Genome sequencing as a first-line genetic test in familial dilated cardiomyopathy

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Purpose: We evaluated genome sequencing (GS) as an alternative to multigene panel sequencing (PS) for genetic testing in dilated cardiomyopathy (DCM).

Methods: Forty-two patients with familial DCM underwent PS and GS, and detection rates of rare single-nucleotide variants and small insertions/deletions in panel genes were compared. Loss-of-function variants in 406 cardiac-enriched genes were evaluated, and an assessment of structural variation was performed.

Results: GS provided broader and more uniform coverage than PS, with high concordance for rare variant detection in panel genes. GS identified all PS-identified pathogenic or likely pathogenic variants as well as two additional likely pathogenic variants: one was missed by PS due to low coverage, the other was a known disease-causing variant in a gene not included on the panel. No loss-of-function variants in the extended gene set met clinical criteria for pathogenicity. One BAG3 structural variant was classified as pathogenic.

Conclusion: Our data support the use of GS for genetic testing in DCM, with high variant detection accuracy and a capacity to identify structural variants. GS provides an opportunity to go beyond suites of established disease genes, but the incremental yield of clinically actionable variants is limited by a paucity of genetic and functional evidence for DCM association.

Keywords: Familial dilated cardiomyopathy; Panel sequencing; genome sequencing; Genetic testing; Molecular diagnosis

INTRODUCTION

Dilated cardiomyopathy (DCM) is a common heritable heart muscle disorder that frequently has a genetic etiology.1 Although long lists of disease-associated genes have been compiled,1 genetic testing yields positive results in relatively few individuals and has not been recommended as part of routine patient care.2 Knowing genotype status has enormous potential benefit for families, permitting tailored surveillance strategies and early detection of individuals at risk.3 The lack of results for most DCM families represents an unmet clinical need and a major roadblock for implementation of personalized therapy.

In recent years, next-generation sequencing has facilitated genetic testing by enabling high-throughput evaluation of multiple genes, including underinvestigated large genes with hundreds of coding exons. Available methods include multigene panel sequencing (PS), exome sequencing (ES), and genome sequencing (GS). PS uses libraries enriched for protein-coding regions of disease-associated genes. There is generally high sequence coverage and comparative studies with Sanger sequencing have found excellent reproducibility for variant detection.4 PS is widely used by clinical diagnostic laboratories with cardiomyopathy panel sizes increasing over time from <20 genes to >100 genes.5,6 The finite number of...
Committee. However, are increasingly implicated in human disease and enables gaps, particularly for high-probability disease genes. In addition to protein-coding sequences, GS uniquely provides information about the vast tracts of noncoding sequences that are increasingly implicated in human disease and enables high-resolution structural variant (SV) detection. However, because GS typically has a lower overall sequencing depth than PS and ES, its potential sensitivity for pathogenic variant (PV) screening has been questioned. Golbus and colleagues have recently reported promising results for GS in a pilot study of 11 DCM patients. A detailed appraisal of the role of GS for DCM genetic testing is now timely and warranted.

Here we compare PS and GS in a cohort of patients with familial DCM. We determined the concordance of PS and GS for rare variant detection, evaluated loss-of-function (LOF) variants in an extended gene panel, and performed the first comprehensive evaluation of SVs in DCM. Our data show that GS is a reliable method for screening established DCM disease genes as well as providing a wealth of sequence information for ongoing data mining in “unsolved” cases.

MATERIALS AND METHODS

Study subjects
Forty-two patients (19 [45%] males), aged 18 to 82 (mean 50) years with familial DCM were recruited from St Vincent’s Hospital and by referral from collaborating physicians. The clinical characteristics of study probands are provided in Supplementary Table S1. Familial DCM was defined by the presence of DCM and/or early (<35 years) sudden unexplained death in two or more individuals in the absence of another heritable cardiac or systemic cause. Probands and participating first-degree relatives provided informed written consent and were evaluated by history and physical examination, electrocardiogram (ECG), and transthoracic echocardiography. All study subjects were of self-reported European ancestry. Protocols were approved by St Vincent’s Hospital Human Research Ethics Committee.

