

## Journal Pre-proof

Prevalence and evolution of right ventricular dysfunction among different genetic backgrounds in dilated cardiomyopathy

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## **Prevalence and evolution of right ventricular dysfunction among different genetic backgrounds in dilated cardiomyopathy**

*Short title: RVD in genetically determined DCM*

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**Abstract (250/250 words)**

**Background:** Titin (*TTN*) related dilated cardiomyopathy (DCM) has a higher likelihood of left ventricular reverse remodeling (LVRR) compared to other genetic etiologies. No data regarding the evolution of right ventricular dysfunction (RVD) according to genetic background is available.

**Methods:** Consecutive 104 DCM patients with confirmed pathogenic genetic variants (51 *TTN* related DCM; 53 other genetic DCM) and a control group of 139 patients with negative genetic testing and available follow-up data at 12-24 months were analyzed. RVD was defined as a right ventricular fractional area change (RVFAC) <35%. The main study end-point was the comparison of the evolution of RVD and the delta change of RVFAC throughout the follow-up according to etiology. A composite of

**Results:** In the *TTN* related DCM cohort, the prevalence of RVD at baseline was 35% (36/104) and at follow-up was 45% (47/104). In the other genetic DCM cohort, the prevalence of RVD at baseline was 30% (28/93) and at follow-up was 40% (37/93). In the control group, the prevalence of RVD at baseline was 15% (21/139) and at follow-up was 20% (28/139). The delta change of RVFAC was significantly greater in the *TTN* related DCM cohort compared to the other genetic DCM cohort and the control group.

**Conclusions:** The evolution of RVD and the delta change of RVFAC are significantly greater in *TTN* related DCM compared to other genetic DCM and the control group.

**Keywords:** dilated cardiomyopathy, right ventricular dysfunction, fractional area change, genetic background

## Brief Summary

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## Introduction

Dilated cardiomyopathy (DCM) is a primary heart muscle disease defined by left- or bi-ventricular systolic dysfunction in the absence of abnormal loading conditions or significant coronary artery disease [1;2]. A specific genetic background is identified in up to 40% of DCM patients, with 40 to 60 causative genes involved in determining the clinical phenotype [3;4]. Among these, truncating variants in the titin (*TTN*) gene represent the most prevalent etiology, accounting for 11 to 25% of genetically determined DCM [4].

Recently, considerable efforts have been devoted to characterizing the clinical phenotype of *TTN* related DCM. Evidence suggests that *TTN* truncating variants are associated with milder forms of DCM and a higher likelihood left ventricular reverse remodeling (LVRR) with guideline-directed medical treatment (GMT) [5-7].

So far, no data are available about the prevalence and evolution of right ventricular (RV) involvement in patients affected by *TTN* related DCM. Right ventricular dysfunction (RVD) is identifiable in approximately 30% of DCM patients at the initial clinical presentation [8;9], with a

high rate of RVD recovery following 6-12 months of GMT [10]. However, differences in the prevalence and progression of RVD according to genetic background have not been explored.

The aim of this study was to assess the prevalence and evolution of RVD in patients with *TTN* related DCM compared to other pathogenic genetic variants and DCM patients with no genetic determinants.

## Methods

### Inclusion and exclusion criteria

All consecutive patients enrolled to the Trieste Heart Muscle Disease Registry, Italy [11], from January 1995 to December 2017, were screened for inclusion. Patients with an available genetic test documenting a pathogenic or likely pathogenic mutation and available follow-up data at 12-24 months were eligible. A control group of genetically tested DCM patients enrolled in the same time-frame, in which genetic testing was either negative or demonstrated a variant of uncertain significance, was also included. The enrolment was considered the first evaluation in our Center.

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## Results

### Study population

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### Prevalence and evolution of right ventricular dysfunction according to genetic background

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**Predictors of right ventricular dysfunction at follow-up**

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**Genetically tested negative DCM cohort**

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## Discussion

7 the prevalence of RVD at clinical presentation is comparable in different genetic DCM subgroups. Second, most patients with *TTN* related DCM and genetically negative DCM improve their RV function with GMT and very rarely develop *de novo* RVD after their index presentation. In contrast, other genetic etiologies are less frequently associated with normalization of RV function and, in a non-negligible number of cases, show a late RV involvement during the natural progression of the disease. Finally the presence of RVD at initial presentation and a genetic background other than *TTN* are independently associated with the persistence RVD at follow-up.

