Data article

Changes in apoptotic gene expression induced by the DNA cross-linkers epichlorohydrin and diepoxybutane in human cell lines

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**ABSTRACT**

Real time quantitative reverse transcription PCR was used to monitor changes in apoptotic gene expression after treating cells with the DNA cross-linkers epichlorohydrin (ECH) and diepoxybutane (DEB). This article presents the data obtained from application of the comparative $C_T$ method to the amplification of twelve apoptotic genes in human MCF10-A cells and eight genes in HUVEC cells. Further insight regarding the significance of these data can be found in "Cross-linking by epichlorohydrin and diepoxybutane correlates with cytotoxicity and leads to apoptosis in human leukemia (HL-60) cells" (Le et al., 2018) [1].

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**Specifications Table**

| Subject area   | Chemistry |
|----------------|-----------|
| More specific subject area | Biochemistry |
| Type of data | Tables |
| How data was acquired | Real time quantitative reverse transcription PCR |
| Data format | Analyzed |

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Experimental factors

The expression of genes involved in apoptosis was analyzed via qRT-PCR after treatment of cells with the cross-linking agents epichlorohydrin and diepoxybutane.

Experimental features

Cells were treated with cross-linkers, and reverse transcription and amplification were performed in a single reaction with a real-time PCR system. The comparative C_T method was used to quantify gene expression in drug-treated versus untreated cells, with actin used as the endogenous control.

Data source location

N/A

Data accessibility

Data are within this article

Value of the data

- Previous studies of the cytotoxic mechanism of DNA cross-linkers have often used cancer cells, which are prone to apoptosis. MCF10-A and HUVEC cells are models of non-cancer cell lines.
- These data provide information about changes in the expression of several genes involved in apoptosis after treating cells with the cross-linkers epichlorohydrin (ECH) or diepoxybutane (DEB), providing insight into the pathways by which cell death results.
- These data suggest mechanistic differences in the modes of action of these structurally related compounds, which are likely to be related to the observed differences in cytotoxicities and carcinogenic potentials. These findings may also be useful in the design of chemotherapeutic cross-linking agents.

1. Data

Results from comparative C_T tests [1,2] for MCF10-A cells treated with ECH (Table 1) or DEB (Table 2) and for HUVEC cells treated with DEB (Table 3) are presented. Target genes are from a human apoptosis array. Positive \( \Delta \Delta C_T \) values indicate downregulation; negative \( \Delta \Delta C_T \) values indicate upregulation.

2. Experimental design, materials and methods

Drug treatment conditions were as follows: 2.0 mM DEB, 48 h and 2.5 mM ECH, 48 h for MCF10-A cells; 0.05 mM DEB, 24 h for HUVEC cells. Total RNA was purified from untreated and drug-treated

Table 1

| Target gene | \( \Delta \Delta C_T \) Mean | \( \Delta \Delta C_T \) SE | t-stat | p-value | Expression | N |
|-------------|---------------------------|-------------------------|--------|---------|------------|---|
| BOK         | 1.457                     | 0.445                   | 3.275  | 0.031   | –          | 5 |
| DIABLO      | 3.606                     | 1.020                   | 3.535  | 0.038   | –          | 4 |
| PUMA        | 4.673                     | 0.543                   | 8.507  | 0.013   | –          | 3 |
| BIM         | –2.189                    | 0.724                   | –3.022 | 0.039   | +          | 5 |
| BAX         | 2.294                     | 0.469                   | 4.593  | 0.013   | –          | 3 |
| BAK1        | 2.840                     | 0.095                   | 29.759 | 0.001   | –          | 3 |
| APAF-1      | 6.479                     | 0.390                   | 16.620 | 0.000   | –          | 6 |
| CASP-9      | 5.859                     | 0.397                   | 14.764 | 0.000   | –          | 6 |
| CASP-8      | 2.785                     | 0.230                   | 12.130 | 0.001   | –          | 4 |
| CASP-2      | 3.949                     | 0.670                   | 5.893  | 0.027   | –          | 3 |
| TANK        | 1.088                     | 0.335                   | 3.245  | 0.031   | –          | 5 |
| BCL-2       | 5.229                     | 0.274                   | 19.074 | 0.003   | –          | 3 |
Reverse transcription and amplification were performed (Qiagen QuantiFast SYBR Green RT-PCR kit) with primers from the Human Apoptosis Primer Library (RealTimePrimers.com). Amplification conditions were as follows: 50 °C for 10 min, 95 °C for 5 min, 50 cycles of 95 °C for 10 s and 58 °C for 45 s in a StepOne Real-Time PCR system (Applied Biosystems).

CT values were determined for each gene of interest, as well as for an internal control (actin). ΔCT values were then calculated by subtracting the CT value for the actin control from the CT value for each gene of interest. To assess the effects of drug treatment on gene expression, the ΔΔCT value was calculated for each gene of interest by subtracting the ΔCT value for untreated cells from the ΔCT value for drug-treated cells (ΔΔCT = ΔCT treated − ΔCT untreated).

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2018.05.133.
Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2018.05.133.

References

[1] P.M. Le, V.L. Silvestri, S.C. Redstone, J.B. Dunn and J.T. Millard, Cross-linking by epichlorohydrin and diepoxybutane correlates with cytotoxicity and leads to apoptosis in human leukemia (HL-60) cells, Toxicol. Appl. Pharmacol. 352 (2018) 19-27. http://dx.doi.org/10.1016/j.taap.2018.05.020.

[2] T.D. Schmittgen, K.J. Livak, Analyzing real-time PCR data by the comparative C_t method, Nat. Protoc. 3 (2008) 1101–1108.