



# Genetics of paediatric cardiomyopathies

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## Purpose of review

Paediatric cardiomyopathy is a rare disease with a genetic basis. The purpose of this review is to discuss the current status of genetic findings in the paediatric cardiomyopathy population and present recent progress in utilizing this information for management and therapy.

## Recent findings

With increased clinical genetic testing, an understanding of the genetic causes of cardiomyopathy is improving and novel causes are identified at a rapid rate. Recent progress in identifying the scope of genetic variation in large population datasets has led to reassessment and refinement of our understanding of the significance of rare genetic variation. As a result, the stringency of variant interpretation has increased, at times leading to revision of previous mutation results. Transcriptome and epigenome studies are elucidating important pathways for disease progression and highlight similarities and differences in pathogenesis from adult cardiomyopathy. Therapy targeted towards the underlying cause of cardiomyopathy is emerging for a number of rare syndromes such as Pompe and Noonan syndromes, and genome editing and induced pluripotent stem cells provide promise for additional precision medicine approaches.

## Summary

Genetics is moving at a rapid pace in paediatric cardiomyopathy. Genetic testing is increasingly being incorporated into clinical care. Although interpretation of rare genetic variation remains challenging, the opportunity to provide management and therapy targeted towards the underlying genetic cause is beginning to be realized.

## Keywords

genetic variant, genome editing, induced pluripotent stem cells, Noonan syndrome, transcriptome

## INTRODUCTION

Cardiomyopathy is a rare disease in the paediatric population, estimated to affect one in 100 000 individuals [1,2]. The causes of cardiomyopathy are diverse and include infectious, environmental and genetic etiologies. Since the original identification of mutations in *MYH7*, a gene encoding the thick filament ATPase  $\beta$  myosin heavy chain, as causative of hypertrophic cardiomyopathy (HCM) 25 years ago, there has been ongoing discovery of genes that cause this disease. The speed of discovery has been enhanced by improved sequencing technologies that allow rapid, efficient and cost-effective testing. As a result, the array of clinically available genetic tests has expanded rapidly. With many of the technical barriers to molecular testing surmounted, the challenge has shifted to improving our interpretation of the consequences of genetic variation.

In addition to mutations that cause isolated or familial cardiomyopathy, inborn errors of metabolism, neuromuscular diseases and genetic syndromes also cause cardiomyopathy in the paediatric population and the differential and diagnostic approach can be complex [3,4]. There is practice

variation in the approach to genetic diagnosis and there is still much to be learned about the genetic basis of paediatric cardiomyopathy. Improved genetic diagnostic capabilities promise novel therapeutic approaches and genome editing technologies create prospects for the future. In this review, we will discuss the recent novel findings and interpretive challenges for genetic testing, highlight some important new genetic discoveries across etiologic categories and present recent progress in utilizing this information for management and therapy.

## Isolated nonsyndromic cardiomyopathy

Mutations in genes encoding sarcomeric proteins are the primary genetic cause of HCM in adults and

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## KEY POINTS

- Paediatric cardiomyopathy is genetically heterogeneous and may be isolated or occur as part of a syndrome, neuromuscular disorder or metabolic disease.
- Enhanced sequencing capabilities allow rapid identification of novel candidate genes or alleles causing cardiomyopathy; proof of causality is more challenging.
- In aggregate, rare genetic variation is relatively common. Understanding the scope of genetic variation in healthy individuals has allowed refinement and increased stringency of interpretation of variant pathogenicity.
- Transcriptome and epigenome analyses are contributing new information to our understanding of paediatric cardiomyopathy and its similarities to and differences from adult cardiomyopathy.
- Management and therapy directed to the underlying genetic cause of cardiomyopathy is becoming available and highlights the promise of precision medicine.

likely the most common cause in children as well [5]. Genetic causes of dilated cardiomyopathy (DCM) are identified less frequently, but include genes encoding sarcomeric, cytoskeletal or desmosomal proteins, amongst others. Restrictive cardiomyopathy (RCM) and arrhythmogenic ventricular cardiomyopathy (AVC) are rarer forms of cardiomyopathy but also are caused by mutations in sarcomeric (RCM) or desmosomal (AVC) genes.

