C	Mis-splicing	CS152769 [DM]	Pathogenic[a]	0.45	273	30.76
in two major	*MYBPC3*	c.639C>A	p.(Tyr213*)	KU319882 (present study)	Pathogenic[a]	0.52	385	32.15
sarcomeric genes	*MYBPC3*	c.649A>G	p.(Ser217Gly)	CM109108 [DM]	Pathogenic[a]	0.52	428	31.85
	MYBPC3	c.1409G>A	p.(Arg470Gln)	CM116865 [DM]	Pathogenic[a]	0.42	469	28.16
	MYBPC3	c.1505G>A	p.(Arg502Gln)	CM981325 [DM]	Pathogenic[a]	0.47	191	28.72
	MYBPC3	c.1564G>A	p.(Ala522Thr)	CM057197 [DM]	Pathogenic[a]	0.49	122	29.78
	MYBPC3	c.2309-2A>G	Mis-splicing	CS043648 [DM]	Pathogenic[a]	0.5	176	29.58
	MYBPC3	c.2311G>A	p.(Val771Met)	CM056362 [DM]	Pathogenic[a]	0.56	128	31.5
	MYBPC3	c.2429G>A	p.(Arg810His)	CM034546 [DM]	Pathogenic[a]	0.24	412	33.22
	MYBPC3	c.3617G>A	p.(Gly1206Asp)	CM057198 [DM]	Pathogenic[a]	0.5	649	30.63
	MYH7	c.2302G>C	p.(Gly768Arg)	CM109192 [DM]	Pathogenic[a]	0.42	271	29.17
	MYH7	c.2507T>C	p.(Ile836Thr)	KU319884 (present study)	Pathogenic[b]	0.5	303	31.87
	MYH7	c.5302G>A	p.(Glu1768Lys)	CM042429 [DM]	Pathogenic[a]	0.57	326	32.63
7 mutations	*MYH6*	c.3883G>C	p.(Glu1295Gln)	rs34935550 (dbSNP)	Pathogenic[b]	0.41	86	27.89
in other genes	*MYH6*	c.5111C>T	p.(Ala1704Val)	KU508434 (present study)	Likely pathogenic[b]	0.47	553	32.91
	MYOM1	c.432-1G>T	Mis-splicing	KU508435 (present study)	Pathogenic[a]	0.51	773	30.67
	MYOM1	c.1655G>A	p.(Gly552Asp)	KU508436 (present study)	Likely pathogenic[b]	0.44	265	32.35
	GLA	c.718_719delAA	p.(Lys240Glufs*9)	CD941686 [DM]	Pathogenic[a]	1	270	32.53
	LAMP2	c.661G>A	p.(Gly221Arg)	CM137777 [DM?]	pathogenic[b]	0.55	115	30.42
	MYOZ2	c.488T>C	p.(Leu163Ser)	rs143345726 (dbSNP)	Likely pathogenic[b]	0.45	319	32.86

Reference nucleotide data: starting with CM/CD/CS for variants annotated in HGMD; starting with KU/rs for variants annotated in NCBI (GenBank, accession number/dbSNP). [a]Mutations annotated in Human Genome Mutation Database (HGMD, http://www.hgmd.org/; release 2015.4) as DM (disease-causing mutations) and nonsense, frameshift or canonical splice site (±2 bp) mutations identified in this study (or annotated only in dbSNP) were classified as 'pathogenic'. [b]The missense mutations not annotated in HGMD and those described as 'DM of questionable pathological relevance' (DM?) were classified as i) 'pathogenic variants' if the pathogenic impact was predicted by all algorithms; ii) 'likely pathogenic variants' if the pathogenic impact was predicted by two out of three algorithms. HCM, hypertrophic cardiomyopathy.

Table V. HCM patients belonging at discovery set that, after NGS analysis, show pathogenic or likely pathogenic variants.

