



Genetic Variants Associated With Cancer Therapy–Induced Cardiomyopathy

BACKGROUND: Cancer therapy–induced cardiomyopathy (CCM) is associated with cumulative drug exposures and preexisting cardiovascular disorders. These parameters incompletely account for substantial interindividual susceptibility to CCM. We hypothesized that rare variants in cardiomyopathy genes contribute to CCM.

METHODS: We studied 213 patients with CCM from 3 cohorts: retrospectively recruited adults with diverse cancers (n=99), prospectively phenotyped adults with breast cancer (n=73), and prospectively phenotyped children with acute myeloid leukemia (n=41). Cardiomyopathy genes, including 9 prespecified genes, were sequenced. The prevalence of rare variants was compared between CCM cohorts and The Cancer Genome Atlas participants (n=2053), healthy volunteers (n=445), and an ancestry-matched reference population. Clinical characteristics and outcomes were assessed and stratified by genotypes. A prevalent CCM genotype was modeled in anthracycline-treated mice.

RESULTS: CCM was diagnosed 0.4 to 9 years after chemotherapy; 90% of these patients received anthracyclines. Adult patients with CCM had cardiovascular risk factors similar to the US population. Among 9 prioritized genes, patients with CCM had more rare protein-altering variants than comparative cohorts ($P \leq 1.98e-04$). Titin-truncating variants (TTNtv) predominated, occurring in 7.5% of patients with CCM versus 1.1% of The Cancer Genome Atlas participants ($P = 7.36e-08$), 0.7% of healthy volunteers ($P = 3.42e-06$), and 0.6% of the reference population ($P = 5.87e-14$). Adult patients who had CCM with TTNtv experienced more heart failure and atrial fibrillation ($P = 0.003$) and impaired myocardial recovery ($P = 0.03$) than those without. Consistent with human data, anthracycline-treated TTNtv mice and isolated TTNtv cardiomyocytes showed sustained contractile dysfunction unlike wild-type ($P = 0.0004$ and $P < 0.002$, respectively).

CONCLUSIONS: Unrecognized rare variants in cardiomyopathy-associated genes, particularly TTNtv, increased the risk for CCM in children and adults, and adverse cardiac events in adults. Genotype, along with cumulative chemotherapy dosage and traditional cardiovascular risk factors, improves the identification of patients who have cancer at highest risk for CCM.

CLINICAL TRIAL REGISTRATION: URL: <https://www.clinicaltrials.gov>. Unique identifiers: NCT01173341; AAML1031; NCT01371981.

Pablo Garcia-Pavia, MD, PhD*
Yuri Kim, MD, PhD*
Maria Alejandra Restrepo-Cordoba, MD*
et al

*Drs Garcia-Pavia, Kim, and Restrepo-Cordoba contributed equally.

†Drs Barton, Aplenc, J. G. Seidman, Ky, Ware, and C. E. Seidman are co-senior authors (see page 39).

Full author list is available on page 39.

Key Words: cardiomyopathies
■ drug therapy ■ genetics ■ medical oncology ■ titin

Sources of Funding, see page 39

© 2019 The Authors. *Circulation* is published on behalf of the American Heart Association, Inc., by Wolters Kluwer Health, Inc. This is an open access article under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits use, distribution, and reproduction in any medium, provided that the original work is properly cited.

<https://www.ahajournals.org/journal/circ>

Clinical Perspective

What Is New?

- This is the first study to consider the association between rare genetic variants in a large set of cardiomyopathy genes and the occurrence of cancer therapy–induced cardiomyopathy (CCM).
- We demonstrated an increased prevalence of rare variants in cardiomyopathy genes, in particular, truncating variants in the *TTN* gene, in adult and pediatric patients who have cancer with CCM.
- We confirmed human genetic data with experimental analyses, showing that anthracyclines induced protracted left ventricular dysfunction in mice with titin-truncating variants, but not in wild-type mice.

What Are the Clinical Implications?

- Our findings show that variants in cardiomyopathy genes contribute to CCM susceptibility among adult and pediatric patients with cancer.
- The identification of genetic risk factors opens new opportunities to define patients at high risk for CCM and associated adverse outcomes.
- Future investigations to define patients who have cancer with high risk for CCM through genetic testing can assess the efficacy of prophylactic cardioprotective drugs and treatment regimens to reduce CCM while providing effective cancer therapy.

Considerable advances in cancer therapies have led to major improvements in long-term survival for many malignancies, but also to unintended side effects, including cardiotoxicity.^{1,2} Cancer therapy–induced cardiomyopathy (CCM), identified as reduced left ventricular ejection fraction (LVEF) with or without signs and symptoms of overt heart failure,³ can occur during, shortly after, or many years beyond cancer treatments and affects the long-term prognosis of patients.^{1,4,5}

Anthracyclines, which are commonly used to treat both solid tumors and hematologic malignancies in children and adults,² cause cardiotoxicity in up to 10% of patients with cumulative dosages of 250 mg/m² but in 65% of patients receiving cumulative dosages >550 mg/m².⁶ Combining anthracyclines with other therapies, such as trastuzumab (an antibody targeting HER-2), can provoke greater cardiotoxicity with depressed LVEF occurring in ≈18% to 34% of treated individuals, and severe, symptomatic heart failure in 2% to 4%.^{3,7} Additional clinical parameters are recognized to contribute to CCM, including female sex, extremes of age, and preexisting cardiac risk factors.² Even when accounting for these factors, predicting individual susceptibility to CCM remains challenging.

Several candidate gene and genome-wide association studies have identified common genetic variants that are associated with CCM through candidate gene analyses and genome-wide association studies.^{2,8–12} Although a recent systemic literature review concluded that the overall evidence supporting variant associations with CCM was limited, genetic data were robust for one intergenic variant (rs28714259) and variants in proximity to 4 other genes.¹³ Rare variants in genes that cause familial cardiomyopathies¹⁴ have also been identified in several small case series and isolated patients with CCM.^{13,15–17}

To better understand the clinical and genetic determinants in CCM, we studied 3 CCM cohorts comprising adult and pediatric patients with diverse malignancies, of whom 90% received anthracyclines. We then corroborated our human findings through cardiac phenotyping of anthracycline-treated mice. From these analyses, we demonstrate the direct and prevalent involvement of variants in genes associated with dilated cardiomyopathy and, in particular, titin-truncating variants (*TTN*ts) in CCM.

METHODS

The data that support the findings of this study are available within the article, the online supplementary files, and publicly available databases. Additional requests, from qualified researchers trained in human subject confidentiality protocols, for anonymized data may be sent to the corresponding authors.

CCM Cohorts, Healthy Volunteer, and Population Controls

Research protocols were reviewed and approved by the institutional ethics board at each participating site. Adult patients with CCM (cohorts A and B), parents of minor patients with CCM (cohort C), and healthy volunteers provided written informed consent. Cohort A includes non-Finnish European patients with CCM retrospectively collected from 6 European heart failure or cardiac transplantation clinics in Spain and the United Kingdom. Cohort B includes prospectively enrolled patients with breast cancer, participating in cardiotoxicity studies of cancer treatments (clinicaltrials.gov NCT01173341). Cohort C includes pediatric patients with newly diagnosed acute myeloid leukemia, enrolled in a clinical therapy trial therapy (AAML1031; clinicaltrials.gov NCT01371981). Cohorts B and C are US patients with non-Finnish European, African, or Asian ancestry, who had prespecified clinical assessments with cardiac imaging (echocardiograms or multigated acquisition scans) before, during, and after chemotherapy. Table 1 provides additional demographic profiles on these cohorts.

CCM was diagnosed irrespective of symptoms based on LVEF to <50 (cohort B) or <53% (cohorts A and C)^{3,18,19} and ≥10% reduction from baseline by echocardiography or <50% and ≥10% reduction from baseline by radionuclide ventriculography, in the absence of established coronary artery disease, cardiomyopathy, primary valvular disease, or uncontrolled hypertension.