### RV dysfunction in DCM

DCM represents the second most common HF etiology with a higher prevalence of RV involvement compared to ischemic heart disease [9]. However, few large-scale studies have previously described the prevalence and prognostic role of RV dysfunction in patients with DCM. Gulati et. al demonstrated, in a cohort of DCM patients investigated with cardiac magnetic resonance (CMR), that up to one third might present with RVD at the first clinical presentation [8]. Furthermore, after adjustment for other established prognostic factors, patients with baseline RVD had a 4-fold increase in cardiovascular mortality or HTx [8]. Nevertheless, our group formerly documented that RVD is a dynamic process in the natural history of DCM and, while most patients normalize their RV function following GMT, persistent or late-onset RVD are strongly associated with poor prognosis [10].

In the present analysis, we develop this understanding by describing, for the first time, difference according to genetic background. Approximately one third of cases presented with RVD, regardless of genetic background. However, we describe a different evolution in *TTN* related DCM patients compared to other genetic pathogenic variants. In fact, most patients in the *TTN* related DCM significantly improved their RV function over time, and only approximately 5% of patients still had RVD after a median of 14 months since diagnosis. On the contrary, patients with other genetic etiologies and RVD at first clinical presentation mostly maintained it during follow-up, and, in a non-negligible number of cases (17.6%; table 2), a subsequent worsening of RV function in the successive two years after the initial presentation was documented. This was supported by the multivariable model, where a genetic background other than *TTN* was strongly and independently associated with the presence of RVD at follow up ( $p=0.001$ ).

This finding is intriguing, and suggests that *TTN* related DCM is rarely a biventricular disease. Indeed, RVD at the first clinical presentation will normalize it in the subsequent clinical course, being likely representing hemodynamic impairment rather than structural disease or being more amenable to treatment. Therefore, appreciating the genetic background in patients presenting with DCM may be important to predict the dynamic evolution and the possible persistence of RVD, [20], which is associated with a poorer global outcome (figure 2).

#### ***TTN* related DCM and cardiac reverse remodeling: a benign mutation?**

*TTN* pathogenic mutations are the most frequent cause of genetically determined DCM, representing almost 1/3 of this cohort [4]. *TTN* related DCM is thought to be associated with a milder phenotype of the disease and a particularly high rate of LVRR with GMT [5-7].

Previous studies have reported that genetically determined DCM patients are less prone to favorable LVRR compared to their genetically negative counterparts [5]. Interestingly, this

difference was not evident in patients with *TTN* mutations compared to genetically negative patients [5].

In our analysis, we confirmed that *TTN* related DCM has a higher incidence of LVRR compared to other genetic etiologies ( $p=0.049$ ). Furthermore, we also demonstrated that RVD recovery is also similar in *TTN* related DCM and genetically negative DCM, reaching approximately 80% in both groups. The latter finding is totally new and assumes that pathogenic *TTN* mutations might lead to a milder form of genetically determined DCM, in whom there is a higher likelihood of global cardiac reverse remodeling with GMT.

#### **Outcomes in genetically determined DCM; a matter of RVD?**

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## Study limitations

This study has the intrinsic limitation of all observational, registry studies. As patients are enrolled from a referral center for cardiomyopathies, the results might not be generalizable for all DCM patients.

The enrolment period was long, starting in 1995, and several important advances in GMT guideline-directed medical treatment occurred in this time.

Brain natriuretic peptides levels were not systematically available and could not be included in the preset analysis. Drug doses were also not available but, importantly, we did not observe any baseline and follow-up differences in rates of prescription.

The multivariable included only 3 variables due to the low number of events, which limited the statistical power of our analysis. However, we performed two sensitivity models where both RVD and the genetic background remained significant.

Tricuspid annular plane excursion (TAPSE) was available only in a minority of patients, and RVD was only defined using RVFAC.

Two-dimensional echocardiography clearly manifests some limitations in the assessment of RV compared to CMR. However, we performed an inter-observer and intra-observer variability analysis that indicated a good performance level (ICC 0.929; 95% CI 0.888-0.958;  $p < 0.001$ ; kappa agreement 0.84 and 0.81 for intra-observer and inter-observer analysis respectively) and we previously reported good correlation between echocardiographic RVFAC and CMR RV ejection fraction in a series of 50 DCM patients [10].

