SPRED1 germline mutations caused a neurofibromatosis type 1 overlapping phenotype

E Pasmant,1,2 A Sabbagh,1,2 N Hanna,1,2 J Masliah-Planchon,2 E Jolly,2 P Goussard,2 P Ballerini,3 F Cartault,4 S Barbarot,5 J Landman-Parker,6 N Soufir,7 B Parfait,1,2 M Vidaud,1,2 P Wolkenstein,8 D Vidaud,1,2 R N F France

Objective: Germline loss-of-function mutations in the SPRED1 gene have recently been identified in patients fulfilling the National Institutes of Health (NIH) diagnostic criteria for neurofibromatosis type 1 (NF1) but with no NF1 (neurofibromin 1) mutation found, suggesting a neurofibromatosis type 1-like syndrome.

Methods: 61 index cases with NF1 clinical diagnosis but no identifiable NF1 mutation were screened for SPRED1 mutation.

Results: We describe one known SPRED1 mutation (c.190C>T leading to p.Arg64Stop) and four novel mutations (c.637C>T leading to p.Gln213Stop, c.272T>C leading to p.Met1Thr, c.468C>T leading to p.Arg16Stop, and c.1048_1060del leading to p.Gly350fs) in five French families. Their NF1-like phenotype was characterised by a high prevalence of café-au-lait spots, freckling, learning disability, and an absence of neurofibromas and Lisch nodules in agreement with the original description. However, we did not observe Noonan-like dysmorphism. It is noteworthy that one patient with the p.Arg16Stop mutation developed a monoblastic acute leukaemia.

Conclusions: In our series, SPRED1 mutations occurred with a prevalence of 0.5% in NF1 patients and in 5% of NF1 patients displaying an NF1-like phenotype. SPRED1 mutated patients did not display any specific dermatologic features that were not present in NF1 patients, except for the absence of neurofibromas that seem to be a specific clinical feature of NF1. The exact phenotypic spectrum and the putative complications of this NF1 overlapping syndrome, in particular haematological malignancies, remain to be further characterised. NIH diagnostic criteria for NF1 must be revised in view of this newly characterised Legius syndrome in order to establish a specific genetic counselling.

Germline mutations in genes involved in the Ras-mitogen activated protein kinase (MAPK) signalling pathway have been reported in several phenotypically overlapping syndromes with autosomal dominant transmission. These observations provided a unifying mechanism—Ras MAPK pathway constitutive activation—leading to neurocardio-facial-cutaneous (NCFC) syndromes (fig 1). These rare diseases include neurofibromatosis 1 (NF1, OMIM 162200), Noonan syndrome (NS, OMIM 168950), LEOPARD syndrome (LS, OMIM 151100), cardio-facio-cutaneous syndrome (CFC, OMIM 115150), and Costello syndrome (CS, OMIM 218040). Predisposition to malignancies is a known feature of NCFC syndromes with the exception of CFC.

NF1 has a birth incidence of ~1/3000 and has been showed to be caused by autosomal dominant loss of function of mutations of the NF1 (neurofibromin 1; OMIM 000267) gene in approximately 95% of patients fulfilling the National Institutes of Health (NIH) clinical diagnostic criteria. NF1 is located in 17q11.2 and contains 60 translated exons distributed over ~350 kb. Most of the NF1 mutations (90–95%) are intragenic mutations (point mutation, splice mutation, small deletion, insertion, or duplication). The remaining NF1 mutations (5–10%) are microdeletions encompassing the entire NF1 gene and its neighbouring genes. The protein encoded by NF1 (neurofibromin) is a Ras-GTPase activating protein (Ras-GAP) that acts as a negative regulator of the Ras-MAPK cascade.

Germline dominant loss-of-function mutations in the SPRED1 (sprouty-related, EVH1 domain containing 1; OMIM 152594) gene have recently been identified in five unrelated families and seven additional patients fulfilling the NIH diagnostic criteria for NF1, although no NF1 mutation was found.3 Remarkably, their phenotype referred as neurofibromatosis type 1-like syndrome (NFLS, OMIM 611431) consisted of multiple café-au-lait spots, axillary freckling, and macrocephaly but without neurofibromas and Lisch nodules. The SPRED1 gene, located in 15q13.2, contains seven coding exons, and encodes the SPRED1 protein. Sprouty (SPRY1, −2, −3, and −4) and SPRED1 (−2, −3) proteins are an evolutionarily conserved family of membrane-associated negative regulators of growth factor induced extracellular signal regulated kinases (ERK) activation.5,6 SPRED1 specifically inhibits mitogen activated protein kinases (MAPK) signalling by suppressing Raf phosphorylation and activation.

