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<th>Genetic Analysis of Cardiac β Myosin Heavy Chain (MHC) Gene in Seven Families with Hypertrophic Cardiomyopathy in Japan</th>
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<td>Author(s)</td>
<td>Hayashi, Ikuo; Ashizawa, Naoto; Oku, Yasuhiko; Ozeki, Shinichiro; Ohtsuru, Akira; Yano, Katsusuke</td>
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Introduction

The cardiomyopathies are classified according to their anatomic and pathophysiologic types, as dilated, hypertrophic and restrictive. The distinctions between these three categories are not absolute, and there is often overlap. Hypertrophic cardiomyopathy is a primary disorder of cardiac muscle characterized by hypertrophy of the left ventricle with preserved or enhanced contraction, in the absence of another cardiac disease, or systemic disease which can produce left ventricular hypertrophy. At the microscopic level, the most characteristic abnormality is the great extent of disorganization of both the cell-to-cell alignment and the regular structure of myofibrils, known as myosite disarray. Secondary myocardial hypertrophy may accompany any type of cardiovascular disorder, such as valvular, hypertensive, ischemic and congenital heart disease. Disarray may also be present in small amounts in secondary myocardial hypertrophy (about 5% of the total tissue area), but in hypertrophic cardiomyopathy it is found as much as 30% of the total tissue area. The chief morphological abnormality in hypertrophic cardiomyopathy is greater thickening of the ventricular septum than the left ventricular free wall. Patients with hypertrophic cardiomyopathy are often asymptomatic or have non specific cardiovascular symptoms, such as dyspnea, chest pain or syncope. The most frightening clinical outcome of hypertrophic cardiomyopathy is sudden cardiac death which can occur even in asymptomatic persons. Another clinical problem is the difficulty to determine which patient is developed from hypertrophic to dilated cardiomyopathy. In over one half of patients hypertrophic cardiomyopathy is familial, while remaining cases appear to be sporadic. Familial hypertrophic cardiomyopathy (FHC) is an autosomal dominant disorder (1, 2) and it is one of the most common forms of inheritable cardiac disease. Significant variability in the clinical and morphological expression among families, and even within the same family, suggest phenotypic heterogeneity of this disease. Recently linkage analysis in large multiplex Caucasian FHC showed a close linkage of affected individuals with the cardiac βM HC locus on the chromosome 14 band q1 (3-5). Missense mutations of the cardiac βM HC locus have been reported among the Japanese with FHC. (6-10). Using various restriction fragment length polymorphism (RFLP) markers, the FHC locus was found to be located on Chromosome 18 (Japanese study) (11) Chromosome 16 (Italian study) (12), and Chromosome 2 (NIH study) (5), indicating genetic heterogeneity. To clarify the frequency of mutations or polymorphisms in the cardiac βM HC gene, we studied 7 unrelated families with HCM by PCR-SSCP analysis. As the recent studies reported that mutations were mainly found in the head or head-rod junction, we selected the exons 3-25 of the cardiac βM HC gene.
Method

Study group

Seven families were identified through an affected family member and underwent extensive medical history and cardiovascular examinations, including 12-lead electrocardiography, M-mode and two-dimensional echocardiographies. The diagnosis of HCM was based on unexplained ventricular hypertrophy in the absence of ather potential causes of ventricular hypertrophy such as systemic hypertension. Patients with apical hypertrophy were excluded from this study.

Genetic DNA extraction

The blood was drawn from family members after informed consent. High-molecular-weight DNAs were prepared from peripheral leucocytes, and these cells were digested using the SDS-protein K method. DNA was extracted with phenol-chloroform, and ethanol precipitate [13]. LV muscle tissue was obtained from the proband 1.1. of family 1. and the sporadic case; T.M. of HCM underwent autopsy.

PCR amplification

Oligonucleotide primers for PCR amplification were synthesized by DNA synthesizer (Cyclon plus, Milligen/Biosearch, Burlington) and obtained from H. Nish et al. Using these sets of primers, genomic DNA was amplified in a thermal cycler (Program Temp Control System PC-700, Astec Inc., Tokyo) under the following conditions: 94°C for 1 minute, 55-60°C for 1 minute, 72°C for 1 minute, and final primer extension time of 4 minutes at 72°C.