DNA sequencing and variant calling
See Supplementary Methods for expanded sequencing methods. Briefly, 42 patient DNA samples were newly sequenced by GS, or previously sequenced using a custom capture kit. 13 All genomic data, including previously published data, were analyzed using a GATK best practices analysis pipeline. Short variants were annotated, filtered and prioritized using Seave. Structural variants (SVs) including copy-number variants were identified using ClinSV (Minoche et al., manuscript in preparation) which uses a combination of discordantly mapping read pairs, split-mapping reads, and depth of coverage changes. A genomic position was defined as “covered” if the sequencing depth had ≥15 high-quality reads. Selected variants were confirmed in probands and evaluated in family members using Sanger sequencing and/or polymerase chain reaction (PCR).

Variant concordance analysis
Variants that passed filters and were located within the genomic regions targeted in PS were included in this analysis. Variant concordance was assessed using bcftools (v1.2) and vcfeval from RTG-Core (Real Time Genomics, v3.4.4). In individual patients, sites at which the frequency of the two predominant alleles was <95% (allowing for sequencing errors) were considered nonbiallelic. The concordance analysis was performed for all single-nucleotide variants (SNVs) and indels, then separately for the subset that were annotated as high or medium impact.

Variant filtration and prioritization
Rare stop gain, splice donor or acceptor site loss, frameshift indels (defined as LOF variants), and missense variants were included if the maximal minor allele frequency (MAF) in the 100 Genomes Project, Exome Sequencing Project, or Exome Aggregation Consortium (ExAC) databases was <1%. Missense variants were then excluded if they were predicted to be benign by both SIFT and PolyPhen2, or annotated as benign in ClinVar. SVs were included if they had population allele frequencies <1% and overlapped with exonic regions from genes of interest (Supplementary Methods). Variants were classified into one of five categories: pathogenic, likely pathogenic, uncertain significance (VUS), likely benign, and benign, according to recommendations for clinical reporting from the American College of Medical Genetics and Genomics (ACMG).

Gene sets analyzed
Three sets of genes were evaluated (Supplementary Table S2). The first set included 67 “panel genes” evaluated by PS. An “extended gene set” was comprised of 406 genes, including reported DCM-associated genes that were not represented on the PS panel, genes with presumptive links to cardiac and skeletal myopathies, and cardiac-enriched genes from the human protein atlas. The third set included a list of 57 genes compiled by the ACMG in which secondary findings are deemed clinically reportable.
RESULTS

PS-identified SNV and indels

PS was performed in 42 probands with familial DCM. Seventy-eight rare (MAF <1%) LOF or potentially damaging missense variants were identified in 37 probands (Table 1). All 78 PS-identified variants were confirmed to be present in probands, and were also investigated in family members, using Sanger sequencing (Supplementary Methods). Twenty-one variants in 21 families (50%) were subsequently deemed pathogenic or likely pathogenic based on ACMG criteria,17 including 14 LOF TTN variants that we have reported previously.12

GS sequencing depth and coverage

GS had an average depth of 34×, covering 97% of the genome, 98% of all exons, and 99% of PS gene exons (Fig. 1a). In comparison, PS had a much higher average read depth (486×) but covered only 91% of its targeted regions (Fig. 1a). GS coverage was compared with a ES dataset obtained in the human NA12878 cell line using the SSv5 capture kit. In this dataset, ES had an average read depth of 150× but covered only 69% of the PS targets (Fig. 1a). Similar results were found in ES datasets for which CREv2 and SSv5 capture kits had been used, with coverage of panel targets only 64 and 56%, respectively (Fig. 1a, Supplementary Table S3). The poor coverage of ES relative to PS highlights the benefit of a comprehensive disease-focused panel, compared with a generic ES design. The remaining causes of the lower coverage of panel genes with PS and ES, when compared with GS, were incompletely or mistargeted exons due to biases in probe design, synthesis, and hybridization (Fig. 1c,d).

We further interrogated the reference sets of gene isoforms used in the design and analysis of target regions. GS data were analyzed with respect to protein-coding transcripts from the comprehensive Ensembl database, reporting 1–31 isoforms per panel gene. In comparison, PS targets included exons and conserved flanking sequences of isoforms from University of California–Santa Cruz (UCSC) knownGene and RefSeq, while ES SureSelect targets were based on subsets of isoforms from UCSC, RefSeq, Gencode, and CCDS databases. Coverage of Ensembl isoforms of panel genes was high (99%) with GS, but was 86% with PS and ranged from 90 to 79% with ES (Fig. 1b, Supplementary Table S3). We found that this was mainly due to an extra 67 kb of Ensembl isoform sequences that were not included on the PS panel and 59 kb not included in ES SSv5 SureSelect targets/exons (Fig. 1e,f). Even with ES at >300× average depth of coverage, sequencing breadth plateaued at 90% for Ensembl exons and 95% for SureSelect targeted exons, which was less than the 99% achieved by GS (Fig. 1g).

