Mutations in the Human Muscle LIM Protein Gene in Families With Hypertrophic Cardiomyopathy

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Background—Muscle LIM protein (MLP) is an essential nuclear regulator of myogenic differentiation. Additionally, it may act as an integrator of protein assembly of the actin-based cytoskeleton. MLP-knockout mice develop a marked cardiac hypertrophy reaction and dilated cardiomyopathy (DCM). MLP is therefore a candidate gene for heritable forms of hypertrophic cardiomyopathy (HCM) and DCM in humans.

Methods and Results—We analyzed 1100 unrelated individuals (400 patients with DCM, 200 patients with HCM, and 500 controls) for mutations in the human CRP3 gene that encodes MLP. We found 3 different missense mutations in 3 unrelated patients with familial HCM but detected no mutation in the DCM group or the controls. All mutations predicted an amino acid exchange at highly conserved residues in the functionally important LIM1 domain, which is responsible for interaction with α-actinin and with certain muscle-specific transcription factors. Protein-binding studies indicate that mutations in the CRP3 gene lead to a decreased binding activity of MLP to α-actinin. All 3 index patients were characterized by typical asymmetrical septal hypertrophy. Family studies revealed cosegregation of clinically affected individuals with the respective mutations in MLP.

Conclusion—Here, we present evidence that mutations in the CRP3/MLP gene can cause HCM. (Circulation. 2003;107:1390-1395.)

Key Words: cardiomyopathy ■ genes ■ hypertrophy

Muscle LIM protein (MLP) is an LIM-only protein that shares structural and functional properties of the cysteine-rich protein (CRP) subfamily. These proteins are composed of 2 LIM domains, defined by a unique double zinc finger structure. It has been suggested that the LIM domain acts as a protein-binding interface. Expression of MLP is confined to skeletal and cardiac muscle. In the myocardium, MLP is expressed at high levels in developing and adult cardiomyocytes.1

MLP acts as an essential promoter of myogenesis, and it may be a cofactor in the regulation of muscle-specific gene expression in skeletal and heart muscle.1 By linking the β-spectrin network to myofibrillar actin filaments, MLP may also stabilize the association of the contractile apparatus with the sarcolemma.2

A murine MLP gene knockout was established to gain further insight into the function of MLP.3 MLP-deficient mice develop 2 different cardiac phenotypes. Thirty-five percent to 65% of the mice develop an early phenotype characterized by 2- to 4-fold increased heart weight and a hypertrophy reaction. They die of rapid progressive congestive heart failure in the second postnatal week. The remaining fraction of animals present with an adult phenotype reminiscent of patients with dilated cardiomyopathy (DCM).

Most cases of hypertrophic cardiomyopathy (HCM) and ≈25% of cases of DCM were estimated to have a genetic cause (see recent reviews4,5). Although several disease genes have been identified, a substantial proportion of familial cases cannot presently be linked to any of the known disease genes. Human CRP3, which encodes MLP, was considered a promising candidate. Therefore, we screened 600 individuals with either DCM or HCM for mutations in CRP3. We found 3 different missense mutations in HCM families that cause amino acid substitutions in a functionally important region of MLP. Furthermore, we investigated whether mutations in...
MLP might cause alterations in its binding characteristics. These protein-binding studies demonstrate that at least 1 of the mutations significantly decreases the capacity of MLP to bind α-actinin.

Methods

Clinical Evaluation
All patients and family members gave informed consent to participate in the study in accordance with the ethical guidelines of Charité University Hospital. Blood samples were drawn for genetic investigation, medical history was taken, and an examination was performed that included a 12-lead ECG and 2D and M-mode echocardiography. All DCM patients had left heart catheterization with selective coronary angiography to exclude coronary artery disease. The diagnosis of DCM was based on World Health Organization criteria. The diagnosis of HCM was based on criteria proposed by McKenna et al.6 Additionally, tissue Doppler imaging (TDI) with determination of septal early (Ea) and late (Aa) diastolic velocities was performed in individuals younger than 60 years old, as described previously.7 Pathological septal indices8 were taken as an additional echocardiographic major criterion for HCM if other causes of diastolic dysfunction (arterial hypertension, coronary artery disease/history of myocardial infarction) could be excluded. Pathological TDI required the presence of 3 indices: septal Ea ≤10 cm/s, an inverse relation of septal early (Ea) and late (Aa) diastolic velocities was performed in individuals younger than 60 years old, as described previously.7 The complete human MLP gene was amplification with mismatch oligonucleotides (sequences, mismatched nucleotides capitalized: 5'-tagtggcaatccgaaagctattg-3' and 5'-ccatagaccatctggtagatcataca-3'). The mutated cDNA was also cloned into the modified pACT2 vector. PCR mutagenesis and cloning were done by standard procedures.7 All constructs were verified by sequencing.

