

ONLINE MUTATION REPORT

FKRP (826C>A) frequently causes limb-girdle muscular dystrophy in German patients

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Limb-girdle muscular dystrophies (LGMD) and congenital muscular dystrophies (MDC) represent two heterogeneous groups of genetic diseases differing in clinical severity and age of onset.¹⁻⁶ Mutations in the *LAMA2* gene can result in either MDC or, more rarely, LGMD.⁷ Laminin $\alpha 2$ forms a link between α -dystroglycan and the basal lamina. α -Dystroglycan is a heavily glycosylated peripheral membrane component of the dystrophin-associated-glycoprotein complex (DAG), whilst β -dystroglycan, derived from the same gene, is a transmembrane protein that links to dystrophin intracellularly. Dystroglycan therefore plays a pivotal role in linking the actin-associated cytoskeleton to components of the extracellular matrix, and disruption of this axis is associated with several forms of muscular dystrophy.⁸ Recently, abnormalities of α -dystroglycan glycosylation have been reported for several forms of MDC and for LGMD2I. A novel gene encoding a putative glycosyltransferase, fukutin-related protein (FKRP), was found to be responsible for both a novel form of MDC (MDC1C) and for LGMD2I.¹⁻⁵ Interestingly, the single homozygous point mutation (826C>A) leading to an amino acid exchange (Leu276Ile) is associated with a relatively benign clinical phenotype,⁹⁻¹⁰ whereas patients compound heterozygous for the 826C>A mutation may show a more severe clinical phenotype. We investigated the frequency of the *FKRP* mutation (826C>A) in 124 LGMD patients and correlated these findings with the clinical phenotype.

METHODS**Patients**

All patients described in this study were examined by one of the coauthors. Most patients described are of German descent and reside in Germany. One patient is Croatian (patient 2 in the table), and one patient (patient 19 in the table) is of German descent, but lives in Hungary.

Consanguinity was not reported. Pedigrees were compatible with autosomal recessive traits. Electromyography of affected muscles in all patients was compatible with chronic myopathy. The clinical findings of all patients are summarised in the table. Diagnostic muscle biopsies were performed in 19 out of 20 patients and showed various degrees of chronic necrotic myopathy without inflammatory or specific structural changes on standard histological examinations. In all samples, the number of necrotic fibers was below 10% of the total. Muscle tissue was available for immunohistochemistry and immunoblotting in all but three patients. Venous blood samples were used for DNA extraction and *FKRP* mutation analysis. Morphological and genetic data are shown in the table, and clinical phenotypes are presented in figure 1. In all patients available for testing brain MRI, pulmonary function and cardiac ultrasound were performed.

Key points

- A novel gene (*FKRP*) was found to be responsible for both a form of congenital muscular dystrophy (MDC1C) and a form of limb-girdle muscular dystrophy (LGMD2I). Our work aimed at investigating the frequency of *FKRP* (826C>A) in a large cohort of limb-girdle muscular dystrophy (LGMD) patients and correlating these findings with the clinical phenotype.
- We present clinical and genetic data of 20 LGMD2I patients from 19 unrelated families. Neurological examinations consisting of diagnostic muscle biopsies including immunohistochemistry and sequence analysis of *FKRP* were performed in this cohort.
- Interestingly, one single point mutation (826C>A) leading to an amino acid exchange (Leu276Ile) was associated with a relatively benign clinical phenotype. We identified the previously described *FKRP* mutation (826C>A) in 20 patients. Thirteen patients were homozygous for the mutation and seven were compound heterozygous. In all patients heterozygous for the 826C>A mutation, a second heteroallelic mutation was detected; two mutations have been described before, four mutations are novel. Interestingly, muscle pain and myoglobinuria were the earliest presenting symptoms in most patients.
- In summary, LGMD2I is frequently caused by a single missense mutation of the *FKRP* gene, namely 826C>A (Leu276Ile). This knowledge may simplify the diagnostic workup for LGMD patients of European origin.