Concordance between GS and PS

GS identified on average 3.8 × 10⁶ SNVs and 1.2 × 10⁶ small indels per proband genome-wide, of which 24,000 were coding and 42 were LOF and rare (MAF <1%). Extensive Sanger sequencing of a subset of 115 SNV and indels in probands and family members showed that GS had an overall very low false-positive rate (0.81%, Supplementary Results).

For the variant concordance analysis between GS and PS, we used the same analytical pipeline and investigated the detection rates of all SNVs and indels in PS-targeted regions irrespective of MAF and read depth. A median of 483 variants per proband were concordant between GS and PS, with 131 variants identified exclusively by GS and 104 variants exclusively by PS (Supplementary Table S4). Seventy-seven percent of GS-specific variants were in positions that had <10 reads on PS, with the majority of these occurring at positions with no reads. In contrast, only 3% variants were missed by GS for the same reason. Variants listed in dbSNP are more likely to be true positives and this was the case for 87% of GS-specific variants but only 31% of the PS-specific variants, suggesting that two-thirds of PS-specific variants were either novel or false positives. Of these PS-specific variants, 22% were multiallelic (vs. 5% in GS) and 53% were located at homopolymers and short tandem repeats, likely resulting from replication slippage. This can occur naturally but more often arises during PCR-mediated DNA replication.20

To further investigate discordant variants, we looked at annotated LOF and missense variants, and manually inspected the read alignments. There was an average of 82 concordant variants per proband, with 11 variants exclusive to GS and 23 variants exclusive to PS (Supplementary Table S5). The most frequent cause of GS-specific variants was inadequate PS read coverage (Supplementary Fig. S1A), followed by missed variants occurring in Ensembl exons that were not represented on the PS panel. An additional 16% of GS-specific variants were present in the PS reads but missed by the variant caller. In contrast, most (84%) of the PS-specific variants were sequencing artifacts due to phasing (Supplementary Fig. S1B). This can occur during cycle-based sequencing when some of the DNA strands fall behind or jump ahead of the cycle.21 Other sources of discordance seen with both GS and PS included amplification of sequencing errors, incorrect variant calls (especially for indels), and ambiguous regions of low mapping quality (Supplementary Fig. S1C). In total, there was an average of 10 likely real LOF and missense variants per person that were missed by PS and 0.3 missed by GS.