The α-actinin construct was pretransformed into the Saccharomyces cerevisiae L40 reporter strain18 by a modified lithium acetate protocol.19 Subsequently, the pretransformed cells were cotransformed with the wild-type or mutant MLP prey plasmid. Selection of transformant colonies was performed on agar plates that lacked leucine and tryptophan. The transformants that appeared after 4 to 5 days' incubation at 30°C were culated in selective medium. Cells were lysed, and β-galactosidase activity was quantified with o-nitrophenyl β-d-galactopyranoside (ONPG) according to the protocol in the “Yeast Protocols Handbook” (BD Biosciences Clontech). Activities were expressed as mean arbitrary units ±SD. The β-galactosidase activity of wild-type MLP was set to 100 arbitrary units. The significance of the difference between the observed activities of wild-type and mutant MLP was tested by the Student t test.

Results

Missense Mutations in the Human MLP Gene
Three different heterozygous missense mutations in CRP3, all located in exon 3, were detected in 3 unrelated patients with familial HCM (Figure 1B). Mutations that predicted a single amino acid exchange were detected in 2 patients: a CTT→CCT mutation in codon 44 that predicted a leucine-to-proline exchange (Leu44Pro) and a TGC→GGC mutation in codon 58 that predicted a cysteine-to-glycine exchange (Cys58Gly). The third mutation affected 3 nucleotides, TCCGAG→AGGGGG, in the 2 adjacent codons 54 and 55, predicting an exchange of serine to arginine and glutamic acid to glycine (Ser54Arg/Glu55Gly). The mutation Leu4Pro was confirmed by an additional NlaIV restriction site generated by the mutation. The mutation Ser54Arg/Glu55Gly was confirmed by additional HinII and BgII digests, and the Cys58Gly mutation was confirmed by an additional BceAI restriction site. None of the described mutations were present in 1000 control chromosomes.

In the largest of the HCM families examined in this study (family C), all known HCM disease genes could be excluded (data not shown). Genetic analysis did not reveal any mutations that predicted amino acid exchanges in the DCM patients.

All mutations were located in the LIM1 domain of MLP (Figures 2A through 2C). An alignment of the corresponding sequences revealed that all mutations affected highly conserved residues (Figure 2A). These residues were completely conserved throughout the entire family of CRPs (CRP1, CRP2, and CRP3). Additionally, the residues showed full conservation across species that included human, mouse, rat, amphibian, fish, and insects. Protein modeling suggested

The images of the models were generated with Molscript,13 Raster3D,14 and Swiss PDB Viewer.15

Yeast 2-Hybrid Assay
The complete human α-actinin-216 and MLP cDNA sequences were amplified by PCR with a human skeletal muscle library (BD Biosciences Clontech) as a template. The cDNAs were cloned into a modified pLexA vector or a modified pACT2 vector, respectively. The MLP Cys58Gly mutation was introduced into the full-length wild-type sequence by PCR amplification with mismatch oligonucleotides (sequences, mismatched nucleotides capitalized: 5'-tagtggcaatccgaaagctattg-3' and 5'-ccatagaccatctggtagatcataca-3'). The mutated cDNA was also cloned into the modified pACT2 vector. PCR mutagenesis and cloning were done by standard procedures.7 All constructs were verified by sequencing.