Table 1. Clinical Characteristics at Baseline and Follow-Up in Patients With CCM in Study Cohorts

Characteristics	Cohort A (n=99)	Cohort B (n=73)	Cohort C (n=41)
Baseline			
Age at chemotherapy onset, y	48.7±17.1	49.6±10.8	10.8±5.6
Male sex, n (%)	33 (33)§	0 (0)§	17 (41)§
Family history of cardiomyopathy, n (%)	3 (3)	0 (0)	NA
Ethnicity, n (%)			
White	99 (100)§	46 (63)§	25 (61)§
Black	0 (0)§	23 (32)§	9 (22)§
Asian	0 (0)§	4 (5)§	3 (7)§
Others	0 (0)§	0 (0)§	4 (10)§
Comorbidities, n (%)			
Current or past smokers	33 (33)	25 (34)	0 (0)
Hypertension	29 (29)	29 (39)	0 (0)
Hypercholesterolemia	27 (27)	17 (23)	0 (0)
Diabetes mellitus	20 (20)	7 (10)	0 (0)
Oncological disease, n (%)			
Breast cancer	51 (52)§	73 (100)§	0 (0)§
Hematological malignancy	38 (38)§	0 (0)§	41 (100)§
Other solid tumor	10 (10)§	0 (0)§	0 (0)§
Exposure to anthracycline, n (%)	91 (91)	58 (79)	41 (100)
Cumulative anthracycline dose, * mg/m ²	300.7±153.2	240±0	488.3±23.4
Exposure to anti-HER2, n (%)	20 (20)§	36 (49)§	0 (0)§
Radiation therapy to chest, n (%)	32 (32)§	47 (64)§	0 (0)§
LVEF before chemotherapy,† %	62.1±5.4§	55.0±4.7§	64.5±5.8§
At CCM diagnosis			
Time from chemotherapy to diagnosis, y	3 (1–9)§	0.7 (0.4–1.2)§	0.3 (0.2–0.4)§
LVEF at CCM diagnosis, %	33.0±10.0§	41.5±5.5§	44.8±6.7§
NYHA functional class III–IV, n (%)	44 (44)§	1 (1.3)§	NA§
Follow-up			
Duration of follow-up, y	4 (1–7)§	1.7 (0.7–3.3)§	2.3 (1.1–3.2)§
Final LVEF, %	47.3±13.2	49.3±8.2	54.8±13.0
LVEF recovery,‡ n (%)	50 (50)	33 (45)	28 (68)
Cardiac transplantation, n (%)	9 (9)	0 (0)	0 (0)
Cardiac death, n (%)	3 (3)	0 (0)	2 (5)

Data are expressed as numbers (%) or mean±SD, except for time from chemotherapy to cardiotoxicity diagnosis and duration of follow-up, which are expressed as median (Q1–Q3). Comorbidities are those present at diagnosis of CCM. Patient characteristics which are significantly different (adjusted *P*-value <0.05 using Fisher exact test for categorical variables and Welch *t* test for continuous variables) between adult cohorts A and B are shown in bold. CCM indicates cancer therapy-induced cardiomyopathy; HER-2, human epidermal growth factor receptor-2; LVEF, left ventricular ejection fraction; and NYHA, New York Heart Association.

*Cumulative anthracycline dose for 7 patients in cohort A is unknown; these patients were excluded from calculation. Fifty-eight patients in cohort B who underwent anthracycline treatment received 240 mg/m². Planned cumulative anthracycline dose for cohort C (492 mg/m² for 40 patients and 342 mg/m² for 1 patient) is noted in the table, but actual dose may have varied, because 17 patients underwent dose modification of unknown quantity during their treatment period.

†LVEF before chemotherapy was available to review in 31, 73, and 41 subjects in cohorts A, B, and C, respectively.

‡LVEF recovery was defined as an absolute increase in LVEF ≥5% with final LVEF ≥50% in the adult cohorts and ≥53% in the pediatric cohort.

§Significant values.

Additional clinical information including follow-up duration and adverse outcomes was obtained from medical and clinical trial records and patient reports. Where prechemotherapy cardiac imaging was absent, patients were included when LVEF was ≤45% and no alternative cause for cardiac dysfunction other

than chemotherapy was identified. LVEF recovery was defined by a final LVEF ≥50% with ≥5% LVEF increase or restoration of LVEF to the baseline value.¹⁸

Healthy volunteers of European ancestry (n=445) were prospectively recruited participants into the U.K. Digital Heart Project

(<https://digital-heart.org/>)²⁰ with no cardiovascular disease or risk factors by self-report and normal cardiac magnetic resonance imaging.

Next-Generation Sequencing and Variant Analysis

Genomic DNA extracted from peripheral blood samples was used to produce DNA-sequencing libraries that were captured and sequenced on Illumina TruSight Cardio Sequencing kit and a custom Agilent array (DCMv5) as described.^{20,21} Variants were identified using the Genome Analysis Tool Kit (GATK) HaplotypeCaller tool following GATK Best Practices.²² Rare variants (minor allele frequency <1.0e−4, assessed in ancestry-matched subjects in the Genome Aggregation Database [gnomAD]²³) were annotated by SnpEFF and GRCh37.68 (also see the [online-only Data Supplement](#)). The cumulative burden of rare variants in cardiomyopathy genes was compared in CCM cohorts with all patients who had breast (n=1042) and lung (n=1011) cancer participating in The Cancer Genome Project (TCGA),²⁴ healthy volunteers, and gnomAD²³ subjects with non-Finnish European, African, and Asian ancestries (combined and in ancestry-specific analyses).

Anthracycline Treatment of Mice

Protocols were reviewed and approved by the Institutional Animal Care and Use Committee at Harvard Medical School (Boston, MA). Wild-type and heterozygous C57BL/6N mice with a titin A-band truncation (Ttn^{tv/+})^{25,26} received 3 doses of intraperitoneal doxorubicin (5 mg/kg) at weekly intervals (≈45 mg/m²). Cardiac function was assessed in vivo at baseline (age=10–14 weeks) and weekly using a digital ultrasound system (Vevo 2100 Imaging System and M5550D transducer; FujiFilm VisualSonics) by an experienced observer blinded to mouse genotype and treatment. Cardiomyocytes from treated and untreated wild-type and Ttn^{tv/+} mice were isolated and sarcomere contractility was measured (see the [online-only Data Supplement Methods](#)).

Statistical Analyses

Cohort and subgroup analyses, and comparisons with TCGA genomic data,²⁴ healthy volunteers, and reference populations²³ were performed by Fisher exact test (2-tailed), binomial test, or Pearson χ^2 test of association for categorical values. Welch *t* test and Kruskal-Wallis rank sum tests were used to assess numerical data. Analyses were conducted using either the Stata SE package (version 14, StataCorp) or the R statistical package (version 3.4.0; <http://www.R-project.org/>).

Additional method details are provided in the [online-only Data Supplement](#).

RESULTS

Patients With CCM

We studied 3 CCM cohorts (Table 1). Cohort A includes 99 patients of European ancestry with hematologic, breast, or other solid-tumor cancer (mean age at treatment=48.7±17.1 years), recruited from heart failure and

cardiac transplant clinics. Two US cohorts were identified through prospective longitudinal cardiac evaluations obtained throughout cancer therapy: Cohort B comprised 73 patients (mean age at treatment=49.6±10.8 years) with European, African, or Asian ancestry, enrolled from breast cancer clinics as part of a prospective study of who developed CCM during treatment; Cohort C comprised 41 pediatric patients with newly diagnosed acute myelogenous leukemia (mean age at treatment=10.8±5.6 years) of diverse ancestries. Although individual treatments varied, 90% of all patients with CCM received anthracycline and 33% of adults received trastuzumab. After normalizing anthracycline doses²⁷ the cumulative equivalent dose was <400 mg/m² in 93.9% of patients in cohort A, 100% of patients in cohort B, and 2.3% of patients in cohort C.

We assessed clinical risk factors for CCM in these cohorts. Seventy-six percent of all patients were CCM were females, predominantly treated for breast cancer. In cohorts A and B the prevalence of cigarette smoking, hypertension, and diabetes mellitus was comparable (*P*=not significant) to that of the general US population,²⁸ but hypercholesterolemia in patients with cancer was less common (*P*=3.0e−09). Three patients in cohort A, without prechemotherapy imaging studies, had family histories of cardiomyopathy of unknown cause. Patients in cohort C were considerably younger (mean age=10.8±5.6 years), without cardiovascular risk factors, and all had normal LVEF at study entry.

The median time after the initiation of cancer treatment to CCM diagnosis in cohort A was 3.0 (range=1–9) years, but 0.3 to 0.7 years for cohorts B and C because of cardiac surveillance during treatment in these 2 cohorts. At CCM diagnosis, the mean LVEF decrease was 23.4±9.2% in cohort A, 13.5±3.3% in cohort B, and 19.7±6.0% in cohort C. Across all cohorts, treatment with high cumulative anthracycline dose (>400 mg/m²) was not associated with poorer left ventricular (LV) dysfunction at CCM diagnosis (mean LVEF=42.0±9.6%). Patients (cohorts A and B) who received trastuzumab without anthracycline had similar cardiovascular risk factors and no significant differences in either baseline or postchemotherapeutic LVEF (mean LVEF decrease=13.9±3.6%) in comparison with patients receiving anthracyclines with or without other agents (mean LVEF decrease=16.7±7.5%). Cardiac recovery occurred in approximately half of patients with CCM from each cohort, but 9% of patients in cohort A underwent cardiac transplantation. Cardiac deaths occurred in 3% of patients in cohort A and in 5% of patients in cohort C.

