Hypertrophic Cardiomyopathy. A Study of the Troponin-T Gene in 127 Spanish Families

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The information available on the correlation between genotype and phenotype and the prognostic implications of different troponin-T gene mutations is sparse and, at times, contradictory. We studied the TNNT2 gene in 127 patients with hypertrophic cardiomyopathy and identified three mutations in patients from four families (3.1%): the Phe87Leu mutation, which has not been previously reported, the Arg278Cys mutation (two families) and the Asp271Ile mutation. Seven carriers of the Phe87Leu mutation (aged 29 to 52 years) were found to have mild hypertrophy (i.e., a wall thickness <16 mm). There were 11 deaths associated with the condition (seven sudden deaths), and four of those who died were aged between 14 and 16 years. No sudden deaths occurred in the other three families. In conclusion, troponin-T mutations were responsible for 3% of the hypertrophic cardiomyopathy cases in our study population. The Phe87Leu mutation was associated with only mild hypertrophy but with a high risk of sudden death.

Key words: Hypertrophic cardiomyopathy. Genetics. Troponin T. Sudden death.

INTRODUCTION

Hypertrophic cardiomyopathy (HCM) is an autosomal dominant hereditary disease caused by over 500 mutations in 11 different genes.1-4 Information about the relationship between genotype and phenotype and the prognosis associated with various mutations in the troponin T gene (TNNT2) is limited and at times contradictory.4,5-13 The aim of this study was to identify mutations in the TNNT2 gene and study the correlations between the genotype and the phenotype.

METHODS

Blood samples were studied from 127 consecutive patients with HCM (mean age, 50 [16] years; 66% men; maximum wall thickness, 18 [5] mm; 28% with obstruction). The patients came from 3 centers: the Hospital Universitario in A Coruña (60 patients), the Hospital Virgen de la Arrixaca (37 patients),
and the Hospital General in Alicante (30 patients). Cardiac evaluation included ECG, echocardiogram, Holter, and an exercise stress test. All the patients gave written informed consent.

Each index patient provided 4 mL of blood, drawn into an EDTA tube. The DNA was extracted and amplified, and TNNT2 exons were analysed by screening with denaturing high-performance liquid chromatography (DHPLC). In the event of an anomalous profile, the exon was sequenced (sequencer: ABI310/ABI3130). Specific primers were designed for the amplification of the fragments of interest.

RESULTS

Eight different alterations were found in 107 exons. Three variants were considered to be causal mutations: Phe87Leu (not previously reported), Arg278Cys and Asp271Ile (Table 1). The Asp271Ile mutation was identified in a Galician family and the Arg278Cys mutation in one family from Murcia and another from Alicante. Both these mutations had already been associated with HCM. The Phe87Leu mutation was considered to be causative as it segregated with the disease, affected a highly conserved residue and was not identified in 140 healthy controls. Table 2 summarizes the clinical characteristics of the carriers.

Clinical Characteristics and Genotype-Phenotype Correlation

Phe87Leu

This mutation was identified in a family with history of sudden death (SD) (Figure 1). In total, 18 persons were affected, with 11 related deaths: 7 SD, 3 due to heart failure and 1 from stroke. Four of those who died were aged between 14 and 16 years and were asymptomatic ([IV.1], [IV.12], [III.31], and [III.39]). Of the 10 patients for whom an echocardiogram was available, 7 had mild hypertrophy (<16 mm); in 2 of these the echocardiogram did not show the hypertrophy and the diagnosis was made at autopsy. Two of the patients with mild hypertrophy had a restrictive pattern. Three patients had a wall thickness >20 mm (maximum, 27 mm [IV.8]). Only the index case [IV.14] had a gradient. Systolic function was conserved, except in one case (ejection fraction, 40% [III.21]). One of the affected members had recurrent

