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Data Article

Small RNA data set that includes tRNA-derived fragments from Jurkat cells treated with camptothecin



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ARTICLE INFO

Article history:

Received 20 December 2017

Received in revised form

15 January 2018

Accepted 18 January 2018

Available online 3 February 2018

ABSTRACT

In this article, we report a small RNA data set obtained from human T cell acute leukemia Jurkat cells, which were treated with the universal apoptotic agent camptothecin. Based on the Annexin-V labeling pattern, we sorted two Jurkat subpopulations in treated cells: one that is sensitive to the drug and the other being relatively more resistant. We report new original data that include the frequency of tRNA-derived fragments (tRF) in drug-sensitive and resistant cells. We also present partially analyzed data to show the origin of reads on tRNAs as well as the borders of the fragments. We believe that this data can benefit the science community working in the field of tRF and/or apoptosis.

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Specifications Table

Subject area	Biology
More specific subject area	Molecular Genetics

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<https://doi.org/10.1016/j.dib.2018.01.050>

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Type of data	Figures and Excel file
How data was acquired	Deep sequencing of total RNAs
Data format	Analyzed data
Experimental factors	Drug treatment and cell sorting
Experimental features	Total RNAs isolated from sorted cells were subjected to deep-sequencing using Illumina platform
Data source location	Izmir, Turkey
Data accessibility	Raw data available at GEO (Accession number GSE35442)

Value of the data

- These data can be used to study drug-induced fragmentation pattern of tRNAs.
- The abundance of tRNA-related fragments in drug-sensitive and resistant cells can be used to study potential tRF-mediated regulation of apoptosis.
- These data are also useful for the researchers interested in the discovery of novel tRNA-related apoptotic markers.

1. Data

We report three pieces of data. The data in Fig. 1 show the percentage of small RNA reads in each sub-population. Panel A in Fig. 2 is a graph of tRNA-derived fragments superimposed onto a representative tRNA. Panel B in Fig. 2 displays the potential 3' cleavage site of tRNA-derived fragments on a

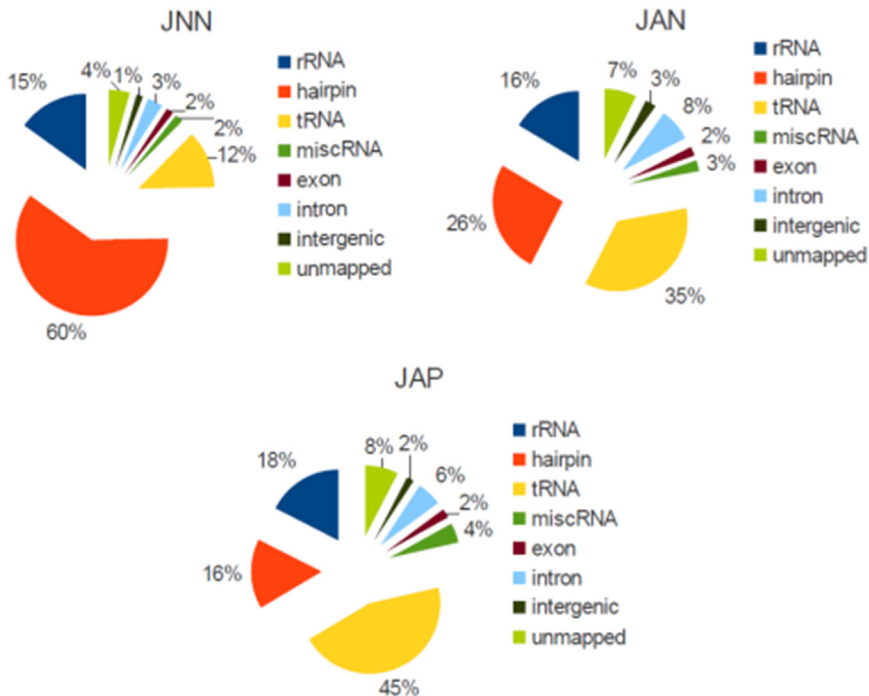


Fig. 1. The percentage of different small RNA populations in the drug-free, control cells (JNN), camptothecin-treated and Annexin V-positive cells (JAP) and camptothecin-treated and Annexin V-negative cells (JAN).