Novel gene discoveries for cardiomyopathy often first occur in adults because of increased disease prevalence in this age group. The genetic architecture of disease in the paediatric population has not been comprehensively studied across all cardiomyopathy phenotypes. Of the cardiomyopathy phenotypes, the genetic basis of HCM is the best understood. *MYH7* and *MYBPC3* are the most common genes with mutations in isolated HCM in adults and the overall diagnostic yield with clinical testing for HCM is high. These two genes appear to account for the largest proportion of paediatric cardiomyopathy cases as well [6]. Single-centre studies indicate that the yield of genetic testing may be higher in paediatric HCM patients than in adults [7<sup>•</sup>]. Two recent studies followed genotype positive, phenotype-negative patients and determined the penetrance of HCM was 6–7% during childhood but cautioned that severe hypertrophy and cardiac events can develop [8,9<sup>••</sup>]. Case reports of multiple mutations in paediatric patients with HCM have led to speculation that early-onset

cardiomyopathy may result from ‘multiple hits’. A recent retrospective review of sarcomere mutation carriers showed that 25% of patients less than 18 years of age had two or more pathogenic or likely pathogenic variants versus 4.8% for adults, but the overall number of paediatric patients studied was small ( $n = 24$ ) [10]. To date, many studies are limited by their single site status and the potential ascertainment bias that occurs at tertiary referral centres. Ascertainment bias also exists because genetic assessment and testing of paediatric cardiomyopathy patients is rarely standardized and comprehensive. Numbers at single sites are relatively small, and comparison of results between centres is difficult because the populations are not identical. A major problem, discussed further below, is that genetic testing interpretation of variant pathogenicity has changed due to new evidence provided by large population-based sequencing datasets [11<sup>••</sup>,12<sup>••</sup>]. Unless retrospective studies reinterpret ‘mutation positive’ patients using updated findings, the likelihood of misclassification is high. Finally, many studies do not age stratify the paediatric patients and this may be important in order to define whether the genetic causes and outcomes are different in infants and preadolescent children as compared with adolescent and adult patients.

HCM is classically defined as a disease of the sarcomere. However, in the paediatric population, causes are more heterogeneous. It is not rare to identify individuals with mutations in *LAMP2* (Danon disease) or *PRKAG2* (cardiac glycogenosis) that result in early, severe hypertrophy. These genetic causes are important to distinguish from sarcomeric mutations because of differences in clinical course and prognosis [13–15]. Similarly, individuals with Noonan syndrome are sometimes diagnosed with this genetic syndrome years after their development of HCM. Because of the increased prevalence of syndromic associations, inborn errors of metabolism, mitochondrial disorders and neuromuscular disease, evaluation by a medical geneticist is highly recommended for all types of cardiomyopathy, especially in younger children [4,16,17].

The underlying genetic cause of DCM is less frequently identified than for other types of cardiomyopathy. Recent data indicate that in the paediatric population, there is no survival difference between familial DCM and idiopathic DCM after adjustment for other factors [18<sup>••</sup>]. However, the majority of patients in this study did not undergo genetic testing and therefore it is unclear whether there might be a survival difference based on genotype. Overall, older age, heart failure and greater left ventricular dilation at diagnosis were independently associated with an increased risk of the combined

endpoint of transplantation and death. Determining whether genotype is predictive of outcome is an important future goal.

Mutations in the large cytoskeletal protein titin have emerged as the most common genetic cause of DCM in adults and have also been shown to be a risk factor for peripartum cardiomyopathy [19,20<sup>■</sup>,21]. The large size of the *TTN* gene, encoding titin, creates challenges for interpretation of rare variants. Progress has been made in identifying protein domains and mutation types that are more likely to be pathogenic if mutated [20<sup>■</sup>,22]. These findings have not been extended to studies in the paediatric population. In analogy to the peripartum cardiomyopathy findings, it will be interesting to determine whether rare variants in *TTN* are identified at a higher rate in paediatric patients with concomitant stressors such as myocarditis, indicating a genetic susceptibility to the development of disease. By extending genetic analyses outside the structural apparatus of the sarcomere, several genes have been identified relatively recently that suggest new mechanisms of disease causation. For example, mutations in the chaperone protein *BAG3* and the splicing factor *RBM20* are each thought to represent approximately 2% of causes in adult idiopathic DCM. The frequency of mutations in these genes in the paediatric population is not known.

### Genetic testing and variant interpretation

Current guidelines recommend genetic testing in children and adults with HCM, and consideration of testing in individuals with DCM or RCM [23–26]. Cardiac surveillance is recommended for first-degree relatives. If genetic testing is positive in the patient, then cascade genetic testing of family members is recommended for risk stratification. We previously identified that at a single institution,

uptake of cardiac surveillance was significantly higher than uptake of genetic testing for known familial mutations [27]. Khouzam *et al.* [28<sup>■</sup>] studied factors associated with underutilization of genetic services and identified specific health beliefs and awareness that were important to facilitate care. Genetic testing is cost-effective as part of the care for families with cardiomyopathy [29<sup>■</sup>] and additional investigation of barriers to incorporation of genetic testing into practice is needed.

