Loss of seryl-tRNA synthetase (SARS1) causes complex spastic paraplegia and cellular senescence

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ABSTRACT

Background Aminoacyl-tRNA synthetases (ARS) are key enzymes catalysing the first reactions in protein synthesis, with increasingly recognised pleiotropic roles in tumourgenesis, angiogenesis, immune response and lifespan. Germline mutations in several ARS genes have been associated with both recessive and dominant neurological diseases. Recently, patients affected with microcephaly, intellectual disability and ataxia harbouring biallelic variants in the seryl-tRNA synthetase encoded by seryl-tRNA synthetase 1 (SARS1) were reported.

Methods We used exome sequencing to identify the causal variant in a patient affected by complex spastic paraplegia with ataxia, intellectual disability, developmental delay and seizures, but without microcephaly. Complementation and serylation assays using patient’s fibroblasts and an Saccharomyces cerevisiae model were performed to examine this variant’s pathogenicity.

Results A de novo splice site deletion in SARS1 was identified in our patient, resulting in a 5-amino acid in-frame insertion near its active site. Complementation assays in S. cerevisiae and serylation assays in both yeast strains and patient fibroblasts proved a loss-of-function, dominant negative effect. Fibroblasts showed an abnormal cell shape, arrested division and increased beta-galactosidase staining along with a senescence-associated secretory phenotype (raised interleukin-6, p21, p16 and p53 levels).

Conclusion We refine the phenotypic spectrum and modes of inheritance of a newly described, ultrarare neurodevelopmental disorder, while unveiling the role of SARS1 as a regulator of cell growth, division and senescence.

INTRODUCTION

Aminoacyl-tRNA synthetases (ARS) are ubiquitously expressed and highly evolutionarily conserved enzymes responsible for esterification of amino acids (AA) to their cognate transfer RNA (tRNA), an essential reaction in decoding mRNA into protein. ARS catalyse a two-step reaction in which the given amino acid is condensed with ATP to form tightly bound aminoacyl adenylate (AA-AMP), with the simultaneous release of pyrophosphate PPI. The activated amino acid is then transferred from AMP to the 3’-end of its cognate tRNA, producing AA-tRNA and AMP.

Mutations in ARS enzymes have been implicated in both recessive and dominant diseases affecting a broad range of tissues. While recessive inheritance is very frequently associated with severe, early onset diseases which impact the central nervous system and other organs, dominant mutations cause specifically late-onset peripheral neuropathies in a restricted list of cytoplasmic ARS genes. It is still unclear why mutations in these ubiquitous enzymes cause such a highly specific phenotype. Seryl-tRNA synthetase 1 (SARS1) is a cytoplasmic ARS enzyme that charges serine onto its cognate tRNAser but also onto the non-cognate selenocysteine tRNAsec. Subsequently, serine-bound tRNAsec undergoes
tRNA conversion of the bound serine to selenocysteine by a 4-step reaction.5

SARS1 is essential for vascular development as shown in a zebrafish model,6 and also in a rapid network formation assay of human umbilical vein endothelial cells.7 This non-canonical function is linked to the UNES domain, a unique domain which has only been found in the C-terminus of vertebrate SARS1. UNES harbours a nuclear localisation signal and can divert a fraction of the SARS1 protein into the nucleus to control the expression of vascular endothelial growth factor A.8

Two recent articles reported homozygous loss-of-function missense mutations in SARS1 in two independent families exhibiting a neurodevelopmental syndrome including microcephaly, intellectual disability, seizures and ataxia,9 together with other anomalies such as cardiomyopathy, deafness and decompensation during fever.10 In this work, we identified a de novo inherited novel pathogenic variant of SARS1 causing a complex spastic paraplegia and ataxia phenotype, thus confirming the recent implication of mutations in this gene in neurological and movement disorders.9,10 Furthermore, this variant illustrates the concept that dominant negative mutations in ARS genes can give rise to phenotypes similar to those caused by recessive mutations, rather than the neuropathies frequently linked to dominantly inherited variants.

Three-dimensional modelling
The domain structure of the SARS1 gene was retrieved from the UniProt database and NCBI. The three-dimensional (3D) structure of wild-type (WT) SARS1 was retrieved from https://www.rcsb.org, and a model of the mutated SARS1 was obtained using the SWISS-MODEL utility on the ExPASy webpage (https://swissmodel.expasy.org). Structures were visualised with PyMOL.

Fibroblast cultures
Patient dermal fibroblasts were generated from a skin biopsy using standard cell culture techniques. Fibroblasts from the patient and age-matched and sex-matched controls were grown in DMEM (Dulbecco's Modified Eagle's Medium)(Ref: 31885-023) containing 1% penicillin/streptomycin and 10% fetal bovine serum (FBS). Cultures were maintained at 37°C under 5% CO2 and 95% humidity.