These protein-binding studies demonstrate that at least 1 of the mutations might cause alterations in its binding characteristics. The complete human MLP gene was amplification with mismatch oligonucleotides (sequences, mismatched nucleotides capitalized: 5'-tagtggcaatccgaaagctattg-3' and 5'-ccatagaccatctggtagatcataca-3'). The mutated cDNA was also cloned into the modified pACT2 vector. PCR mutagenesis and cloning were done by standard procedures.7 All constructs were verified by sequencing. The MLP Cys58Gly mutation was introduced into the full-length wild-type sequence by PCR amplification with mismatch oligonucleotides (sequences, mismatched nucleotides capitalized: 5'-tagtggcaatccgaaagctattg-3' and 5'-ccatagaccatctggtagatcataca-3'). The mutated cDNA was also cloned into the modified pACT2 vector. PCR mutagenesis and cloning were done by standard procedures.7 All constructs were verified by sequencing. The α-actinin construct was pretransformed into the Saccharomyces cerevisiae L40 reporter strain by a modified lithium acetate protocol. Subsequently, the pretransformed cells were cotransformed with the wild-type or mutant MLP prey plasmid. Selection of transformant colonies was performed on agar plates that lacked leucine and tryptophan. The transformants that appeared after 4 to 5 days' incubation at 30°C were culated in selective medium. Cells were lysed, and β-galactosidase activity was quantified with o-nitrophenyl β-d-galactopyranoside (ONPG) according to the protocol in the “Yeast Protocols Handbook” (BD Biosciences Clontech). Activities were expressed as mean arbitrary units ±SD. The β-galactosidase activity of wild-type MLP was set to 100 arbitrary units. The significance of the difference between the observed activities of wild-type and mutant MLP was tested by the Student t test.
changes in the surface charge generated by the mutations found in families A and B compared with wild-type MLP (Figures 3A and 3B) and an alteration in 1 of the zinc ion binding sites generated by the mutation found in family C (Figure 3C), respectively.

A yeast 2-hybrid assay was used to investigate the potential impact of the human MLP(Cys58Gly) mutant on the interaction with the myocardial isoform of human α-actinin (α-actinin-2). Yeast cells that coexpressed α-actinin-2 and the MLP(Cys58Gly) mutant showed significantly reduced β-galactosidase activity compared with cells that coexpressed α-actinin-2 and wild-type MLP (Figure 4). This indicates reduced binding affinity of mutated MLP to α-actinin. Additionally, yeast cells that expressed mutant MLP grew significantly slower on plates that selected for activation of the HIS3 reporter gene (data not shown). To confirm the results of yeast 2-hybrid assays, we also performed blot overlay assays and obtained corresponding results (data not shown).

Figure 1. A, Pedigrees of HCM families A, B, and C. Squares indicate males; circles, females. Open symbols indicate unaffected subjects; solid symbols, affected individuals; slanted bars, deceased individuals; question marks, individuals with unknown disease status; N, individuals not classifiable with respect to affected status; arrows, index patient of each family; SCD next to shaded symbols, sudden cardiac death; +, presence of MLP mutation; and −, absence of MLP mutation. B, Sequence electropherograms of MLP exon 3 representing mutations. Upper panel represents mutant sequence; lower panel, normal sequence. Mutated amino acids are shown above normal amino acid sequence.

Figure 2. A, Alignment of amino acids 37 to 61 of related CRPs. Protein accession numbers represent SWISS-PROT and SWISS-PROT TrEMBL accession numbers, respectively. B, Schematic representation of structure of LIM1 domain of MLP (residues 1 to 61). Boxed residues in A represent mutated residues found in MLP/CRP3 gene in families A, B, and C (see Figure 1). Letters on colored background represent position of mutated conserved residues. Letters in bold italics represent Zn(II) coordinating cysteine/histidine residues. C, 3D model of human MLP LIM1 domain with position of mutated residues colored as in A and B. Dark spheres indicate zinc ions; zinc-coordinating residues 37, 40, and 61 appear in dark gray.
Clinical Findings

In family A, a Leu44Pro mutation was detected in 3 individuals (II:2, II:3, and II:4; Figure 1A). Individual II:2 showed marked midventricular hypertrophy at the age of 28 years. On ECG, he had T-wave inversions in leads I and aVL and deep S V2/V3. Holter ECG revealed ventricular tachycardias of Lown class IVa. His 32-year-old brother (II:3) also showed midventricular hypertrophy. On ECG, he had minor repolarization changes in left ventricular leads. The oldest brother (II:4) had concentric hypertrophy and minor T-wave abnormalities. We found thus-far undetected and uncontrolled moderate arterial hypertension in him. Therefore, this individual’s clinical status was assigned “not classifiable.” All 3 brothers were asymptomatic (clinical data summarized in the Table). The father (I:1) had died at the age of 67 years of cancer. No information with respect to HCM was available on him. Cardiac hypertrophy was excluded in the mother. Individual III:1, the son of II:2, had normal results on cardiac examination.