Gene Variants in Patients With CCM

We previously identified 9 genes with an excess of rare missense and in-frame insertions/deletion or truncating variants among patients with cardiomyopathy.²⁹ Within

Table 2. Burden Analysis of 9 DCM Genes in CCM Cohorts

Gene	Cohort A (n=99)	Cohort B (n=73)	Cohort C (n=41)	All CCM (n=213)	TCGA* Breast/Lung (n=2053)	HVOL† (n=445)	P Values Comparisons of			
							All CCM Versus			NFE‡ CCM (n=170) Versus NFE gnomAD
							TCGA	HVOL	gnomAD‡	
BAG3	1 (1.0%)	2 (2.7%)	0 (0.0%)	3 (1.4%)	18 (0.9%)	4 (0.9%)	0.44 (1)	0.69 (1)	0.44 (1)	0.37 (1)
DSP	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (0.2%)	0 (0.0%)	1 (1)	1 (1)	1 (1)	1 (1)
LMNA	0 (0.0%)	1 (1.4%)	0 (0.0%)	1 (0.5%)	16 (0.8%)	2 (0.4%)	1 (1)	1 (1)	1 (1)	1 (1)
MYH7	3 (3.0%)	0 (0.0%)	0 (0.0%)	3 (1.4%)	35 (1.7%)	5 (1.1%)	1 (1)	0.72 (1)	1 (1)	0.75 (1)
SCN5A	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (0.2%)	1 (0.2%)	1 (1)	1 (1)	1 (1)	1 (1)
TCAP	1 (1.0%)	0 (0.0%)	1 (2.4%)	2 (0.9%)	2 (0.1%)	0 (0.0%)	0.05 (0.45)	0.10 (0.90)	0.07 (0.62)	1 (1)
TNNC1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.1%)	0 (0.0%)	1 (1)	1 (1)	1 (1)	1 (1)
TNNT2	0 (0.0%)	1 (1.4%)	0 (0.0%)	1 (0.5%)	7 (0.3%)	0 (0.0%)	0.55 (1)	0.32 (1)	0.50 (1)	0.34 (1)
TTN	10 (10.0%)	4 (5.5%)	2 (4.9%)	16 (7.5%)	22 (1.1%)	3 (0.7%)	7.36e−08 (6.62e−07)	3.42e−06 (3.08e−05)	5.87e−14 (5.28e−13)	2.03e−10 (1.82e−09)
8 genes (no TTN)	5 (5.1%)	4 (5.5%)	1 (2.4%)	10 (4.7%)	86 (4.2%)	12 (2.7%)	0.72	0.25	0.01	0.21
9 genes	15 (15.1%)	8 (11%)	3 (7.3%)	26 (12.2%)	108 (5.3%)	15 (3.4%)	1.98e−04	3.90e−05	1.78e−06	6.98e−06

The number of subjects with variants in each gene is noted in the table, and percentages are noted in parentheses (%). Types of variants analyzed for each gene: all protein-altering variants (BAG3, LMNA, TCAP, TNNC1, TNNT2), missense variants and in-frame deletion or insertion only (MYH7), frameshift variant, stop-gained, splice-donor, and splice-acceptor variants only (DSP, SCN5A, TTN). P values were calculated via Fisher exact test for all CCM vs breast and lung cancer TCGA participants (TCGA) and healthy volunteers (HVOL) and binomial test for all CCM vs gnomAD.²³ Bonferroni corrections are provided in parentheses. Significant values are shown in bold. CCM indicates cancer therapy-induced cardiomyopathy; and DCM, dilated cardiomyopathy.

*TCGA denotes all breast and lung cancer participants (n=2053) in The Cancer Genome Atlas.²⁴

†HVOL denotes 445 healthy volunteers without cardiovascular disease based on detailed evaluations.

‡gnomAD denotes reference population with African American, non-Finnish European, and East Asian ancestries.

§NFE denotes non-Finnish Europeans ancestries. The subanalyses of NFE patients with CCM are compared with NFE gnomAD reference population n≥113482.

||Significant values.

See Table II in the online-only Data Supplement for subanalyses of patients with CCM and reference populations stratified by ancestry.

these prespecified genes, we examined rare variants (defined as minor allele frequency <1.0e−4) among ancestry-matched reference populations,²³ CCM cohorts, healthy volunteers, and all breast and lung cancer participants in TCGA²⁴ (Table 2). Because anthracyclines are highly effective and widely used to treat these malignancies,⁶ we expect that most TCGA participants received this chemotherapeutic agent. The prevalence of rare protein-altering variants across all 9 genes was significantly higher in a combined CCM cohort than in unselected lung and breast cancer TCGA participants ($P=1.98e-04$), healthy volunteers ($P=3.90e-05$), and reference populations ($P=1.78e-06$). Although patients with CCM had rare variants in several established dilated cardiomyopathy (DCM) genes (BAG3, LMNA, MYH7, TCAP, TNNT2, and TTN), only variants in TTN, which encodes titin, were significantly increased. TTNts were highly enriched in all patients with CCM (n=16; 7.5%) in comparison with unselected breast or lung TCGA participants (combined, $P=7.36e-08$ and Table I in the online-only Data Supplement), healthy volunteers ($P=3.42e-06$), and the reference population ($P=5.87e-14$). Subanalyses of patients with CCM and the reference population stratified by ancestry (Table II in the online-only Data Supplement), although limited by small numbers, confirmed the observed enrichment of TTNts in all patients with CCM. TTNts that are significantly

increased in patients with DCM^{20,30} reside in exons that are highly expressed in LV tissues, especially those that encode the A-band and distal I-band.³¹ TTNts identified in patients with CCM shared these characteristics (Table 3).

We extended these analyses to include 40 other genes that have been implicated in cardiomyopathies.²⁹ Variants in these genes account for a very small fraction of unselected patients with cardiomyopathy. There was no significant difference in the prevalence of all rare protein-altering variants (minor allele frequency <1.0e−4; Tables III and IV in the online-only Data Supplement) or variants predicted as damaging (Tables V and VI in the online-only Data Supplement) in patients with CCM in each cohort or the combined CCM cohort, in comparison with healthy volunteers or in the reference population. For individual genes, the prevalence of rare variants was nominally increased only in FKRP (encoding fukutin-related protein); recessive FKRP mutations cause several forms of muscular dystrophies with cardiac involvement.³²

Clinical Outcomes in Adult Patients Who Have CCM With or Without TTNts

Patients with CCM in cohorts A and B were predominantly women (81%), with breast cancer (73%), with traditional cardiovascular risk factors, who received

Table 3. Summary of TTNtv Identified From All 3 Cohorts With CCM

Variant	Impact	TTN Band	Affected Exon	PSI of Affected Exon	Cancer Type	Chemotherapy	LVEF at CCM (Change)	Follow-Up, y	Adverse Outcome
chr2:179399704 c.101638G>T	Nonsense (p.Glu33880X)	M	359	1	Breast	Epirubicin	30% (NA)	14	HF
chr2:179400742 c.100731dupA	Frameshift (p.Ser33578IlefsTer15)	A	358	0.99	Breast	Doxorubicin + Trastuzumab	37% (24%)	4	VT, HF
chr2:179410112 c.95722+2delT	Splicing	A	345	0.99	Endometrial	Doxorubicin	20% (NA)	5	HF
chr2:179414849 c.91715dupA	Frameshift (p.Asn30572fs)	A	338	0.98	Breast	Epirubicin	42% (NA)	5	HF
chr2:179422284 c.60512-2A>C	Splicing	A	330	0.96	Breast	Doxorubicin + Trastuzumab	43% (17%)	2.2	None
chr2:179425091 c.85768C>T	Nonsense (p.Arg28590X)	A	327	0.95	Breast	Doxorubicin	35% (NA)	2	HF, VT, transplantation
chr2:179428124 c.82734dupA	Frameshift (p.Val27579SerfsTer15)	A	327	0.95	Non- Hodgkin lymphoma	Doxorubicin	29% (NA)	2	None
chr2:179432234 c.78625G>T	Nonsense (p.Glu26209X)	A	327	0.95	Non- Hodgkin lymphoma	Doxorubicin	34% (NA)	3	HF
chr2:179435679 c.75179delA	Frameshift (p.Asn25060fs)	A	327	0.95	Breast	Doxorubicin + Trastuzumab	44% (12%)	3.4	None
chr2:179441250 c.69715+6T>C	Splicing	A	326	0.95	Breast	Trastuzumab	38% (12%)	0.4	None
chr2:179446855 c.66240delA	Frameshift (p.Asp22081MetfsTer31)	A	316	0.86	Bone sarcoma	Doxorubicin	25% (NA)	6	HF
chr2:179453355 c.63096delT	Frameshift (p.His21032fs)	A	305	0.97	AML	Daunorubicin+ Mitoxantrone	36% (22%)	2.8	None
chr2:179478777 c.49345+2T>C	Splicing	A	263	0.89	AML	Daunorubicin+ Mitoxantrone	50% (18%)	0.8	None
chr2:179571683 c.29042-2A>C	Splicing	I	102	0.88	Breast	Doxorubicin	35% (15%)	1.6	None
chr2:179604819 c.13141G>T	Nonsense (p.Glu4381X)	I	49	0.95	Breast	Doxorubicin	31% (30%)	6	HF
chr2:179631116 c.9693_9694delCT	Frameshift (p.Tyr3232CysfsTer5)	I	41	1	Breast	Epirubicin	45% (NA)	6	HF

Variants are defined based on the meta-transcript (LRG_391_t1 / ENST00000589042) that incorporates all exons in described TTN isoforms (including fetal and noncardiac isoforms) with the exception of exons that are unique to the novex transcripts.