RT-PCR and qRT-PCR
RNA was extracted from patient and control fibroblasts using the RNeasy Mini Kit (QIAGEN). Total RNA quantity and quality were assessed by 0.8% agarose gel electrophoresis and NanoDrop spectrophotometry. cDNA was synthesised using the SuperScript IV kit (Life Technologies) following the manufacturer’s instructions. cDNA was amplified by PCR using primers designed with Primer3 using the whole coding sequence of SARS1 (NM_001330669) (forward: GGAACGGCTCTCATCAGTA; reverse: AGGAGACCAACTCAGGAAG). Products were separated by agarose gel electrophoresis (3%), purified (QiAquick Gel Extraction Kit, QIAGEN) and sequenced by the Sanger method using standard methodology. cDNA PCR products were cloned into pCMV-Tag2 plasmid using standard methods, and several colonies were extracted for DNA and sequenced to isolate WT and mutated sequences. qRT-PCR was performed in a LightCycler 480 device using SYBR Green I Master Mix (Roche). All reactions were performed in triplicate. Each gene mRNA level was normalised to that of H36B4 using the 2-ΔΔCT method. A two-sided Student’s t-test was used to compare the expression ratios of patients and controls. Data are presented as the mean±SD. All primers are shown in online supplemental table 1.

Immunofluorescence
Fibroblasts from the index patient and three age-matched and sex-matched controls were seeded on coverslips and cultured in a 6-well plate (200 000 per well) at 37°C for 24 hours. Coverslips were fixed with 4% paraformaldehyde, blocked and incubated overnight with mouse anti-α-tubulin (dilution 1/10 000, Ref: ab80779, Abcam) and rabbit anti-SARS1 (dilution 1/10, Ref: ab183025, Abcam) primary antibodies. Slides were incubated with goat antirabbit IgG Alexa Fluor 488 (dilution 1/1000, Ref: A-21428, Dako) and antimouse IgG Alexa Fluor 647 (dilution 1/1000, Ref: A-21236, Dako) secondary antibodies. DAPI (4',6-diamidino-2-phenylindole) was used to stain cell nuclei. Confocal microscopy images were acquired with a Leica TCS SL laser scanning confocal spectral microscope using a 63× objective. Images were treated using Fiji software.

Western blot analysis
For western blot analyses, fibroblasts were homogenised in RIPA (Radioimmunoprecipitation assay) buffer (150 mM NaCl, 1% (w/v) Nonidet P40, 0.5% (v/v) sodium deoxycholate, 0.1% sodium dodecyl-sulfate (SDS) (w/v), 50 mM Tris-HCl, pH
In vitro analysis of SARS1 activity

To analyse hSARS serylation activity, we prepared S100 extracts from S. cerevisiae yeast and fibroblasts (see S. cerevisiae yeast S100 preparation). These crude enzymatic preparations were then used in rRNA aminoacylation assays with 14C-radio labelled serine (Serine, L-[3-14C] PerkinElmer Ref NEC827050UC, Lot 236182 52.4 µCi/mmol ; 50 µCi/mL). All reactions were carried out at 30°C for yeast extracts and 37°C for fibroblast extracts under the following conditions: 50 mM HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), KOH buffer pH 7.5, 20 mM KCl, 15 mM MgCl2, 4 mM DTT (Dithiothreitol), 5 mM ATP, 0.1 mg/mL BSA, 440 µM total yeast tRNA and 74 µM of [14C] serine. tRNA concentration was 22 µM. Data were corrected according to the extract’s concentration. Ten microtitre aliquots from a 62 µL reaction mixture were spotted onto Whatman paper and quenched with 5% trichloroacetic acid (TCA) at various time intervals. After three TCA washes, papers were washed three times with ethanol and dried. Radioactivity was measured in a Beckman LS 6500 scintillation counter with a toluene-based scintillant. The reaction times were 2, 4, 8, 16, 24, 32 min for yeast extracts and 2, 8, 60, 180, 360 min for fibroblasts extracts. Experiments were performed five times independently.