Immunohistochemistry

Serial 10 μ m cross-sections were obtained in a cryostat, placed on gelatinised slides and fixed with acetone for 1 min. Commercially available monoclonal antibodies to α -dystroglycan (Clone VIA4-1, Upstate Biotechnology, Lake Placid, NY, USA) and merosin (MAB 1922, Chemicon, Temecula, Canada) were used at conditions recommended by the suppliers. This was followed by incubation with secondary biotin-conjugated anti-mouse IgG (Amersham, Pharmacia Biotech, Uppsala, Sweden) and streptavidin-coupled Cy3 (Dianova, Hamburg, Germany).

Abbreviations: DAG, dystrophin-associated-glycoprotein complex; *FKRP*, fukutin-related protein; LGMD, limb-girdle muscular dystrophy; MDC, congenital muscular dystrophy

Clinical and genetic findings of 20 LGMD2I patients from 19 independent families

No	Sex	Age at onset	Disease duration	Age at exam	Initial symptoms	Distribution of weakness (MRC)	Average CK levels (normal value <80 U/l)	Biopsy muscle	Protein analysis IHC		Mode of inheritance	FKRP analysis
									Mer	α DG		
1*	F	5	35	40	Myalgia, exercise-induced muscle cramps, calf hypertrophy, proximal leg weakness	4/5 proximal arm muscles, 3/5 proximal leg muscles, 4-5/5 foot extensors	350	Biceps brachii	n.d.	n.d.	Homozygous	826C>A
2	M	8	4	12	Muscle cramps, fatigability during exercise	4/5 proximal arm weakness, 3/5 proximal leg muscles, scoliosis	4800	Rectus femoris	n.d.	n.d.	Homozygous	826C>A
3*	M	10	25	35	Myalgia, exercise-induced muscle cramps, calf hypertrophy	3-4/5 proximal arm muscles, 3-4/5 proximal leg muscles	750	Biceps brachii	+	-	Homozygous	826C>A
4	M	14	21	35	Stress induced rhabdomyolysis, mild proximal leg weakness	4/5 proximal arm muscles, 4/5 proximal leg muscles	900	Vastus lateralis	+	n.d.	Homozygous	826C>A
5	F	14	17	31	Calf hypertrophy, proximal leg weakness	4/5 proximal leg muscles, 4/5 foot extensors	2500	Tibialis anterior	-	-	Homozygous	826C>A
6	F	15	31	46	Myalgia, muscle cramps, calf hypertrophy	4/5 proximal leg muscles (knee flexors), foot extensor 4-5/5	1000	Biceps brachii	+	-	Homozygous	826C>A
7	F	15	15	30	Proximal leg weakness	4/5 proximal arm muscles, 3/5 proximal leg muscles, 4/5 foot extensors	1000	Biceps brachii	-	(-)	Homozygous	826C>A
8	M	16	11	27	Stress induced myalgia, calf hypertrophy	4/5 proximal arm muscles, 3-4/5 proximal leg muscles, 4/5 foot extensors	1000	Vastus lateralis	-	-	Homozygous	826C>A
9	M	17	21	38	Exercise-induced rhabdomyolysis, proximal leg weakness	4/5 proximal arm muscles, 3/5 proximal leg muscles, 3/5 foot extensors	1000	Vastus lateralis	-	-	Homozygous	826C>A
10	M	17	19	36	Exercise-induced rhabdomyolysis, proximal leg weakness	4/5 proximal arm muscles, 3-4/5 proximal leg muscles	2000	Tibialis anterior	-	-	Homozygous	826C>A
11	M	17	11	28	Stress induced myalgia and rhabdomyolysis, no paresis	No paresis	4600	Deltoides	(-)	-	Homozygous	826C>A
12	F	20	26	46	Myalgia, proximal leg weakness	4/5 proximal arm muscles, 3/5 proximal leg muscles, 1/5 foot extensors, 3/5 foot flexors	500	Tibialis anterior	+	n.d.	Homozygous	826C>A
13	F	25	23	48	Muscle cramps, proximal leg weakness	3-4/5 proximal leg muscles, 4-5 foot extensor	200	Vastus lateralis	+	-	Homozygous	826C>A
14	M	3	10	13	Malignant hyperthermia-like reaction, proximal leg weakness	4/5 proximal leg muscles	5600	Tibialis anterior	-	-	Compound heterozygous	826C>A, 362T>A
15	F	9	20	29	Myalgia, calf hypertrophy, proximal leg weakness	4/5 proximal arm muscles, 2-3/5 proximal leg muscles, 1/5 foot extensors, 3/5 foot flexors	760	Tibialis anterior	(-)	-	Compound heterozygous	826C>A, 1054C>G
16	F	12	20	32	Myalgia, proximal leg weakness	3-4/5 proximal arm muscles, 2-3/5 proximal leg muscles, 4/5 foot extensors	1000	Biceps brachii	+	-	Compound heterozygous	826C>A, 919T>A
17	F	12	19	31	Stress induced myalgia and rhabdomyolysis, walks on tiptoes, proximal leg weakness	4/5 proximal arm muscles, 3/5 proximal leg muscles, 4/5 foot extensors	2000	Biceps brachii	+	-	Compound heterozygous	826C>A, 1486T>A, (341C/G)
18	M	15	25	40	Proximal leg weakness, calf hypertrophy	3-4/5 proximal leg muscles, 4/5 foot extensors	1200	Vastus lateralis	+	-	Compound heterozygous	826C>A, 1486T>A, (341C/G)
19	F	20	22	42	Calf hypertrophy, could never run fast	4-5/5 proximal arm muscles, 3-4/5 proximal leg muscles	4000	n.d.	n.d.	n.d.	Compound heterozygous	826C>A, 1475delC
20	F	32	13	45	Proximal leg weakness	3/5 proximal arm muscles, 2-3/5 proximal leg muscles, 1/5 foot extensors, 3/5 foot flexors	1300	Tibialis anterior	+	n.d.	Compound heterozygous	826C>A, 899T>C

