Data in Brief 8 (2016) 360–363

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data in support of qPCR primer design and verification in a Pink1 −/− rat model of Parkinson disease

Cynthia A. Kelm-Nelson [a,*], Sharon A. Stevenson [b], Michelle R. Ciucci [a,c,d]

[a] Department of Surgery, Division of Otolaryngology, University of Wisconsin-Madison, Madison, WI, USA
[b] Department of Zoology, University of Wisconsin-Madison, Madison, WI, USA
[c] Neuroscience Training Program, University of Wisconsin-Madison, Madison, WI, USA
[d] Department of Communication Sciences and Disorders, University of Wisconsin-Madison, Madison, WI, USA

ARTICLE INFO

Article history:
Received 6 April 2016
Received in revised form
12 May 2016
Accepted 24 May 2016
Available online 30 May 2016

ABSTRACT

Datasets provided in this article represent the *Rattus norvegicus* primer design and verification used in *Pink1* −/− and wildtype Long Evans brain tissue. Accessible tables include relevant information, accession numbers, sequences, temperatures and product length, describing primer design specific to the transcript amplification use. Additionally, results of Sanger sequencing of qPCR reaction products (FASTA aligned sequences) are presented for genes of interest. Results and further interpretation and discussion can be found in the original research article "Atp13a2 expression in the periaqueductal gray is decreased in the *Pink1* −/− rat model of Parkinson disease" [1].

Specifications table

Subject area	*Biology*
More specific subject area	*Neurobiology of disease*

DOI of original article: http://dx.doi.org/10.1016/j.neulet.2016.04.003
* Correspondence to: Department of Surgery, Division of Otolaryngology, 1300 University Avenue, 483 Medical Sciences Center, University of Wisconsin-Madison, Madison, WI 53706, USA. Tel.: +1 608 262 6122; fax: +1 608 262 6356.
E-mail address: CAKelm@wisc.edu (C.A. Kelm-Nelson).

http://dx.doi.org/10.1016/j.dib.2016.05.056

Type of data	*Tables*
How data was acquired	National Center for Biotechnology Information (NCBI) Primer Blast was used to design primers and Sanger sequencing was used for primer confirmation.
Data format	*Raw*
Experimental factors	Netprimer® (PREMIER Biosoft, Palo Alto, CA, USA) was used to examine secondary structure of all primers designed through NCBI Primer Blast to avoid primer products. Non-template controls were run with each primer pair to check for formation of primer-dimers and non-specific amplification products.
Experimental features	Specificity for each primer pair was confirmed using melt curve analysis; all primer runs yielded single peak melt curves indicating amplification of single gene products. Furthermore, the qPCR reaction product for each gene was sequenced using Sanger sequencing with both forward and reverse primers at the University of Wisconsin Biotechnology Center to confirm that sequences match intended targets.
Data source location	*Madison, Wisconsin, USA*
Data accessibility	*Data are within this article*

Value of the data

- **Data presented here allows for experimental replication.**
- **Data can be used as a benchmark for other researchers using rat brain tissue.**
- **Primers can then be manufactured and used in alternative models of Parkinson disease and then compared to this data set.**

1. Data

Table 1 describes the rat (*Rattus norvegicus)* primer information including gene name, gene abbreviation, GenBank® accession numbers, experimental primer sequences, melt temperature and product length (base pairs) for each gene (*Pink1*, *Asyn*, *Th*, *D1*, *D2*, *Atp13a2*, *Gba*, *Cflar*, *Gabrb2*, *Gad1*, *Gad2*) as well as reference genes (*Gapdh*, *βactin*).

Table 2 describes the results of Sanger sequencing of qPCR reaction product for each amplification product from the University of Wisconsin Biotechnology Center. Confirmed results presented are FASTA sequences confirmed through NCBI Nucleotide BLAST software.

2. Experimental design, materials and methods

Netprimer (PREMIER Biosoft, Palo Alto, CA, USA) was used to examine secondary structure of all primers designed through NCBI Primer Blast to avoid primer products (Table 1). The Pink1 gene primer was used based on a previous publication [2]. Non-template controls were run with each primer pair to check for formation of primer-dimers and non-specific amplification products. Specificity for each primer pair was confirmed using melt curve analysis; all primer runs yielded single peak melt curves indicating amplification of single gene products. Furthermore, the qPCR reaction product for each gene was sequenced using Sanger sequencing with both forward and reverse primers at the University of Wisconsin Biotechnology Center (Table 2). FASTA sequences were entered into the NCBI Nucleotide BLAST software to confirm that sequences matched intended targets.

Table 1
Rattus norvegicus primer information.