Genetic testing is probabilistic and results must be interpreted in the context of the patient and family history. Choosing the proper genetic testing requires an understanding of the genes associated with specific cardiomyopathy phenotypes, variable presentations, diagnostic yields of available tests and the a priori probability of a positive result [10,29<sup>■</sup>,30]. Ideally, a medical geneticist, genetic counsellor or other medical provider well versed in cardiovascular genetics and molecular testing should review the interpretation of results. Increasing the genetic literacy among cardiovascular genetic care providers is necessary to improve the provision of care to this patient population [31<sup>■</sup>].

In 2015, the American College of Medical Genetics and Genomics and the Association for Molecular Pathology released standards for the interpretation of genetic variants identified by clinical testing [32]. These standards delineate five potential interpretations for molecular testing results (Table 1) and are intended to improve the consistency of variant interpretation. Interpretation of variants is rapidly evolving, as widespread sequencing efforts and public databases such as the Exome Aggregation Consortium (<http://exac.broadinstitute.org>), and the 1000 Genomes Project Exome Sequencing Project (<http://evs.gs.washington.edu/EVS>) lend insight into the frequency of rare variants in the population and allow comparison to

**Table 1.** Interpretation of genetic testing results

Variant classification	Criteria
Pathogenic	Predicted null variant in gene where loss of function is known disease mechanism; de-novo variant; absent in population databases or MAF very low; cosegregation in multiple families; computational predictions support deleterious effect; functional data support deleterious effect
Likely pathogenic	Criteria similar to pathogenic but with less supporting evidence such as fewer available families for cosegregation data, contradictory computational predictions or weaker functional data
Variant of uncertain significance	Very low population frequency or absent from databases but lacking cosegregation, computational, and/or functional evidence for pathogenicity
Likely benign	Allele frequency greater than expected for disease incidence; allele identified in young, healthy individuals; no effect in functional assays; lack of segregation in family members; and/or mutation type not consistent with known disease mechanism
Benign	MAF >5% in ExAC or ESP OR 2 or more of the likely benign criteria

ESP, exome sequencing project; ExAC, Exome Aggregation Consortium; MAF, minor allele frequency. For detailed criteria, see Richards *et al.* [32].

cardiomyopathy cohorts [11<sup>22</sup>,12<sup>22</sup>,33,34]. These studies have highlighted that rare genetic variation is, in aggregate, much more common than anticipated and is present to a substantial degree within healthy individuals. There has been a significant effort to reassess past interpretation of genetic variation in cardiomyopathy patients. In some cases, this has led to a revision of previous clinical genetic test reports and serves as a reminder that it is imperative to assess testing results in the context of the dynamic family history and to update interpretations frequently. ClinVar (<https://www.ncbi.nlm.nih.gov/clinvar/>) is an important resource for reporting human genetic variation and phenotypes. It allows the deposition of supporting evidence and assertion criteria that aid in the communication about interpretation of human variation and health status. ClinGen (<https://www.ncbi.nlm.nih.gov/clinvar/docs/clingen/>) reviews data about genotype–phenotype relationships from ClinVar and additional sources and generates a report, including medical actionability. These resources represent important efforts to share genetic and clinical information to inform variant interpretation.

### **Integrative genomics: the transcriptome in paediatric cardiomyopathy**

In addition to novel discoveries at the gene level, there have been important new discoveries resulting from the assessment of the transcriptome in patients with cardiomyopathy. DCM and heart failure in adults is molecularly characterized by transcriptional alterations in metabolic networks; in addition, there are distinct mRNA splicing patterns, including activation of embryonic splicing patterns and alterations in RBM20-mediated splicing in diseased hearts [35<sup>22</sup>,36<sup>22</sup>,37–39]. Far less is known about the transcriptome in paediatric hearts. Although animal models indicate that foetal and neonatal gene expression differs from adult hearts, the temporal shifts in transcriptional profiles have not been well characterized in paediatric patients. Several recent studies investigate the molecular findings in explanted hearts from children with heart failure and demonstrate age-related differences. Paediatric patients with DCM showed a differential adaptation of the  $\beta$ -adrenergic signalling pathway when compared with adults with DCM or nonfailing controls [40]. Specifically, downregulation of  $\beta$ 1 and  $\beta$ 2-adrenergic receptors is identified in children, whereas  $\beta$ 2-adrenergic receptor expression is maintained in adults. Differences in the phosphorylation status of phospholamban are also noted in children versus adults [40]. Phosphodiesterase isoform expression and responsiveness to phosphodiesterase

inhibition also differed in paediatric versus adult samples [41<sup>22</sup>,42]. Defining normal transcriptional profiles during infancy and other paediatric age ranges is important to better understand how to optimize treatment approaches.