*Patients 1 and patient 3 are sibs.

 α DG, α -dystroglycan; CK, creatine kinase; IHC, immunohistochemistry; Mer, merosin; MRC, Medical Research Council; +, normal; (-), mildly reduced; -, reduced; --, severely reduced or missing; n.d., not done.

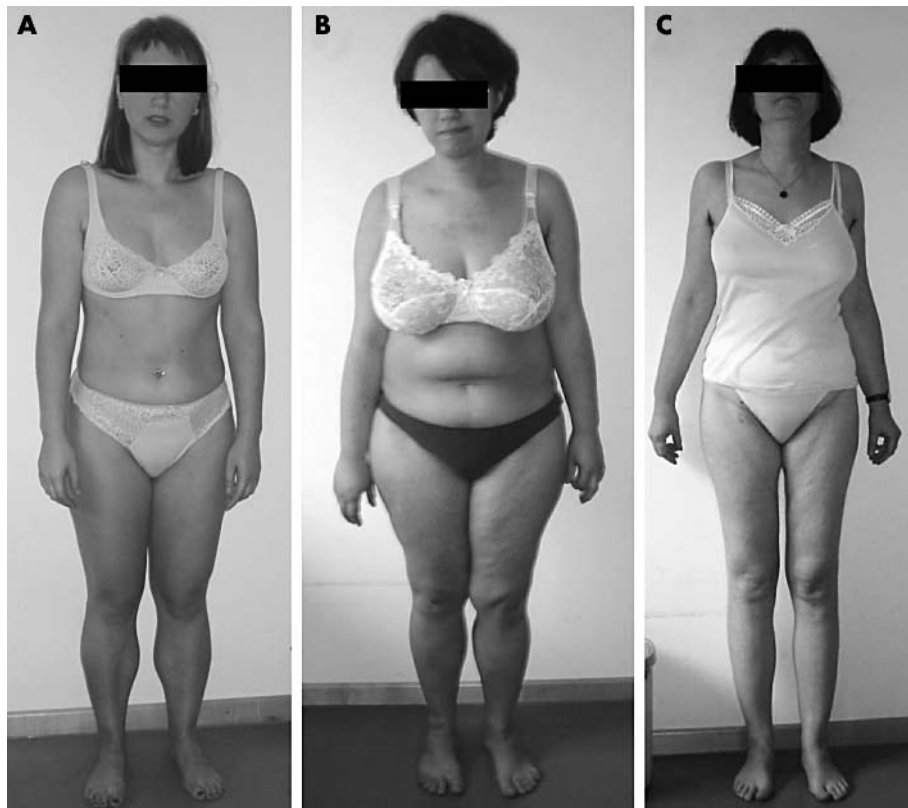


Figure 1 Clinical phenotype of independent LGMD2I patients according to the table (A is patient 5, B is patient 17, C is patient 12). Patients are homozygous (A, C) or compound heterozygous (B) for the *FKRP* Leu276Ile mutation. Calf hypertrophy is seen in some (A, B) but not all patients (C).

