De novo desmin-mutation N116S is associated with arrhythmogenic right ventricular cardiomyopathy

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Received July 16, 2010; Revised September 2, 2010; Accepted September 3, 2010

INTRODUCTION

Arrhythmogenic right ventricular cardiomyopathy (ARVC) is an inherited heart muscle disease, frequently accompanied by sudden cardiac death and terminal heart failure. Genotyping of ARVC patients might be used for palliative treatment of the affected family. We genotyped a cohort of 22 ARVC patients referred to molecular genetic screening in our heart center for mutations in the desmosomal candidate genes JUP, DSG2, DSC2, DSP and PKP2 known to be associated with ARVC. In 43% of the cohort, we found disease-associated sequence variants. In addition, we screened for desmin mutations and found a novel desmin-mutation p.N116S in a patient with ARVC and terminal heart failure, which is located in segment 1A of the desmin rod domain. The mutation leads to the aggresome formation in cardiac and skeletal muscle without signs of an overt clinical myopathy. Cardiac aggresomes appear to be prominent, especially in the right ventricle of the heart. Viscosimetry and atomic force microscopy of the desmin wild-type and N116S mutant isolated from recombinant Escherichia coli revealed severe impairment of the filament formation, which was supported by transfections in SW13 cells. Thus, the gene coding for desmin appears to be a novel ARVC gene, which should be included in molecular genetic screening of ARVC patients.

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the two major types of cell adhesion junctions in cardiomyocytes providing mechanical attachment between cells and located at the intercalated disc. Multiple mutations were described in genes encoding for desmocollin 2 (DSC2), desmoglein 2 (DSG2), plakophilin 2 (PKP2), plakoglobin (JUP) and desmoplakin (DSP) (reviewed in 7). Recently, there have been repeated reports on compound and digenic heterozygosity of desmosomal gene variations contributing to ARVC (8–10). Although the association of the dominant form of ARVC with mutations in desmosomal genes is well documented, in the majority of ARVC patients, no mutations were found among these genes.

Recessive inherited forms of human ARVC associated with palmo-planar keratoderma and woolly hair are also associated with mutations in the genes coding for plakoglobin (11), desmocollin 2 (12) and desmoplakin (13, 14). Another recessive plakophilin 2 splice mutation identified in an ARVC proband with no signs of cutaneous abnormalities was described by Awad et al. (15).

Desmin is the typical intermediate filament (IF) protein expressed by cardiac, skeletal and smooth muscle cells. It serves as a mechanical integrator of neighboring Z-discs in the sarcomere and also as an important structural component of the intercalated disc by binding to desmosomal plaque proteins. Mutations in the desmin gene are associated with severe human diseases, including diverse forms of myotubular myopathies and/or dilated cardiomyopathy (16, 17). Right-sided heart failure in desmin gene mutation carriers has occasionally been reported in the literature (18, 19), van Tintelen et al. (20) recently reported that patients fulfilling ARVC task force criteria carry a mutation in the head domain of desmin. Thus, DES appears to be another candidate gene carrying mutations in inherited forms of ARVC.

Here we report screening of an ARVC cohort on the prevalence of mutations in desmosomal proteins and desmin. We provide further evidence on functional consequences of a novel mutation identified in the desmin 1A segment of the rod domain for the development of ARVC.

RESULTS

Mutation detection

The desmosomal genes DSG2, DSC2, PKP2, JUP and DSP, in addition to the DES gene of 22 unrelated ARVC index patients, were analyzed for gene variations by sequencing and denaturing high-pressure liquid chromatography (dHPLC). In addition, patient #5 included in the study was screened only for mutations in PKP2 and DES. According to the novel task force criteria (21), 12 of these patients were classified as definite, 7 as borderline and 4 as possible ARVC. Of note, six of the seven transplanted patients were classified as definite, whereas the explanted heart of the seventh patient was not available for pathological examination (Table 1).

Overall, 16 variants in DSG2 (4 ×), DSC2 (3 ×), PKP2 (6 ×), DSP (2 ×) and DES (1 ×) were identified in 16 patients (Table 2). The variants identified included 10 missense, 3 nonsense and 2 deletion/insertion variants predicting an amino acid frameshift. Of note, we did not find any variant relevant for ARVC in the gene JUP.