In addition to these investigations in DCM patients, RNA-Seq was recently performed on a cohort of paediatric RCM patients and compared with other forms of adult cardiomyopathy and controls [43<sup>22</sup>]. This identified molecular pathway dysregulation that was common to the cardiomyopathies, as well as those unique to RCM. Transcripts selectively induced in RCM include many known and novel G-protein coupled receptors linked to calcium handling and contractile regulation. In-depth comparisons of alternative splicing implicate RBM20 as a potential mediator of alternative splicing in RCM. Interestingly, the disruption of alternative splicing patterns in paediatric RCM occurs in the inverse direction as in adult DCM. Taken together, these initial investigations of the paediatric cardiomyopathy transcriptome indicate that although there are molecular signatures that overlap with adult cardiomyopathy, phenotype and age-specific profiles exist that can provide useful mechanistic data for possible intervention.

### **Epigenetics and paediatric cardiomyopathy**

MicroRNAs (miRNAs), noncoding RNAs that consist of 18–22 nucleotides, are important regulators of gene expression at the posttranscriptional level and act as important modulators of cardiac hypertrophy, heart failure and fibrosis [44]. A study of miRNAs in mouse models has shown that overexpression can result in cardiac hypertrophy and heart failure and that deletion can be protective. Upregulation of specific miRNAs can also be seen in patients with heart failure [45]. For these reasons, combined with the fact that miRNAs are relatively stable in the blood, miRNAs have generated interest as circulating biomarkers for use in clinical care. To date, miRNAs have not been well studied in paediatric cardiomyopathy patients, but an early study indicates that children with heart failure have unique miRNA profiles [46]. Long noncoding RNAs (lncRNAs) are another group of RNA molecules that play important roles in development and disease through their function in the regulation of transcriptional and posttranscriptional events. For example, the mitochondrial lncRNA LIPCAR identified patients undergoing cardiac remodelling who were independently at risk for future cardiovascular deaths [47]. Identifying miRNAs and lncRNAs that are important in the paediatric population and understanding developmental-specific regulation may



**Table 2.** Noonan syndrome and other RASopathies

Gene	% of patients	Comments
<i>PTPN11</i>	50%	Also causes NSML
<i>SOS1</i>	10–15%	High prevalence of ectodermal abnormalities
<i>RAF1</i>	5%	HCM in >80%; also causes NSML
<i>RIT1</i>	5%	High incidence of congenital heart disease; HCM in 70%
<i>KRAS</i>	2%	Also associated with CFC syndrome
<i>BRAF</i>	1–2%	Usually seen in CFC syndrome
<i>NRAS</i>	<1%	
<i>A2ML1</i>	Unknown	Candidate
<i>LZTR1</i>	Unknown	Candidate
<i>RASA2</i>	Unknown	Candidate
<i>SOS2</i>	Unknown	Candidate; ectodermal defects
<i>RRAS</i>		Candidate; Noonan like syndrome
<i>HRAS</i>		Costello syndrome; activating mutations
<i>MAP2K1</i>	2%	CFC syndrome
<i>MAP2K2</i>		CFC syndrome
<i>SHOC2</i>	2%	Noonan-like syndrome
<i>CBL</i>		Noonan-like syndrome

CFC, cardiofaciocutaneous syndrome; NSML, Noonan syndrome with multiple lentigenes. Table compiled from [51,52] and GeneReviews.

provide additional insight into epigenetic mechanisms in paediatric cardiomyopathy.

### Towards novel disease-specific therapeutics

Precision medicine is increasingly viewed as a means to establish individualized management and therapeutic plans that will lead to improved outcomes. In paediatric cardiomyopathy, a first step towards precision medicine is understanding the underlying cause of the patient's disease. Recent progress in disease-specific therapeutics has produced some exciting results. For example, infants with Pompe disease are now treated with enzyme replacement therapy (ERT) in order to ameliorate HCM. Early diagnosis is critical in order to optimize outcomes [48]. There is recent evidence that the development of HCM is not limited to the classic infantile-onset disease and that Pompe disease represents a continuum [49]. An interesting recent report also showed the successful use of ERT for storage caused by a *PRKAG2* mutation [50].