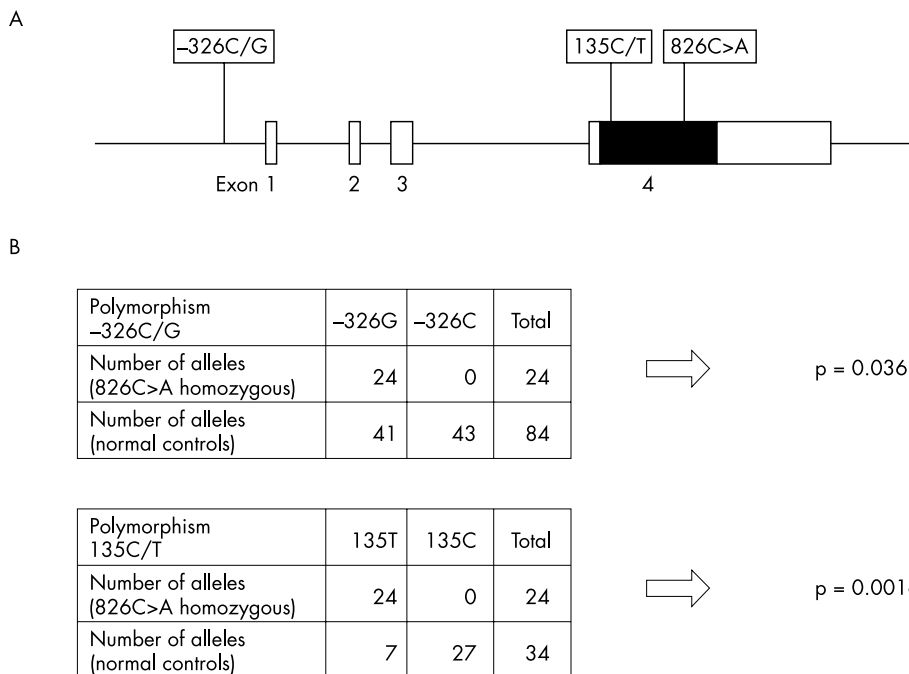


Figure 2 Analysis of two polymorphisms at the *FKRP* gene locus reveals a common core founder haplotype of the 826C>A allele. (A) Exons 1–4 are indicated by boxes and the coding region is represented by a filled black box. The newly identified polymorphism -326C/G is located upstream of the transcriptional start site in the promoter region. The intragenic polymorphism 135C/T has been described previously.² (B) Fisher’s exact two-tailed test reveals a common haplotype carrying -326G, 135T, and 826A.

