ONLINE MUTATION REPORT

Clinical and genetic characteristics of α cardiac actin gene mutations in hypertrophic cardiomyopathy

J Mogensen, A Perrot, P S Andersen, O Havndrup, I C Klausen, M Christiansen, P Bross, H Egeblad, H Bundgaard, K J Osterziel, G Haltern, H Lapp, P Reinecke, N Gregersen, A D Børglum

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Hypertrophic cardiomyopathy (HCM) is a dominantly inherited disease defined by unexplained myocardial hypertrophy. The prevalence is about 0.2% in the general population. The condition is characterised by a heterogeneous disease expression, and common symptoms include angina, dyspnoea, palpitations, syncope, and exercise limitation. Hypertrophic cardiomyopathy is a frequent cause of sudden cardiac death in young people.[1] More than 200 mutations associated with the disease have been identified in sarcomeric contractile protein genes: *TNNT2* (troponin T), *MYL3* (essential myosin light chain), *MYBPC3* (myosin binding protein C), *MYL2* (regulatory myosin light chain), *MYH7* (β myosin heavy chain), *TPM1* (α tropomyosin), *ACTC* (α cardiac actin), and *TNNI3* (troponin I).[2–4]

In addition, mutations recently have been reported in two non-sarcomeric genes.[5–7]

Mutations in *ACTC* have also been reported to cause the inherited form of idiopathic dilated cardiomyopathy (DCM). It has been suggested previously that *ACTC* mutations that affect sarcomere contraction lead to HCM, whereas *ACTC* mutations that affect force transmission from the sarcomere to the surrounding syncytium lead to DCM.[3 8]

We report the clinical and genetic characteristics of *ACTC* mutations in 206 consecutive patients with HCM.

Key points

- The study aimed to investigate the prevalence and clinical characteristics of α cardiac actin mutations (*ACTC*) in 206 consecutive families with hypertrophic cardiomyopathy (HCM) Mutation analysis was performed by SSCP analysis and direct sequencing. In addition, the likely impact of *ACTC* mutations on sarcomeric function was investigated by analysis of the crystal structure of the actin protein
- The prevalence of *ACTC* mutations was 1.5%. Two novel mutations were identified. Available phenotypic information in carriers of *ACTC* mutations suggested a heterogeneous clinical appearance that ranged from unaffected cases to patients with severe disease presentation
- Examination of the crystal structure of actin showed that amino acids mutated in HCM were exposed to the surface domain of actin that interacts with myosin
- *ACTC* mutations are rare in HCM, and no specific genotype–phenotype correlation is apparent. The localisation of *ACTC* mutations in conserved and functional important regions of the gene substantiate the current hypothesis that *ACTC* mutations in HCM affect sarcomeric contraction, whereas *ACTC* mutations in dilated cardiomyopathy affect force transmission

MATERIALS AND METHODS

Informed consent was obtained from each participant in accordance with local institutional review committee guidelines.

We investigated 206 consecutive Caucasian probands with HCM from Germany (n = 146) or Denmark (n = 60) by mutation analysis of *ACTC*. We physically and genetically investigated relatives of probands who carried *ACTC* mutations. The diagnosis of HCM was based on the presence of unexplained myocardial hypertrophy.[3 9 10] In brief, a person was defined as having HCM if the maximal left ventricular wall thickness by echocardiography or cardiac magnetic resonance scan was ⩾13 mm or the electrocardiogram (ECG) showed major Q wave abnormalities, left ventricular hypertrophy, or marked repolarisation alterations. One patient (pedigree B, participant I-1) was diagnosed with HCM on the basis of results obtained by cardiac catheterisation and cardiac magnetic resonance scans. Participants were suspected of having HCM if their ECG showed incomplete bundle branch block and right axis deviation (pedigree A, participants III-2 and II-3). We classified the phenotype of all participants before DNA analysis.