GS detection of pathogenic/likely pathogenic variants in panel genes

GS data underwent further filtering to identify rare LOF or potentially damaging missense variants in panel genes. GS successfully detected the 78 prioritized PS variants, including all 21 of the pathogenic and likely pathogenic variants. A frameshift variant, SGCB p.M1Gfs, in family AF (Table 1), identified by GS and confirmed by Sanger sequencing, was missed by PS due to lack of coverage.
| Proband ID | Gene | Variant | Variant type | ACMG classification | Detection method |
|------------|------|---------|--------------|---------------------|------------------|
| AA-II-3    | TTN  | c.7282A>T, p.R2431S | SNV; missense | VUS                 | X                |
| BA-II-3    | MYH6 | c.502G>A, p.D168N | SNV; deletion/duplication | Pathogenic | X                |
| AA-II-4    | TTN  | c.3616C>T, p.D1207fs | SNV; missense | VUS                 | X                |
| AI-II-2    | TTN  | c.502G>A, p.D168N | SNV; deletion | Pathogenic         | X                |
| AM-I-7     | DMD  | c.8209-4T>C | SNV; splice | VUS                 | X                |
| AA-I-4     | TTN  | c.1.2delAT, p.M1Gfs | INDEL; frame shift deletion | Likely pathogenic | X                |
| AI-II-4    | TTN  | c.9772T>C, p.V3258H | SNV; missense | VUS                 | X                |
| AA-I-4     | TTN  | c.4481T>C, p.P1494S | SNV; missense | VUS                 | X                |
| AA-I-4     | TTN  | c.47692C>T, p.R15848H | SNV; stop codon | Likely pathogenic | X                |
| AA-I-4     | DMD  | c.2945C>T, p.R982* | SNV; missense | VUS                 | X                |
| AA-I-4     | TTN  | c.86830G>A, p.D29489N | SNV; missense | VUS                 | X                |
| AA-I-4     | MYH6 | c.1092+2>T, c.1092+3delTTCAGTA | INDEL; splice deletion | Pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Pathogenic         | X                |
| BA-I-3     | TTN  | c.471191C>T, p.R15713C | SNV; missense | VUS                 | X                |
| BA-I-3     | NEB  | c.159500G, p.G5282* | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.1.2delAT, p.M1Gfs | INDEL; frame shift deletion | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | SYNE1| c.233150C, p.R7772Q | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.159500G, p.G5282* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.25336A>G, p.K845E | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.23467T>C, p.R7846M | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.4302C>G, p.R1434C | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30327G>T, p.M1011R | SNV; missense | VUS                 | X                |
| BA-I-3     | TTN  | c.30485C>T, p.T10162M | SNV; stop codon | Likely pathogenic | X                |
| BA-I-3     | TTN  | c.139000>T, p.E4634* | SNV; stop codon | Likely pathogenic | X                |
| Proband ID | Gene | Variant | Variant type | ACMG classification | Detection method |
|------------|------|---------|--------------|---------------------|------------------|
| PS WGS    | XIRP2 | Chr2:167868183-168522158del | SV; deletion | VUS | X X |
|           | MYH7  | c.1578_1600A | SNV; splice | VUS | X X |
|           | SONGA | c.3305C>A, p.S1102Y | SNV; missense | VUS | X X |
|           | NC    | c.717C>A, p.T239* | SV; stop codon | VUS | X X |
| DO-I-4    | TTN   | c.74880_74883dupACA, p.P24962fs | INDEL; frameshift insertion | Pathogenic | X X |
|           | BMD   | c.428C>T, p.S143F | SNV; missense | Likely benign | X |
|           | NKX2-5 | c.552C>G, p.I184M | SNV; missense | Likely pathogenic | X |
|           | SCN5A | c.3305C>A, p.S1102Y | SNV; missense | VUS | X X |
|           | ASB15 | c.1207G>T, p.G403* | SNV; stop codon | VUS | X X |
|           | TTN   | c.104878C>T, p.R34960C | SNV; missense | VUS | X X |
|           | FRMD3 | Chr9:85906635-85962244del | SV; deletion | VUS | X X |
|           | RYR1  | c.13328-13348dupGGGGCCCTTGCGAA, p.GGPFRPE4443-4449dup | INDEL; in-frame deletion | Likely benign | X X |
|           | AMG   | American College of Medical Genetics and Genomics, DCM: dilated cardiomyopathy, INDEL: small insertion or deletion, PS: targeted panel sequencing, SNV: single-nucleotide variant, SV: structural variant, VUS: variant of unknown significance, GS: genome sequencing | | | |

# Potential disease-causing variants are shown in bold

# Variant identified by candidate gene screening
LOF variants in an extended gene set

To further explore the GS data, we compiled an extended set of 406 genes with proven and putative links to cardiomyopathy (Supplementary Table S2). GS successfully identified a reported likely pathogenic missense variant, p.I184M, in the NKX2-5 gene (Table 1). An additional 17 LOF variants in 14 families were evaluated (Table 2), all of which were validated by Sanger sequencing, but none met ACMG criteria for pathogenicity.

Five variants, in the FLNC, ANO5, ACADVL, TRIM63, and PDE4DIP genes, were present in all (two or more) family members with DCM in the respective kindreds (Supplementary Fig. S2). In family DF (negative after PS testing), a FLNC p.C2369* variant was identified. Variants in FLNC, which encodes the actin-binding protein filamin C, have been associated with cardiac and skeletal myopathies. Filamin C deficiency causes cardiac developmental defects in zebrafish and neonatal death in homozygous mice, while heterozygous mice carrying a human FLNC p.W2710X PV show skeletal myopathy. To date, there is no definitive animal model evidence that heterozygous filamin C loss-of-function results in DCM. Although the nonsense FLNC variant was present in both affected individuals in family DF (II-1, II-2), it was also present in two unaffected siblings aged...
### Table 2: WGS-identified LOF variants in the extended gene set