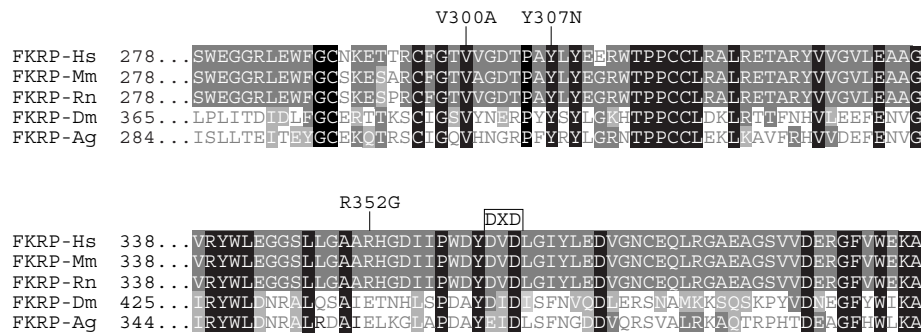


Figure 3 Multiple sequence alignment of FKRP homologues. Partial amino acid sequence alignment of FKRP homologues of *Homo sapiens* (FKRP_Hs: NP_077277), *Mus musculus* (FKRP-Mm: NP_775606), *Rattus norvegicus* (FKRP_Rn: XP_218425), *Drosophila melanogaster* (FKRP_Dm: NP_611531), and *Anopheles gambiae* (FKRP_Ag: XP_314789). The conserved DXD motif between glycosyltransferases is boxed. Identical amino acid residues are colored white on black background; conserved residues in $\geq 60\%$ are shown in white on dark grey, residues similar in $\leq 40\%$ are in white on light grey. Residues not conserved are shown in dark grey on white. Positions of FKRP mutations V300A, Y307N, and R352G are indicated above the sequence alignment.

Mutation analysis of the FKRP gene

Venous blood samples were obtained from the patients as well as from their affected and unaffected family members, if available. Genomic DNA was isolated using a blood and tissue culture DNA extraction kit according to the manufacturer's recommendations (Qiagen, Hilden, Germany). A total of 124 patients (81 patients from the University of Munich, 33 patients from the University of Bonn, and 10 patients from other centers) with so far unclassified LGMD were screened for the FKRP (826C>A) mutation. Muscle biopsies were taken in all but seven patients, and screened for deficiencies in dystrophin, sarcoglycans, dysferlin, caveolin-3, and calpain-3 by standard immunohistochemical and immunoblotting methods. No abnormalities were found except for a mild or moderate reduction of calpain-3 on immunoblots of 29 patients. However, mutations in CAPN3 were excluded in these patients by direct sequencing of all exons, and calpain-3 deficiency was therefore considered to be secondary.

A PCR fragment encompassing the common 826C>A mutation was amplified using primers 3F[5'-ACCAGCCTCTTCTGCAGACC-3'] and 4R[5'-CCTTCTCCCATACGAAGC-3']. Standard PCR conditions were applied as follows: initial melting at 95°C for 5 min; followed by 32 cycles at 52°C for 90 s, 72°C for 3 min, and 94°C for 1 min; and a final extension at 72°C for 7 min. The resulting 532 bp fragment was purified using the NucleoSpin Extract kit (Macherey-Nagel, Düren, Germany), digested with the restriction endonuclease BfaI (New England Biolabs, Frankfurt, Germany), and the resulting fragments separated on 2% agarose gels by electrophoresis. The mutant fragment (826C>A) remains uncut, whereas wild-type DNA is digested into two fragments of 168 and 364 bp length. To confirm the presence of homozygous as well as heterozygous FKRP (826C>A), the same PCR product was sequenced using an Applied Biosystems model 3100 Avant DNA sequencer and fluorescein-labeled dideoxy terminators (Perkin-Elmer, Foster City, CA, USA). Moreover, the frequency of FKRP (826C>A) was tested in 300 healthy controls (600 control chromosomes).

For homozygous as well as heterozygous carriers of FKRP (826C>A), the entire coding region (exon 4 with adjacent sequences of intron 3 and adjacent sequences of 3'-untranslated region) and the promoter region were sequenced using the following primers:

- PRO-1S 5'-TTACACAGCCCTCCTCCG-3'
- PRO-1R 5'-GCCGCCATCTTGAGCAAT-3'
- FKRP-1F 5'-AAAGGGAATTGAGAAAGAGC-3'

- FKRP-1R 5'-GCAGGAAGGAGTCTACCAG-3'
- FKRP-2F 5'-TCGAGGCATTTGACAACGCGG-3'
- FKRP-2R 5'-CCGAGAGGTTGAAGAGGT-3'
- FKRP 3F 5'-ACCAGCCTCTTCTGCAGACC-3'
- FKRP-3R 5'-GTTGCAGCCGAACCACTCCA-3'
- FKRP-4F 5'-ATCTACTTGGAGGACGTGGGCAA-3'
- FKRP-4R 5'-CCTTCTCCCATACGAAGC-3'
- FKRP-5R 5'-GCTCACACAGAGCTTCTCC-3'