Non-synonymous polymorphisms found in the screened genes and already published in GenBank and/or the Ensembl SNP database (www.gene_cards.org, www.ensembl.org) with an allele frequency of at least 3% were not considered as disease-causing and are shown in Supplementary Material, Table S1. The human gene mutation databases [www.fsm.it/cardmoc, www.arvcdatabase.info (21)] were checked for entry of all variations/mutations found in this study.

Since there was evidence that, especially in genes coding for cardiac type II cadherins, sequence variants were misinterpreted (10, 22–24), we checked all but one (DSG2 p.M1I) sequence variants reported here in at least 320 anonymous blood donors used as controls.

Desmoglein 2 (DSG2). We identified, by mutation screening of a 36-year-old ARVC patient (#1), who underwent heart transplantation (HTx) in the meantime, a G to A transition at codon 392 of DSG2, leading to the substitution of valine for isoleucine (p.V392I). This mutation was also identified in one brother who, up to now, is clinically unaffected (age 45 years). There was a history of SCD within the family. The DSG2 p.V392I mutation was previously reported and the affected amino acid is conserved among mammals (25). From recently published data, the genotype–phenotype relationship appears to be demonstrated for this variant (9, 26).

In patient #13, we identified sequence variants c.3G>A (p.M1I) and c.1480G>A (p.D494M). The mutation p.M1I was previously found in an ARVC patient (25), whereas the variant p.D494M was classified as an undetermined variant in an ARVC database (21). Two brothers of this patient #13 were diagnosed to have ARVC and one of them was transplanted. One of them was tested only to find both mutations. M1I was not tested in blood donor controls, because this position will skip the initiation of translation at the proper position. In addition, a predicted in-frame start site at codon 179 will lead to loss of the leader sequence, which is essential for proper intracellular trafficking of the protein.

The variant E713K was found in patient #15. However, we found the presence of this variant in 4 out of 86 blood donors. We consider this variant therefore as a polymorphism not associated with ARVC (22).

Desmocollin 2 (DSC2). The variant c.2687_2688insGA (p.A897KfsX901; previously published as p.E896fsX900) was identified in the DSC2 gene of a 34-year-old man (patient #14) with positive ARVC family history and was identified in an ARVC database (21). Two brothers of this patient #13 were diagnosed to have ARVC and one of them was transplanted. One of them was tested only to find both mutations. M1I was not tested in blood donor controls, because this position will skip the initiation of translation at the proper position. In addition, a predicted in-frame start site at codon 179 will lead to loss of the leader sequence, which is essential for proper intracellular trafficking of the protein.

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Desmocollin 2 (DSC2). The variant c.2687_2688insGA (p.A897KfsX901; previously published as p.E896fsX900) was identified in the DSC2 gene of a 34-year-old man (patient #14) with positive ARVC family history and was reported previously as a mutation (27). However, in agreement with other studies (10,26,28), we classified this variant as a polymorphism as the variant was found in 12 out of 395 blood donors.

In a 62-year-old patient (patient #22), we identified the novel homozygous deletion c.1912_1917delAGAA (p.Q638fsX647). The brother of patient #22 died suddenly at the age of 27 due to cardiac death. This deletion is predicted to skip the transmembrane domain of desmocollin 2.
Plakophilin 2 (PKP2). In our study, six ARVC patients (26%) with different PKP2 variations/mutations were identified. The variation p.D26N was already described as an unclassified variant by van Tintelen et al. (29). Genotyping of 363 blood donors recognized this variation as a single-nucleotide polymorphism (SNP) as 10 individuals had the same variation.

The mutation p.Q726X (6) was found in a 64-year-old HTx candidate (patient #2) only. Sequence data of the affected families were available.

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The mutation p.Q726X (6) was found in a 64-year-old HTx candidate (patient #10) diagnosed to have ARVC. The mutation was not inherited by the patient’s single daughter, who was not clinically affected by cardiomyopathy. The family declined further testing despite a family history of SCD: two brothers (aged 44 and 55) and two nephews (both aged 17) of the patient died suddenly.

Furthermore, a 62-year-old male HTx candidate (patient #5) was identified as a carrier of the mutation p.R79X (6), leading to the premature termination of translation. This mutation was also recently identified in a Scandinavian ARVC population (30), and segregation with ARVC was shown in a Dutch patient cohort (29).