S. cerevisiae yeast S100 preparation

Cells were grown in 500 mL SDC-leu-Ura on a rotary shaker at 30°C and harvested when OD600 = 1 by centrifugation at 5000 × g for 5 min at 4°C. The pellet was resuspended in 5 mL of lysis buffer containing 50 mM Na-HEPES pH 7, 30 mM KCl, 10% glycerol, 0.1 mM EDTA, 5 mM β-mercaptoethanol and protease inhibitors tablet (Roche). One volume of glass beads (Ø 0.25–0.5 mm, Roth) was added and cell lysis was performed with a FastPrep-24 apparatus (6 × 1 min at 6.5 m/s, with 1 min on ice between each cycle). Cells debris were removed by centrifugation at 500 × g for 10 min at 4°C and the supernatant is centrifuged at 100 000 × g for 1 hour. The resulting soluble fraction (S100) is recovered, then dialysed O/N against the storage buffer (same as for fibroblasts extracts). Strains used were hSARS, hSARS + hSARSmut or WT (see online supplemental table 2).

β-Galactosidase staining

Fibroblasts from the index patient and two controls were seeded on coverslips and cultured in a 6-well plate (200 000 per well) at 37°C for 24 hours. Staining was performed following the manufacturer’s instructions (Senescence Cells Histochemical Staining Kit, Sigma). Photos were taken using a Nikon Eclipse 80i microscope, 10× objective and NIS-Elements BR software.

RESULTS

Data availability

The authors confirm that the data supporting the findings of this study are available within the article and its online supplemental materials.

Clinical description and genetic findings

The patient is an early adolescent Caucasian male with no relevant family history, born at term after an uneventful pregnancy and...
with a normal neonatal period. He started having focal seizures as a toddler, frequently precipitated by fever, which lasted up to 10 min and on some occasions were followed by brief postictal paresis. Seizures did not respond to phenobarbital or valproate monotherapy but were eventually controlled with combination of valproate and lamotrigine at middle childhood. He remained seizure-free despite AED withdrawal at late childhood. Electroencephalograms were normal or showed infrequent multifocal spikes. Serial brain MRI at the beginning of adolescence showed subtle and non-progressive punctiform frontal subcortical hyperintensities. MRS was normal. Funduscropy and electroretinogram were normal, but visual evoked potentials showed bilateral increased latencies with normal amplitudes.

He had a global developmental delay, with late acquisition of independent walking at early childhood, motor clumsiness and delayed speech, being able to produce only a few bisyllables during early childhood. Early clumsiness evolved to overt signs of spastic paraparesis that worsened slowly during middle childhood but subsequently remained stable. He underwent surgery for strabismus just before early adolescence. The most recent exam showed prominent and symmetrical signs of spasticity in the lower limbs, with hyper-reflexia, bilateral ankle clonus and right Babinski sign, and a wide-base unstable gait. He showed no dysmorphic traits, and head growth was normal. Relevant complementary exams included repeatedly normal plasma and cerebrospinal fluid amino acid profiles (serine: 125 μM, normal value 89–165; glycine: 236 μM, normal value 147–299; cysteine: 28 μM, normal value 24–54).

WES in our patient, followed by variant prioritisation using an in-house bioinformatics pipeline that uses interactome networks based on the clinical presentation (in standard HPO terms),12 revealed a candidate heterozygous deletion variant in SARS1. The variant (chr1:109778053_109778055delGGT, hg19) causes the ablation of a canonical splice site (c.969_969+2delGGT) in the boundary of exon 7 and intron 7. This variant was prioritised due to: (i) its absence from gnomAD13 and other databases of control individuals (ExAC, 1000 Genomes); (ii) being a canonical splice site variant in a predicted loss-of-function intolerant gene and (iii) being located in a gene (SARS1) previously associated with similar clinical presentation as our patient (OMIM #617709). After cosegregation analysis in the parents, this variant was found to be de novo. Patient fibroblast cDNA sequencing showed that this change causes the inclusion of 16 intronic bp into the cDNA, which results in the in-frame insertion of 5 amino acids (p.Lys323_Ile324InsSerArgTrpValArg) (figure 1A,B, online supplemental figure 1).

### Structural and functional characterisation

The deletion is located in evolutionarily conserved motif 2 (residues 291–329) of the SARS1 aminoacylation domain (online supplemental figure 2). A 3D model analysis showed that the inserted residues perturbed the secondary structure of SARS1 by disrupting an important β-strand and displacing the side chain of Phe321 (figure 1C,D). Residue Phe321 is predicted to be important for the recognition of the adenosine ring (A ring) of the AMP molecule through stacking interactions,14 15 suggesting that this variant may affect the overall aminoacylation activity of SARS1. Furthermore, L-serine binding to residue 325 could also be compromised.14 15

In higher eukaryotes, binding of the aminoacylation reaction intermediate analogue (Ser-325) in the active site induces conformational change and tightening of the tRNA binding domain as well as structural ordering of insertions I and II. These conformational changes are necessary to correctly execute the aminoacylation activity and are likely impaired by this mutation.14–16

We next assessed the effects of the variant on protein stability by western blot analysis, using a polyclonal antibody against human SARS1 (Ref: ab183025, Abcam). Results indicate that the insertion did not significantly change SARS1 levels in the patient’s fibroblasts (figure 1E).

