Familial Left Ventricular Noncompaction
Associated With a Novel Mutation in the Alpha-
cardiac Actin Gene

_{Miocardiopatía no compactada familiar asociada con una mutación nueva en el gen de la alfa-actina cardiaca_}

To the Editor,

Left ventricular noncompaction (LVNC) is characterized by multiple prominent ventricular trabeculations and deep intertrabecular recesses.¹ A familial background is found in 18% to 50% of adults and the estimated prevalence in echocardiographic studies is 0.014% to 1.300%.² Its genetic bases are heterogeneous,¹⁻³ with only two reported mutations in the alpha-cardiac actin gene (ACTC1)⁴: ACTC1⁴M271V and ACTC1⁴E101K with additional apical hypertrophic cardiomyopathy, restrictive filling, and septal defects.⁴ As in other inherited familial conditions, the finding of a pathogenic mutation can be very valuable when screening at-risk relatives.⁵

Herein we present a family with LVNC caused by the novel heterozygous ACTC1¹²⁸⁹⁷ mutation, which exhibited different clinical features and courses in the affected family members, namely isolated LVNC, LVNC associated with atrioseptal defect, and restrictive cardiomyopathy associated with atrioseptal defect.

A 9-month-old girl underwent heart transplantation in another hospital because of a restrictive cardiomyopathy with dilated atria, depressed left ventricular ejection fraction, and an associated small ostium secundum atrioseptal defect (proband, Figure, IV:1). At hospital discharge, the presence of a previously unsuspected LVNC was reported in the macroscopic evaluation of the heart. No histologic evaluation was carried out and no samples from the explanted heart were kept for further examination. A comprehensive workup, approved by the local research ethics committee, was offered to her first-degree relatives and the family tree was accordingly expanded. This evaluation included electrocardiogram, echocardiography, and blood sampling for genetic studies. Cardiac magnetic resonance imaging, exercise testing, and Holter-electrocardiogram were performed at cardiologist discretion. LVNC was defined following Jenni’s (telesystolic noncompacted/compacted myocardium > 2 by echocardiography) and/or Petersen’s criteria (telediastolic noncompacted/compacted > 2.3 by cardiac magnetic resonance imaging).⁶

Sanger sequencing (MYH7, myosin binding protein C3, Nkx2.5, and ACTC1 genes) was performed in genomic DNA of the maternal

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**Figure**. Familial pedigree. ACTC1, alpha-cardiac actin gene; LVNC, left ventricular noncompaction; LVH, left ventricular hypertrabeculation; MI, myocardial infarction; NE, not evaluated; OS-ASD, ostium secundum atrioseptal defect; RCM, restrictive cardiomyopathy. Circles denote females, squares males. Red symbols represent affected individuals. *Macroscopic evaluation at heart transplantation.
<table>
<thead>
<tr>
<th>Pedigree position</th>
<th>Sex/Age, y</th>
<th>Clinical history</th>
<th>ECG</th>
<th>Echocardiography</th>
<th>CMRI</th>
<th>Holter</th>
<th>Exercise testing</th>
<th>Genetics: heterogeneous ACTC1&lt;sup&gt;1289T&lt;/sup&gt; mutation</th>
</tr>
</thead>
<tbody>
<tr>
<td>II:3</td>
<td>F/59</td>
<td>Asymptomatic</td>
<td>Normal</td>
<td>Normal</td>
<td></td>
<td>—</td>
<td>—</td>
<td>Non carrier</td>
</tr>
<tr>
<td>II:4</td>
<td>M/66</td>
<td>Dyspnea, NYHA class I-II/IV</td>
<td>SR, first degree AV block, QS in the inferior leads</td>
<td>One year before this study, in another center: echocardiography within normal limits</td>
<td>LVEF, 36%; moderately impaired RV EF</td>
<td>—</td>
<td>—</td>
<td>Normal Carrier</td>
</tr>
<tr>
<td>III:2</td>
<td>F/33</td>
<td>Asymptomatic</td>
<td>Normal</td>
<td>Normal</td>
<td></td>
<td>—</td>
<td>—</td>
<td>Non carrier</td>
</tr>
<tr>
<td>III:4</td>
<td>F/32</td>
<td>Previous clinical history: OS-ASD repaired at 10 years of age; one miscarriage (hydranops)</td>
<td>Normal</td>
<td>Three years before this study, in another center: echocardiography within normal limits</td>
<td>LVNC; LVEF, 48%; intramyocardial LGE at the inferior wall and posterior septum</td>
<td>—</td>
<td>—</td>
<td>Carrier</td>
</tr>
<tr>
<td>III:5</td>
<td>M/37</td>
<td>Asymptomatic</td>
<td>Normal</td>
<td>Normal</td>
<td></td>
<td>—</td>
<td>—</td>
<td>Non carrier</td>
</tr>
<tr>
<td>III:6</td>
<td>M/31</td>
<td>Dyspnea, NYHA class II/IV</td>
<td>SR, nonspecific ventricular activation delay</td>
<td>LVNC; spheric-shaped dilated LV (65/52 mm); LVEF, 25%; restrictive filling pattern; severe mitral regurgitation; normal-sized RV with preserved RV EF</td>
<td>LVNC; dilated LV; LVEF 27%; prolapse of posterior mitral left with severe mitral regurgitation.</td>
<td>—</td>
<td>—</td>
<td>Carrier</td>
</tr>
<tr>
<td>IV:1</td>
<td>F/3</td>
<td>Heart transplantation at 9 months of age because of refractory heart failure; no further clinical events</td>
<td>SR at 150 bpm; left atrial and LV hypertrophy and inespecific alteration in the ventricular repolarization</td>
<td>Before heart transplantation: dilated LV (36/27 mm) and LVEF, 46%; restrictive filling pattern; severe-moderate mitral and tricuspid regurgitation; moderate pulmonary hypertension; OS-ASD, 5 mm</td>
<td>At heart transplantation: LV hypertrabeculation</td>
<td>—</td>
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<td>Carrier</td>
</tr>
</tbody>
</table>