We isolated genomic DNA from all participants, including controls, from peripheral blood samples, and we amplified *ACTC* by polymerase chain reaction (PCR) with intronic primers, as previously described.[3] We analysed PCR products by single strand conformation polymorphism (SSCP) and heteroduplex analysis of exons 2, 3, and 4 with a precast 12.5% polyacrylamide gel at 4°C and 20°C (Multiphor gel apparatus; Pharmacia Biotech, Uppsala, Sweden). We visualised bands with silver staining and analysed abnormal conformers by direct sequencing.[11] Because of difficulties in obtaining reproducible SSCP analysis of exons 1, 5, and 6, we subjected these exons to direct sequencing with standard protocols. We established the haplotypes of families A and B with analysis of a highly polymorphic short tandem repeat localised within *ACTC*.[3] We performed Msl I restriction enzyme cleavage of DNA from family A according to the manufacturer's manual (New England Biolabs, Beverly, MA, USA).

RESULTS

Genetic investigations

The proband of family A (individual II-1) had an 1153A→G nucleotide substitution in exon 3, which resulted in a Tyr166Cys amino acid exchange. Subsequent mutation analysis of this proband's relatives identified three additional carriers of the mutated allele (fig 1 and table 1).

The proband of family B (individual I-1) had a 283A→C nucleotide substitution in exon 5, which resulted in a Met305Leu amino acid substitution (fig 1 and table 1). The

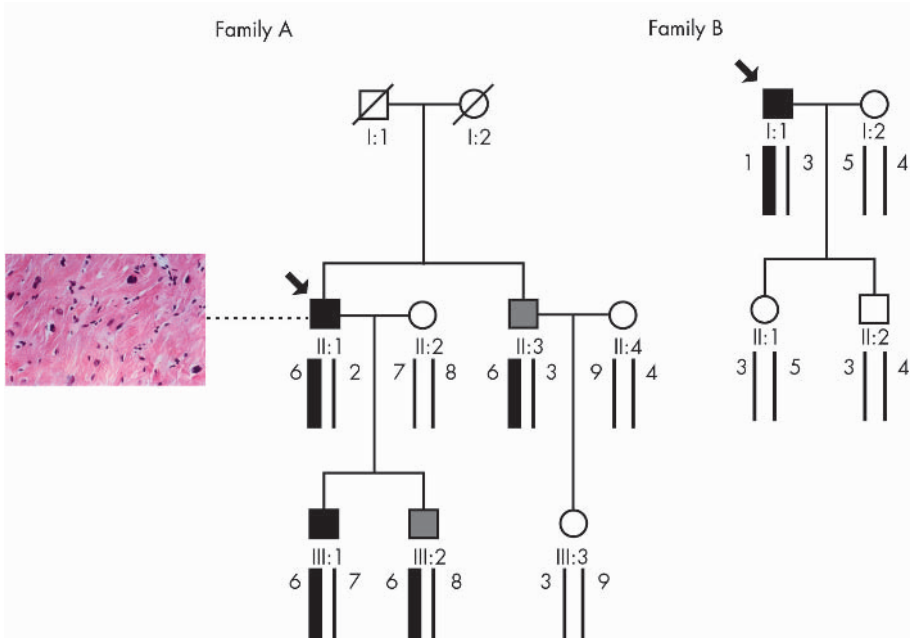

Figure 1 Pedigree drawing of families A and B, who carried *ACTC* Tyr166Cys and Met305Cys amino acid substitutions, respectively. The tissue section shown was part of the intraventricular septum removed by transaortical myectomy from individual II-1 of family A and stained with haematoxylin and eosin. The histology showed myocyte hypertrophy and disarray consistent with a diagnosis of HCM.[15] Alleles defined by the short tandem repeat polymorphism within *ACTC* shown in roman numbers. □ men without HCM; ■ men who fulfilled diagnostic criteria for HCM; ■ men suspected of having HCM; ○, healthy women; / deceased; ▌normal genotype of ACTC, ▌ACTC mutation that segregates with allele 6 in family A and allele 1 in family B.