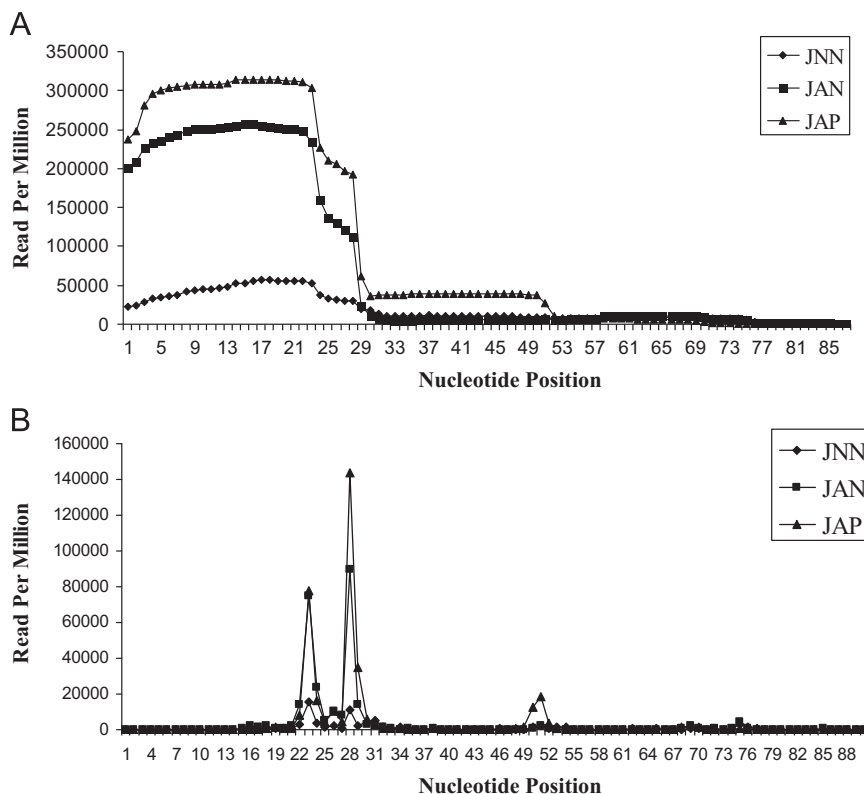


Fig. 2. Camptothecin-induced tRNA fragmentation in Jurkat cells. (A) Cloning frequency of each nucleotide on a representative tRNA. (B) The position of 3' terminus of tRNA-derived fragments relative to their 5' terminus.

representative RNA. Expression levels of tRNA-derived fragments are listed in a supplementary Microsoft Excel Table ([Supplementary Table 1](#)).

2. Experimental design, materials and methods

Jurkat cells were treated with camptothecin (8 μ M for 4 h) or incubated in media (control). A subpopulation of cells remained resistant to apoptosis despite the treatment with 128-fold drug concentration. Each population was sorted using Annexin-V-conjugated magnetic beads, resulting in three types of cells: (1) untreated control cells (JNN, Jurkat negative negative); (2) drug-treated but Annexin-V-negative cells (JAN, Jurkat apoptosis negative); and (3) drug-treated, apoptosis, Annexin-V-positive cells (JAP). Total RNAs isolated from each sample type were subjected to deep-sequencing and reads were blasted to the human genome to identify the read frequency of tRNA-derived sequences [1].

Acknowledgements

This work was supported by the Scientific and Technical Research Council of Turkey (107T475 to BA).

Transparency document. Supplementary material

Transparency document associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2018.01.050>.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2018.01.050>.

Reference

- [1] I. Erdogan, M.I. Cosacak, A. Nalbant, B. Akgul, Deep sequencing reveals two Jurkat subpopulations with distinct miRNA profiles during camptothecin-induced apoptosis, *BIORXIV* (2017) 237099.