AML indicates acute myeloid leukemia; CCM, cancer therapy–induced cardiomyopathy; HF, heart failure hospitalization; LVEF, left ventricular ejection fraction; NA, not available; PSI, proportions spliced in; TTNtv, titin-truncating variant; and VT, ventricular tachycardia.

anthracyclines (86.6%) or trastuzumab (33%), and with follow-up between 8.4 months and 18 years (Table 1). We defined the clinical courses among patients who have CCM with TTNtv and compared risk factors for CCM and outcomes among patients with and without TTNtv (Table 4 and Tables VII through IX in the online-only Data Supplement). At diagnosis of CCM, the mean LVEF of patients with (34.9±7.4) and without TTNtv (36.8±9.5; *P*=not significant) were comparable; however, patients with TTNtv had more heart failure hospitalizations and atrial fibrillation (*P*=0.003 for each) than those without TTNtv. Recovery occurred in both groups, although the final mean LVEF was more depressed in patients with TTNtv (39.6±14.2 versus 48.9±10.8; *P*=0.03).

Modeling CCM in TTNtv Mice

Given the multiple variables that can influence cardiotoxicity in human patients, we assessed whether TTNtv increased susceptibility to anthracycline-induced cardiomyopathy in an experimental model. Doxorubicin was administered (3 doses of 5 mg/kg at weekly intervals; cumulative=45 mg/m²) to genetically identical mice, with the exception of the absence (wild-type) or presence (Ttn^{tw/+}) of a heterozygous A-band titin truncation in one gene copy.^{25,26} Untreated Ttn^{tw/+} mice have normal LV function (not significantly different from wild-type mice) and anthracycline administration comparably depressed LV function in both genotypes at week 4 after treatments (Figure). However, at week 8, LV function recovered to baseline in wild-type mice but remained

Table 4. Comparisons of Risk Factors and Outcomes in Adult Patient Who Has CCM With and Without TTNtv

Clinical Characteristics	TTNtv (n=14)	Non-TTNtv (n=158)	P Value*
Baseline			
Male sex, n (%)	2 (14.3)	31 (19.6)	1
Comorbidities, n (%)			
Current or past smokers	3 (21.4)	55 (34.8)	0.39
Hypertension	4 (28.6)	54 (34.2)	0.78
Hypercholesterolemia	6 (42.9)	38 (24.1)	0.20
Diabetes mellitus	2 (14.3)	25 (15.8)	1
Oncological treatments, n (%)			
Doxorubicin ± other	13 (92.9)	136 (86.1)	0.70
At CCM diagnosis			
LVEF at CCM diagnosis, %	34.9±7.4	36.8±9.5	0.38
NYHA functional class III–IV, n (%)	6 (42.9)	39 (24.7)	0.2
Follow-up			
Last LVEF, %	39.6±14.2	48.9±10.8	0.03‡
LVEF recovery, n (%)	6 (42.9)	77 (48.7)	0.78
On neurohormonal blockers,† n (%)	10 (71.4)	121 (76.6)	0.74
Atrial fibrillation, n (%)	5 (35.7)	10 (6.3)	0.003‡
Heart failure–related hospitalization, n (%)	9 (64.3)	39 (24.7)	0.003‡
Cardiac transplantation, n (%)	2 (14.3)	7 (4.4)	0.16
Aborted sudden cardiac death, n (%)	1 (7.1)	6 (3.8)	0.45
Cardiac death, n (%)	0 (0.0)	3 (1.9)	1
Death from all cause, n (%)	0 (0.0)	5 (3.2)	1

CCM indicates cancer therapy–induced cardiomyopathy; LVEF, left ventricular ejection fraction; NYHA, New York Heart Association; and TTNtv, titin-truncating variant.

*P values were calculated using the Fisher exact test for categorical variables and the Welch t test for continuous variables.

†Number of patients who were taking at least one of β -blockers, angiotensin-converting enzyme inhibitors/angiotensin receptor blockers, or mineralocorticoid receptor antagonists. No data were available to review for 1 of the patients with TTNtv.

‡Significant values.

depressed through week 12 in *Ttn*^{tv/+} mice ($P=0.0004$ versus wild-type). Functional analyses in isolated cardiomyocytes confirmed that LV dysfunction reflected cell autonomous effects of anthracyclines (Figure B). Histological analysis of cardiac tissues from anthracycline-treated wild-type or *Ttn*^{tv/+} mice were comparable and showed no significant increase in fibrosis or apoptosis in comparison with untreated mice.

DISCUSSION

We demonstrate an increased prevalence of DCM-associated gene variants, predominantly TTNtv, in adult patients who have cancer and pediatric patients who have acute myelogenous leukemia with CCM relative to

controls. Although the majority of the patients with CCM have European ancestry, the frequency of cardiomyopathy variants in other patients with CCM who have other ancestries was not significantly different (Table II in the online-only Data Supplement). TTNtv were identified in 16 of 213 CCM cases (7.5%), a considerably higher prevalence than in unselected breast and lung cancer TCGA participants (1.1%, $P=7.36e-08$) or healthy volunteers (0.7%, $P=3.42e-06$) and enriched in comparison with ancestry-matched reference populations ($P=5.87e-14$). Because cardiac status is not recorded for TCGA participants, these data provide conservative estimates of the burden of TTNtv in CCM. Further support that TTNtv contribute to CCM is derived from a mouse model of CCM: anthracycline-treated *Ttn*^{tv/+} mice and isolated cardiomyocytes had protracted LV and cellular dysfunction in comparison with wild-type.

Clinical outcomes among patients with CCM showed considerable variability, but cardiac function improved in 45% to 68% of adult and pediatric patients. Recovery occurred in 83 adults and 28 children, and was not significantly correlated ($P\geq 0.5$) with preexisting cardiovascular risk factors in adults, TTNtv, high (>400 mg/m²) anthracycline dose, or trastuzumab therapy. However, adult patients who have CCM with TTNtv had more heart failure hospitalizations and atrial fibrillation, as occurs in patients with DCM caused by TTNtv,^{33,34} and cardiac function was worse in patients with than in patients without these variants.

In addition to TTNtv, our analyses identified rare protein-altering variants in 5 genes previously studied in patients with DCM.²⁹ Mutations in *BAG3*, *LMNA*, *MYH7*, and *TNNT2* are established autosomal dominant causes of DCM.^{14,35} *TCAP* mutations are occasionally identified in patients with DCM,³⁶ but more commonly cause a recessive form of limb-girdle muscular dystrophy.³⁷ Despite the low prevalence of variants in these genes across all CCM cohorts (4.7%), their critical roles in myocyte biology imply that variants identified here may contribute to an individual's risk for CCM.

The increased burden of rare variants, including TTNtv, indicate that genetics is an important component in CCM susceptibility and adverse outcomes. We demonstrate that genetics is associated with CCM susceptibility across different cancer types and treatment regimens, in particular, those including anthracycline and trastuzumab (Table 1). Genetic variants in previously identified cardiomyopathy genes were increased among adult cancer survivors with overt CCM and severe clinical courses, and among prospectively studied adult and pediatric patients with mild CCM identified during ongoing cancer treatment. It is notable that heart failure, cardiac transplantation, aborted sudden death, and cardiac death occurred years after completion of chemotherapy regimens in some patients with CCM (Table 4), an observation that underscores the

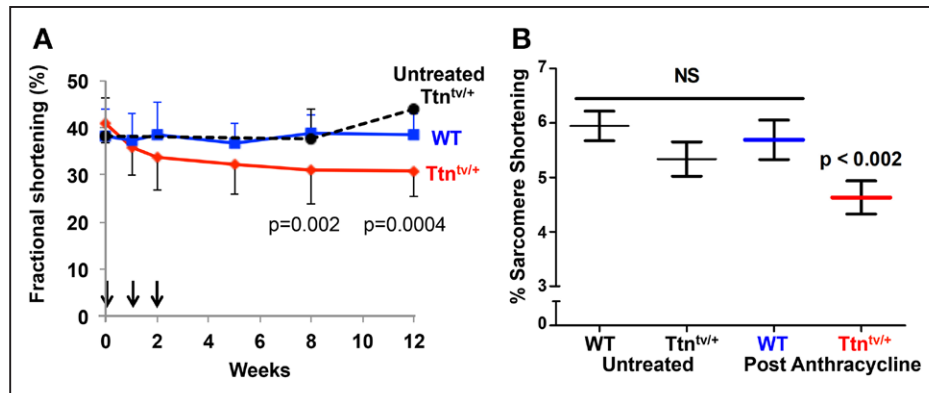


Figure. Persistent cardiac dysfunction in *Ttn*^{fl/+} mice after anthracycline treatment.