Gene	Gene abbreviation	Accession number	Direction	Sequences	T (°C)	Product (bp)
Gapdh glyceraldehyde-3-phosphate dehydrogenase	*Gapdh*	NM_017008.4	Forward Reverse	GGATACTGAGAGCAAGAGAGA TTATGGGGTCTGGGATGGAA	59	106
Actb actin, beta	*βactin*	NM_031144.3	Forward Reverse	TGTGGATTGGTGGCTCTATC AGAAAGGGTGTAAAACGCAG	59	149
Pink1 PTEN induced putative kinase 1	*Pink1*	Primers created from Dave et al. [2]	Forward Reverse	CATGGCTTTGGATGGAGAGT TGGGAGTTTGCTCTTCAAGG	58	n/a
Snca synuclein, alpha (non-A4 component of amyloid precursor)	*Asyn*	NM_019169.2	Forward Reverse	TCAGCCCAGAGCCTTTCAC AGCCACAACTCCCTCCTTG	58	165
Th tyrosine hydroxylase	*Th*	NM_012740.3	Forward Reverse	CTTTGACCCAGACACAGCA TGGATACGAGAGGCATAGTTC	59	123
Drd1 dopamine receptor D1	*D1*	NM_012546.2	Forward Reverse	GCTGGCTCCCTTTCTTCATC CACCCAAACCACACAAACAC	60	111
Drd2 dopamine receptor D2	*D2*	NM_012547.1	Forward Reverse	TCCTTGACCTTCCTCTTGGG CCTGACACTGATGTTGCCTG	60	188
Atp13a2 ATPase type 13A2	*Atp13a2*	NM_001173432.1	Forward Reverse	CTTCTCTCTGTCTGGCTTCC TCCTCAGTCCGTTGGTGTAG	60	95
Gba glucosidase, beta, acid	*Gba*	NM_001127639.1	Forward Reverse	GAGCAGAGTGTTCGGTTAGG GATTCAGGGCAAGGTTCCAG	60	115
Cflar CASP8 and FADD-like apoptosis regulator	*Cflar*	NM_001033864.2	Forward Reverse	GTGCTGCTGATGGAGATTGG CTCTTGTCCTTGGCTACCTTG	60	107
Gabrb2 gamma-aminobutyric acid (GABA) A receptor, beta 2	*Gabrb2*	NM_012957.2	Forward Reverse	GGTGCTTTGTCTTTGTCTTTATGG CGCATCTTCTCGTTGTTGG	61	130
Gad1 glutamate decarboxylase 1	*Gad1*	NM_017007.1	Forward Reverse	GACACTTGAACAGTAGAGACCC TGTAGGACGCAGGTTGGTAG	61	116
Gad2 glutamate decarboxylase 2	*Gad2*	NM_012563.1	Forward Reverse	CCAGGCTCATCGCATTCAC GCACTCACCAGGAAAGGAAC	61	190

Table 2
Results of Sanger sequencing of qPCR reaction product.

Gene	FASTA (Aligned Sequence)
Gapdh	ATCCCAACTCGGCCCCCAACACTGAGCATCTCCCTCACAATTTCCATCCCAGACCCCCATAA
βactin	AGATGTGGATCAGCAAGCAGGAGTACGATGAGTCCGGCCCCTCCATCGTGCACCGCAAATGCTTCTAGGCGGACTGTTAC
PINK1	CTCTTCTCATTTTTCCCGACCAC
Asyn	GGGGAAAACAGGAGGAATCAGAGTTCTGCGGAAGCCTAGAGAGCCGTGTGGAGCAAAGATACATCTTTAGCCATGGATGT
Th	CCAGCCTGTGTACTTTGTGTCCGAGAGCTTCAATGACGCCAAGGACAAGCTCAGG
D1	GGCTCCCTTTCTTCATCTCGAACTGTATGGTGCCCTTCTGTGGCTCTGAGGAGACCCAGCCAT
D2	TTCCTTGACCTTCCTCTTGGGCACAGAAACTAGCTCAGTGGTCGAGCACACCCTGATCGCTGG
Atp13a2	CGGTGTCTAAGGGGGCACCCTTCCGCCAGCCGCTCTACACCAACGGACTGAGGAA
Gba	GCAACTGTTACCACGTCAATTCCATG
Cflar	CTGATGGAGATTGGGGAGAATTTGAATCAATCTGATGTATCCTCCTTAATTT
Gabrb2	TCTTCTTTGGGAGAGGACCCCAGCGCCAAAAGAAAGCAGCTGAGAAAGCTGCTAATGCCAACAACGAGAAGATGCG
Gad1	GCATCTTCCACGCCTTCGCCTGCAACCTCCTCGAACGCGGGAGCGGATCCTAATACTACCAACCTGCGTCCTACAA
Gad2	GCCTTGGGGATCGGAACAGACAGCGTGATTCTGATTAAATGTGATGAGAGAGGGAAAATGATCCCATCTGACCTTGAAAG

Transparency document. Supplementary material

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.05.056.

References

[1] C.A. Kelm-Nelson, S.A. Stevenson, M.R. Ciucci, Atp13a2 expression in the periaqueductal gray is decreased in the Pink1 −/− rat model of Parkinson disease, Neurosci. Lett. 621 (2016) 75–82.
[2] K.D. Dave, et al., Phenotypic characterization of recessive gene knockout rat models of Parkinson's disease, Neurobiol. Dis. 70 (0) (2014) 190–203.