Once a novel missense mutation was detected in a patient, the patient's relatives and 50 healthy normal controls were screened by restriction digest and direct sequencing of PCR products. Mutations tested were Val121Glu (362T>A), Val300Ala (899T>C), and Arg352Gly (1054C>G). A PCR fragment encompassing 362T>A was amplified using primers 2F and 2R. The resulting 468 bp fragment was purified and then digested with the restriction endonuclease BalI (Promega, Mannheim, Germany). The mutant fragment (362T>A) remains uncut, whereas wild-type DNA is digested into two fragments of 198 and 270 bp length. A PCR fragment encompassing 899T>C was amplified using primers 3F and 4R. The resulting 532 bp fragment was purified and then digested with the restriction endonuclease SacII (MBI Fermentas, St. Leon-Rot, Germany). Mutant DNA (899T>C) is digested into three fragments of 68, 174, and 290 bp length whereas wild-type DNA is digested into two fragments of 68 and 464 bp length. A PCR fragment encompassing 1054C>G was amplified using primers 3F and 4R. The resulting 532 bp fragment was reamplified using primer 352s (TACCTCTACGAGGAGCGCTGGACGC) and mismatch primer 352as (TCCCATGGGATGATGTCCCCGCGGC; mismatch indicated by bold letter). The resulting 161 bp fragment was purified and digested with the restriction endonuclease Eco52I (MBI Fermentas, St. Leon-Rot, Germany). Mutant DNA (1054C>G) is digested into two fragments of 135 and 26 bp length whereas wild-type DNA remains uncut.

Furthermore, we determined the frequency of two intra-genic polymorphisms, -326C/G (promoter) and 135C/T (exon 4¹) in mutant (826C>A) and normal alleles by direct sequencing (fig 2). Alleles of patient 3, the brother of patient 1, were not used for the calculation. For statistical analysis Fisher's two-tailed exact test was employed to ascertain whether individual polymorphisms were linked to 826C>A.

Sequence comparison

To compare the amino acid sequences of human FKRP with FKRP homologues from other species, sequences were

accessed through public domains (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi>) and aligned with FASTA software. The accession numbers are: *Homo sapiens* (NP_077277), *Mus musculus* (NP_775606), *Rattus norvegicus* (XP_218425), *Drosophila melanogaster* (NP_611531), and *Anopheles gambiae* (XP_314789).

RESULTS

Clinical data

We identified *FKRP* (826C>A) either homozygously or compound heterozygously in 20 patients from 19 unrelated families. A summary of the clinical, morphological, and genetic findings for all patients is shown in the table and in figure 1.

Onset of symptoms occurred from 3 to 32 years of age, with a mean age of 15 ± 7 years. Mean disease duration was 19 ± 7 years and mean age at examination was 34 ± 10 years. In 15 out of 20 (75%) patients, myalgia and rhabdomyolysis were the first signs of the disease. Patients frequently complained about muscle cramps, predominantly in calf muscles, and exercise-induced muscle pain. In one patient (patient 14), a malignant hyperthermia-like reaction along with myoglobinuria (CK levels up to 23 000 U/l, normal value <80 U/l) during adenotomy (general anaesthesia, application of succinylcholine) represented the first sign of muscle disease at the age of 3 years. This reaction was not investigated further, and there is no report of malignant hyperthermia in the relatives of patient 14. The phenotype is variable: some patients (patients 4, 5, 6, and 11) do not suffer from severe paresis even decades after the onset of symptoms, while others are more severely affected. All patients are still able to walk without support. However, some patients (patients 7, 9, 12, 15, 16, 17, and 20) show difficulties in walking and climbing stairs because of marked proximal leg weakness. Distribution of weakness was mainly proximal, affecting the hip girdle more than the shoulder girdle. In most patients, foot extensors became affected with ongoing disease. Calf hypertrophy was noted in eight out of 20 patients. Lumbar lordosis, scoliosis, and scapular winging were not commonly found, and none of the patients showed facial weakness, tongue hypertrophy, or contractures.

CK levels were examined on several occasions and were found to be elevated 4- to 60-fold in our patients (CK mean 1800 ± 1600 U/l). The highest CK levels were found during episodes of myoglobinuria, but levels never returned back to normal values. Most of the patients with a disease duration of more than 20 years showed less dramatic CK elevations as compared to patients with a shorter disease duration. Brain MRI scans were performed in 12 out of 20 patients and showed no abnormalities. Pulmonary function and cardiac ultrasound were carried out in all patients. Two patients (patients 3 and 9) showed mildly to moderately impaired cardiac function (ejection fraction: patient 3: 55%, patient 9: 38%), while in one patient vital capacity was mildly reduced to 80% (patient 1).