A, Untreated *Ttn*^{fl/+} mice have left ventricular function comparable with wild-type (WT) mice.^{25,26} Intraperitoneal doxorubicin (5mg/kg) was administered (arrows) to WT and *Ttn*^{fl/+} mice ($n=15$ per genotype) in 3 successive weekly doses (cumulative dose=45 mg/m²). Serial echocardiograms showed persistent significantly depressed systolic function (mean fractional shortening \pm SD) in *Ttn*^{fl/+} in comparison with WT mice ($P=0.0004$). **B**, Isolated cardiomyocytes ($n\geq 52$ per group) were studied 12 weeks after initial doxorubicin injection. Cardiomyocytes from doxorubicin-treated *Ttn*^{fl/+} mice had significantly depressed contractility ($P<0.002$) in comparison with cardiomyocytes from doxorubicin-treated WT mice or untreated mice. NS indicates not significant.

need for continued cardiac surveillance in patients with CCM.

These data establish a genetic relationship between DCM and CCM. Cardiomyopathy variants were found in 12.2% of patients with CCM (Table 2), whereas these occur in $\approx 40\%$ of patients with familial and sporadic DCM.^{31,38–40} Whether broader genomic analyses may uncover additional genetic contributors to CCM is worthy of study. TTNts are significantly prominent in DCM, occurring in 15% of ambulatory and 25% of end-stage patients,^{30,31,34,38} but are rarely identified in childhood-onset DCM,⁴¹ whereas here we identified TTNts in 8.1% of adults and 5.0% of children with CCM. TTNts found in patients with CCM, like those in patients with DCM, disrupted exons that are constitutively expressed in the heart and are overrepresented in the A-band (Table 3). TTNts also occur in $\approx 15\%$ of patients with peripartum cardiomyopathy²¹ and in $\approx 10\%$ of individuals with alcoholic cardiomyopathy,⁴² findings that imply additional cardiovascular stress can unmask the deleterious cardiac effects of TTNts. Consistent with this supposition, in vitro analyses of human isogenic cardiomyocytes (derived from induced pluripotent stems cells) demonstrate that titin provides an essential mechanical connection that propagates diastolic traction stresses from β -cardiac myosin during sarcomere formation. Cardiomyocytes with TTNts have diminished reassembly of sarcomeres after stress in comparison with cells without TTNts.⁴³ We suggest that chemotherapy, like pregnancy and excessive alcohol, is an important provocation that is poorly tolerated by TTNts, a conclusion that is supported both by these human data and by analyses of anthracycline-treated TTNt mice.

We recognize several limitations in this study. Given the demographic profiles of the cohorts studied here, further analyses of patients with diverse ancestries are needed. Cohort A was retrospectively recruited

after diagnosis of CCM, and these patients had more severe phenotypes and longer durations of follow-up than the prospectively identified patients in cohorts B and C. Because breast cancer was the most common diagnosis in adult patients with CCM and all pediatric cases had acute myelogenous leukemia, these findings may not be relevant to other cancers and other treatment regimens. All patients had individual chemotherapy dosages and additional treatments based on clinical practice and treatment protocols. These and other variables may influence susceptibility to CCM. This study compared the frequency of TTNts among patients with CCM to the frequency of TTNts in a large cohort of patients with cancer participating in TCGA, some fraction of whom likely developed CCM. A limitation of our study is that we do not know which TCGA subjects developed CCM, potentially affecting the accuracy of the TTNt frequency estimate in the CCM-free cancer cohort. A more ideal comparison group would have been patients treated with chemotherapy who did not develop cardiomyopathy. While recognizing these issues, we suggest that enrichment of protein-altering variants and TTNts across all cohorts strongly supports the conclusion that genetics, like high-dose anthracycline and combination therapy, and cardiovascular risk factors contribute to CCM.

Current strategies to diagnose CCM focus on imaging and circulating biomarkers^{1,2,18,44–46} and treatment guidelines are limited, often recommending interruption or discontinuation of chemotherapy that can negatively impact the survival of patients with cancer. The identification of genetic risk factors opens new opportunities to identify patients with cancer at high risk for CCM and to assess the efficacy of prophylactic cardioprotective drugs and treatment regimens.^{47–49} Future investigations will determine if early recognition of patients who have cancer with high CCM risk through genetic testing

can optimize cancer and cardiovascular treatments to reduce CCM while providing effective cancer therapy.

ARTICLE INFORMATION

Received September 12, 2018; accepted March 7, 2019.

The online-only Data Supplement is available with this article at <https://www.ahajournals.org/doi/suppl/10.1161/circulationaha.118.037934>.

Authors

Pablo Garcia-Pavia MD, PhD*; Yuri Kim, MD, PhD*; Maria Alejandra Restrepo-Cordoba*; Ida G. Lunde, PhD; Hiroko Wakimoto, MD, PhD; Amanda M. Smith, BA; Christopher N. Toepfer, PhD; Kelly Getz, PhD; Joshua Gorham, MSc; Parth Patel, MD; Kaoru Ito, MD, PhD; Jonathan A. Willcox, PhD; Zoltan Arany, MD, PhD; Jian Li, PhD; Anjali T. Owens, MD; Risha Govind, MSc; Beatriz Nuñez, MD; Erica Mazaika, MSc; Antoni Bayes-Genis, MD; Roddy Walsh, PhD; Brian Finkelman, MD, PhD; Josep Lupon, MD, PhD; Nicola Whiffin, PhD; Isabel Serrano, MD; William Midwinter, BSc; Alicja Wilk, BSc; Alfredo Bardaji, MD, PhD; Nathan Ingold; Rachel Buchan, MSc; Upasana Tayal, PhD, MRCP; Domingo A. Pascual-Figal, MD, PhD; Antonio de Marvao, PhD, MRCP; Mian Ahmad, PhD; Jose Manuel Garcia-Pinilla, MD, PhD; Antonis Pantazis, MD; Fernando Dominguez, MD, PhD; A. John Baksi, PhD, MRCP; Declan P. O'Regan, PhD; Stuart D. Rosen, MD; Sanjay K. Prasad, MD; Enrique Lara-Pezzi, PhD; Mariano Provencio, MD, PhD; Alexander R. Lyon, PhD; Luis Alonso-Pulpon, MD, PhD; Stuart A. Cook, PhD; Steven R. DePalma, PhD; Paul J.R. Barton, PhD†; Richard Aplenc, MD, PhD†; Jonathan G. Seidman, PhD†; Bonnie Ky, MD, MSCE†; James S. Ware, PhD, MRCP†; Christine E. Seidman, MD†

Correspondence

Pablo Garcia-Pavia, MD, PhD, Department of Cardiology, Hospital Universitario Puerta de Hierro, Manuel de Falla, 2; 28222 Madrid, Spain; or Christine E. Seidman, MD, Departments of Medicine & Genetics, NRB Room 256, Harvard Medical School, 77 Ave Louis Pasteur, Boston, MA 02115. Email pablogpavia@yahoo.es or cseidman@genetics.med.harvard.edu

Affiliations

Hospital Universitario Puerta de Hierro, Madrid, Spain (P.G.-P., M.A.R.-C., F.D., L.A.-P.). Centro de Investigación Biomédica en Red Enfermedades en Cardiovascular Diseases (CIBERCV), Madrid, Spain (P.G.-P., M.A.R.-C., A.B.-G., J. Lupon, D.A.P.-F., J.M.G.-P., F.D., E.L.-P., L.A.-P.). University Francisco de Vitoria, Pozuelo de Alarcón, Madrid, Spain (P.G.-P.). Harvard Medical School, Boston, MA (Y.K., I.G.L., H.W., C.N.T., J.G., P.P., K.I., J.A.W., S.R.D., J.G.S., C.E.S.). Massachusetts General Hospital, Boston (Y.K.). Oslo University Hospital and University of Oslo, Norway (I.G.L.). Perelman School of Medicine and University of Pennsylvania Health System, Philadelphia (A.M.S., K.G., Z.A., J. Li, A.T.O., B.F., R.A., B.K.). University of Oxford (C.N.T.). National Heart & Lung Institute, Imperial College London, UK (R.G., E.M., R.W., N.W., W.M., A.W., N.I., R.B., U.T., A.d.M., M.A., A.P., A.J.B., S.D.R., S.K.P., E.L.-P., A.R.L., S.A.C., P.J.R.B., J.S.W.). Royal Brompton & Harefield NHS Foundation Trust, London, UK (R.G., E.M., R.W., N.W., W.M., A.W., N.I., R.B., U.T., A.d.M., M.A., A.P., A.J.B., S.D.R., S.K.P., A.R.L., P.J.R.B., J.S.W.). Hospital Universitario Puerta de Hierro, Universidad Autónoma de Madrid, Spain (B.N., M.P.). Hospital Universitario Germans Trias i Pujol, Badalona, Spain (A.B.-G., J. Lupon). MRC London Institute of Medical Sciences, Imperial College UK (N.W., D.P.O., S.A.C., J.S.W., C.E.S., A.d.M.). Hospital Universitario de Tarragona Joan XXIII. IISPV, Rovira Virgili University, Spain (I.S., A.B.). Hospital Universitario Virgen de la Arrixaca, University of Murcia, Spain (D.A.P.-F.). Centro Nacional de Investigaciones Cardiovasculares, Madrid, Spain (E.L.-P.). National Heart Centre Singapore and Duke-National University of Singapore (S.A.C.). Howard Hughes Medical Institute, Chevy Chase, MD (S.R.D., C.E.S.). Brigham and Women's Hospital, Boston MA (P.P., C.E.S.). Hospital Universitario Virgen de la Victoria, IBIMA, Malaga, Spain (J.M.G.-P.).