Two novel PKP2 mutations were identified in our study; the mutation p.Q220X (patient #11) creates a premature stop codon, whereas p.D601EfsX55 (patient #21) generates a pre-mature, terminated protein exhibiting a modified C-terminus. The mutation p.R811S within exon 12 (patient #18) was recently described (28). No additional genotype–phenotype data of the affected families were available.

Desmoplakin (DSP). In patient #16, we identified the variant causing the amino acid substitution p.N1726K within the gene coding for desmoplakin. We identified this variant also in 2 out of 380 blood donors. This variant is already registered in an ARVC database (21).

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Desmin (DES). In our cohort, we identified a mutation in the DES gene in a single ARVC patient (#2) only. Sequence data of the affected families were available.

In our cohort, we identified another novel polymorphism R798Q, which was found in 7% of blood donors.
analysis of DES revealed the missense mutation p.N116S (Fig. 1), whereas we did not find any variant among the desmosomal genes (JUP, DSG2, DSC2, PKP2, DSP). The patient history revealed several episodes of syncope, and task force criteria for ARVC were fulfilled [right ventricular end-diastolic diameter (RVEDD) = 45 mm, left ventricular end-diastolic diameter = 52 mm, biopsy with fibro-fatty replacement, electrocardiography with T-wave inversion in V4, V5 and V6]. The patient was transplanted at the age of 17 due to terminal heart failure. The patient was re-transplanted at the age of 21, because the donor heart was actually rejected.

Due to the identified DES mutation, the patient was also examined for skeletal muscle disease. At the age of 19, the patient started to complain of exercise-induced muscle pain, fatigability and weakness when walking uphill or climbing stairs. Neurological examination at the age of 20 revealed only a slight proximal weakness of the lower extremities and that her standing up from a squatting position was slowed.

Cardiac and skeletal muscle pathology of the desmin-mutation carrier. Immunohistochemical studies of myocardial sections revealed accumulation of desmin and myotilin immunoreactive aggresomes in the RV and left ventricle (LV) of the DES N116S heart after HTx. Of note, the aggresome formation appeared to be more prominent in the RV compared with the LV myocardium. In contrast in myocardial sections of a non-failing control heart, an even distribution of immunoreactive aggresomes in the RV and left ventricle was observed (Fig. 2).

Skeletal muscle biopsy from the quadriceps muscle was performed at the age of 19. Light microscopic studies were unremarkable with the exception of type I fiber predominance and some diffusely distributed rounded atrophic fibers. There were no inflammatory infiltrations, necroses, basophilic regenerating fibers, centrally located nuclei or structural changes of muscle fibers. Morphological studies revealed a diameter of type 1 fibers between 11 and 76 µm (normal: 30–70 µm) and diameter of type 2 fibers between 14 and 67 µm, thus indicating an unspecific fiber atrophy (see Supplementary Material, Figure). Immunohistochemical stainings of skeletal muscle revealed some fibers with intracellular desmin and myotilin-positive aggresomes typically seen in patients with myofibrillar myopathies (Fig. 3).

N116 of desmin is located within the IA segment of the rod domain in the amino acid motif ‘LNDR’, which is absolutely conserved in the IF protein family (31, 32). Of note, there was no history of ARVC or arrhythmias within the family, which was supported by DNA sequencing of her parents and her sister. Thus, the DES-variant N116S in this patient was found to be a spontaneous mutation.

Viscosimetric measurements of desmin mutant protein. Specific viscosity of the N116S mutation on desmin filament formation was investigated using in Escherichia coli, expressed, purified full-length WT and mutant as well as various mixtures of desmin (75:25 and 50:50, respectively; Fig. 4). WT desmin exhibited an increase of specific viscosity was supported by DNA sequencing of her parents and her sister. Thus, the DES-variant N116S in this patient was found to be a spontaneous mutation.

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expression vector-transfected (Fig. 5C) and -untransfected controls (Fig. 5A).