To assess SARS1 aminoacylation activity, we performed serylation enzymatic assays using the patient’s fibroblasts compared with sex-matched and age-matched controls (n=3). In brief, we measured radioactivity in fibroblast S100 extracts of the index case and controls at different time points during a 6-hour incubation with 14C-radiolabelled L-serine. Five independent assays performed in duplicate were carried out. Mutant fibroblasts showed reduced (−30%) aminoacylation activity (figure 1F). After ACMG/AMP criteria evaluation,17 and taking into account both de novo segregation (PS2) and enzymatic analysis (PS3), this variant is classified as pathogenic.

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**Figure 1** Seryl-tRNA synthetase 1 (SARS1) de novo variant features.
(A) Family tree. Square: male, circle: female, black symbol: affected individual, white symbols: unaffected individuals, WT: wild-type allele. (B) Representation of variant c.969_969+2delGGT impacting on SARS1 splicing. Disruption of exon 7 donor site leads to the use of an alternative AG donor site located 17–18 bases downstream. This results into the inclusion of 16 intronic bp into the coding sequence, and consequently in the in-frame insertion of 5 amino acids. (C) Primary and secondary structure elements of SARS1. Both sequences are shown starting at F(Phe) 316. WT residues: black; inserted residues: blue. Underlined residues correspond to those being part of the conserved motif 2, present in class II aminoacyl-tRNA synthetases. The two residues in red correspond to F321 and E325 that are involved in ATP and serine recognition, respectively. Below each sequence (letters in grey), secondary structure elements are shown (β=β-strand, α=α-helix and =loop region). (D) Three-dimensional model (based on 4L87, modelled with PyMol) showing the ATP/AMP-Ser binding region of SARS1. Cyan: WT model; dark blue: motif 2; red: mutated region (insertion); pink: AMP-serine analogue. (E) Western blot analysis showing SARS1 and γ-tubulin protein levels in fibroblasts from the patient and age-matched controls (n=3). γ-Tubulin was used as a loading control. (F) SARS1 serylation assays in control and patient-derived fibroblast S100 extracts. tRNA concentration was 22 μM. Data were corrected according to the extract’s concentration. Experiments were performed five times independently.
Analysis of hSARS and its mutant in S. cerevisiae yeast revealed dominant-negative effects

To further study the effect of the mutation, we performed complementation studies in the yeast strain Schizosaccharomyces pombe, which harbours a SARS1 homologue (seryl-tRNA synthetase SES1, YDR232w). This is an essential gene, thus a plasmid copy of the SES1 must be provided on deletion to sustain growth of the haploid strain. We thus constructed a centromeric yeast plasmid (pRS316-γSARS) carrying the URA3 auxotrophic marker and the SES1 gene, including ORF and promoter regions. Subsequently, the SES1 ORF was replaced by either human WT SARS1 cDNA (plasmid pRS316-hSARS) or the mutant version of hSARS (plasmid pRS316-hSARSm) (figure 2A).

Spore analysis showed that substituting SES1 for WT human SARS (hSARS) allowed the generation of viable strains, with similar growth capacities figure 2B, indicating that human SARS1 can compensate for SES1 absence. In contrast, the mutant plasmid carrying the insertion identified in our patient (hSARSm), did not allow the generation of viable haploid strains, meaning that mutant hSARSm1 is not functional in yeast (online supplemental figure 3). However, when the hSARS strain was cotransformed with a plasmid expressing hSARSm1 (emulating heterozygosis), an important growth defect was observed, strongly suggesting a dominant negative effect of hSARSm over the WT SARS1 form (figure 2A).

To assess hSARS aminoacylation activity, we performed similar seryl-tyrosine assays as those performed in fibroblasts, using yeast extracts transfected with hSARS, or cotransfected with hSARS+hSARSm. S100 extracts were incubated with \(^{14}C\)-radio-labelled L-serine for 30 min. Interestingly, the hSARS+hSARSm strain showed a 30% lower activity than hSARS alone, consistent with previous results in fibroblasts, and again suggesting a dominant negative effect of hSARSm over hSARS (figure 2B).