| Family ID | Gene | Variant | ExAC variant frequency; PLi score | Notes | Segregation* |
|-----------|------|---------|-----------------------------------|-------|--------------|
| **Families "unsolved" after PS** |
| AJ        | RYR2 | c.8209-4T>C | Absent; 1.00 | Ryanodine receptor 2, SR protein involved in Ca^{2+} homeostasis. KO mice (-/-): embryonic lethal, (-/-): adults, normal baseline EF, ↓ contraction post-TAC; cKO mice (-/-): adults, transient ↓ contraction. CPVT families with exon 3 deletion: DCM in a subset of individuals | 1/1 affected |
| AT        | MYO1B | c.1692+1_1692+29del | Absent; 0 | Myosin 1B, Z-disc protein. KO mice (-/-): embryonic lethal, disordered myofibrils | 1/2 affected |
| BF        | BDKRB1 | p.R282* | 0.002883; 0.07 | Bradykinin receptor B1. KO mice (-/-): adults, mild ventricular dilation, normal EF | 2/3 affected |
| BG        | TTN | p.R255* | 0.001450; 0 | Myosin binding protein H-like, sarcomeric protein. KO mice (-/-): adults, DCM; p.R255* variant: altered MyBP-HL localization in transfected neonatal mouse cardiomyocytes | 1/3 affected |
| BP        | RYR2 | c.14757-7_14757-6delICinsAT | Absent; 1.00 | Ryanodine receptor 2 (see above) | 2/3 affected |
| SCN4A     | Y600* | | Absent; 0.01 | a4 subunit, voltage-gated sodium channel. KO mice (-/-): adults, no heart defects reported | 1/3 affected |
| MYBPHL    | p.R255* | | 0.001450, 0 | Myosin binding protein H-like, sarcomeric protein. KO mice (-/-): adults, DCM; p.R255* variant: altered MyBP-HL localization in transfected neonatal mouse cardiomyocytes | 1/3 affected |
| **Families with identified pathogenic/likely pathogenic variants** |
| AM        | ADRA1A | RRHQA341-345* | Absent; 0 | α1A adrenoceptor. KO mice (-/-): adults, normal EF | 3/8 affected |
| PLEC      | Q2360* | | 0.0002591; 0.02 | Plecit, cytoskeletal protein. KO mice (-/-): neonatal death, Z-disc disorganization | 1/12 unaffected |
| BK        | TRIM63 | p.Q247* | 0.000486; 0 | Tripartite motif containing 63, E3 ubiquitin ligasep.Q247* variant: transfected cells, ↓autoubiquitination; transgenic mice, adults, ↑ LV mass, ↑ LVEDD, normal EF | 1/2 affected |
| BR        | TLL2 | p.V441* | Absent; 0 | Tolloid like 2, zinc-dependent metalloprotease. KO mice (-/-): adults, no heart defects reported | 1/2 affected |
| CS        | ANO5 | p.N64fs | 0.001027; 0 | Anoctamin 5, transmembrane protein. KO mice (-/-): adults, normal EF (baseline, isoproterenol stress) | 1/6 affected |
| CZ        | PDE4D | p.C18* | 0.0000698; NA | Phosphodiesterase 4D interacting protein, A-kinase anchoring protein, contributes to phosphorylation of cMyBPC and cTNI | 4/4 affected |
| DO        | SYNE2 | p.A6022A* | Absent; 0 | Spectrin repeat-containing nuclear envelope protein 2, nuclear membrane protein. KO mice (-/-): adults, normal EF | 2/2 affected |
| EA        | ASB15 | p.G403* | 0.0000906; 0 | Ankyrin repeat and SOCS box containing 15, involved in muscle differentiation and protein turnover | 2/3 affected |
| MO        | ACADVL | c.1077_+1G>T | Absent; 0 | | 1/3 affected |
52 (II-4, II-5) and 45 years, respectively, and it was classified as a VUS. In family CS, all affected individuals carried a likely pathogenic LOF TTN variant and an ANO5 p.N64fs variant. ANO5 encodes anoctamin 5, a transmembrane protein with putative calcium-activated chloride channel activity. Homozygosity for LOF ANO5 variants in human subjects has been associated with limb girdle and Miyoshi muscular dystrophies. This phenotype is not present in Ano5 knockout mice and none of the CS family members had overt skeletal myopathy. Despite good family cosegregation, the ANO5 variant was called a VUS. In family MO, individuals with a pathogenic LOF TTN variant also carried a splice acceptor site variant, ACADVL c.1077+_1G>T. The latter has been associated with a 36% reduction in very long chain acyl-CoA dehydrogenase activity but this level is predicted to be tolerated. Affected individuals in family BK had a likely pathogenic missense MYH7 variant as well as a TRIM63 p.Q274* variant, both of which have proposed associations with hypertrophic cardiomyopathy. The two variant carriers (II-3, II-4) clearly had DCM with one also showing left ventricular hypertrophy. This nonsense TRIM63 variant has been associated with reduced autoubiquitination in transfected cells, and increased left ventricular mass in transgenic mice. The four affected individuals tested in family CZ all carried a PDE4DIP p.C18* variant in addition to a pathogenic missense MYH7 variant. PDE4DIP encodes an A-kinase anchoring protein that is involved in phosphorylation of the sarcomeric proteins, cMyBPC and cTNNI. This variant could plausibly modulate sarcomere kinetics but was classified as a VUS due to a lack of compelling evidence supporting PDE4DIP loss of function as a DCM mechanism.