Atomic force microscopic imaging of desmin filaments. At a relatively low surface coverage with desmin, distinct differences between the WT and the mutant desmin could be identified (Fig. 6A and B). Both desmin variants exhibited straight linear filaments that self-assemble into a protein network structure. In addition, the N116S desmin showed distinct superimposed coiled-filament morphology. At larger surface coverage, the N116S variant also exhibited larger fibrous protein aggregates that could be identified in atomic force microscopy (AFM) topography and phase images (Fig. 6C and D).

Thus, our in vitro AFM data are in accordance with the in situ histological findings and underline that the mutation
N116S leads to distinct disturbances of desmin filament formation and aggresome formation. N116S is therefore a pathogenic variant causing the cardiac and skeletal muscle phenotype of the ARVC patient.

**DISCUSSION**

ARVC is an inherited cardiomyopathy, which is believed to be caused mainly by mutations in proteins of the cardiac desmosomes. However, up to now, three other non-desmosomal genes were reported to carry mutations associated with ARVC in rare cases. One is the gene encoding the cardiac ryanodine receptor 2 (RYR2) (34, 35), which mediates intracellular calcium release during excitation–contraction coupling. Another study characterized promotor mutations in the transforming growth factor beta-3 gene associated with ARVC (36). However, the impact and significance of these mutations remain unclear. The third gene defect concerns
Figure 5. Immunofluorescence microscopy of desmin-transfected SW13 cells and staining by anti-desmin antibody. Desmin WT and N116S cDNA were cloned into pLPCX expression vector for transfection. The filamentous network formation was observed in SW13 cells transfected with desmin WT (D), whereas the aggresome formation was found in cells transfected with the mutant desmin N116S (E). As a control, no staining was observed in untransfected cells (A) and transfected with the vector pLPCX (C). Anti-desmin staining of untransfected SW13 is shown in (B). Scale bar = 50 μm.

Figure 6. AFM topview images of WT and N116S mutated desmin filaments. (A) AFM topography image of low coverage WT desmin yielding a network of straight linear filaments. (B) Low coverage of N116S mutated desmin results in an analogous desmin filament network and a superimposed coiled superstructure (see inset). (C) AFM topographs of N116S desmin yielding a filament network structure with larger protein aggregates. (D) Corresponding AFM phase image of (C) representing relative material contrast of N116S desmin unveiling a filament network structure with large filamentous protein aggregates. Vertical color scale is 1 nm for all topography images.
the transmembrane protein 43 (TMEM43) which is predicted to be an integral inner nuclear membrane protein with currently unknown function (37).

Although mutations in desmosomal genes were found in a considerable number of cases in ARVC patients, the genetic examination does not lead to the identification of relevant mutations in the majority of ARVC cases (4, 5). Here we present data of the genes JUP, DSG2, DSC2, DSP and PKP2 in patients referred to our heart center for genetic screening due to ARVC. All patients were classified according to the novel task force criteria (Table 1) (38). In about 30% of the patients, we identified mutations in these desmosomal genes.

In DSG2, we identified three previously published mutations/variations. V392I located within a functional and conserved cadherin domain has already been identified earlier as a pathogenic mutation in several English (9, 25) and Dutch (26) ARVC patients. However, in contrast to Syrris et al. (25), Bause et al. (9) and Bhuiyan et al. (26) who did not find the mutation in 200, 250 and 150 healthy controls, respectively, we found this mutation once in 338 blood donors (0.3%). As this frequency is comparable with the estimated prevalence of ARVC, we have classified this variant as a mutation (Table 2). However, the disease association of p.V392I should be confirmed in future studies.

In this study, the previously described mutation DSG2 p.M1I (25) and the currently undetermined variant p.D494M (21) were identified in an 18-year-old patient (#13), with a definite diagnosis of ARVC, including a positive family history with a severe clinical phenotype. In contrast, Syrris et al. (25) identified the p.M1I mutation within a proband aged 14 years with features of ARVC, who stayed clinically stable during 10 years of follow-up after ICD implantation. In that study relatives identified as carriers for the family typical mutation presented variable disease expression. The mutation p.M1I is predicted to abolish translation initiation and protein export thus causing a haplo-insufficiency with unknown effects on cell function and intercellular cell contact.