TABLE 1. Results of the Genetic Study of the TNNT2 Gene

<table>
<thead>
<tr>
<th>Exon/Intron</th>
<th>Nucleotide Change</th>
<th>Amino Acid Change</th>
<th>Carriers, No.</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intron 3</td>
<td>Del5pb</td>
<td>Intronic variant</td>
<td>35</td>
<td>Does not affect protein</td>
</tr>
<tr>
<td>Exon 8</td>
<td>TCT&gt;TCC</td>
<td>Ser69Ser</td>
<td>15</td>
<td>Does not affect protein</td>
</tr>
<tr>
<td>Exon 9</td>
<td>AAG&gt;AAA</td>
<td>Lys97Lys</td>
<td>1</td>
<td>Does not affect protein</td>
</tr>
<tr>
<td>Exon 9</td>
<td>ATC&gt;ATT</td>
<td>Ile106Ile</td>
<td>46</td>
<td>Does not affect protein</td>
</tr>
<tr>
<td>Exon 14</td>
<td>AAG&gt;AGG</td>
<td>Lys253Arg</td>
<td>6</td>
<td>Polymorphism described</td>
</tr>
<tr>
<td>Exon 8</td>
<td>TTT&gt;CTT</td>
<td>Phe87Leu</td>
<td>1</td>
<td>New mutation</td>
</tr>
<tr>
<td>Exon 15</td>
<td>AAC&gt;ATC</td>
<td>Asp271Ile</td>
<td>1</td>
<td>Mutation described</td>
</tr>
<tr>
<td>Exon 16</td>
<td>CGC&gt;TGC</td>
<td>Arg278Cys</td>
<td>2</td>
<td>Mutation described</td>
</tr>
</tbody>
</table>

Figure 1. Family tree of A8 with Phe87Leu mutation in TNNT2.

In general, the younger affected members of the family were asymptomatic and over half the affected members aged between 40 and 50 years had dyspnea (NYHA II-III). The family and genetic study led to implantation of automated defibrillators for primary prevention in 2 affected members [III:36 and IV:3]. The mutation was not identified in 6 members with a normal phenotype.

This mutation was identified in two families, M92 and A16 (Figure 2 and Table 2). Of the 8 carriers, 4 fulfilled the diagnostic criteria for HCM (A16: II:1; M92: I:1, I:2, II:5), 1 had a doubtful phenotype (M92: II:2) and 3 had a normal echocardiogram and ECG (M92: II:3 and II:4, A16: III:1) (Table 2). These families had no history of adverse events related with the disease.

One of the carriers in family M92 had very marked hypertrophy (40 mm) (II:5), which contrasted with the normal phenotype of this patient’s siblings who were carriers. His father (I:2) had moderate hypertrophy and his mother (I:3) had mild hypertrophy. In order to attempt to clarify the relationship between genotype and phenotype in family M92, sequencing was made of another 8 sarcomeric genes (MYH7, MYBPC3, alpha tropomyosin, actin, TNNI2, TNNC1, and the myosin light chains) in the proband. The patient with severe hypertrophy (II:5) carried an Asp 928Asn mutation in the beta myosin heavy chain (MYH7), which was also present in his father (I:2), aunt (I:1) and cousins (II:1 and II:2). Three of the 4 carriers of this mutation were affected (I:1, II:1 and II:2). Thirteen of the 48 carriers of other mutations had a normal phenotype (12.5%); this was in line with the high frequency of the Arg278Cys mutation in these families (25%). The high prevalence of normal phenotypes in this genotype-phenotype relationship suggests that there are other factors involved in the expression of the phenotype, such as the presence of other mutations or modifier genes (I:1, II:1, II:2). One of the 4 carriers had a normal ECG and a normal echocardiogram (I:1) (Table 2). The families with the Arg278Cys mutation did not have a history of adverse events related with the disease. For the family with severe hypertrophy, IAD, no medical treatment was prescribed.
The Arg278Cys mutation was identified in 2 families. This mutation has been reported in 11 families from various countries. The mutation affects an amino acid located at the binding site of troponin I and C. Including our two families, there are now 36 carriers. The penetrance is incomplete, and hypertrophy, which becomes evident at advanced ages (50 years), is usually mild (17 mm). Reports exist of 11 SD, most in persons older than 60 years of age, although 2 cases occurred in young persons without ventricular hypertrophy. Six of the 11 SD happened in the same family, so there might have been some additional unidentified risk factor.

We identified a family with the Asp271Ile mutation; only one case has been previously reported, and we do not have the clinical data. Three carriers in our family had a mild phenotype, and in one of these there was atrial communication. The data currently available do not allow the risk profile to be established.

Our study confirms that carriers of the mutations in TNNT2 can develop mild phenotypes, as has been indicated previously, and that mutations exist that are associated with a very high risk of SD, as is the case of the Phe87Leu mutation. In these cases, genetic analysis is a very useful clinical tool. A few patients with severe phenotypes might carry double mutations, or the phenotype could be the consequence of the involvement of unknown modulating agents. We have also confirmed that some mutations in TNNT2, such as Arg278Cys, can cause late onset HCM. In these cases, the risk of SD may be greater in patients of a certain age.

In conclusion, mutations in the TNNT2 gene caused 3% of cases of HCM in our population. The Phe87Leu mutation is associated with mild hypertrophy and a high risk of SD. The Arg278Cys mutation is associated with mild hypertrophy, incomplete penetrance and a high risk in older carriers. The presence of double mutations should be suspected in persons with severe forms of the disease.

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REFERENCES