Immunohistochemistry

The histological changes were characteristic of a muscular dystrophy in all patients. Immunohistochemistry revealed a variable reduction of α -dystroglycan in most patients (table). However, the degree of α -dystroglycan reduction did not clearly correlate with the severity of clinical symptoms nor with the age of onset. Immunohistochemistry for merosin showed a reduction in seven out of 15 examined patients.

Genetic analysis

In a cohort of 124 LGMD patients (81 patients from Munich neurological department, 33 patients from Bonn neurological department, and 10 from other departments) the previously

described *FKRP* mutation 826C>A (Leu276Ile) was identified in 20 patients, of which 13 were homozygous for the mutation and seven were compound heterozygotes (table). None of the homozygous individuals was the offspring of consanguineous marriages. In all patients heterozygous for the 826C>A mutation we were able to detect a second heteroallelic mutation by sequence analysis (table). Two of these mutations were previously described (919T>A resulting in Tyr307Asn¹⁰; 1486T>A resulting in Stop496Arg¹¹). Interestingly, in two of our patients the latter mutation was associated with Ala114Gly (341C/G) which was also seen in patients from Tunisia.¹¹ Four mutations are novel: 1475delC is predicted to result in a frameshift close to the termination codon which may cause an elongation of the amino acid chain. None of the three novel missense mutations Val121Glu (362T>A), Val300Ala (899T>C), and Arg352Gly (1054C>G) were found in 100 normal alleles each. Val300 and Tyr307 are highly conserved across species, while Val121 and Arg352 are only conserved among mammals, but not in insects (fig 3).

To evaluate the hypothesis that the *FKRP* mutation 826C>A is due to a founder effect, a previously described polymorphism in exon 4 (135C/T)¹ and a polymorphism in the promotor region (-326C/G) were analysed. Both polymorphisms were identified homozygously in all patients homozygously harboring the *FKRP* (826C>A) mutation. A Fisher's exact test indicated strong linkage disequilibrium for both polymorphisms when *FKRP* (826C>A) alleles were compared to controls (fig 2). Moreover, *FKRP* (826C>A) was identified heterozygously in one out of 300 healthy controls (600 control chromosomes).

DISCUSSION

In this study, we present clinical and genetic data of 20 LGMD2I patients from 19 unrelated families. The severity of muscular dystrophies due to *FKRP* mutations is described to vary remarkably, ranging from severe MDC to mild LGMD of adulthood. In this study, the average clinical phenotype is relatively mild and includes patients presenting with muscle pain, myoglobinuria, and elevated CK levels only. This is partly due to a sampling bias since more affected patients (patient 2), who presented with a more severe phenotype, initially went to pediatric, not neurologic departments, and only patients carrying the frequent mutation *FKRP* (826C>A) were included. Similarly, previous studies have reported a more benign LGMD phenotype to be associated with this mutation.^{2,9} Remarkably, early onset of symptoms does not necessarily lead to a severe phenotype. Compared to another recent series of *FKRP* 826C>A (Leu276Ile) patients,⁹ our patients only rarely showed signs of impaired pulmonary or cardiac function even decades after disease onset. Interestingly, muscle pain and myoglobinuria were noted as the first symptoms in the majority of our patients. Therefore, diagnostic workup of myoglobinuria should include examination for *FKRP* (826C>A) if CK levels remain elevated between episodes. Of note, a malignant hyperthermia-like reaction occurred during anaesthesia in one patient. Although we cannot exclude that this is a coincidental finding, particular caution should be exercised when LGMD2I patients undergo operations.