Variant p.D494M affected a conserved amino acid among mammals (Pan troglodytes, Canis lupus familiaris, Bos taurus, Mus musculus, Rattus norvegicus, data not shown) located immediately behind the cadherin domain 4 of desmoglein 2. Because no haplotype analysis has been performed yet it is unknown whether the p.M1I and p.D494M variants affect the same DSG2 allele. Due to the severe clinical phenotype of patient #13, carrying the M1I mutation, the additional p.D494M variant might have an impact as a modifier.

In DSG2, a novel homozygous deletion mutation p.Q638LfsX647 was identified in a 62-year-old female with definite diagnosis of ARVC. A recessive desmosomal mutation has already been reported in non-syndromic ARVC (15). To assess the significance of the mutation, e.g. the origin and mode of inheritance, further genotyping of family members and haplotype analysis could not be realized yet. Substitution of the amino acid glutamine by histidine at position 638 of desmocollin 2 has been reported twice in US collectives of ARVC probands. However, the authors of the studies differently assessed the significance of the mutation. Den Haan et al. (39) classified p.Q638H as a non-conserved desmosomal protein variant, whereas Xu et al. (8) regarded it as a desmosomal gene mutation. Deletion mutation p.Q638LfsX647 identified in this study relates to the same gene locus but is predicted to cause a frameshift. The predicted protein missed the typical cadherin transmembrane domain because a premature stop codon shortened the protein by 256 amino acids at the C-terminus. The effect on intercellular contact, desmosome formation and possibly functional compensation by other (desmosomal) proteins remains to be determined.

Two novel PKP2 mutations Q220X and D601EfsX55 were also identified. In agreement with the data from Gerull et al. (6), most of the identified PKP2 mutations in our cohort were frameshift mutations or premature stop codons. We also found that the PKP2 mutation Q726X did not lead to a truncated version of PKP2, because the mutated short version of PKP2 was not detectable by western blotting in myocardial extracts of the patient’s explanted heart (data not shown).

The variant p.R811S was previously reported to be pathogenic (28). Although we did not identify p.R811S in 397 blood donors, we classified it as a genetic variant of unknown significance (GUS), since it is not conserved among mammals and does not affect a known functional domain of plakophilin 2.

In DSP, we identified the gene variation p.G2844V located within the C-terminal part of desmoplakin. The C-terminus of desmoplakin contains the amino acid repeat GSRS (40) wherein variation p.G2844V affects the glycine of the sixth repeat. Although the importance of the repeats is not yet clarified, there is evidence that the C-terminus of desmoplakin encompasses sequences critical for binding to IFs (41). Although the variant was located within a functionally relevant protein region and was not identified in controls, it was classified as a GUS, since it was not identified in two family members who died of SCD. Whether the variant is a rare polymorphism or a family-specific gene variation is currently not known.

We further analyzed in this cohort desmin as a candidate gene, which is functionally related to the intercalated disc and speculated that desmin, which is a cytoskeletal filament protein located in the myocardial z- and intercalated disc and connected to the desmosomal plaque proteins via desmoplakin (41), might also carry mutations in ARVC patients. This approach was supported by a recent report on ARVC cases in a family affected by desmin-related myopathy. However, linkage analysis of that family indicated that the genetic defect was located on chromosome 10 (42) and not related to mutations in desmin, which is coded by 2q35. Further evidence of an association of mutations in DES with ARVC was recently published by van Tintelen et al. (20). However, they found the mutation p.S13F in DES, which is located outside of the rod in the N-terminal head domain of desmin in a large family. The mutation was frequently associated with a myopathy and with a broad spectrum of cardiomyopathies. The desmin aggresome formation was also found within the myocardium. More than 50% of the family members presented dilated or hypertrophic cardiomyopathy with conduction delay phenotypes, whereas ARVC was found in only two cases. Patients with a predominantly LV phenotype experienced a RV failure during the course of the
disease. Interestingly, conduction delays were found to be early signs of the disease.

The same group published two other mutations in DES p.N342D and p.R454W, which were located in the segment 2B and in the tail domain of desmin, respectively. However, patients carrying these mutations presented biventricular dilatation (43). The authors found that carriers of the p.N342D allele present a predominantly RV cardiomyopathy, myopathy and a LV dilatation during the course of the disease. The mutation p.N342D was previously known to be associated with an isolated skeletal muscle phenotype (44). Biventricular dilatation was found in the carrier of p.R454W with unknown skeletal muscle involvement. This mutation was detected previously in the non-helical tail domain of desmin and was linked to a hypertrophic obstructive cardiomyopathy with later onset of a myopathy (45). Thus, the clinical phenotype of ARVC-related DES mutations differs considerably.

