Data in Brief 12 (2017) 616–623

Contents lists available at ScienceDirect

Data in Brief

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

Data Article

Data on the exon-intron organization of genes coding for B-cell receptor-like proteins

Sergey Y. Morozov*, Anna V. Pankratenko,
Anastasia K. Atabekova, Andrey G. Solovyev

Department of Virology and A. N. Belozersky Institute of Physico-Chemical Biology,
Lomonosov Moscow State University, 119992 Moscow, Russia

ARTICLE INFO

Article history:
Received 19 October 2016
Received in revised form
26 April 2017
Accepted 3 May 2017
Available online 6 May 2017

Keywords:
B-cell receptor protein
Gene organization
Exons
Introns
Unikonts
Bikonts

ABSTRACT

B-cell receptor-associated protein (BAP) family plays important roles in the ER homeostasis and stress responses of eukaryotic cells [1]. We reported the analysis of plant BAP-like (PBL) genes and the encoded proteins of higher land plants [2]. The origin and functional divergence of these genes among all eukaryotes, however, are poorly studied, which impedes our understanding of the functional relationships and diversity among BAP-like proteins. One possible reason for the potential functional diversity may be the differences in the exon-intron structure of PBL genes. In this study, we first performed analysis of the exon-intron organization of these genes in the genome sequences of the Viridiplantae species in addition to previously published data on Angiosperms [2]. To further address the distribution of BAP-like genes in other eukaryotes, we extended our dataset to include the representative genes encoded by non-plant bikonts and unikonts [3].

DOI of original article: http://dx.doi.org/10.1016/j.biochi.2016.10.009

* Corresponding author.
E-mail address: morozov@genebee.msu.su (S.Y. Morozov).

http://dx.doi.org/10.1016/j.dib.2017.05.011

Specifications Table

Subject area	*Biology*
More specific subject area	*Phylogenomics*
Type of data	*Table*
How data was acquired	*Gene sequence organizations and protein parameters were derived using ExPASy software, NCBI, Dendrome and Phytozome databases (see below)*
Data format	*Analyzed*
Experimental factors	*Amino acid and nucleotide sequences were retrieved from NCBI, Dendrome and Phytozome databases (see below).*
Experimental features	*Gene and protein sequences were derived using NCBI, Dendrome and Phytozome databases (see below)*
Data source location	NCBI: http://www.ncbi.nlm.nih.gov/ Phytozome v11: http://www.phytozome.net/ ExPASy: http://www.expasy.org/tools/ Dendrome: http://dendrome.ucdavis.edu/
Data accessibility	*With this article*

Value of the data

- The BAP-like genes are usually combined in small gene families and encoded by all well-studied eukaryotic taxons belonging to bikonts and unikonts.
- Data on BAP-like gene organizations enable researchers to compare how these genes evolved during progression of different eukaryotic branches resulted, particularly, in appearance of mammals and flowering plants.
- Data on BAP-like proteins and genes are intriguing to understand their unique features in different taxons.
- Data on gene organizations enable researchers to infer the possible ranges of time frames in the drastic divergence events (particularly, intron gain and loss) of BAP-like genes.

1. Data and experimental design

Annotation information was obtained for 29 representative genes in bikonts (Table 1) and 81 genes in unikonts (Table 2) [1-3]using Blast2GO program.

2. Materials and methods

Annotation of the predicted genes and proteins was mined at the National Center for Biotechnology Information database (NCBI) and Phytozome database, version 11. Additional annotation of other predicted BAP-like proteins and genes was extracted from The UniProt Knowledgebase database (http://www.uniprot.org/).