Unfortunately, the low number of patients for each single pathogenic mutation did not allow us to draw any conclusions regarding the possible prevalence of RV involvement in single specific mutations, and this should be pursued in the future.

### Conclusions

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**Acknowledgements.** # k u #ku 7

**Sources of finding:** V

**Disclosures.** V

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**Table 1: Baseline characteristics of the study population.**

Characteristics	Genetically positive cohort (n=104)	<i>TTN</i> related DCM (n=51; 49%)	Other genetic DCM (n=53; 51%)	P value
<b>Age (years) (0)</b>	42±15	47±14	37±15	<b>0.002</b>
<b>Male sex (%) (0)</b>	78 (75%)	40 (78%)	38 (71%)	0.500
<b>Time since HF diagnosis (months) (6)</b>	1 (0-8)	1 (0-8)	1 (0-7)	0.82
<b>Hypertension (%) (0)</b>	22 (21.2%)	12 (23.5%)	10 (18.8%)	0.635
<b>SBP (mmHg) (10)</b>	119±16	119±18	120 ± 16	0.712
<b>NYHA III-IV (%) (0)</b>	13 (12.5%)	6 (11.8%)	7 (13.2%)	1.000

<b>Beta-blockers (%) (0)</b>	86 (82.7%)	46 (95.8%)	40 (83.3%)	0.091
<b>ACEI/ARBs/ARNI (%) (0)</b>	95 (89.4%)	47 (92.2%)	46 (86.8%)	0.527
<b>Loop diuretics (%) (0)</b>	52 (50%)	23 (45.3%)	29 (54.7 %)	0.220
<b>CRT (during follow up) (%) (0)</b>	10 (9.6%)	5 (9.8%)	5 (9.4%)	1.000
<b>ICD (during follow up) (%) (0)</b>	44 (42.3%)	25 (49%)	19 (35.8%)	0.234
<b>HR (bpm) (12)</b>	76±17	78±19	73±18	0.053
<b>QRS length (ms) (31)</b>	102±24	103±19	101±28	0.734
<b>LBBB (%) (0)</b>	10 (9.6%)	6 (11.7%)	4 (7.5%)	0.740
<b>Echocardiography</b>				
<b>LVEF (%) (2)</b>	33±10	33±11	34±10	0.400
<b>iLVEDD (mm/m<sup>2</sup>) (5)</b>	34±6	34±6	35±5	0.059
<b>iLVEDV (ml/m<sup>2</sup>) (6)</b>	94±32	93±33	94±34	0.295
<b>LAESA (cm<sup>2</sup>) (12)</b>	25±8	26±8	24±8	0.240
<b>RVFAC (%) (0)</b>	39±11	42±11	35±11	<b>0.011</b>
<b>RVD (%) (0)</b>	30 (28.8%)	11 (21.6%)	19 (35.8%)	0.132
<b>Moderate-severe MR (%) (0)</b>	34 (32.7%)	19 (37.3%)	15 (28.3%)	0.404

P values are referred to the comparison between *TTN* related DCM and other genetic DCM and reported in bold when significant (i.e. <0.05). In the first column, the number in parentheses represents the overall number of genetically tested positive patients with missing data.

DCM= dilated cardiomyopathy; SBP= systolic blood pressure; NYHA =New York Heart Association; ACEI: angiotensin-converting enzyme inhibitors; ARB= angiotensin receptor blockers; ARNI= angiotensin receptor neprilysin inhibitor; CRT= cardiac resynchronization therapy; ICD= implantable cardiac defibrillator; HR= heart rate; LBBB= left bundle branch block; LVEF= left ventricular ejection fraction; iLVEDD= indexed left ventricular end-diastolic diameter; iLVEDV= indexed left ventricular end-diastolic volume; LAESA= left atrial

end-systolic area; RVFAC= right ventricular fractional area change; RVD= right ventricular dysfunction; MR= mitral regurgitation.