Whereas treatment of HCM in Pompe disease uses replacement of the deficient enzyme, new therapy in Noonan syndrome and Noonan syndrome

with multiple lentigenes (NSML, formerly LEOPARD syndrome) is directed at correcting the dysregulation of RAS-MAPK signalling. Mutations in *PTPN11* are the most common cause of Noonan syndrome, resulting in constitutive activation of the protein. New genes causing Noonan syndrome and related RASopathies continue to be identified (Table 2) [51,52]. In contrast, in NSML, mutations in *PTPN11* render the protein catalytically impaired. Greater than 80% of patients with NSML have HCM that is caused by hyperactivation of the AKT/mTOR pathway. Thus, mutations in the same gene can both cause HCM but via different mechanisms. This has important therapeutic implications.

The ability to prevent HCM was investigated in a mouse model of NSML by early treatment with the mTOR inhibitor rapamycin. Mice treated early did not develop HCM, and those treated at later stages demonstrated reversal of disease [53]. Recently, the first trial of a mTOR inhibitor was reported in an infant with NSML and rapidly progressive HCM. Therapy was initiated with a goal of halting progression of hypertrophy and outflow tract obstruction until transplant [54]. Pathway-specific inhibitors allow therapeutics to be tailored to the underlying genetic cause of disease.

Antagomirs, molecules used to inhibit miRNAs, have shown promise in animal models for inhibiting the development and progression of cardiomyopathy. For example, blocking profibrotic miRNAs with antagomirs in a mouse model of HCM resulted in decreased interstitial fibrosis and increased cardiac function. The development of antagomirs for therapeutic use in heart failure is reported in preclinical development [55].

Finally, the ability to perform genome editing has generated substantial enthusiasm about the ability to 'correct' mutations and restore normal function. When paired with research using human-induced pluripotent stem cells (iPSCs), these new technologies provide opportunities to understand the consequence of a pathogenic variant in the context of the patient's individual genetic variation. For example, recent studies of *TAZ* variants causing Barth syndrome using gene replacement and genome editing in iPSC demonstrated the necessity and sufficiency of the variants for phenotypes including sarcomere assembly and myocardial contraction abnormalities [56]. Human engineered cardiac tissues from a patient with a *BRAF* mutation recapitulated the HCM phenotype, providing a cell culture approach to study disease mechanisms and therapies *in vitro* [57]. Genome editing capabilities have also generated specific interest as a mechanism to correct a mutant allele encoding a structural component of the sarcomere in isolated

nonsyndromic cardiomyopathy. In a mouse model of HCM, adenoviral constructs were used to silence the mutant allele but not the wild-type allele, ameliorating the disease phenotype [58]. In another study using iPSCs, a mutation in phospholamban was shown to impair cardiomyocyte contractility and targeted genetic correction of the mutation rescued this defect [59]. These studies illustrate the power of combining iPSC and genome editing to understand the functional significance of genetic variation.

## CONCLUSION

Cardiomyopathy is not a single disease but multiple diseases with different underlying causes. Understanding the genetic basis of disease is a critical first step to design patient-specific management and therapy. Improving our ability to interpret genetic variation is necessary to properly assign causality. Ongoing investigation of the transcriptome and epigenome in paediatric patients will provide novel information about disease progression and outcome and may provide novel targets for therapeutic intervention. Genome editing and induced pluripotent stem cells provide novel tools to investigate genetic variation. Several disease-specific or gene-specific approaches have emerged and have promising results.

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## Conflicts of interest

None.

## REFERENCES AND RECOMMENDED READING

Papers of particular interest, published within the annual period of review, have been highlighted as:

- of special interest
- of outstanding interest

1. Lipshultz SE, Sleeper LA, Towbin JA, *et al.* The incidence of pediatric cardiomyopathy in two regions of the United States. *N Engl J Med* 2003; 348:1647–1655.
  2. Nugent AW, Daubeney PE, Chondros P, *et al.* The epidemiology of childhood cardiomyopathy in Australia. *N Engl J Med* 2003; 348:1639–1646.
  3. Tariq M, Ware SM. Importance of genetic evaluation and testing in pediatric cardiomyopathy. *World J Cardiol* 2014; 6:1156–1165.
  4. Ware SM. Evaluation of genetic causes of cardiomyopathy in childhood. *Cardiol Young* 2015; 25(Suppl 2):43–50.
  5. Morita H, Rehm HL, Menesses A, *et al.* Shared genetic causes of cardiac hypertrophy in children and adults. *N Engl J Med* 2008; 358:1899–1908.
  6. Kaski JP, Syrris P, Esteban MT, *et al.* Prevalence of sarcomere protein gene mutations in preadolescent children with hypertrophic cardiomyopathy. *Circ Cardiovasc Genet* 2009; 2:436–441.
  7. Loar RW, Bos JM, Will ML, *et al.* Genotype-phenotype correlations of hypertrophic cardiomyopathy when diagnosed in children, adolescents, and young adults. *Congenit Heart Dis* 2015; 10:529–536.
- This study analyses yield of testing in patients diagnosed with HCM less than 21 years of age and finds genotype-positive patients have an increased left ventricular wall thickness.
8. Jensen MK, Havndrup O, Christiansen M, *et al.* Penetrance of hypertrophic cardiomyopathy in children and adolescents: a 12-year follow-up study of clinical screening and predictive genetic testing. *Circulation* 2013; 127:48–54.
  9. Vermeer AM, Clur SB, Blom NA, *et al.* Penetrance of hypertrophic cardiomyopathy in children who are mutation positive. *J Pediatr* 2017. [Epub ahead of print]
- This study assesses the follow-up cardiac event in predictively tested children who are genotype positive and finds a relatively low rate (6.7%) but do identify significant cardiac events.
10. Bales ND, Johnson NM, Judge DP, Murphy AM. Comprehensive versus targeted genetic testing in children with hypertrophic cardiomyopathy. *Pediatr Cardiol* 2016; 37:845–851.
  11. Walsh R, Thomson KL, Ware JS, *et al.* Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. *Genet Med* 2017; 19:192–203.
- This study illustrates the difficulty of variant interpretation in light of massive amounts of new sequencing data in control populations.
12. Lek M, Karczewski KJ, Minikel EV, *et al.* Analysis of protein-coding genetic variation in 60,706 humans. *Nature* 2016; 536:285–291.
- Tour de force analysis of human genetic variation including a majority of genes that do not yet have established disease phenotypes.
13. Thevenon J, Laurent G, Ader F, *et al.* High prevalence of arrhythmic and myocardial complications in patients with cardiac glycogenosis due to PRKAG2 mutations. *Europace* 2017; 19:651–659.
  14. Fu L, Luo S, Cai S, *et al.* Identification of LAMP2 mutations in early-onset Danon disease with hypertrophic cardiomyopathy by targeted next-generation sequencing. *Am J Cardiol* 2016; 118:888–894.
  15. Maron BJ, Roberts WC, Arad M, *et al.* Clinical outcome and phenotypic expression in LAMP2 cardiomyopathy. *JAMA* 2009; 301:1253–1259.
  16. Badertscher A, Bauersfeld U, Arbenz U, *et al.* Cardiomyopathy in newborns and infants: a broad spectrum of aetiologies and poor prognosis. *Acta Paediatr* 2008; 97:1523–1528.
  17. Kindel SJ, Miller EM, Gupta R, *et al.* Pediatric cardiomyopathy: importance of genetic and metabolic evaluation. *J Cardiac Fail* 2012; 18:396–403.
  18. Rusconi P, Wilkinson JD, Sleeper LA, *et al.* Differences in presentation and outcomes between children with familial dilated cardiomyopathy and children with idiopathic dilated cardiomyopathy: a report from the Pediatric Cardiomyopathy Registry Study Group. *Circ Heart Fail* 2017; 10:pii: e002637.
- Large multisite evaluation of nearly 1000 paediatric patients with idiopathic or familial DCM shows no survival difference between groups. Older age, presence of heart failure and greater dilation are independently associated with outcome.
19. Ware JS, Li J, Mazaika E, *et al.* Shared genetic predisposition in peripartum and dilated cardiomyopathies. *N Engl J Med* 2016; 374:233–241.
  20. Deo RC. Alternative splicing, internal promoter, nonsense-mediated decay, or all three: explaining the distribution of truncation variants in titin. *Circ Cardiovasc Genet* 2016; 9:419–425.
- Development of a computational model to predict the effect of rare variants in titin.
21. Herman DS, Lam L, Taylor MR, *et al.* Truncations of titin causing dilated cardiomyopathy. *N Engl J Med* 2012; 366:619–628.
  22. Burke MA, Cook SA, Seidman JG, Seidman CE. Clinical and mechanistic insights into the genetics of cardiomyopathy. *J Am Coll Cardiol* 2016; 68:2871–2886.
  23. Authors/Task Force m. Elliott PM, Anastakis A, Borger MA, *et al.* 2014 ESC Guidelines on diagnosis and management of hypertrophic cardiomyopathy: the Task Force for the Diagnosis and Management of Hypertrophic Cardiomyopathy of the European Society of Cardiology (ESC). *Eur Heart J* 2014; 35:2733–2779.
  24. Charron P, Heron D, Gargiulo M, *et al.* Genetic testing and genetic counselling in hypertrophic cardiomyopathy: the French experience. *J Med Genet* 2002; 39:741–746.
  25. Gersh BJ, Maron BJ, Bonow RO, *et al.* 2011 ACCF/AHA guideline for the diagnosis and treatment of hypertrophic cardiomyopathy: executive summary: a report of the American College of Cardiology Foundation/American Heart Association Task Force on Practice Guidelines. *J Am Coll Cardiol* 2011; 58:2703–2738.
  26. Hershelberger RE, Siegfried JD. Update 2011: clinical and genetic issues in familial dilated cardiomyopathy. *J Am Coll Cardiol* 2011; 57:1641–1649.