PCR-SSCP analysis

The PCR-SSCP analysis and the silver staining method were performed as described by S. Hoshino et al. [14]. Formamide dye (80% formamide, 20 mM EDTA, 0.01% bromophenol blue, pH 8.0) was added to an aliquot of PCR products (0.1-0.2 μg) to obtain the final concentration of 50% formamide. Samples were heat-denatured at 96°C for 5 minutes, and rapidly cooled on ice. The samples were electrophoresed in two sets of 8% polyacrylamide gels (0.1 cm width, 0.4 TBE, acrylamide:bisacrylamide = 30:1) with and without 10% glycerol in 0.4 TBE (1×TBE: 89 mM Tris-borate, 89 mM boric acid, 2 mM EDTA, pH 8.0) at 12 V/cm for 3-7 hours at room temperature. DNA fragments were visualized by a silver staining kit (Daiichi Chemical Co. Ltd., Tokyo) according to the manufacturer's instructions.

Result

There were no unusual DNA fragments detected except that which was detected on exons 3 and 21. Figure 1 shows the result of the PCR-SSCP analysis of exon 21. In all affected members of family 1. (indicated by an asterisk), an unusual slow-migrating DNA fragment was observed under the condition of 10% glycerol containing gel. This unusual slow-migrating DNA fragment was also found in the DNA from LV muscle of proband 1.1. In exon 3, under the condition without glycerol containing gel, an unusual slow-migrating DNA fragment was observed in proband S.S. of family S (number 1) and proband I.I. of family I.
Fig 2: PCR-SSCP analysis of the cardiac β MHC gene. PCR products of the exon 3 of the β MHC gene were analyzed as in Fig 1. Lane 1-7 show the each proband of FHCM. Asteric(*)lanes indicated additional migrating DNA fragment.

Fig 3: M-mode and two-dimensional echocardiograms in the parasternal long-axis view (top: sporadic HCM Pt; T.M., bottom: proband I.I.). LV cavity enlargement and the impairment of LV ejection was observed simultaneously with less thickness of IVS.

Fig 4: Histological specimen from sporadic HCM Pt; T. M. (left) and proband I.I.(right). The myocardial cell enlargement and disarray was shown accompanied by prominent fibrosis (H.E. ×40).
Discussion

FHCM is a primary disorder of cardiac muscle that has an autosomal dominant pattern of inheritance (1, 2). In some families, the cardiac β MHC gene might be a crucial loci of HCM. Cardiac β MHC gene that encode regions of the MHC polypeptide consists of forty exons (Fig. 5). The MHC polypeptide has two functional domains, a globular head region (exon 3-22) and an elongated rod region (exon 23-40). The head region is important for myocardial function. Since the mutations were reported in the head or head-rod junction, we selected the exons 3-25 of the cardiac β MHC genes in our study. In exon 21, all affected members of one family (proband I.1) showed an identical pattern of aberrantly migrating bands. In exon 3, we found polymorphism and probable point mutation in one patient with sporadic HCM (Pt; T.M). To confirm this mutation in cardiac tissue, PCR-SSCP was carried out using cardiac muscles obtained at autopsy. The same additional migration band was also found. Interestingly, both proband I.1 and Pt; T.M developed lethal congestive heart failure with LV dilatation as confirmed by autopsy. It is not clear whether these point mutations may lead HCM to diastolic-phase HCM (15-17). These observations suggest that the mutation or polymorphism in the β MHC gene exists and may cause HCM in some Japanese families. The mechanism by which mutations in the cardiac β MHC genes produce cardiac hypertrophy is still unknown. This study suggested that different mutations in the cardiac β MHC gene may cause similar clinical disease. The positive data was detected only in two lethal cases with diastolic-phase HCM, although the number of investigated families was small. To ascertain whether mutations in the same genetic locus are responsible for FHCM in other families, further investigations are required. Recently Perryman M.B et al. reported the missense mutation in exon 13 of the β MHC gene in the messenger RNA isolated from a right ventricular endomyocardial biopsy (18). We are now confirming the mutation of genomic DNA mentioned above using direct sequencing and assessing the transcription of a mutant β MHC gene allele into messenger RNA of the LV myocardium derived from autopsy. In conclusion, genetic analysis of the cardiac β MHC gene using PCR-SSCP might be useful for screening of hypertrophic cardiomyopathy.

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References


Fig 5: Exon map adapted from Jaenicke et al (1990). A representation of the cardiac β MHC gene.