Structural variants

Because GS sequence coverage extends beyond exonic regions, comprehensive genome-wide evaluation of SVs is possible. Using our in-house pipeline, ClinSV, we detected an average of 5379 SVs, including 4470 copy-number variants per proband, of which 232 were rare (MAF < 1%), and 23 that were rare and overlapped genic regions. When the 67 panel genes were evaluated, one rare SV was identified. This was a complex BAG3 deletion/duplication that included the BAG domain and is likely to have a loss-of-function effect (Fig. 2a, Table 3). This BAG3 SV was confirmed to be present in the proband using Sanger sequencing, segregated with DCM in family AA (Supplementary Fig. S2), and was deemed to be pathogenic. Numerous truncating BAG3 variants have been reported in DCM patients, with many cosegregating with disease in families. Eight SVs were found in the extended gene set, all of which were validated by independent sequencing methods (Supplementary Methods and Results), but none met ACMG criteria for pathogenicity or were likely primary causes of DCM (Fig. 2b, Table 3). For example, in the proband from family BG we identified a rare whole-gene duplication of triadin (TRDN; Fig. 2b), a developmentally regulated core member of the ryanodine receptor complex, whose copy number has been conserved in mammals.
Although present in 4 of the 6 other affected family members (Supplementary Fig. S2), this variant was also seen in 4 unaffected family members, and was classified as a VUS. The remaining SVs mostly showed incomplete segregation with disease, occurred in families with other identified pathogenic/likely pathogenic variants, overlapped with SVs reported in population databases, or were in genes with unknown relevance to DCM, and were all classified as VUS.

Value of GS in additional family members

In two large kindreds that remained unsolved after PS and GS testing of the proband, we undertook GS in additional family members. In family BP (Supplementary Fig. S2), a MYBPHL p.R255* variant was identified in three family members but not in the proband. One of these, I-1, had been diagnosed with DCM and first-degree atrioventricular block at 84 years of age. The other two variant carriers included an asymptomatic 56-year-old male (II-1), and a 42-year-old female with ventricular ectopy (II-6), neither of whom had DCM.

MYBPHL has been recently described as a DCM disease gene, with homozygous and heterozygous knockout mice showing DCM and conduction-system abnormalities. The same MYBPHL p.R255* variant was seen in a family with early-onset DCM and in an unrelated individual with left ventricular dilation. The mutant MyBP-HL protein was function-altering, with reduced expression in human cardiomyocytes and abnormal myofilament localization in transfected neonatal mouse cardiomyocytes. In family BG

