Data Article

Data on the expression of SRPK1a in mammals

Metaxia Vlassia a, Konstantinos A. Kyritsis b, Ioannis S. Vizirianakis b, Thomas Giannakouros c, Michalis Aivaliotis d, e, Eleni Nikolakaki c, *

a Institute of Biosciences & Applications, National Centre for Scientific Research “Demokritos”, Athens, Greece
b Laboratory of Pharmacology, Department of Pharmacy, Aristotelian University, Thessaloniki, Greece
c Laboratory of Biochemistry, Department of Chemistry, Aristotelian University, Thessaloniki, Greece
d Laboratory of Biological Chemistry, School of Medicine, Aristotelian University, Thessaloniki, Greece
e Functional Proteomics and Systems Biology (FunPATH)-Center for Interdisciplinary Research and Innovation (CIRI-AUTH), Thessaloniki, Greece

A R T I C L E   I N F O

Article history:
Received 11 April 2019
Received in revised form 27 May 2019
Accepted 25 June 2019
Available online 3 July 2019

Keywords:
SR protein kinase
SRPK1
SRPK1a
Mammals
Phylogenetics

A B S T R A C T

SRPK1 is an evolutionary conserved protein kinase that specifically phosphorylates its substrates at serine residues located within arginine-serine-rich (RS) domains. We have previously reported the existence of a second less abundant isoform in humans, SRPK1a, which is formed from alternative splicing of the SRPK1 gene and contains an insertion of 171 amino acids at its N-terminal domain (Nikolakaki et al., 2001). In the NCBI database SRPK1a is annotated as a related to SRPK1-mRNA sequence coding for protein CAC39299.1. Here, we present data on the conservation of the extra sequence of SRPK1a in mammals. Furthermore, the retrieved sequences were comparatively analyzed and data on their evolutionary origin and relationships are also presented.

© 2019 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).
Table 1 is an alignment of the additional SRPK1a mRNA 23-535nt region (Nikolakaki et al., 2001)[1], not found in SRPK1, against RNA-Seq reads of erythroid cell populations [2]. Fig. 1 is a conservation-based colored alignment of partial SRPK1a sequences that contain only the additional N-terminal part of the kinase, in mammals. Table 2 is a list of peptides originated from in silico trypsin digestion of SRPK1a 22-534nt translated region that returned a match in PRIDE database [3,4]. Fig. 2 is a phylogenetic tree obtained by Maximum Likelihood method in MEGA6 [5].

1. Data

Table 1 is an alignment of the additional SRPK1a mRNA 23–535nt region (Nikolakaki et al., 2001)[1], not found in SRPK1, against RNA-Seq reads of erythroid cell populations [2]. Fig. 1 is a conservation-based colored alignment of partial SRPK1a sequences that contain only the additional N-terminal part of the kinase, in mammals. Table 2 is a list of peptides originated from in silico trypsin digestion of SRPK1a 22-534nt translated region that returned a match in PRIDE database [3,4]. Fig. 2 is a phylogenetic tree obtained by Maximum Likelihood method in MEGA6 [5].

2. Experimental design, materials and methods

Sequence similarity searches and multiple sequence alignments were performed using the NCBI tools: Sequence Read Archive (SRA) BLASTN [6], BLASTP [7] and COBALT [8], respectively. The GeneDoc tool [9] was employed for conservation-based color visualizations of the alignments and production of the alignment figures. The PeptideMass tool in default settings [10] was used to retrieve in silico specific

| Gene    | Accession_ID | mRNA_region | GSE_ID     | SRA_ID        | Cell_type        | No of_RNA-Seq_reads (100%) |
|---------|--------------|-------------|------------|---------------|------------------|-----------------------------|
| SRPK1a  | AJ318054.1   | 23–535      | GSE53635   | SRX398536     | proerythroblast   | 27                          |
| SRPK1a  | AJ318054.1   | 23–535      | GSE53635   | SRX398537     | early_basophilic  | 7                           |
| SRPK1a  | AJ318054.1   | 23–535      | GSE53635   | SRX398538     | late_basophilic   | 6                           |
SRPK1a peptide sequences, following in silico trypsin digestion of the human SRPK1a mRNA (AJ318054.1) 22-534nt segment translated into protein (sequence included within the arrows in Fig. 1). The resulting peptides were then used as queries in the PRIDE database [3,4]. Evolutionary analyses and drawing of the phylogenetic tree were conducted by the Maximum Likelihood method in MEGA6 [5]. Annotations of organisms were done manually, based on the known classification of the organisms described in the COBALT output.

Fig. 1. Conservation-based colored sequence alignment, drawn using the GeneDoc program [9]. Nomenclatures are according to organism names. The corresponding accession numbers in the NCBI protein database are shown in Fig. 2. Coloring scale: red, blue, and grey, for 100%, 80% and 60% sequence conservation, respectively. Arrows denote the starting and ending amino acid residues (glycine and alanine, respectively) of the additional sequence which is found only in SRPK1a and is omitted in SRPK1.
Table 2

*In silico* trypsin digestion of SRPK1a 22–534 translated region. Below are shown the resulting peptides that returned a match in PRIDE database (PRD000004, human plasma proteome; PXD001383, chromatin-associated and soluble human transcription factor complexes; PXD000593, human CDK family protein complexes), as well as the local alignment identity score of SRPK1a (CAC39299.1) with the PRIDE peptide matches using BLASTP [7].