presence of the mutation in proband B was confirmed by a Msl1 restriction enzyme assay, which cleaved the wildtype allele, as expected, and left the mutated allele intact. To diminish the possibility that the *ACTC* mutations identified (Tyr166Cys and Met305Leu) were common polymorphisms, 150 control chromosomes were investigated by SSCP analysis (exon 3) or direct sequencing (exon 5). No sequence variations were identified, which confirmed the result of previous SSCP analyses of controls of exon 3 (300 chromosomes) and exon 5 (870 chromosomes).[8] These observations are in accordance with the fact that cardiac actin is a highly conserved protein throughout evolution including the Tyr166 and Met305 amino acids that are conserved in the 37 vertebrate and invertebrate actins that are part of the protein alignment database.[12] Compared with the original sequence published more than a decade ago , five silent homozygous base changes were seen in all 206 individuals investigated (exon 2, 274T→G; intron 3, 1089G→C; exon 4, 1488T→C and 1532C→T; and exon 6, 284T→C), which is likely to reflect the contemporary, more accurate method of sequencing. Others have performed mutation analysis of *ACTC* in the context of DCM and identified a total of eight silent single nucleotide polymorphisms in populations of Asian and South African origin, respectively.[13 14]

Table 1 Clinical features of families A and B

Pedigree	Age (years)	Sex	Symptoms	Electrocardiogram findings	Echocardiogram findings	Phenotypic assignment	*ACTC* genotype
A							
II-1	51	Man	Angina Dyspnoea (New York Heart Association grade III)	Atrial fibrillation	HCM Septum 18 mm Systolic anterior movement of mitral valve Left ventricle outflow tract gradient at rest 35 mm Hg	HCM	Tyr166Cys
III-1	27	Man	No	Incomplete right bundle branch block	HCM Septum 15 mm	HCM	Tyr166Cys
III-2	24	Man	No	Incomplete right bundle branch block and right axis deviation	Normal	Suspected HCM	Tyr166Cys
II-3	47	Man	No	Incomplete right bundle branch block and right axis deviation	Normal	Suspected HCM	Tyr166Cys
B							
I-1	61	Man	Angina Dyspnoea (New York Heart Association grade II)	Atrial fibrillation	Not obtainable*	HCM	Met305Leu

* Cardiac catherisation showed apical systolic obstruction and normal left ventricular function and coronary arteries.

Clinical investigations

The proband of family A was diagnosed with HCM at the age of 51 years. He had severe symptoms of angina and dyspnoea (New York Heart Association (NYHA) class III) (fig 1, table 1). An echocardiogram showed septal hypertrophy of 18 mm, mild mitral regurgitation, systolic anterior movement of the mitral valve, and a left ventricle outflow tract gradient of 35 mm Hg at rest, which increased to 60 mm Hg after the Valsalva manoeuvre. Transaortal myectomy abolished the outflow tract obstruction and gave considerable symptomatic improvement. Part of the left ventricular septum was removed by transaortal myectomy and stained with haematoxylin and eosin. Histology of the removed myocardium showed myocyte hypertrophy and myofibrillar disarray consistent with a diagnosis of HCM[15] (fig 1). The proband's mother, individual I-2, had dyspnoea on exertion, which had started in her late twenties. She later developed atrial fibrillation and mitral regurgitation and died of congestive heart failure at the age of 50 years. The remaining relatives had no symptoms of disease, but the echocardiogram of participant III-1 showed septal hypertrophy of 15 mm. In addition, the electrocardiograms of participants III-2 and II-3 had minor abnormalities in terms of incomplete right bundle branch block and right axis deviation, while their echocardiograms were within the upper normal range of the maximal left ventricular wall thickness (both 12 mm).

The proband of family B was diagnosed at the age of 61 years. He had symptoms of angina on exertion and dyspnoea (NYHA II) (fig 1, table 1). Images of the heart by echocardiography were unobtainable, but cardiac catheterisation showed apical systolic obliteration of the left ventricle consistent with a diagnosis of apical HCM. This finding was confirmed by a cardiac magnetic resonance scan, which showed a maximal left ventricular wall thickness of 14 mm. He had no family history of cardiac disease, and subsequent physical examination and mutation analysis of his children did not identify additional disease carriers.