Acknowledgments

We thank the patients and physicians who participated in enrollment, in particular, Drs J. Segovia, C. Mitroi, M. Gomez-Bueno, F. Hernandez, A. Gamis, L. Sung, T. Alonzo, and S. Meshinchi. We also recognize many years of scientific guidance from Professor J. G. Guig.

Sources of Funding

This work was supported in part by grants from the Instituto de Salud Carlos III (ISCIII; PI15/01551, PI17/01941, and CB16/11/00432 to Drs Garcia-Pavia and Alonso-Pulpon, and IF17/00003 to Dr Restrepo-Cordoba), the Spanish Ministry of Economy and Competitiveness (SAF2015-71863-REDT to Dr Garcia-Pavia), the John S. LaDue Memorial Fellowship at Harvard Medical School (to Dr Kim), Wellcome Trust (107469/Z/15/Z to Dr Ware), Medical Research Council (intramural awards to Drs Cook and Ware; MR/M003191/1 to Dr Tayal), National Institute for Health Research Biomedical Research Unit at the Royal Brompton and Harefield National Health Service Foundation Trust and Imperial College London (to Drs Barton, Cook, and Ware), National Institute for Health Research Biomedical Research Centre at Imperial College London Healthcare National Health Service Trust and Imperial College London (to Drs O'Regan, Cook, Prasad, and Ware), Sir Henry Wellcome Postdoctoral Fellowship (to Dr Toepfer), Rosetrees and Stonegate Imperial College Research Fellowship (to Dr Whiffin), Fondation Leducq (to Drs Cook, C.E. Seidman, and J.G. Seidman), Health Innovation Challenge Fund award from the Wellcome Trust and Department of Health (UK; HICF-R6-373; to Drs Cook, Barton, and Ware), the British Heart Foundation (NH/17/1/32725 to Dr O'Regan; SP/10/10/28431 to Dr Cook), Academy of Medical Sciences SGL015/1006 (to Dr de Marvao), Alex's Lemonade Stand Foundation (to Dr Getz), National Institutes of Health (to Dr Aplenc: U01CA097452, R01CA133881, and U01CA097452; to Dr Arany: R01 HL126797; to Dr Ky: R01 HL118018 and K23-HL095661; to Dr J.G. Seidman and C.E. Seidman: 5R01HL080494, 5R01HL084553), and the Howard Hughes Medical Institute (to Dr C.E. Seidman). The Universitario Puerta de Hierro and Virgen de la Arrixaca Hospitals are members of the European Reference Network on Rare and Complex Diseases of the Heart (Guard-Heart; <http://guard-heart.ern-net.eu>). This publication includes independent research commissioned by the Health Innovation Challenge Fund (HICF), a parallel funding partnership between the Department of Health and Wellcome Trust. The Centro Nacional de Investigaciones Cardiovasculares (CNIC) is supported by the Ministry of Economy, Industry and Competitiveness and the Pro CNIC Foundation, and is a Severo Ochoa Center of Excellence (SEV-2015-0505). Grants from ISCIII and the Spanish Ministry of Economy and Competitiveness are supported by the Plan Estatal de I+D+I 2013–2016 – European Regional Development Fund (FEDER) “A way of making Europe.” The views expressed in this work are those of the authors, and the funding institutions played no role in the design, collection, analysis, or interpretation of the data or in the decision to submit the manuscript for publication.

Disclosures

Drs C. E. and J. G. Seidman are founders and own shares in Myokardia Inc, a startup company that is developing therapeutics that target the sarcomere. James S. Ware receives grant support and honoraria from Myokardia. Myokardia had no involvement in this study. The other authors report no conflicts.

REFERENCES

- Zamorano JL, Lancellotti P, Rodriguez Munoz D, Aboyans V, Asteggiano R, Galderisi M, Habib G, Lenihan DJ, Lip GY, Lyon AR, Lopez Fernandez T, Mohty D, Piepoli MF, Tamargo J, Torbicki A, Suter TM; ESC Scientific Document Group. 2016 ESC Position Paper on cancer treatments and cardiovascular toxicity developed under the auspices of the ESC Committee for Practice Guidelines: the Task Force for cancer treatments and cardiovascular toxicity of the European Society of Cardiology (ESC). *Eur Heart J*. 2016;37:2768–2801. doi: 10.1093/eurheartj/ehw211
- Armenian SH, Lacchetti C, Barac A, Carver J, Constine LS, Denduluri N, Dent S, Douglas PS, Durand JB, Ewer M, Fabian C, Hudson M, Jessup M, Jones LW, Ky B, Mayer EL, Moslehi J, Oeffinger K, Ray K, Ruddy K, Lenihan D. Prevention and monitoring of cardiac dysfunction in survivors of adult cancers: American Society of Clinical Oncology Clinical Practice Guideline. *J Clin Oncol*. 2017;35:893–911. doi: 10.1200/JCO.2016.70.5400
- Plana JC, Galderisi M, Barac A, Ewer MS, Ky B, Scherrer-Crosbie M, Ganame J, Sebag IA, Agler DA, Badano LP, Banchs J, Cardinale D, Carver J, Cerqueira M, DeCara JM, Edvardsen T, Flamm SD, Force T, Griffin BP, Jerusalem G, Liu JE, Magalhães A, Marwick T, Sanchez LY, Sicari R, Villarraga HR, Lancellotti P. Expert consensus for multimodality imaging evaluation of adult patients during and after cancer therapy: a report from the American Society of Echocardiography and the European Association of Cardiovascular Imaging. *Eur Heart J Cardiovasc Imaging*. 2014;15:1063–1093. doi: 10.1093/ehjci/jeu192
- Curigliano G, Cardinale D, Suter T, Plataniotis G, de Azambuja E, Sandri MT, Criscitello C, Goldhirsch A, Cipolla C, Roila F, ESMO Guidelines Working Group. Cardiovascular toxicity induced by chemotherapy,