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**Fig. 2 Structural variants identified in dilated cardiomyopathy (DCM) probands.** Schematics showing protein locations and relative size of deletions and duplications in a BAG3, and b 8 genes in the extended gene set. Protein domains are named and highlighted with colors, dashed vertical lines denote exon boundaries, and codons are numbered.
| Family ID | Gene | Variant | Database of Genomic Variants | Notes | Segregation |
|----------|------|---------|-----------------------------|-------|-------------|
| AA       | BAG3 | Chr10:121436136-121436726 del, Chr10:121436139-121436799 dup (g.30254-30844 del, 30257-30917 dup); involves exon 4 (aa.357-533) including BAG domain | Overlap with 2 larger dup, 1 in unaffected subject | BCL associated athanogene 3, chaperone protein. KO mice (-/-); neonatal death Human ventricle: decreased BAG3 expression in heart failure | 3/3 affected, 1/1 unaffected |
| BG       | TRDN | Chr6:123509665-124330720 dup (821.1 kb); includes TRDN (complete gene) and NKAIN2 (exon 1) | Similar dup in >10 DD patients + unaffected subjects | Triadin, SR protein involved in Ca\(^{2+}\) homeostasis. Tg mice (5-fold overexpression): ↓ contraction | 5/7 affected, 4/4 unaffected |
| C        | CTNNA3 | Chr10:68286145-68513397 del (227.3 kb); loss of exon 10 (aa 428-458) including vinculin-like domain. >40 overlapping deletions, known CNV hotspot | | α\(^3\) catenin, intercalated disc protein. KO mice (-/-): adult DCM | 4/6 affected, 4/17 unaffected |
| FK       | FRMD3 | Chr9:85906635-85962244 del (55.6 kb); loss of exons 5-12 (aa 125-357, includes partial FERM domain, peptide and lipid-binding regions) | Overlap with 3 del/dup | FERM domain-containing protein 3, cytoskeletal protein | 4/4 affected, 1/4 unaffected |
| HB       | HPS3 | Chr3:148874313-148882670 del (g.31943-40298 del, 8.4 kb); loss of exon 9-14 (aa.504-863), no identified domains Overlap with 1 larger dup in 2 DD cases | | Hermansky–Pudlak syndrome 3 protein | 1/2 affected, 1/2 unaffected |
| BL       | DSC2 | Chr18:28681558-28686269 del (g.37617-42327 del, 4.7 kb); loss of first exon + promoter | Absent | Desmocollin 2, desmosomal protein. KO mice (-/-): embryonic lethal | 2/2 affected |
| BR       | SCN1B | Chr19:35531062-35531134 del (g.14470-14543 del, 73b in 3' UTR) | Absent | β1 subunit, voltage-gated sodium channel | 1/3 affected, 1/9 unaffected |
| DD       | XIRP2 | Chr2:167868183-168522158 del/dup (654 kb); del from exon 3/dup (includes whole gene + translocated del segment) | Similar del (exon 4 on), multiple smaller CNV in same region | Xin actin-binding repeat-containing protein 2, intercalated disc protein. KO mice (-/-): postnatal death, ( +/-): normal EF. Human ventricle: expression levels increased (early) or reduced (late) with myocardial stress | 2/2 affected, 1/2 unaffected |
| FQ       | AK1  | Chr9:130621906-130645663 dup (238 kb); includes complete gene Overlap with 3 full-gene dup/multiple small del, in unaffected subjects | | Adenylate kinase 1, enzyme involved in energy metabolism | 2/2 affected |

CNV copy-number variant; DCM dilated cardiomyopathy, DD developmental delay, EF ejection fraction, KO knockout, PS panel sequencing, SR sarcoplasmic reticulum

aDatabase includes diverse patient and control cohorts

bSegregation analysis did not include phenotype-negative variant carriers aged less than 40 years
(Supplementary Fig. S2), GS in two of the proband’s aunts (II-2, II-4) identified a novel LOF TTN variant. Sanger sequencing of this variant in all family members confirmed its absence from the proband and presence in three affected siblings.

**Overall yield of GS and reportable secondary findings**

The yield of pathogenic/likely pathogenic variants was increased from 21 families (50%) with PS, to 24 families (57%) following GS analysis of panel genes and preliminary mining of the extended gene panel. Interrogation of the ACMG 57-gene list\(^{17}\) (Supplementary Table S2) yielded three significant secondary findings. In the family BG proband, we found a common function-altering GLA p.D313T variant associated with Fabry disease\(^{37}\) that did not segregate with DCM in the family (Supplementary Fig. S2). Two other probands were heterozygous carriers of common missense MUTYH variants that are annotated as pathogenic in ClinVar and associated with increased cancer risk.

**DISCUSSION**

Our data support GS as a viable method for genetic testing in familial DCM with high detection accuracy for rare SNVs and indels in disease-associated genes. These findings concur with recently reported results for GS-based testing in hypertrophic cardiomyopathy\(^{36}\) and extend pilot data for GS in DCM.\(^{11}\) A compelling argument in favor of GS as a first-line testing method is its potential for ongoing data mining in unsolved cases. However, in an initial analysis we found that surprisingly few variants in an extended gene set data met clinical criteria for pathogenicity.

Despite a lower overall sequencing depth than PS (and ES), GS gave superior SNV and indel detection with less risk of variants being missed due to sequence gaps. GS’s broad and uniform sequence coverage, even across exons targeted specifically by PS, results from sample preparation methods that avoid capture bias\(^{37}\) and a lack of constraint to predefined sets of transcript isoforms and target regions. Some GS-identified variants in panel genes were missed by PS because different gene reference sets were used. This limitation of PS could potentially be reduced by optimized probe design and comprehensive representation of tissue-specific isoforms.\(^{6}\) The poor ES coverage observed over PS regions was recapitulated using three different exome capture kits, in data generated from two laboratories. Even at 300× depth, ES failed to achieve the same breadth of coverage as 34× GS. Importantly we show that on target ES performance can be good, but often the target does not correspond to the nearby exon, resulting in potentially missed pathogenic variants.