Analysis of actin crystal structure

Actins are major constituents of the thin filaments in the muscle sarcomere. They generate force within the sarcomere in companion with myosin and transmit force from the sarcomere to the surrounding syncytium by the thin filament. Previous studies of *ACTC* mutations in families with either HCM or the hereditary form of DCM has led to the hypothesis that *ACTC* mutations in force generating domains lead to HCM, while *ACTC* mutations in force transmitting domains lead to DCM.[3 8] This hypothesis has been further supported by analysis of a transgenetically modified mouse carrying *ACTC* mutations in both force transmitting and force generating domains, as the hearts of these mice had features of both HCM and DCM.[16]

Analysis of the ultrastructure of the actin molecule showed that the novel (Tyr166, Met305) and previously reported (Ala295) actin amino acids mutated in HCM were situated around the five stranded β sheet in the lower part of subdomain 3 of the actin molecule[16] (fig 2). The side chains of all three amino acids are exposed to the surface that interacts with myosin and situated in close proximity to residues directly involved in interaction with myosin.[17] The mutations lead to replacement of a polar side chain with a hydrophobic side chain or vice versa (Met305Leu and Ala295Ser) and the removal of an aromatic ring (Tyr166Cys) that may distort the adjacent surface area. This may well influence the surface that interacts with myosin and thereby impair force generation. In addition, Tyr166 is involved in the interactions between actin monomers, and Met305 forms part of the hydrophobic binding pocket for the adenosine moiety of the associated ATP and ADP.[18] Monomeric actin binds ATP and assembles into fibres after ATP–ADP hydrolysis. Disturbances of the nucleotide binding pocket or the actin–actin interchain interactions are likely to impair fibre assembly, which could result in disorganisation of the actin fibres and thus further decrease force generation within the sarcomere.

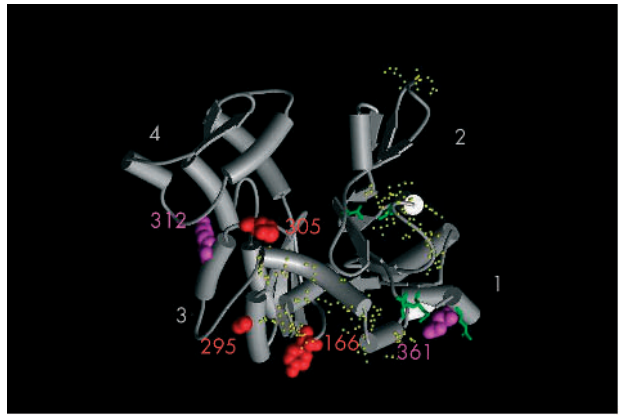

Figure 2 Schematic representation of actin monomer based on the crystal structure of the actin, prepared with WebLab ViewerLite (Molecular Simulations, San Diego, CA, USA)[18] Putative binding sites to myosin are shown in yellow.[19] The Tyr166 and Met305 amino acid mutated in families A and B, as well as the Ala295 previously reported to be mutated in HCM, shown in red. All HCM mutations are localised at the actin surface that interacts with myosin. Two amino acids previously reported to cause DCM (Arg312 and Glu361) are shown in purple.[8] Amino acid differences between α cardiac actin and γ enteric actin expressed in a transgenic *ACTC* knock out mouse highlighted in green.[16]

DISCUSSION

We identified two novel and one previously reported *ACTC* mutation in 3/206 (1.5%) Caucasian HCM patients of Northern European origin.[3] The rare finding of *ACTC* mutations was consistent with previous reports that identified three mutations in 368 patients with HCM and no mutations in 421 patients with HCM.[20–22]

Conventional page gel SSCP analysis was used for mutation analysis of three exons of *ACTC*. This method is presumed to be less sensitive than direct sequencing and more recent methods developed for mutation screening.[22] The frequency of *ACTC* mutations in our study, however, was similar to that in other studies, and it is unlikely therefore, that the SSCP method we used missed a significant number of mutations. Although the number of affected participants was limited in this study, the two amino acid substitutions identified (Tyr166Cys and Met305Leu) were believed to be disease causing mutations, because all clinically affected individuals were mutation carriers, no sequence variations were identified in ethnically matched control individuals, both mutations changed highly conserved amino acids, and both mutations were likely to change protein–protein interactions on the basis of analysis of the crystal structure of actin.

The phenotypes associated with the Tyr166Cys and Met305Leu amino acid substitutions seemed to be heterogeneous. Both probands of families A and B had reduced exercise capacity and symptoms of disease in contrast with the remaining asymptomatic mutation carriers of family A. In addition, the proband of family A had pronounced hypertrophy of the septum that needed myectomy compared with the mild or absent hypertrophy of the remaining participants who carried the mutated allele.