- targeted agents and radiotherapy: ESMO Clinical Practice Guidelines. *Ann Oncol*. 2012;23(suppl 7):vii155–vii166. doi: 10.1093/annonc/mds293
5. Armenian SH, Xu L, Ky B, Sun C, Farol LT, Pal SK, Douglas PS, Bhatia S, Chao C. Cardiovascular disease among survivors of adult-onset cancer: a community-based retrospective cohort study. *J Clin Oncol*. 2016;34:1122–1130. doi: 10.1200/JCO.2015.64.0409
 6. Swain SM, Whaley FS, Ewer MS. Congestive heart failure in patients treated with doxorubicin: a retrospective analysis of three trials. *Cancer*. 2003;97:2869–2879. doi: 10.1002/cncr.11407
 7. Hahn VS, Lenihan DJ, Ky B. Cancer therapy-induced cardiotoxicity: basic mechanisms and potential cardioprotective therapies. *J Am Heart Assoc*. 2014;3:e000665. doi: 10.1161/JAHA.113.000665
 8. Wells QS, Veatch OJ, Fessel JP, Joon AY, Levinson RT, Mosley JD, Held EP, Lindsay CS, Shaffer CM, Weeke PE, Glazer AM, Bersell KR, Van Driest SL, Karnes JH, Blair MA, Lagrone LW, Su YR, Bowton EA, Feng Z, Ky B, Lenihan DJ, Fisch MJ, Denny JC, Roden DM. Genome-wide association and pathway analysis of left ventricular function after anthracycline exposure in adults. *Pharmacogenet Genomics*. 2017;27:247–254. doi: 10.1097/FPC.0000000000000284
 9. Wojnowski L, Kulle B, Schirmer M, Schlüter G, Schmidt A, Rosenberger A, Vonhof S, Bickeböller H, Toliat MR, Suk EK, Tzvetkov M, Kruger A, Seifert S, Kloess M, Hahn H, Loeffler M, Nürnberg P, Pfreundschuh M, Trümper L, Brockmüller J, Hasenfuss G. NAD(P)H oxidase and multidrug resistance protein genetic polymorphisms are associated with doxorubicin-induced cardiotoxicity. *Circulation*. 2005;112:3754–3762. doi: 10.1161/CIRCULATIONAHA.105.576850
 10. Visscher H, Ross CJ, Rassekh SR, Sandor GS, Caron HN, van Dalen EC, Kremer LC, van der Pal HJ, Rogers PC, Rieder MJ, Carleton BC, Hayden MR; CNMDS Consortium. Validation of variants in SLC28A3 and UGT1A6 as genetic markers predictive of anthracycline-induced cardiotoxicity in children. *Pediatr Blood Cancer*. 2013;60:1375–1381. doi: 10.1002/pbc.24505
 11. Blanco JG, Leisenring WM, Gonzalez-Covarrubias VM, Kawashima TI, Davies SM, Relling MV, Robison LL, Sklar CA, Stovall M, Bhatia S. Genetic polymorphisms in the carbonyl reductase 3 gene CBR3 and the NAD(P)H:quinone oxidoreductase 1 gene NQO1 in patients who developed anthracycline-related congestive heart failure after childhood cancer. *Cancer*. 2008;112:2789–2795. doi: 10.1002/cncr.23534
 12. Wang X, Liu W, Sun CL, Armenian SH, Hakonarson H, Hageman L, Ding Y, Landier W, Blanco JG, Chen L, Quiñones A, Ferguson D, Winick N, Ginsberg JP, Keller F, Neglia JP, Desai S, Sklar CA, Castellino SM, Cherrick I, Dreyer ZE, Hudson MM, Robison LL, Yasui Y, Relling MV, Bhatia S. Hyaluronan synthase 3 variant and anthracycline-related cardiomyopathy: a report from the Children's Oncology Group. *J Clin Oncol*. 2014;32:647–653. doi: 10.1200/JCO.2013.50.3557
 13. Linschoten M, Teske AJ, Baas AF, Vink A, Dooijes D, Baars HF, Asselbergs FW. Truncating Titin (TTN) variants in chemotherapy-induced cardiomyopathy. *J Card Fail*. 2017;23:476–479. doi: 10.1016/j.cardfail.2017.03.003
 14. 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. doi: 10.1016/j.jacc.2016.08.079
 15. van den Berg MP, van Spaendonck-Zwarts KY, van Veldhuisen DJ, Gietema JA, Postma A, van Tintelen JP. Familial dilated cardiomyopathy: another risk factor for anthracycline-induced cardiotoxicity? *Eur J Heart Fail*. 2010;12:1297–1299. doi: 10.1093/eurjhf/hfq175
 16. Shipman KE, Arnold I. Case of epirubicin-related cardiomyopathy in familial cardiomyopathy. *J Clin Oncol*. 2011;29:e537–e538. doi: 10.1200/JCO.2011.34.8052
 17. Wasielewski M, van Spaendonck-Zwarts KY, Westerink ND, Jongbloed JD, Postma A, Gietema JA, van Tintelen JP, van den Berg MP. Potential genetic predisposition for anthracycline-associated cardiomyopathy in families with dilated cardiomyopathy. *Open Heart*. 2014;1:e000116. doi: 10.1136/openhrt-2014-000116
 18. Cardinale D, Colombo A, Bacchiani G, Tedeschi I, Meroni CA, Veglia F, Civelli M, Lamantia G, Colombo N, Curigliano G, Fiorentini C, Cipolla CM. Early detection of anthracycline cardiotoxicity and improvement with heart failure therapy. *Circulation*. 2015;131:1981–1988. doi: 10.1161/CIRCULATIONAHA.114.013777
 19. Narayan HK, Finkelman B, French B, Plappert T, Hyman D, Smith AM, Margulies KB, Ky B. Detailed echocardiographic phenotyping in breast cancer patients: associations with ejection fraction decline, recovery, and heart failure symptoms over 3 years of follow-up. *Circulation*. 2017;135:1397–1412. doi: 10.1161/CIRCULATIONAHA.116.023463
 20. Schafer S, de Marvao A, Adami E, Fiedler LR, Ng B, Khin E, Rackham OJ, van Heesch S, Pua CJ, Kui M, Walsh R, Tayal U, Prasad SK, Dawes TJ, Ko NS, Sim D, Chan LL, Chin CW, Mazzarotto F, Barton PJ, Kreuchwig F, de Kleijn DP, Totman T, Biffi C, Tee N, Rueckert D, Schneider V, Faber A, Regitz-Zagrosek V, Seidman JG, Seidman CE, Linke WA, Kowalik JP, O'Regan D, Ware JS, Hubner N, Cook SA. Titin-truncating variants affect heart function in disease cohorts and the general population. *Nat Genet*. 2017;49:46–53. doi: 10.1038/ng.3719
 21. Ware JS, Li J, Mazaika E, Yasso CM, DeSouza T, Cappola TP, Tsai EJ, Hilfiker-Kleiner D, Kamiya CA, Mazzarotto F, Cook SA, Halder I, Prasad SK, Pisarcik J, Hanley-Yanez K, Alharethi R, Damp J, Hsieh E, Elkayam U, Sheppard R, Kealey A, Alexis J, Ramani G, Safirstein J, Boehmer J, Pauly DF, Wittstein IS, Tohan V, Zucker MJ, Liu P, Gorcsan J 3rd, McNamara DM, Seidman CE, Seidman JG, Arany Z; IMAC-2 and IPAC Investigators. Shared genetic predisposition in peripartum and dilated cardiomyopathies. *N Engl J Med*. 2016;374:233–241. doi: 10.1056/NEJMoa1505517
 22. Cingolani P, Platts A, Wang le L, Coon M, Nguyen T, Wang L, Land SJ, Lu X, Ruden DM. A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of *Drosophila melanogaster* strain w1118; iso-2; iso-3. *Fly (Austin)*. 2012;6:80–92. doi: 10.4161/fly.19695
 23. Genome Aggregation Database (gnomAD). <https://gnomad.broadinstitute.org/>. Accessed March 19, 2019.
 24. National Institutes of Health: National Cancer Institute. The Cancer Genome Atlas Program. <http://cancergenome.nih.gov/>. Accessed March 18, 2019.
 25. Lunde IGW, Burke MA, Sououli V, Linke WA, Gorham J, Conner D, Christensen G, Seidman JG, Seidman CE. Titin A-band truncation in mice causes stress-induced dilated cardiomyopathy. *Eur J Heart Fail* 2015;17:31.
 26. Lunde I.G.W., Burke MA, Sououli V, Linke WA, Gorham J, Conner D, Christensen G, Seidman JG, Seidman CE. Proximal titin A-band truncation causes dilated cardiomyopathy in response to increased afterload in mice. *Eur Heart J*. 2015;36:521.
 27. Keefe DL. Anthracycline-induced cardiomyopathy. *Semin Oncol*. 2001;28(4 suppl 12):2–7.
 28. Benjamin EJ, Blaha MJ, Chiuve SE, Cushman M, Das SR, Deo R, de Ferranti SD, Floyd J, Fornage M, Gillespie C, Isasi CR, Jiménez MC, Jordan LC, Judd SE, Lackland L, Lichtman JH, Lisabeth L, Liu S, Longenecker CT, Mackey RH, Matsushita K, Mozaffarian D, Mussolino ME, Nasir K, Neumar RW, Palaniappan L, Pandey DK, Thiagarajan RR, Reeves MJ, Ritchey M, Rodriguez CJ, Roth GA, Rosamond WD, Sasson C, Towfighi A, Tsao CW, Turner MB, Virani SS, Voeks JH, Willey JZ, Wilkins JT, Wu JH, Alger HM, Wong SS, Muntner P; American Heart Association Statistics Committee and Stroke Statistics Subcommittee. Heart disease and stroke statistics-2017 update: a report from the American Heart Association. *Circulation*. 2017;135:e146–e603. doi: 10.1161/CIR.0000000000000485
 29. Walsh R, Thomson KL, Ware JS, Funke BH, Woodley J, McGuire KJ, Mazzarotto F, Blair E, Sella A, Taylor JC, Minikel EV, Exome Aggregation Consortium, MacArthur DG, Farrall M, Cook SA, Watkins H. Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. *Genet Med*. 2017;19:192–203. doi: 10.1038/gim.2016.90
 30. Roberts AM, Ware JS, Herman DS, Schafer S, Baksi J, Bick AG, Buchan RJ, Walsh R, John S, Wilkinson S, Mazzarotto F, Felkin LE, Gong S, MacArthur JA, Cunningham F, Flannick J, Gabriel SB, Altshuler DM, Macdonald PS, Heinig M, Keogh AM, Hayward CS, Banner NR, Pennell DJ, O'Regan DP, San TR, de Marvao A, Dawes TJ, Gulati A, Birks EJ, Yacoub MH, Radke M, Gotthardt M, Wilson JG, O'Donnell CJ, Prasad SK, Barton PJ, Fatkin D, Hubner N, Seidman JG, Seidman CE, Cook SA. Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. *Sci Transl Med*. 2015;7:270a6. doi: 10.1126/scitranslmed.3010134
 31. Herman DS, Lam L, Taylor MR, Wang L, Teekakirikul P, Christodoulou D, Conner L, DePalma SR, McDonough B, Sparks E, Teodorescu DL, Cirino JM, Banner NR, Pennell DJ, Graw S, Merlo M, Di Lenarda A, Sinagra G, Bos JM, Ackerman MJ, Mitchell RN, Murry CE, Lakdawala NK, Ho CY, Barton PJ, Cook SA, Mestroni L, Seidman JG, Seidman CE. Truncations of titin causing dilated cardiomyopathy. *N Engl J Med*. 2012;366:619–628. doi: 10.1056/NEJMoa1110186
 32. Wahbi K, Meune C, Hamouda el H, Stojkovic T, Laforêt P, Bécanne HM, Eymard B, Duboc D. Cardiac assessment of limb-girdle muscular dystrophy 21 patients: an echography, Holter ECG and magnetic resonance imaging study. *Neuromuscul Disord*. 2008;18:650–655. doi: 10.1016/j.nmd.2008.06.365
 33. Hoorntje ET, van Spaendonck-Zwarts KY, Te Rijdt WP, Boven L, Vink A, van der Smagt JJ, Asselbergs FW, van Wijngaarden J, Hennekam EA, Pinto YM, Lekanne Deprez RH, Barge-Schaapveld DQCM, Bootsma M,