In family B, 3 individuals were found to have the Ser54Arg/Glu55Gly mutations (II:2, II:3, and II:4). Individual II:2 reported exertional dyspnea and palpitations at the age of 44 years. He had marked concentric left ventricular hypertrophy with severely impaired diastolic compliance, first-degree AV block, and ST-segment depressions in left anterior ECG leads. Holter ECG revealed paroxysmal atrial fibrillation and ventricular tachycardias (Lown class IVb). Individual II:3 reported exertional dyspnea; echocardiography revealed pathological septal TDI indices in the absence of hypertrophy. Individual II:4 reported palpitations and angina. On ECG, she had left ventricular hypertrophy with repolarization changes and deep S V2/V3 (fulfilling 1 major plus 1 minor ECG criterion of HCM). On echocardiography, she showed regional hypertrophy in the proximal septum; normal indices were recorded on TDI. The father (I:1) had died of sudden death at the age of 77 years. He had reported palpitations and shortness of breath before his death. No echocardiographic data were available on him. Individuals I:2, II:1, and III:1 showed no pathological results on cardiac examination.

In family C, a Cys58Gly mutation was found in individual III:2, in his 2 cousins (III:6 and III:8), and in the son (IV:2) of individual III:6. HCM was diagnosed in III:2 at the age of 56 years. Transaortic subvalvular myectomy (Morrow procedure) was performed because of severe outflow tract obstruction 1 year later. ECG revealed left bundle-branch block and a Sokolow-Lyon Index of 4.8 mV. Individuals III:3, III:4, III:5, and II:1 (all more than 60 years old) were clinically unaffected, but arterial hypertension was diagnosed in III:3. A cousin (III:6) of the index patient also had HCM with marked asymmetrical septal hypertrophy and moderate outflow tract obstruction. ECG showed repolarization changes in left ventricular leads. His 42-year-old son (IV:2) reported no symptoms. On echocardiography, he showed pathological septal TDI indices in the presence of borderline septal wall thickness. Arterial hypertension was excluded. Individual III:8 reported paroxysmal palpitations. Echocardiography revealed concentric septal hypertrophy in the presence of...
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velocities; Ea and Aa, early diastolic (Ea) and late diastolic (Aa) tissue Doppler velocities; Ht, hypertension; and Hptr., marked hypertrophy.

diameter; IVS, maximal interventricular wall thickness; PWT, maximal posterior wall thickness; Peak E and Peak A Velocity, peak early (E) and late (A) transmitral filling velocities; Ea and Aa, early diastolic (Ea) and late diastolic (Aa) tissue Doppler velocities; Ht, hypertension; and Hptr., marked hypertrophy.

Discussion

We identified 3 different missense mutations in human CRP3 coding for MLP in 3 families with HCM. The mutations are located in the functionally important LIM1 domain, which affects highly conserved residues. Genetically affected individuals showed mild symptoms and a great variation in the extent of hypertrophy.

For better characterization of individuals without hypertrophy, we performed TDI. This method is able to detect early pathological changes in the heart.8 Because the probands in the study of Nagueh et al were all less than 60 years old,8 and myocardial velocities decrease with age,9 we applied this method only to those individuals less than 60 years old. All 3 indices required to fulfill the criterion of “pathological TDI values” have been established as sensitive and specific markers of mutation-positive subjects without left ventricular hypertrophy.8

The mutation-carrying individuals II:3 in family B and IV:2 in family C showed pathological TDI indices in the basal septal wall without apparent septal hypertrophy. None of the individuals without mutation presented pathological TDI indices. Individual II:4 in family B had normal TDI but ECG changes that fulfilled 1 major plus 1 minor ECG criterion for HCM.6 Therefore, she was classified as affected.

We consider these sequence alterations as disease-causing mutations rather than rare polymorphisms for 7 different reasons:

1. All clinically affected relatives of the 3 families had the respective mutation, whereas relatives with normal cardiac findings did not. This shows cosegregation of the mutations with the disease. Additionally, all known HCM disease genes were excluded in the largest HCM family.

2. The presence of 3 different mutations in 3 unrelated HCM families within the same exon of CRP3 makes the possible explanation of rare polymorphisms highly unlikely.