27. Miller EM, Wang Y, Ware SM. Uptake of cardiac screening and genetic testing among hypertrophic and dilated cardiomyopathy families. *J Genet Counsel* 2013; 22:258–267.
  28. Khouzam A, Kwan A, Baxter S, Bernstein JA. Factors associated with uptake of genetics services for hypertrophic cardiomyopathy. *J Genet Counsel* 2015; 24:797–809.
- One of the first studies in the United States to assess patient, family and caregiver reasons for utilization of genetic testing for cardiomyopathy.
29. Alfares AA, Kelly MA, McDermott G, *et al.* Results of clinical genetic testing of 2,912 probands with hypertrophic cardiomyopathy: expanded panels offer limited additional sensitivity. *Genet Med* 2015; 17:880–888.
- This assessment of clinical genetic testing results for HCM includes a cohort of children with HCM. In addition to providing diagnostic yields, this manuscript assesses cost savings associated with clinical genetic testing.
30. Ouellette AC, Mathew J, Manickaraj AK, *et al.* Clinical genetic testing in pediatric cardiomyopathy: is bigger better? *Clin Genet* 2017. [Epub ahead of print]
  31. Mital S, Musunuru K, Garg V, *et al.* Enhancing literacy in cardiovascular genetics: a scientific statement from the American Heart Association. *Circ Cardiovasc Genet* 2016; 9:448–467.
- This provides a guideline for careproviders of patients with cardiovascular genetic conditions. The need for additional training in order to maximize the benefits of genetic medicine is emphasized.
32. Richards S, Aziz N, Bale S, *et al.* Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med* 2015; 17:405–424.
  33. Nouhravesh N, Ahlberg G, Ghouse J, *et al.* Analyses of more than 60,000 exomes questions the role of numerous genes previously associated with dilated cardiomyopathy. *Mol Genet Genom Med* 2016; 4:617–623.
  34. Walsh R, Buchan R, Wilk A, *et al.* Defining the genetic architecture of hypertrophic cardiomyopathy: re-evaluating the role of nonsarcomeric genes. *Eur Heart J* 2017. [Epub ahead of print]
  35. Burke MA, Chang S, Wakimoto H, *et al.* Molecular profiling of dilated cardiomyopathy that progresses to heart failure. *JCI Insight* 2016; 1:pii: e86898.
- Transcriptional profiling at different disease stages identifies a molecular signature for heart failure using a mouse model.
36. Liu Y, Morley M, Brandimarto J, *et al.* RNA-Seq identifies novel myocardial gene expression signatures of heart failure. *Genomics* 2015; 105:83–89.
- A small study in patients analysing molecular signature for heart failure in one ischemic and two DCM patients.
37. Maatz H, Jens M, Liss M, *et al.* RNA-binding protein RBM20 represses splicing to orchestrate cardiac premRNA processing. *J Clin Invest* 2014; 124:3419–3430.
  38. Kong SW, Hu YW, Ho JW, *et al.* Heart failure-associated changes in RNA splicing of sarcomere genes. *Circ Cardiovasc Genet* 2010; 3:138–146.
  39. Lara-Pezzi E, Gomez-Salainero J, Gatto A, Garcia-Pavia P. The alternative heart: impact of alternative splicing in heart disease. *J Cardiovasc Trans Res* 2013; 6:945–955.
  40. Miyamoto SD, Stauffer BL, Nakano S, *et al.* Beta-adrenergic adaptation in paediatric idiopathic dilated cardiomyopathy. *Eur Heart J* 2014; 35:33–41.
  41. Nakano SJ, Miyamoto SD, Movsesian M, *et al.* Age-related differences in phosphodiesterase activity and effects of chronic phosphodiesterase inhibition in idiopathic dilated cardiomyopathy. *Circ Heart Fail* 2015; 8:57–63.
- This study highlights that children are not just little adults. The profiles of paediatric DCM patients treated with phosphodiesterase inhibitors were distinct from adults.