We screened 22 unrelated patients referred to our institute for genetic screening on ARVC-related mutations. We identified in DES in a single 17-year-old ARVC patient, who survived several syncopes and was transplanted in our center, the novel missense mutation p.N116S. Of note, the family history did not provide further evidence that the cardiomyopathy of the patient was inherited. This was supported by the results of the genetic testing in members of the family, which revealed that this mutation was indeed a spontaneous mutation not found in other relatives. Therefore, we could not prove the pathogeneity of the mutation by co-segregation analysis within the family tree.

However, the identified mutation is located in segment 1A of the rod domain of desmin. This part of the molecule is involved in elongation of the filament and the dimer formation (31, 32). Two other mutations were published in this part of desmin. The mutation p.E108K was claimed to be the first mutation ever found in segment 1A in a patient with dilated cardiomyopathy (17). The amino acid E108 is part of the heptad, which appears to be responsible for the hydrophobic seam connecting the desmin α-helices within the filament’s supercoil. Another mutation of segment 1A (p.E114del) was recently identified in a Uruguayan family affected by myopathy and severe cardiomyopathy. Members of this family displayed arrhythmias, conduction block and SCD. The deletion of codon 114 was supposed to disturb the filament formation, since the heptade of the coiled-coil will be impaired (46).

The mutation p.N116S, which was identified in our study, belongs to the consensus sequence ‘LNDR’, which is absolutely conserved in IF proteins among eukaryotes. Even the lamin sequence of the coelenterate Hydra vulgaris contains this motif in its rod domain.

We cloned the full-length cDNA of desmin in E. coli, introduced the mutation and purified the protein for in vitro analysis of the protein function. We found that the mutated protein revealed impaired filament formation measured by viscosimetry. We further transfected the cDNAs of WT and mutated desmin in SW13 cells, which do not contain endogeneous desmin. SW13 transfected with the WT desmin revealed the filament formation, whereas the mutant p.N116S produced desmin aggresomes within the cytoplasm. The data found in vitro and in cell culture were in close correlation with the histological examinations of skeletal and cardiac muscle of the ARVC patient, which revealed that desmin deposits were present in both muscle systems. Of note, the RV myocardium of the explanted failing heart revealed an apparently higher density of desmin aggresomes compared with the LV.

Mutations recently published in association with ARVC were partly tested in in vitro test systems. The mutation p.R453W was analysed by viscosimetry and failed to form filaments. However, in combination with the WT protein p.R453W leads to final blockade of the capillary. This mutant also formed aggresomes in SW13 cells (45). The mutation p.N342D was not checked by viscosimetry but still revealed a lack of filament network formation in SW13 cells (44). The ARVC-related DES mutation p.S13F was characterized in vitro by transfection experiments in SW13 cells and leads to the aggresome formation, which was also found in myocardial tissues of mutation carriers (20,47). We compared the profile of our viscosimetric data with that of other mutations and found that the mutant p.N116S revealed a time course comparable to the mutant p.A357P. However, this mutant was published in association with a myopathy (17,48). Therefore, the clinical phenotype of DES mutations is currently not predictable from in vitro characterizations of desmin.

As a consequence of the in vitro findings in desmin, the patient was examined after HTx on a skeletal myopathy as well. Although the histological examination of the skeletal muscle biopsies uncovered an aberrant desmin aggregation and unspecific fiber atrophy, clinical examination of the patient did not provide an overt myopathy. Thus, the histopathological findings of the skeletal muscle can be interpreted as subclinical alterations.

In conclusion, genotyping of variants in desmosomal proteins analyzed in this study leads to the identification of disease-causing mutations in a minority of ARVC patients. Thus, additional genes will be identified, which cause ARVC. We could further provide evidence that a novel mutation in DES causes the phenotype of ARVC. Mutations in DES cause a broad spectrum of myopathies and especially cardiomyopathies, which might be associated with rhythm disorders, conduction delays and RV failure. Of note, mutations displaying an arrhythmogenic and/or RV phenotype are found in all domains of the protein and are not located in hotspots.