In the present study, we confirmed the existence of loss-of-function mutations of SPRED1 and the characterisation of a NCFC syndrome with an NF1 overlapping phenotype. We identified three nonsense mutations, one missense mutation, and one frameshift deletion of SPRED1 among 61 families fulfilling NIH diagnostic criteria for NF1 but with no identifiable NF1 mutation. We then developed a molecular diagnostic algorithm for individuals displaying an NF1-like phenotype tailored to routine clinical practice.

PATIENTS, MATERIALS, AND METHODS

Patients
A database devoted to NF1 has been established in France thanks to a grant from the French Clinical Research Program (coordinator: Professor P Wolkenstein, Henri Mondor Hospital, Créteil, France)
Germline mutations in key components of the Ras-mitogen activated protein kinase (MAPK) signalling pathway cause neuro-cardio-facial-cutaneous (NCFC) syndromes. NF1, neurofibromatosis 1.

Figure 1  A schematic of Ras signalling.

DNA and RNA extraction

High molecular weight DNA was prepared by standard proteinase K digestion followed by phenol–chloroform extraction from whole blood leucocytes. Total RNA was extracted from whole blood leucocytes by using the acid–phenol guanidium method. The quality of the nucleic acids was determined by electrophoresis through agarose gels and staining with ethidium bromide (DNA and RNA), and the 18S and 28S RNA bands were visualised under ultraviolet light (RNA).

The somatic leukaemia DNA was extracted from bone marrow of patient II:1 in family 4 (showing 85% of blastic cells) upon diagnosis of acute leukaemia.

**SPRED1** mutation screening

We performed **SPRED1** mutation screening at both RNA and genomic DNA levels. Mutational screening of **SPRED1** was carried out on RNA through the following procedure. After reverse transcription with Superscript II RNase H-Reverse Transcriptase (Invitrogen, Cergy-Pontoise, France), two overlapping PCR fragments were generated by Taqman PCR Core Reagent Kit (Applied Biosystems, Courtaboeuf, France). Mutation screening was performed with the ABI BigDye terminator sequencing kit (Applied Biosystems) on an ABI Prism 3130 automatic DNA sequencer (Applied Biosystems). Sequences were aligned with Seqscape analysis software (Applied Biosystems). The primer oligonucleotide sequences and PCR conditions are available upon request.

Sequences were aligned with Seqscape analysis software (Applied Biosystems) on an ABI Terminator v3.1 cycle sequencing kit (Applied Biosystems). The primer oligonucleotide sequences and PCR conditions are available upon request.
quantified to copy number. The primer oligonucleotide sequences and PCR conditions are available upon request. All PCR reactions were performed with an ABI Prism 7900 Sequence Detection System (Applied Biosystems) and the SYBR Green PCR Core Reagents kit (Applied Biosystems). Experiments were performed in triplicate for each data point.

RESULTS

Germline DNAs molecular analysis

Forty-nine index cases with no identifiable NF1 mutation from the French NF1 database were screened for mutation in the SPRED1 gene. Two SPRED1 heterozygous nonsense mutations were identified at both DNA and RNA levels: one known mutation (family 1: c.190C>T leading to p.Arg64Stop) and one novel mutation (family 2: c.637C>T leading to p.Gln213Stop) (fig 2).

SPRED1 mutational analysis of an additional set of 12 index cases selected from routine genetic counselling on the basis of their NF1-like phenotype (presence of café-au-lait spots and/or freckling and absence of neurofibroma and Lisch nodule), identified three novel heterozygous mutations: one missense mutation (family 3: c.2T>C leading to p.Met1Thr), one nonsense mutation (family 4: c.46C>T leading to p.Arg16Stop), and one frame-shift deletion (family 5: c.1048_1060del leading to p.Gly350fs) (fig 2).

In families 1, 2, and 3, the SPRED1 mutations were present in all affected individuals and were absent in three tested unaffected relatives (family 1: individual II:1, family 2: I:1, and family 3: I:1) (table 1). In families 4 and 5 the propositus showed SPRED1 mutations.

The clinical features of SPRED1 tested individuals of families 1, 2, 3, 4, and 5 are displayed in table 1.