Loss of SARS1 activity causes cellular senescence

Further functional analysis indicated that the patient’s fibroblasts proliferated very slowly, reaching confluence at least four times slower than controls (figure 3A). Mutant fibroblasts showed abnormal shape, being more enlarged and rounded than controls, with nuclear structural alterations such as micronuclei and abnormal mitosis, suggesting an underlying cell division defect (figure 3B). The distribution of WT and mutant SARS1 was consistent with a previously reported, mainly cytosolic pattern with some nuclear localisation. Moreover, β-gal staining revealed increased senescence in patient’s fibroblasts compared with controls (figure 3D). We thus set out to investigate the main molecular effectors of cellular senescence and DNA damage, such as phosphorylated histone H2AX (γ-H2AX). Indeed, western blot analysis showed an increase of γ-H2AX levels in patient’s fibroblasts compared with controls (n=5). SARS1 and SARS2 genes were also quantified. All experiments were performed three times, independently. The values are represented as the means±SD, and Student’s t-test was performed (*p<0.05; **p<0.01; ***p<0.001).

DISCUSSION

In this study, WES identified for the first time a de novo variant in SARS1, challenging the described recessive mode of inheritance, in a patient affected with complex spastic paraparesis with ataxia, seizures and intellectual disability. Two recent articles reported homozygous missense mutations in SARS1 also in close proximity to the active site (c.514G>A, p.Asp172Asn and c.638G>T, p.Arg213Leu), in two families affected by a neurodevelopmental syndrome including microcephaly, ataxia, seizures, moderate intellectual disability and other anomalies such as...
cardiomyopathy, deafness and decompensation during fever.9–10 Alterations in the central nervous system, such as MRI abnormalities including leukencephalopathy, ataxia and seizures, have been reported in both cytoplasmic and mitochondrial ARS-related diseases.3–4,19–20

In this report, we showed that (i) SARS1 activity was significantly decreased both in patient’s fibroblasts and in the ‘heterozygous’ yeast strain; (ii) mutated SARS1 protein did not substitute SES1 activity in yeast and (iii) cell growth was impaired both in patient fibroblasts, and in the yeast strain expressing simultaneously WT and mutated SARS1 forms, emulating our heterozygous patient. These results, together with the presence of five healthy SARS1 loss-of-function variant carriers in the gnomAD database, suggest that this mutation operates through a dominant negative effect, arguing against a haploinsufficiency mechanism. Interestingly, a very recent work described a recurrent de novo pathogenic variant in NARS1, which produced a protein lacking the ATP-binding domain.21 This observation, in addition to our work, strongly suggests that mutations impacting the ATP-binding domain function can yield dominant-negative mutation effects.

In addition, functional characterisation of the patient’s primary fibroblasts indicated severe growth defects and cellular senescence, in combination with a SASP signature. It is intriguing that the opposite mechanism, an overexpression of SARS1 in a transformed BG/HeLa cell line resulted in increased levels of p21, p16 and β-gal and less telomerase recruitment to telomeres, also leading to cellular senescence,22 indicating that a tight regulation of SARS1 levels is pivotal for homeostatic control of cell growth and cell cycle. Thus, SARS1 emerges as the only known tRNA synthetase with such a non-canonical, specific function in cellular senescence. Our results further strengthen the notion that SARS1 dysfunction results into increased senescence levels, and show for the first time how it can be induced by impairing serylation activity, instead of modifying SARS1 expression.

In a more global perspective, tRNA metabolism is closely associated with lifespan and ageing through regulation of processes such as tRNA transcription, modification/transformation of tRNAs, aminocacylation or the effect of the previous on global transcription. As illustrative examples, C. elegans models in which two tRNA synthetase genes were downregulated resulted into increased lifespan (LARS2,21 LARS124), whereas decreased lifespan was observed in several Drosophila models with inactivation or decreased expression of GARS1, MARS2 or MARS1.25

Along these lines, there is previous evidence connecting precocious senescence and neurodevelopmental phenotypes in the literature, including a developmental delay disorder caused by mutations in ALKBH8, a methyltransferase that acts on the wobble uridine base of several tRNA.26,27 Alkbh8-deficient mouse embryonic fibroblasts showed increased β-gal levels, heterochromatin foci and senescence-associated secretory phenotype markers.28 Another tRNA methyltransferase gene, NSUN2, whose recessive loss-of-function mutations cause intellectual disability (OMIM: 611091) is also associated with senescence: NSUN2-knockdown human fibroblasts showed repressed cell proliferation and accelerated replicative senescence.17–18

In summary, we report a novel dominant-negative mutation in SARS1 and a novel mode of inheritance, underscoring the need for caution in interpreting variants in ARS enzyme genes according to inheritance modes, with important implications for genetic diagnosis and counselling. Furthermore, we unveil pivotal roles of this enzyme in the control of cell growth and senescence, underlying the neurodevelopmental phenotypes of affected patients.
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