In addition to the frequent mutation Leu276Ile (826C>A), six additional *FKRP* mutations were identified. Two of these mutations were previously described, and four are novel. The Stop496Arg mutation has been found in the original Tunisian LGMD2I pedigree.¹¹ Similar to the Tunisian patients, this mutation was found on the same allele as Ala114Gly in two of our patients. In an earlier report,¹ Ala114Gly was considered to be pathogenic. However, Ala114Gly was found homozygously in normal Tunisian controls,¹¹ and also in one

normal German control (data not presented). Therefore, Ala114Gly should be considered as a rare polymorphism, while Stop496Arg is likely to represent the pathogenic mutation in our and the Tunisian patients.¹¹ Similarly to Stop496Arg, the novel mutation 1475delC close to the termination codon may cause an elongation of the amino acid chain by several missense codons. We hypothesise that the three novel missense mutations (Val121Glu, Val300Ala, and Arg352Gly) constitute pathogenic changes, since (i) they were not detected in 100 normal alleles, (ii) they affect highly conserved amino acid residues (Val300Ala) or alter the charge of the residue (Val121Glu, Arg352Gly), (iii) they are heteroallelic to Leu276Ile, and (iv) they lead to the typical clinical and biochemical alterations. However, functional studies of mutant FKRP would need to be undertaken to firmly prove the pathogenic nature of these mutations.¹²

The frequent mutation Leu276Ile (826C>A) was found to be associated with two intragenic polymorphisms in all cases and may therefore constitute an old founder allele. This is partly at variance with a previous study that found evidence for several founders through haplotyping using two extragenic, polymorphic repeats spanning 3 cM of the *FKRP* region.² However, two rare alleles of D19S606 that appeared to be in linkage disequilibrium with the mutation were observed, suggesting it may have arisen on a limited number of occasions. Therefore, further studies on a larger number of mutant alleles including both intra- and extragenic, polymorphic markers need to be undertaken to determine whether Leu276Ile (826C>A) has arisen several times, or whether it appeared only once. In the latter case, this event may have happened a long time ago to allow for the observed heterogeneity of close, extragenic markers through recombination events and to explain the Europe-wide distribution of the mutation. Interestingly, Leu276Ile (826C>A) has also been observed in the Hutterites, an endogamous population that emigrated from Europe to North America several hundreds of years ago.¹³ Haplotyping of the Hutterite Leu276Ile (826C>A) allele may help to better understand the history of the mutation.

Overall, LGMD2I appears to be one of the most common muscular dystrophies in adult patients, within the range of LGMD2A (calpainopathies), LGMD2B (dysferlinopathies), and LGMD2C-F (sarcoglycanopathies). Although we did not undertake epidemiological studies and a sampling bias needs to be considered, LGMD2I due to Leu276Ile (826C>A) alone is responsible for 19% (15 out of 81) and 18% (six out of 33) of so far unclassified LGMD in two German cohorts (from the neurology departments of Munich and Bonn, respectively). This is in keeping with a recent study that identified LGMD2I in 11% of all LGMD2 patients.¹⁴ A previous study from the UK identified one Leu276Ile (826C>A) mutant allele in 200 normal control chromosomes,² whereas we identified one mutant allele in 600 control chromosomes in Germany. Therefore, Leu276Ile (826C>A) was detected at a similar frequency in the general populations of both Germany and the UK. Accordingly, a prevalence for LGMD2I could be estimated that is within the range of other, more frequent muscular dystrophies.¹⁵ However, epidemiological studies are warranted to prove this hypothesis.

So far, accurate diagnosis of LGMD was based on a muscle biopsy and subsequent immunohistochemical and immunoblotting examinations of the tissue in most cases. This was partly caused by the large phenotypic variability of most forms of LGMD and the large clinical overlap among different forms. Furthermore, few patients carry recurrent mutations of LGMD genes, while many carry rare or novel mutations. The findings presented in our and other studies suggest that LGMD2I is frequent in adult patients and usually, at least in Europe, caused by a single missense mutation of the *FKRP*

gene, namely Leu276Ile (826C>A). This may simplify the diagnostic workup at least for some patients. In male patients, the high prevalence of dystrophinopathies (Becker muscular dystrophy) and the overlap of clinical findings with LGMD2I may still make a muscle biopsy, early in the diagnostic process, necessary. In contrast, we propose to test directly for *FKRP* (Leu276Ile) in female LGMD patients using a blood sample prior to undertaking a muscle biopsy.

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