Molecular analysis of the somatic leukaemic cells of patient II:2 (family 4)

In order to test the tumour suppressor gene hypothesis, SPRED1 molecular analysis was performed on the leukaemic cells DNA of patient II:2 of family 4. No somatic additional SPRED1 alteration (including point mutation and loss of heterozygosity) was observed.

DISCUSSION

The purpose of this study was to confirm the recently identified loss-of-function mutations of SPRED1 in a new NF1 overlapping syndrome8 (named NFLS) and to specify its phenotype and incidence. We confirmed one known mutation (p.Arg64Stop) described in the original paper of Brems et al8 and reported four novel mutations (p.Gln213Stop, p.Met1Thr, p.Arg16Stop, and p.Gly350fs) in five French families fulfilling NIH NF1 diagnostic criteria. Similar to the mutation p.Gln213Stop previously reported by Brems et al,8 the nonsense mutation p.Gln213Stop found in family 2 also affected exon 7 of SPRED1. The missense mutation c.2T>C (leading to p.Met1Thr) identified at both DNA and RNA levels (ruling out a putative RNA decay) at the initiation codon in exon 2 abolished initiation of translation at the normal start site. Although the first new potential AUG codon downstream of the mutation at the position corresponding to methionine 21 could conceivably be used as an in-frame initiation codon, the loss of 20 amino acids from the Ena/vasodilator stimulated phosphoprotein (VASP) homology (EVH-1) N-terminal functional domain of SPRED1 would probably result in a non-functional protein. It is notable that most of the reported mutations of SPRED1 affect the EVH-1 domain.8 Nonetheless, the precise consequences of the p.Met1Thr mutation at the protein level remain to be determined by experimental means.

The frame shift deletion p.Gly350fs affected the C-terminus SPROUTY-like (SPR) domain of SPRED1, like p.Ser383fs previously reported.1 These five mutations may result in a loss of function of SPRED1, known to inhibit the Ras-MAPK cascade, consistent with the concept that NCFC syndromes are caused by aberrant activation of this pathway.

The mechanism of inheritance in the two large families 1 and 2 (with five and seven affected and mutated individuals, respectively) was compatible with an autosomal dominant
<table>
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<th>Family</th>
<th>Subject</th>
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<th>Sex</th>
<th>Age bracket (years)</th>
<th>Weight (kg)</th>
<th>Length (cm)</th>
<th>Head circumference (cm)</th>
<th>CAL spots &lt;1.5 cm</th>
<th>&gt;1.5 cm</th>
<th>Axillary freckling</th>
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CAL, café-au-lait; F, female; M, male; U, unknown; WT, wild type for SPRED1 mutational analysis; --, negative.

No SPRED1 deletion was found using real-time PCR based gene dosage in any of the patients tested.
LEOPARD syndrome, and NF1 have a higher risk of haematological malignancies, including acute myeloid leukaemia (AML) and the rare disorder juvenile myelomonocytic leukaemia (JMML). With regards to these observations, SPRED1 seemed to be a good candidate gene for leukaemia predisposition. However, molecular analysis of the tumour DNA did not show additional somatic SPRED1 alteration (including point mutation and loss of heterozygosity), in contradiction to the Knudson two-hit model for tumour suppressor genes. Considering our observation and the data implicating hyperactive Ras in the pathogenesis of JMML, as well as the role of SPRED1 in modulating signals from haematopoietic growth factor receptors to Ras, it would be of interest to screen SPRED1 for mutation in the ~20% of JMML cases showing no mutations in either KRAS, NRAS, PTPN11, or NF1 so as to confirm its putative implication in leukaemogenesis.

In conclusion, SPRED1 mutations were present in 0.5% of all NF1 cases and in 5% of NF1 patients displaying an NF1-like phenotype. SPRED1 mutated patients did not display specific dermatologic features not present in NF1 patients, except for the absence of neurofibromas that seem to be a specific clinical feature of NF1. NIH diagnostic criteria for NF1 must now take into account these new data to actualise guidelines and to establish a specific genetic counselling. Further studies will be necessary to characterise the frequency of SPRED1 mutations, the exact phenotypic spectrum (including learning disability), and the putative complications (in particular haematological malignancies) of this Legius syndrome caused by a new mechanism through which Ras-MAPK signalling is deregulated. These findings also emphasise the need to test families with NF1-like phenotype with no NF1 and SPRED1 mutations for additional genes involved in the Ras-MAPK pathway.

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Competing interests: None.

REFERENCES