Limitations of the study
We provided data on a limited cohort size from a single heart center and did not present clinical data on the control cohort of blood donors, since personal data were not available due to binding of the DNA samples. In this study, we could also not exclude large genomic duplications or inversions. Cellular and animal models bearing variations may be helpful in future to examine the impact on cellular level to some extent.

MATERIAL AND METHODS

Patient cohort
We included 23 unrelated ARVC patients (16 males, 7 females) aged between 17 and 73 years. Nineteen patients
(about 80%) were from the Heart and Diabetes Center North Rhine Westphalia (HDZ-NRW), Germany. Of these patients, 22 were screened for all desmosomal genes causing ARVC and the gene DES, whereas patient #5 was screened only for mutations in PKP2 and DES due to compliance problems. Patients were classified according to the revised task force criteria for ARVC (38) (Table 1). In addition, ARVC diagnosis of six patients who received HTx in our center was confirmed by pathological structural examination of the explanted heart, since we analysed a considerable number of index patients with terminal heart failure (Supplementary Material, Table S1). The carrier of the DES mutation was additionally examined for a myopathy by histology of a skeletal muscle biopsy from the M. quadriceps.

All members included in the study were of Caucasian origin. Written informed consent was obtained from all participants. The study was approved by the local ethics committee.

Mutation detection

Blood samples were collected from the affected individuals and DNA was extracted from white blood cells using standard techniques (Illustra™ blood genomic Prep Mini Spin Kit, GE Healthcare, Buckinghamshire, UK). Mutation screening of five desmosomal genes was performed by direct sequencing. The desmin gene was screened by dHPLC.

The genomic sequences used to design the primers were obtained from sequences in the GenBank database on the NCBI website (www.ncbi.nih.gov/projects/genome/guide/human). Based on the published sequence of plakophilin 2 (NM_024422), plakoglobin (NM_004572), desmoplakin (NM_004415), desmocollin 2 (NM_024422), desmoglein 2 (NM_001943) and desmin (NM_1927), amplification and sequencing of the exonic and adjacent intronic sequences were carried out following standard protocols. After amplification, PCR products were purified and labeled using the BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems, CA, USA) and sequenced in both directions on an ABI 310 genetic analyzer. Sequencing electropherograms were inspected manually and analyzed with Variant Reporter Software v1.0 (Applied Biosystems).

DES mutation screening was done by dHPLC using a DNASEp column with a WAVE DNA Fragment Analysis System (Transgenomic Inc., NE, USA) as described previously (35). The analytical temperatures for each exon are available from the authors upon request. Exons with aberrant, temperature-modulated heteroduplex profile were sequenced in both directions.

For all mutations, at least 640 chromosomes from ethnically matched, healthy individuals were genotyped using TaqMan SNP genotyping assay (Applied Biosystems) according to the manufacturer’s protocol.

Tissue immunohistochemistry

Immunofluorescence studies were performed on 5 µm thick frozen serial sections of left and RV heart muscle tissue provided after HTx or of skeletal muscle tissue (M. quadriceps), respectively. The following primary antibodies were used in this study: (i) mouse monoclonal anti-desmin antibody D33 (dilution 1:500; M0760, DakoCytomation, Germany) and (ii) mouse monoclonal anti-myotilin antibody (dilution 1:20; NCL-MYOTILIN, Leica Microsystems, UK). As secondary antibody sheep anti-mouse IgG biotinylated antibody (RPN1001, GE Healthcare Bio-Sciences AB, Sweden) in combination with Cy2-conjugated streptavidin (both dilution 1:100) (016-220-084, Jackson Immunoresearch, USA) was used. Immunostaining was performed according to the recommendations of the manufacturers. Staining was evaluated with a laser scanning spectral confocal microscope (Leica TCS SP2, Leica Microsystems, Germany).