Coverage uniformity gives GS a distinctive advantage for identification of SVs, which account for 0.5–1% of heritable interindividual sequence differences (compared with 0.1% for SNVs).\(^{8}\) Although SVs are increasingly implicated in human disorders,\(^{8}\) we found relatively few pathogenic SVs in cardiomyopathy-associated genes. These results may be skewed by ascertainment bias because DCM associations of panel genes have predominantly been established by profiling SNVs and indels. SVs often involve pairs of flanking low copy repeats.\(^{8}\) Known DCM-associated genes may lack these regions and hence be less susceptible to structural rearrangements. Extending our analysis to 406 cardiac-enriched genes resulted in the discovery of only 8 additional SVs, none of which were clearly causative of DCM. One of the challenges in evaluating SVs is assessment of their functional effects, especially for those variants that involve complex or partial duplications and deletions. Intuitively, changes in gene copy number would impact on gene “dose,” but this is not necessarily the case and a number of adaptive mechanisms may result in dosage compensation.\(^{9}\) Even full-gene or balanced duplications and deletions can have unpredictable effects if there is disruption of local or long-range genomic architecture that involves gene-regulatory sequences.

To improve GS yield, more genetic information is needed to identify patterns of differential variant prevalence in cases and controls, recurrent variant types, and PV hotspots. Equally, more experimental data are required to identify function-altering variants and to show that these functional effects have plausible links to disease causation. In the ACMG criteria\(^{17}\) segregation of variants in affected family members provides support for DCM association, but the level of evidence can increase to moderate or strong with larger family sizes and/or multiple families.

Segregation analysis in familial DCM relies on the assumption of single driver PV but this is increasingly open to question.\(^{38}\) As genetic evaluation has shifted from gene candidate screening studies to genome-wide analyses, it is not uncommon to find multiple rare variants in family probands\(^{39}\) and, as seen with families BG and BP, the number of potential function-altering variants in any one family can increase as more individuals are studied. These combinations of variants may have additive, synergistic, or neutralizing effects, and each person’s total burden of rare and common variants may determine threshold levels for myocardial dysfunction.

Should GS be used as a first-line genetic test for DCM or reserved for PS-negative cases? The answer to this question is currently unknown and involves a dynamic interplay between cost and yield (Supplementary Fig. S3). Currently, the cost of GS-based clinical testing is more than double that of PS. With increasing customer demand and technical efficiencies, the operational costs of both GS and PS are likely to decrease over time. For PS, these reductions will be offset by the ongoing need to design and optimize new probe sets as new disease genes are discovered. The manpower costs of expert clinical reporting are essentially equivalent for PS and GS because the same suites of disease genes are generally evaluated, but these costs may rise as the spectrum of reportable genes and variants expands. The turnaround time for GS is equivalent or faster than routine PS (or ES), because of the time required for targeted sequence capture, together with delays incurred by waiting for samples to be pooled. Recent data have shown that...
fast-tracked ES-based genetic testing in acutely ill pediatric patients is however feasible and cost-saving, due to expedited diagnosis and management.\(^{40}\) GS is a storehouse of medically relevant information that extends beyond identification of rare disease-causing variants, much of which cannot be obtained from PS or ES. For example, polygenic risk scores derived from suites of common variants (often in noncoding regions) may predict an individual’s risk of DCM complications, and pharmacogenomic associations may guide drug selection and doses.

Comprehensive economic models need to be developed that consider variables such as cost per test, number of tests ordered, yield of tests, requirement for secondary testing of probands, cascade testing of family members, and the impact of genotype information on requirements for clinical surveillance of family members. Genotype-based early interventions may also impact more broadly on long-term health outcomes and costs, potentially impacting hospitalization rates, device implantation, drug administration, workforce productivity, and use of social services. Compelling health economics data would provide a powerful argument to insurance companies or governments for the overall benefits of genetic testing and the preferred testing modality.

**ELECTRONIC SUPPLEMENTARY MATERIAL**

The online version of this article (https://doi.org/10.1038/s41436-018-0084-7) contains supplementary material, which is available to authorized users.

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**DISCLOSURE**

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