3. Neither of the MLP mutations was present in 500 controls or 400 patients with DCM. χ² Analysis showed a significant difference of the frequency of MLP mutations in HCM patients compared with controls (P=0.0061). This argues for disease-causing mutations.

4. Further evidence for the significance of the MLP mutations comes from an alignment with the altered sequences. All the mutations predicted amino acid exchanges of highly conserved residues. We found that the altered residues were conserved throughout the family of CRPs both in humans and across species, including avian and invertebrate species.

5. Modeling suggested that the mutations detected in families A and B alter the electrostatic surface of the protein. The mutation Leu44Pro should not cause a

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NYHA class indicates New York Heart Association functional classification; Path. ECG, pathological ECG; LVEDD/LVESD, left ventricular end-diastolic/end-systolic diameter; IVS, maximal interventricular wall thickness; PWT, maximal posterior wall thickness; Peak E and Peak A Velocity, peak early (E) and late (A) transmitral filling velocities; Ea and Aa, early diastolic (Ea) and late diastolic (Aa) tissue Doppler velocities; Ht, hypertension; and Hptr., marked hypertrophy.

borderline arterial hypertension. ECG recordings were normal. Two uncles, homozygotic twins (II:5 and II:6), and 1 cousin (III:9) of the index patient had died of sudden cardiac death in early childhood. The 44-year-old daughter (IV:1) of the index patient had normal results on cardiac examination.
A gross change in net charge, but proline is likely to both alter and fix the carbon backbone of the molecule in a region where flexibility may be important to function.\textsuperscript{12} The Cys58Gly mutation is likely to change the shape of the zinc pocket; the black sphere representing the Zn\textsuperscript{2+} ion is clearly more exposed in the image of the mutant molecular surface than in the wild type (Figure 3C). Therefore, all mutations appear likely to affect structural and/or functional properties of the LIM1 domain.

6. MLP-knockout mice exhibit a cardiomyopathy phenotype that resembles the phenotype of cardiomyopathies in humans. Other characteristics of these mice are typical features of HCM; ultrastructural analysis of MLP-deficient hearts showed a dramatic disruption of cardiac myofibrillar organization, including myofibrillar disarray.

7. All mutations were localized in the functionally important amino-terminal LIM domain (LIM1) of MLP. The LIM1 domain of MLP is responsible for binding to \(\alpha\)-actinin, an actin-binding protein associated with the Z-lines of the myofibrils.\textsuperscript{2} We hypothesized that the mutations influence the interaction of MLP with \(\alpha\)-actinin, and we searched for confirming evidence. Our finding that the binding affinity of the MLP(Cys58Gly) mutant to \(\alpha\)-actinin was significantly impaired in yeast 2-hybrid assays supports this idea. Considering the observations that MLP binds the Z-line protein \(\alpha\)-actinin and \(\beta\)-spectrin at the sarcomlemma, we hypothesize that the impaired interaction of mutant MLP with \(\alpha\)-actinin results in the disturbed myocyte cytoarchitecture observed in HCM patients.

In the present study, we present several lines of evidence suggesting that human \textit{CRP3} is a novel HCM-causing gene. Additional evidence should be provided by linkage analysis in larger families. Beyond that, work needs to be done to investigate the mechanisms by which MLP mutations may influence myocardial cytoarchitecture and hypertrophy.

\textbf{Conclusions}

This is the first report describing \textit{CRP3} mutations in humans. Our data provide strong evidence that human \textit{CRP3} coding for MLP is a novel disease gene that causes HCM.

\textbf{Acknowledgments}

This study was supported in part by Charité research grants, a Max-Delbrück-Centrum Research Fellowship (C. Geier), and the Deutsche Forschungsgemeinschaft (Dr Fürst). We thank the participating families. We are indebted to Dr. A. Hansen, Dr. S. Jander, and Dr. W. Zeh for support in examining family members and to U. Weihrauch and P. Schirmacher for technical assistance. We thank Dr. G. Nürnberg for linkage calculations.

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_Circulation_. 2003;107:1390-1395; originally published online March 3, 2003;
doi: 10.1161/01.CIR.0000056522.82563.5F

_Circulation_ is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
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Print ISSN: 0009-7322. Online ISSN: 1524-4539

The online version of this article, along with updated information and services, is located on the World Wide Web at:

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