42. Nakano SJ, Sucharov J, van Dusen R, *et al.* Cardiac adenylyl cyclase and phosphodiesterase expression profiles vary by age, disease, and chronic phosphodiesterase inhibitor treatment. *J Card Fail* 2017; 23:72–80.
  43. Rindler TN, Hinton RB, Salomonis N, Ware SM. Molecular characterization of pediatric restrictive cardiomyopathy from integrative genomics. *Sci Rep* 2017; 7:39276.
- The first transcriptome analysis in RCM patients demonstrates abnormal splicing profiles in RBM20 target genes and identifies novel pathway dysregulation.
44. Kumarswamy R, Thum T. Noncoding RNAs in cardiac remodeling and heart failure. *Circ Res* 2013; 113:676–689.
  45. Bauters C, Kumarswamy R, Holzmann A, *et al.* Circulating miR-133a and miR-423-5p fail as biomarkers for left ventricular remodeling after myocardial infarction. *Int J Cardiol* 2013; 168:1837–1840.
  46. Stauffer BL, Russell G, Nunley K, *et al.* miRNA expression in pediatric failing human heart. *J Mol Cell Cardiol* 2013; 57:43–46.
  47. Kumarswamy R, Bauters C, Volkman I, *et al.* Circulating long noncoding RNA, LIPCAR, predicts survival in patients with heart failure. *Circ Res* 2014; 114:1569–1575.
  48. van Gelder CM, Hoogeveen-Westerveld M, Kroos MA, *et al.* Enzyme therapy and immune response in relation to CRIM status: the Dutch experience in classic infantile Pompe disease. *J Inher Metab Dis* 2015; 38:305–314.
  49. Lee DH, Qiu WJ, Lee J, *et al.* Hypertrophic cardiomyopathy in Pompe disease is not limited to the classic infantile-onset phenotype. *JIMD Rep* 2014; 17:71–75.
  50. Austin SL, Chiou A, Sun B, *et al.* Alglucosidase alfa enzyme replacement therapy as a therapeutic approach for a patient presenting with a PRKAG2 mutation. *Mol Genet Metab* 2017; 120:96–100.
  51. Aoki Y, Niihori T, Inoue S, Matsubara Y. Recent advances in RASopathies. *J Hum Genet* 2016; 61:33–39.
  52. El Bouchikhi I, Belhassan K, Zohra Moudif F, *et al.* Noonan syndrome-causing genes: molecular update and an assessment of the mutation rate. *Int J Pediatr Adolesc Med* 2016; 3:133–142.
  53. Marin TM, Keith K, Davies B, *et al.* Rapamycin reverses hypertrophic cardiomyopathy in a mouse model of LEOPARD syndrome-associated PTPN11 mutation. *J Clin Invest* 2011; 121:1026–1043.
  54. Hahn A, Lauriol J, Thul J, *et al.* Rapidly progressive hypertrophic cardiomyopathy in an infant with Noonan syndrome with multiple lentigines: palliative treatment with a rapamycin analog. *Am J Med Genet A* 2015; 167A:744–751.
- The first patient to receive RAS-MAPK pathway specific therapy in an attempt to halt progression of HCM.
55. van Rooij E, Kauppinen S. Development of microRNA therapeutics is coming of age. *EMBO Mol Med* 2014; 6:851–864.
  56. Wang G, McCain ML, Yang L, *et al.* Modeling the mitochondrial cardiomyopathy of Barth syndrome with induced pluripotent stem cell and heart-on-chip technologies. *Nat Med* 2014; 20:616–623.
  57. Cashman TJ, Josowitz R, Johnson BV, *et al.* Human engineered cardiac tissues created using induced pluripotent stem cells reveal functional characteristics of BRAF-mediated hypertrophic cardiomyopathy. *PLoS One* 2016; 11:e0146697.
  58. Jiang J, Wakimoto H, Seidman JG, Seidman CE. Allele-specific silencing of mutant Myh6 transcripts in mice suppresses hypertrophic cardiomyopathy. *Science (New York, NY)* 2013; 342:111–114.
  59. Stillitano F, Turnbull IC, Karakikes I, *et al.* Genomic correction of familial cardiomyopathy in human engineered cardiac tissues. *Eur Heart J* 2016; 37:3282–3284.
- Genome editing used to correct phospholamban mutation.