No. of patient (gender)	Age at onset (years)	LVWT (mm)	AICD (yes, no)	Family history of HCM/SCD (yes, no/yes, no)	Other medical (recurrent or episodic) issues	LVEF (%)	Mutations
#890 (F)	72	<15[a]	No	No/no	Aortic root enlargement History of hypertension; Intermittent LBBB	~50	***LAMP2*: c.661G>A p.(Gly221Arg)**
#892 (F)	30	19	No	No/no	LGE at CMR imaging; hypercholesterolemia; NSVT	61	*MYBPC3*: c.1505G>A p.(Arg502Gln) *MYBPC3*: c.1564G>A p.(Ala522Thr) *MYBPC3*: c.2311G>A p.(Val771Met)
#894 (M)	6	24	No	No/no	T2DM	60	*MYBPC3*: c.2429G>A p.(Arg810His)
#895 (M)	58	<15[b]	Yes	Yes/no	None	26	*MYBPC3*: c.2309-2A>G
#898 (F)	1	11	No	Yes/no	None	70	*MYH7*: c.5302G>A p.(Glu1768Lys)
#902 (F)	25	19	Yes	No/no	Hypothyroidism PVC, NSVT	64	*MYH7*: c.2507T>C p.(Ile836Thr)
#903 (F)	52	18	Yes	No/no	Myasthenia gravis, T2DM, HepC, PVC, PACs, PSVT, SND	59	***MYOZ2*: c.488T>C p.(Leu163Ser)**
#905 (M)	30	NA	Yes	Yes/no	H-tx	NA	*MYH7*: c.2302G>C p.(Gly768Arg) ***MYOM1*: c.1655G>A p.(Gly552Asp)**
#906 (F)	58	15	No	No/no	None	NA	*MYBPC3*: c.3617G>A p.(Gly1206Asp)
#907 (M)	37	<15[a]	No	No/no	ECG abnormalities	60	***MYOM1*: c.432-1G>T**
#908 (M)	20	<15[b]	No	Yes/no	H-tx, T2DM	50	***MYH6*: c.5111C>T p.(Ala1704Val)**
#909 (M)	31	<15[a]	No	Yes/no	None	75	*MYBPC3*: c.1409G>A p.(Arg470Gln)
#910 (F)	17	23	No	No/no	None	76	*MYBPC3*: c.639C>A p.(Tyr213*)
#913 (M)	12	19	No	No/no	Angiokeratomas right ear hearing loss Visual impairment hypothyroidism, AF, NSVT	60	*MYBPC3*: c.649A>G p.(Ser217Gly) ***GLA*: c.718_719delAA p.(Lys240Glufs*9)** ***MYH6*: c.3883G>C p.(Glu1295Gln)**
914 (M)	22	34	Yes	No/no	HOCM, LGE at CMR imaging, NSVT	65	*MYBPC3*: c.506-2A>C

Bold font indicates mutations in *MYH6* and in genes encoding non-TTm proteins that would not been identified without NGS analysis. [a]Diagnosis of borderline HCM; [b]original diagnosis of borderline HCM has been modified in dilated cardiomyopathy. PAC, premature atrial contractions; H-tx, heart transplantation; T2DM, type 2 diabetes mellitus; LVWT, left ventricular wall thickness; SND, sinus node dysfunction; AF, atrial fibrillation; hep C, hepatitis C; LBBB, left bundle branch block; AICD, automatic implantable cardioverter defibrillator; LVEF, left ventricular ejection fraction; SCD, sudden cardiac death; LGE, late gadolinium enhancement; CMR, cardiac magnetic risonance; NSVT, non-sustained ventricular tachycardia; PVC, premature ventricular contractions; HOCM, hypertrophic obstructive cardiomyopathy; PSVT, paroxysmal supraventricular tachycardia; NA, not available; NGS, next generation sequencing; HCM, hypertrophic cardiomyopathy.

number of genes, including some which encode for proteins different from myofilaments of the sarcomere and 3 genes responsible for the HCM phenocopy. Moreover, through a combined strategy with Sanger sequencing, we ensured a depth of coverage >20X for each target nucleotide; other studies (15,33) have reported a higher coverage depth, but only as a general mean coverage.

According to the training set analysis, we observed only one false-negative: our non-identified mutation is located into a short homopolymer region that, as has already been reported (31), represents a DNA motif particularly prone to this error, as in these regions, there is not a linear correlation of pH between signal-generated and the number of nucleotides incorporated; the only false-positive call *MYH7*:c.136T>C was already reported in another study (32) and it is located in the first coding exon that had inappropriate coverage and hence, was necessarily analyzed by Sanger sequencing.