| Gene | Accession number | *In silico* digestion position | Tryptic peptide | PRIDE database tryptic peptide match Accession ID | BLASTP top result | BLASTP identity score (%) |
|------|------------------|--------------------------------|----------------|-----------------------------------------------|-------------------|---------------------------|
| SRPK1a | AJ318054.1 | 94–113 | RPPPARPLTRPETPAHPAR | PRD000004 | SRPK1a (CAC39299.1) | 95 |
| SRPK1a | AJ318054.1 | 138–156 | QAPQPGLPGLHPLGQR | PXD0001383 | SRPK1a (CAC39299.1) | 100 |
| SRPK1a | AJ318054.1 | 157–171 | LLSSTFALHPSLPA | PXD0001383 | SRPK1a (CAC39299.1) | 100 |
| SRPK1a | AJ318054.1 | 80–92 | ALGPLQGPAKG | PXD0001383; PXD000593 | SRPK1a (CAC39299.1) | 100 |
Fig. 2. Molecular Phylogenetic analysis by the Maximum Likelihood method. The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model [11]. The tree with the highest log likelihood (−6947.2720) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (above the branches). The analysis involved 49 amino acid sequences (the corresponding accession numbers in the NCBI protein database, are indicated; see also Fig. 1). All positions containing gaps and missing data were eliminated. There were a total of 605 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [5].

Acknowledgements

M.V. (NCSR “Demokritos”) acknowledges support of this work by the projects: “INSPIRED-The National Research Infrastructures on Integrated Structural Biology, Drug Screening Efforts and Drug target functional characterization” (MIS 5002550) implemented under the Action “Reinforcement of the Research and Innovation Infrastructure”, and “SANITURA-Target Identification and Development of Novel Approaches for Health and Environmental Applications” (MIS 5002514) implemented under the
Action for the Strategic Development on the Research and Technological Sectors, both funded by the Operational Programme “Competitiveness, Entrepreneurship and Innovation” (NSRF 2014–2020) and co-financed by Greece and the European Union (European Regional Development Fund).

**Conflict of interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

**References**

[1] E. Nikolakaki, R. Kohen, A.M. Hartmann, S. Stamm, E. Georgatsou, T. Giannakouros, Cloning and characterization of an alternatively spliced form of SR protein kinase 1 that interacts specifically with scaffold attachment factor-B, J. Biol. Chem. 276 (43) (2001) 40175–40182.

[2] H. Pimentel, M. Parra, S.L. Gee, N. Mohandas, L. Pachter, J.G. Conboy, A dynamic intron retention program enriched in RNA processing genes regulates gene expression during terminal erythropoiesis, Nucleic Acids Res. 44 (2) (2016) 838–851.

[3] J.A. Vizcaíno, E.W. Deutsch, R. Wang, A. Csordas, F. Reisinger, D. Rios, J.A. Dianes, Z. Sun, T. Farrah, N. Bandeira, P.A. Binz, I. Xenarios, M. Eisenacher, G. Mayer, L. Gatto, A. Campos, R.J. Chalkley, H.J. Kraus, J.P. Albar, S. Martinez-Bartolomé, R. Apweiler, G.S. Omenn, L. Martens, A.R. Jones, H. Hermjakob, ProteomeXchange provides globally coordinated proteomics data submission and dissemination, Nat. Biotechnol. 32 (3) (2014) 223–226.

[4] J.A. Vizcaíno, A. Csordas, N. Del-Toro, J.A. Dianes, J. Griss, I. Lavidas, G. Mayer, Y. Perez-Riverol, F. Reisinger, T. Ternent, Q.W. Xu, R. Wang, H. Hermjakob, 2016 update of the PRIDE database and its related tools, Nucleic Acids Res. 44 (22) (2016) 11033.

[5] K. Tamura, G. Stecher, D. Peterson, A. Filipski, S. Kumar, MEGA6: molecular evolutionary genetics analysis version 6.0, Mol. Biol. Evol. 30 (12) (2013) 2725–2729.

[6] S.F. Altschul, W. Gish, W. Miller, E.W. Myers, D.J. Lipman, Basic local alignment search tool, J. Mol. Biol. 215 (3) (1990) 403–410.

[7] S.F. Altschul, T.L. Madden, A.A. Schaffer, J. Zhang, Z. Zhang, W. Miller, D.J. Lipman, Gapped BLAST and PSI-BLAST: a new generation of protein database search programs, Nucleic Acids Res. 25 (17) (1997) 3389–3402.

[8] J.S. Papadopoulos, R. Agarwala, COBALT: constraint-based alignment tool for multiple protein sequences, Bioinformatics 23 (9) (2007) 1073–1079.

[9] K.B. Nicholas, H.B.J. Nicholas, GeneDoc: a Tool for Editing and Annotating Multiple Sequence Alignments, Distributed by the author, 1997, http://www.psc.edu/biomed/genedoc.

[10] E. Gasteiger, A. Gattiker, C. Hoogland, I. Ivanyi, R.D. Appel, A. Bairoch, ExPASy: the proteomics server for in-depth protein knowledge and analysis, Nucleic Acids Res. 31 (13) (2003) 3784–3788.

[11] D.T. Jones, W.R. Taylor, J.M. Thornton, The rapid generation of mutation data matrices from protein sequences, Comput. Appl. Biosci. 8 (3) (1992) 275–282.