**Table 2: Evolution of right ventricular dysfunction and rates of left ventricular reverse remodelling of the study population at follow-up.**

Characteristics	<i>TTN</i> related DCM (n=51; 49%)	Other genetic DCM (n=53; 51%)	P value
<b>LVRR (%)</b>	19/51 (37.2%)	10/53 (18.8%)	<b>0.049</b>
<b>RVFAC (%) (0)</b>	46±7	36±10	<b>&lt;0.001</b>
<b>RVD (%) (0)</b>	3 (5.9%)	19 (35.8%)	<b>&lt;0.001</b>
<b>Persistent RVD (%) (0)</b>	2/11 (18.1%)	13/19 (68.4%)	<b>0.004</b>
<b>Incident RVD (%) (0)</b>	1/40 (2.5%)	6/34 (17.6%)	0.09

Significant p values are reported in bold. In the first column, the number in parentheses represents the overall number of genetically tested positive patients with missing data

RVD= right ventricular dysfunction; LVRR= left ventricular reverse remodelling. **Persistent RVD**= patients who presented RVD both at baseline and follow up; **Incident RVD**= patients with a normal RV function at baseline who developed RVD subsequently at follow-up. See supplementary table S2 for complete characteristics at follow-up of the study population.

**Table 3: Multivariable analysis for persistence or incidence of RV dysfunction at follow-up.**

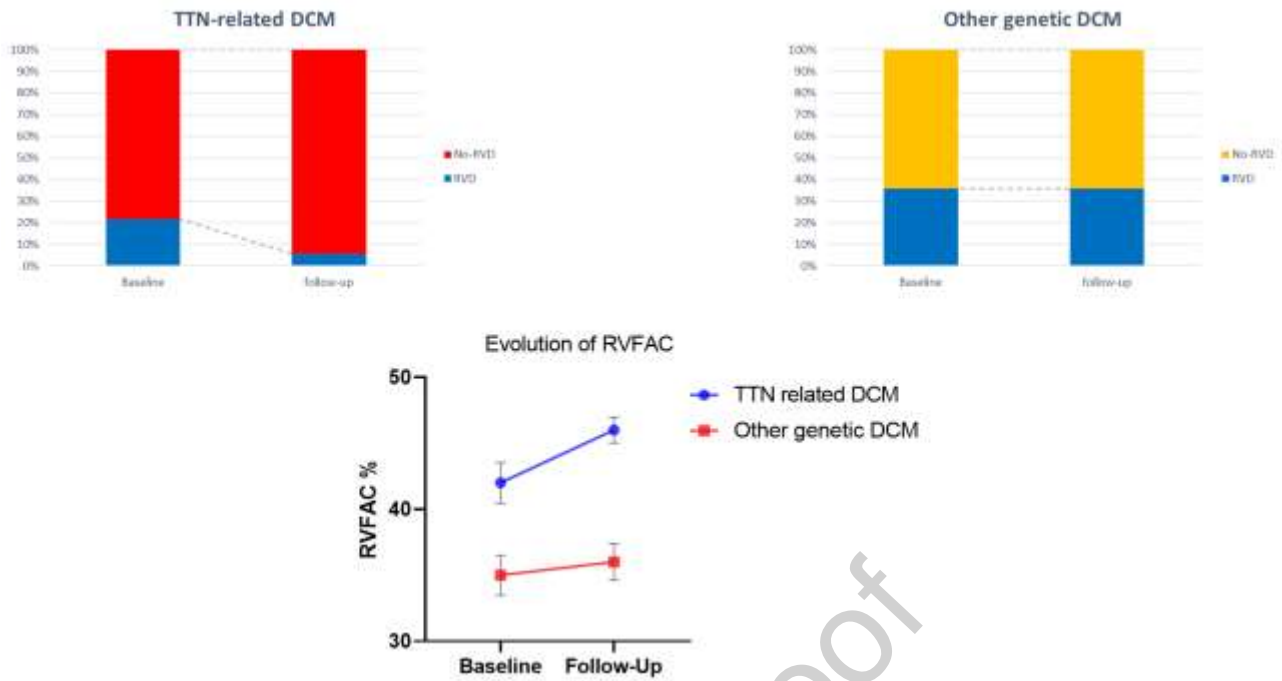
	OR	95% CI	P value
<b>Other genetic DCM vs <i>TTN</i> related DCM</b>	16.458	3.095-87.513	<b>0.001</b>
<b>LVEF (%)</b>	0.962	0.902-1.025	0.231
<b>RV dysfunction at baseline (%)</b>	6.776	1.976-23.239	<b>0.002</b>

Significant p values (i.e.<0.1) are reported in bold. DCM= dilated cardiomyopathy; LVEF= left ventricular ejection fraction; RV= right ventricular. The univariable analysis is reported in supplementary table S3.