Our target NGS panel, applied to the training set encompassing 73 patients, allowed the identification of 15 additional mutations in 11 patients (Table III); these mutations were characterized in genes originally not analyzed by Sanger sequencing: 10 belong to genes encoding proteins of the sarcomere different from (TTms) and, of these, 4 are mutant alleles of the *MYOM1* gene that have previously been associated with HCM in a single study (7). One out of 10 patients, that originally showed wild-type status after Sanger analysis, carried 2 pathogenic alleles in the *MYL2* gene that could support the molecular diagnosis of hereditary HCM, whereas for the remaining 10 out of 63 patients, the newly identified mutation (that represents the co-occuring mutation together with other already described as causative of HCM) could contribute as a modifier of the clinical picture in the affected patients of each HCM family (3,16,22,33); for example, the WPW electrocardiographic pattern of patient #748 (female), that carries a mutant allele in the genes *LAMP2* (X-linked) and *MYH7*, has already been documented by Cheng *et al* (34) in some patients with Danon disease and mutation in the *LAMP2* gene.

Our target NGS panel, applied to the discovery set, allowed the identification of 20 mutations in 15 patients (Table V). If the molecular characterization of these patients was performed with the older diagnostic workflow, a mutant allele would have been identified only in 11 patients, as the analysis of *LAMP2* and *GLA* genes would have had to be specifically requested and the Sanger assay did not include the screening of the *MYOM1*, *MYOZ2* and *MYH6* genes.

The evaluation of the discovery set, even though it is represented by only 15 patients with mutations, seems to suggest that the presence of only one mutant allele in genes encoding non-TTm proteins (*LAMP2*, *MYOM1* and *MYOZ2*) is associated with a milder HCM status: 2 out of 3 patients had a diagnosis of borderline HCM and none of these 3 patients had a family history of HCM or SCD; at the same time, mutations in genes encoding TTm proteins have been identified in all patients that had a family history of HCM and in only one patient with a diagnosis of borderline HCM. Consistent with the findings of larger studies on genotype-phenotype correlations (35,36), although this study did not have this objective, we found that patients without myofilament mutations, encompassing a female subject with single mutant allele in the *LAMP2* (X-linked) gene, show a less severe phenotype.

Interestingly, among the 26 patients of which we report the clinical data, 4 out of 10 HCM subjects with concomitant mutations in genes encoding TTm and non-TTm proteins have also had a history of atrial fibrillation; although, this small sample can only suggest a trend, when the arrhythmia was compared between this subset of patients and the remaining 16 subjects carrying mutations in genes encoding TTm (13 patients) or non-TTm proteins (3 patients) only, the distribution was significantly different (Fisher's exact test, $p<0.05$).

Our data suggest that the screening of new genes using the NGS methodology increases the number of identified mutations. In particular, the discovery set has allowed us to increase the diagnostic yield from 58 to 79%. Additionally, with respect to the Sanger sequencing, the genotyping of the discovery set with NGS methodology has allowed a reduction in turn-around-time for HCM of approximately 75%.

Therefore, in our new diagnostic workflow, including the screening of genes encoding non-TTm proteins, despite the drawback represented by the need to combine targeted NGS and Sanger sequencing in order to obtain a depth of coverage >20X for each target nucleotide, the use of the Ion PGM system has showed the following advantages: i) an important decrease in the turn-around-time; ii) an increase in the diagnostic yield; iii) the detection of multiple mutations, or single mutant alleles in genes encoding non-TTm proteins, that contribute to better defining the genetic and phenotypic heterogeneity of HCM: mutations in genes encoding only non-TTm proteins seem to show a milder HCM status, whereas co-occuring mutations of genes encoding TTm and non-TTm proteins could explain the wide variability of the HCM phenotype.

Given the complexity of target NGS methodology, and as previously suggested by the guidelines of the American College of Medical Genetics and Genomics (37), when the genetic test is requested for clinical diagnostic purposes, this technique should be performed by highly specialized laboratories, i.e., laboratories with ISO9001 certification and possibly with the professional accreditation (in Italy SIGU-CERT, Italian Society of Human Genetics certification program).

The target NGS methodology, by permitting a more rapid analysis of a large number of causative genes, may prove to be useful in unveiling the significant genetic heterogeneity of this complex disease that, conjugated with the broad phenotypic heterogeneity, may improve genetic counselling and the clinical management of patients.

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Appendix

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