Cloning and mutagenesis

The full-length cDNA of desmin wild-type (Des WT) was amplified by polymerase chain reaction (PCR) using SC319574 vector DNA (human desmin cDNA in pCMV6-AC; OriGene, USA) as a template and complementary primers. The DES N116S (Des N116S) mutation was introduced by two-step PCR (overlap extension approach [49]), with the use of oligonucleotides containing the adenine-to-guanine transition at nucleotide position 347. For expression in E. coli BL21 (DE3) cells (Invitrogen, USA), amplified Des WT and N116S cDNA fragments were cloned into the bacterial T7 promoter expression vector pET100/D-TOPO (Invitrogen), which fuses a His6 and Xpress epitope tag to the N-terminus of inserted fragments. For transfection of SW13 cells, both Des WT and N116S cDNA were cloned into the eukaryotic CMV promoter expression vector pLPCX (Clontech, USA) using pET100/D-Des WT or pET100/D-Des N116S as a template in addition to modified sequence-specific primers to generate a C-terminal Clal restriction site during PCR. Fragments were cloned first into pCRII-TOPO (Invitrogen) followed by subcloning into pLPCX using EcoRI and Clal restriction sites. The accuracy of all clones was controlled by sequencing.

Protein expression and purification

Recombinant protein expression in E. coli BL21 was induced according the recommendations of the manufacturers and verified by SDS–PAGE.

Recombinant desmin WT and N116S proteins were isolated from inclusion bodies as described previously (50) with the modification that the pellet finally was dissolved in 8 M urea, 10 mM Tris–HCl (pH 8.0), 100 mM Na2HPO4, 15 mM β-mercaptoethanol. Purification under denaturing conditions via Ni-NTA affinity chromatography (Ni-NTA agarose; Qiagen, Germany) was performed according to the manufacturer’s instructions. For further purification, proteins were dialysed against the target buffer 8 M urea, 20 mM Tris–HCl (pH 7.5) and 1 mM DTT and supplied to a HiTrap DEAE Sepharose Fast Flow column (GE Healthcare Bio-Sciences AB). Proteins were eluted by a linear salt gradient (0–0.3 mM NaCl). Fractions were analyzed by SDS–PAGE and those containing pure desmin WT or N116S were pooled. Protein concentrations were measured by the method of Bradford (51). As determined by anti-desmin immunoblot analysis,
both vectors generated a single protein of the expected 52 kDa size (data not shown).

**In vitro IF assembly and viscosity measurements**

Purified, recombinant desmin WT and N116S were dialyzed stepwise against two set of buffer, that is, 4 mM urea, 5 mM Tris—HCl (pH 8.4) and 2 mM urea and 5 mM Tris—HCl (pH 8.4), for 1 h at room temperature and finally for overnight at 4°C against 5 mM Tris—HCl (pH 8.4), 1 mM EDTA and 0.1 mM EGTA, all buffers containing 1 mM DTT. Before use, the recombinant protein samples were dialyzed for 1 h at room temperature against assembly buffer [5 mM Tris—HCl (pH 8.4), 1 mM DTT] (52). Desmin forms stable tetramers in assembly buffer, as reported (53). Viscosity measurements were performed at a protein concentration of 1 mg/ml in an Ostwald viscometer (Cannon, USA) with a sample volume of 1 ml at 22°C. Assembly studies were performed as described (52). Assembly of IFs was induced at the 10 min time point by the addition of 1/10 volume of assembly start buffer [0.2 mM Tris—HCl (pH 7.0) and 0.5 mM NaCl leading to the final concentration of 25 mM Tris—HCl (pH 7.5), 50 mM NaCl]. Specific viscosity (ηsp) was calculated by ηsp = (t_f − t_b)/t_b (t_f is the flow time of the sample and t_b the flow time of the buffer) (52). The flow time was measured before (time point 0, 5 and 9 min), 1 min after assembly start and then every 5 min over a period of 1 h.

**Transient transfection of cultured cells and immunofluorescence staining**

Desmin- and vimentin-free human adrenocortical carcinoma cells SW13 (ATCC, USA) (33) were used for recombinant desmin cDNA transfection in a cell culture assay. Cells were cultivated in Leibovitz’s L-15 medium supplemented with 10% FCS, 1% penicillin/streptomycin and 1% amphotericin B in T-75 flasks without filters (no air exchange) in a 5% CO2 incubator at 37°C.

Forty-eight hours after cDNA transfection, cells were fixed with the Ruhr-University Bochum, Germany.

**REFERENCES**