The clinical findings associated with *ACTC* mutations described in previous studies further strengthen the impression of variable disease expression (table 2). The first study to

Table 2 Clinical profile associated with previous reported *ACTC* mutations

		Patients				
Mutation	Carriers of mutations	Phenotype positive	Symptomatic	Abnormal electrocardiogram	Ventricular arrhythmia	Abnormal echocardiogram
Ala295Ser[3]	14	13	3	13	1*	9**
Pro164Ala[20]	1	1	1	1	1†	1††
Ala331Pro[20]	1	1	1	1	0	1††
Glu99Lys[20]	7	6	6	7	2‡	6‡‡

* Episodes of non-sustained ventricular tachycardia accompanied by syncope. † ventricular fibrillation and cardiac arrest. ‡ one with ventricular fibrillation and cardiac arrest and one with ventricular tachycardia. ** Seven with wall hypertrophy and two with end stage dilation. †† Septal and apical hypertrophy. ‡‡ Five with predominant apical hypertrophy and one with septal hypertrophy.

report on *ACTC* mutations identified an Ala295Ser amino acid substitution in a large Danish pedigree.[3] Only a few of the affected people had symptoms of disease, including two with end stage dilated HCM and one with tachycardia caused by a Wolff-Parkinson-White syndrome, which preceded a later development of ventricular hypertrophy. The remaining carriers of the mutation, except one, fulfilled the diagnostic criteria for HCM, but none had symptoms of disease. The Ala295Ser mutation seemed to be associated with a high penetrance, diverse phenotypes, a relatively low morbidity, and no sudden deaths. These findings were different from those reported recently by Olson *et al*.[19] They identified three novel *ACTC* mutations, of which two occurred *de novo* and one appeared in a family with seven disease carriers (table 2). Both *de novo* mutations were associated with early onset and severe disease expression, as is the case in patients who also have *de novo* mutations in other cardiac sarcomeric contractile protein genes.[23] Most of the family members who carried the Glu99Lys mutation were reported to have symptoms of disease. Two had experienced ventricular arrhythmia, of which one had been resuscitated from cardiac arrest (no age reported). The predominant finding on echocardiograms in this family was that most of the affected members had apical hypertrophy of the myocardium.

The heterogeneous disease expression associated with *ACTC* mutations in this study accords well with the results of recent studies that investigated the clinical expression of mutations in other genes associated with HCM.[23] Environmental factors and individual genetic backgrounds are likely to modify the phenotype of mutation carriers.[24]

Conclusion

Mutations of the *ACTC* gene in patients with HCM are rare, and no gene specific phenotype is apparent. Localisation of *ACTC* mutations in conserved and functionally important regions of the gene substantiate the hypothesis that *ACTC* mutations in patients with HCM affect sarcomere contraction, whereas *ACTC* mutations in patients with DCM affect force transmission from the sarcomere to the surrounding syncytium.

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Authors' affiliations

J Mogensen, I C Klausen, H Egeblad, Department of Cardiology, Skejby University Hospital, Brendstrupgaardsvej, DK-8200 Aarhus N, Denmark
J Mogensen, P Bross, N Gregersen, Research Unit for Molecular Medicine, Skejby University Hospital, Brendstrupgaardsvej, DK-8200 Aarhus N, Denmark
A Perrot, K J Osterziel, Charité/Franz-Volhard-Klinik, Max Delbrück Center for Molecular Medicine, 13125 Berlin, Germany
P S Andersen, M Christiansen, Department of Clinical Biochemistry, Statens Serum Institut Copenhagen, DK-2300 Copenhagen S, Denmark
O Havndrup, H Bundgaard, Department of Medicine B 2141, Heart Center, University of Copenhagen, DK-2100 Copenhagen Ø, Denmark
G Haltern, H Lapp, Heart Center Wuppertal, University Witten/Herdecke, 42283 Wuppertal, Germany
P Reinecke, Institute of Pathology, Heinrich Heine University, 40225 Düsseldorf, Germany
A D Børglum, Danish Center for Human Genome Research, Institute of Human Genetics, Bartholin Building, University of Aarhus, DK-8000 Aarhus C, Denmark

Conflicts of interest: None declared.

Correspondence to: Dr J Mogensen, Department of Cardiology, Skejby University Hospital, Brendstrupgaardsvej, DK-8200 Aarhus N, Denmark; jens.mogensen@dadlnet.dk

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