**Table 4: Prevalence of RV dysfunction in genetically positive and genetically negative DCM at follow-up.**

	Genetically negative DCM (n=139)	<i>TTN</i> related DCM (n=51)	Other genetic DCM (n=53)	P value
<b>RVFAC (%)</b>	44±8	46±7	36±10	<b>&lt;0.001 *£</b>
<b>RVD (%)</b>	11 (7.8%)	3 (5.9%)	19 (35.8%)	<b>&lt;0.001 *£</b>
<b>Persistent RVD</b>	7/40 (17.5%)	2/11 (18.1%)	13/19 (68.4%)	<b>0.004 £;</b> <b>&lt;0.001*</b>
<b>Incident RVD at follow-up</b>	4/99 (4.1%)	1/40 (2.5%)	6/34 (17.6%)	<b>0.01 *</b>

Only significant p values (i.e. < 0.05) are reported. \*=genetically negative DCM vs other genetic DCM; £=*TTN* related DCM vs other genetic DCM. DCM= dilated cardiomyopathy; RVFAC= right ventricular fractional area change; RVD= right ventricular dysfunction;



**Fig 1. Evolution of RVFAC and prevalence of RV dysfunction at baseline and follow-up in the two genetic cohorts.**

RVFAC= Right ventricular fractional area change; DCM= Dilated Cardiomyopathy. In blue patients affected by *TTN* related DCM, in red patients affected by other genetic DCM. Data are mean and Standard Error of the mean.

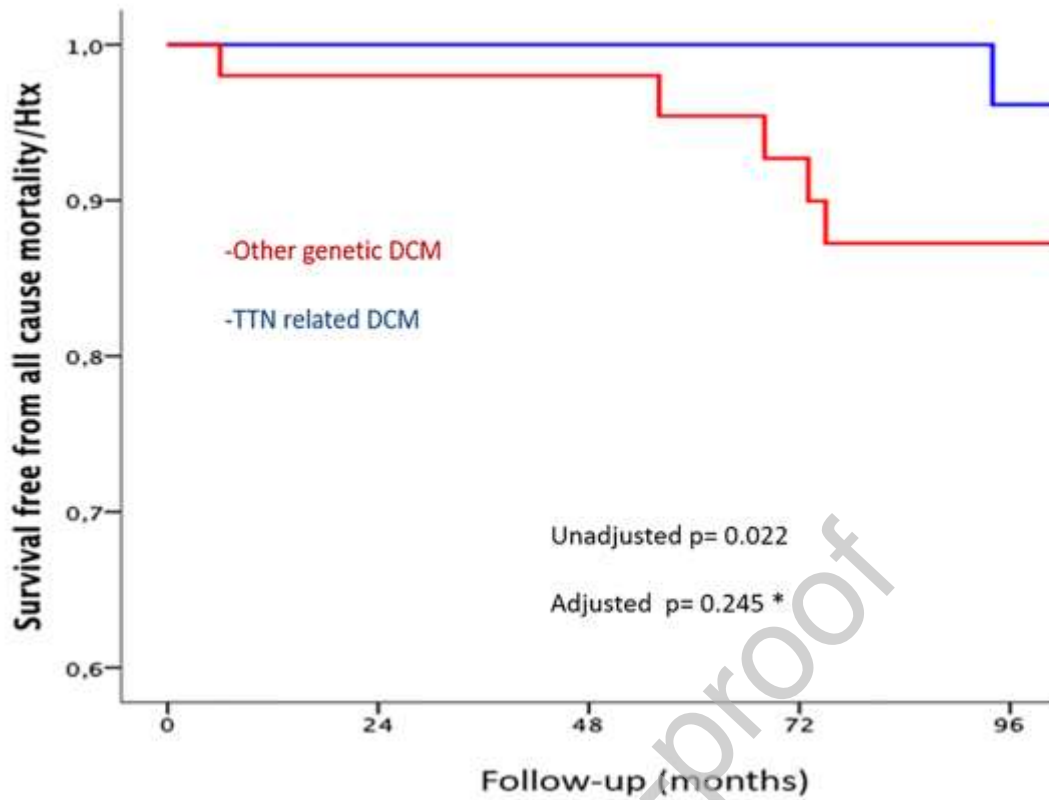


Fig. 2 KM survival curves for all-cause mortality/Htx. The baseline was intended as the 14 [10-18] month evaluation.

Htx= heart transplantation; DCM= dilated cardiomyopathy. In blue TTN-related DCM, in red other genetic DCM. \* p value adjusted for right ventricular dysfunction at follow-up.