ACTC1, alpha-cardiac actin gene; AVB: atrioventricular block; CMRI, cardiac magnetic resonance imaging; ECG, electrocardiogram; F, female; LGE, late gadolinium enhancement; LV, left ventricle; LVEF, left ventricular ejection fraction; LVNC, left ventricular noncompaction; M, male; MI, myocardial infarction; NE, not evaluated; NYHA, New York Heart Association; OS-ASD, ostium secundum atrioseptal defect; RV, right ventricle; RVEF, right ventricular ejection fraction; SR: sinus rhythm.

proband’s uncle since the proband was initially not available for mutation screening. The heterozygous ACTC1I289T mutation was identified and cascade genetic studies were undertaken in the remaining relatives. No additional mutation was found in any of the other screened genes. The Table shows the results of the family study in affected (II:4, III:4, III:6 and IV:1) and nonaffected individuals (no additional family members were available for the study).

Gene sequencing yielded the presence of the heterozygous ACTC1I289T mutation, not present in the National Center for Biotechnology list of single nucleotide polymorphisms in the ACTC1 gene. Although hundreds of variants have been identified in sarcomeric and desmosomal genes, only a few polymorphisms and < 30 mutations causing any kind of cardiomyopathy have been described in the ACTC1 gene, suggesting that changes in the ACTC1 gene are poorly tolerated. Actin is essential for cell morphology, adhesion, and migration. This novel variant alters a preserved amino acid residue (I289) in the protein, replacing a nonpolar (isoleucine) with another polar and noncharged (threonine) aminoacid, thus causing moderate modifications in the physico-chemical properties related to the hydrophobicity, charge, polarity, and mass of the protein (Grantham distance 89 [0-215]). The prediction of in silico (SIFT [Sorting Intolerant from Tolerant], Polyn phen-2, and Pmut) analyses neither confirmed nor ruled out its pathogenicity (unconclusive results with low confidence). The preserved I289 amino acid residue maps to subdomain 3, important for the stability and polymerization of the actin filaments and next to the myosin binding site, possibly disrupted by the presence of the ACTC1I289T mutation. Furthermore, our ACTC1I289T mutation cosegregated perfectly with the LVNC phenotype, with a 100% penetrance in the individuals available for the study.

We acknowledge that a more thorough genetic study could have included many other genes. Nonetheless, we considered it finished in terms of cost-effectiveness for three reasons: a) our results were consistent with a previous study linking LVNC and septal defects due to ACTC1 mutation; b) the variant strongly cosegregated with the phenotype, and c) the molecular consequences of the variant were considered probably pathogenic. Further functional information obtained from animal models may be valuable to confirm the causal role of the ACTC1I289T mutation.

In summary, we offer the phenotypical description of a family with LVNC caused by the highly penetrant, novel, heterozygous ACTC1I289T mutation. Remarkably, in the literature this is the third ACTC1 mutation causing LVNC, and associated ostium secundum atrioseptal defect in some affected family members.

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María Rodríguez-Serrano, a,b Diana Domingo, a,b,c Begoña Igual, d Ana Cano, e Pilar Medina, f and Esther Zorio g,e,c

aServicio de Cardiología, Hospital Universitario y Politécnico La Fe, Valencia, Spain
bDepartamento de Medicina, Universidad de Valencia, Valencia, Spain
cGrupo Acreditado en Hemostasia, Trombosis, Arteriosclerosis y Biología Vascular, Instituto de Investigación Sanitaria La Fe, Valencia, Spain

dUnidad de Imagen Cardiaca, ERESA, Valencia, Spain
eSección de Cardiología Pediátrica, Servicio de Pediatría, Hospital Universitario y Politécnico La Fe, Valencia, Spain
f Corresponding author:
E-mail address: zorio_est@gva.es (E. Zorio).

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Improvement in Hemodynamics and Contractility With Multipoint Left Ventricular Pacing in Cardiac Resynchronization Therapy

Mejoría hemodinámica y de la contractilidad con la estimulación multipunto del ventrículo izquierdo en la terapia de resincronización cardíaca

To the Editor,

Heart failure is a leading cause of morbidity and mortality in Western countries. Bipolar ventricular pacemakers have been used to treat heart failure since the 1990s.1 Over the last decade, randomized studies,2,3 have demonstrated the benefit of cardiac resynchronization therapy (CRT) and helped to establish its indications. This therapy has been shown to increase survival and decrease hospitalizations in patients with heart failure, left ventricular (LV) dysfunction, and prolonged QRS, in particular in those with complete left bundle branch block.4 Unfortunately, a significant number of patients (30%-40%) have no response to CRT.5 This lack of response could be explained by inappropriate pacing site selection, suboptimal device programming, or absence of dysynchronous basal LV contraction.6 Another limitation could be that pacing from a single LV point is incapable of generating a coordinated mechanical activation. Quadripolar electrodes would allow LV pacing from 2 points far