- Regieli J, Hoedemaekers YM, Jongbloed JDH, van den Berg MP, van Tintelen JP. The first titin (c.59926 + 1G > A) founder mutation associated with dilated cardiomyopathy. *Eur J Heart Fail*. 2018;20:803–806. doi: 10.1002/ehf.1030
34. Tayal U, Newsome S, Buchan R, Whiffin N, Walsh R, Barton PJ, Ware JS, Cook SA, Prasad SK. Truncating variants in titin independently predict early arrhythmias in patients with dilated cardiomyopathy. *J Am Coll Cardiol*. 2017;69:2466–2468. doi: 10.1016/j.jacc.2017.03.530
 35. Garcia-Pavia P, Cobo-Marcos M, Guzzo-Merello G, Gomez-Bueno M, Bornstein B, Lara-Pezzi E, Segovia J, Alonso-Pulpon L. Genetics in dilated cardiomyopathy. *Biomark Med*. 2013;7:517–533. doi: 10.2217/bmm.13.77
 36. Hayashi T, Arimura T, Itoh-Satoh M, Ueda K, Hohda S, Inagaki N, Takahashi M, Hori H, Yasunami M, Nishi H, Koga Y, Nakamura H, Matsuzaki M, Choi BY, Bae SW, You CW, Han KH, Park JE, Knöll R, Hoshijima M, Chien KR, Kimura A. Tcap gene mutations in hypertrophic cardiomyopathy and dilated cardiomyopathy. *J Am Coll Cardiol*. 2004;44:2192–2201. doi: 10.1016/j.jacc.2004.08.058
 37. Moreira ES, Wiltshire TJ, Faulkner G, Nilforoushan A, Vainzof M, Suzuki OT, Valle G, Reeves R, Zatz M, Passos-Bueno MR, Jenne DE. Limb-girdle muscular dystrophy type 2G is caused by mutations in the gene encoding the sarcomeric protein telethonin. *Nat Genet*. 2000;24:163–166. doi: 10.1038/72822
 38. Cuenca S, Ruiz-Cano MJ, Gimeno-Blanes JR, Jurado A, Salas C, Gomez-Diaz I, Padron-Barthe L, Grillo JJ, Vilches C, Segovia J, Pascual-Figal D, Lara-Pezzi E, Monserrat L, Alonso-Pulpon L, Garcia-Pavia P; Inherited Cardiac Diseases Program of the Spanish Cardiovascular Research Network (Red Investigación Cardiovascular). Genetic basis of familial dilated cardiomyopathy patients undergoing heart transplantation. *J Heart Lung Transplant*. 2016;35:625–635. doi: 10.1016/j.healun.2015.12.014
 39. Haas J, Frese KS, Peil B, Kloos W, Keller A, Nietsch R, Feng Z, Müller S, Kayvanpour E, Vogel B, Sedaghat-Hamedani F, Lim WK, Zhao X, Fradkin D, Köhler D, Fischer S, Franke J, Marquart S, Barb I, Li DT, Amr A, Ehlermann P, Mereles D, Weis T, Hassel S, Kremer A, King V, Wirsz E, Isnard R, Komajda M, Serio A, Grasso M, Syrris P, Wicks E, Plagnol V, Lopes L, Gadgaard T, Eiskjær H, Jørgensen M, Garcia-Giustinianni D, Ortiz-Genga M, Crespo-Leiro MG, Deprez RH, Christiaans I, van Rijsingen IA, Wilde AA, Waldenstrom A, Bolognesi M, Bellazzi R, Mörrner S, Bermejo JL, Monserrat L, Villard E, Mogensen J, Pinto YM, Charron P, Elliott P, Arbustini E, Katus HA, Meder B. Atlas of the clinical genetics of human dilated cardiomyopathy. *Eur Heart J*. 2015;36:1123–135a. doi: 10.1093/eurheartj/ehu301
 40. Tayal U, Prasad S, Cook SA. Genetics and genomics of dilated cardiomyopathy and systolic heart failure. *Genome Med*. 2017;9:20. doi: 10.1186/s13073-017-0410-8
 41. Fatkin D, Herman L, Benson D, Felkin C, Barton L, Walsh P, Canda R, Ware J, Roberts A, Chung W, Smoot L, Bornauun H, Keogh A, Macdonald P, Hayward C, Seidman J, Roberts A, Cook S, Seidman CE. Titin truncating mutations: a rare cause of dilated cardiomyopathy in the young. *Progress in Pediatric Cardiology*. 2016;40:41–45.
 42. Ware JS, Amor-Salamanca A, Tayal U, Govind R, Serrano I, Salazar-Mendiguchía J, García-Pinilla JM, Pascual-Figal DA, Nuñez J, Guzzo-Merello G, Gonzalez-Vioque E, Bardaji A, Manito N, López-Garrido MA, Padron-Barthe L, Edwards E, Whiffin N, Walsh R, Buchan RJ, Midwinter W, Wilk A, Prasad S, Pantazis A, Baski J, O'Regan DP, Alonso-Pulpon L, Cook SA, Lara-Pezzi E, Barton PJ, Garcia-Pavia P. Genetic etiology for alcohol-induced cardiac toxicity. *J Am Coll Cardiol*. 2018;71:2293–2302. doi: 10.1016/j.jacc.2018.03.462
 43. Chopra A, Kutys ML, Zhang K, Polacheck WJ, Sheng CC, Luu RJ, Eyckmans J, Hinson JT, Seidman JG, Seidman CE, Chen CS. Force generation via β -cardiac myosin, titin, and α -actinin drives cardiac sarcomere assembly from cell-matrix adhesions. *Dev Cell*. 2018;44:87–96.e5. doi: 10.1016/j.devcel.2017.12.012
 44. Biasillo G, Cipolla CM, Cardinale D. Cardio-oncology: gaps in knowledge, goals, advances, and educational efforts. *Curr Oncol Rep*. 2017;19:55. doi: 10.1007/s11912-017-0610-9
 45. Christenson ES, James T, Agrawal V, Park BH. Use of biomarkers for the assessment of chemotherapy-induced cardiac toxicity. *Clin Biochem*. 2015;48:223–235. doi: 10.1016/j.clinbiochem.2014.10.013
 46. Sawaya H, Sebag IA, Plana JC, Januzzi JL, Ky B, Tan TC, Cohen V, Banchs J, Carver JR, Wiegers SE, Martin RP, Picard MH, Gerszten RE, Halpern EF, Passeri J, Kuter I, Scherrer-Crosbie M. Assessment of echocardiography and biomarkers for the extended prediction of cardiotoxicity in patients treated with anthracyclines, taxanes, and trastuzumab. *Circ Cardiovasc Imaging*. 2012;5:596–603. doi: 10.1161/CIRCIMAGING.112.973321
 47. Bianco CM, Al-Kindi SG, Oliveira GH. Advanced heart failure therapies for cancer therapeutics-related cardiac dysfunction. *Heart Fail Clin*. 2017;13:327–336. doi: 10.1016/j.hfc.2016.12.005
 48. Payne DL, Nohria A. Prevention of chemotherapy induced cardiomyopathy. *Curr Heart Fail Rep*. 2017;14:398–403. doi: 10.1007/s11897-017-0353-9
 49. Vallakati A, Konda B, Lenihan DJ, Baliga RR. Management of cancer therapeutics-related cardiac dysfunction. *Heart Fail Clin*. 2018;14:553–567. doi: 10.1016/j.hfc.2018.06.004