Data in Brief

Expression data of HeLa cells treated with CENP-E siRNA or Eg5 siRNA in the presence of BubR1 siRNA

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ABSTRACT

The molecular mechanism responsible for cell fate after mitotic slippage is unclear. We investigated the postmitotic effects of different mitotic aberrations (Ohashi et al. [1]), misaligned chromosomes produced by CENP-E siRNA (siCENP-E), and monopolar spindles resulting from Eg5 siRNA (siEg5) (Miki et al. [2]). To determine which signaling pathways contribute to the postmitotic effect of siCENP-E in the presence of siBubR1 (siCENP-E + siBubR1) compared with siEg5 + siBubR1, we performed comprehensive gene expression analysis using microarray comparisons [1]. The microarray data have been deposited in NCBI’s Gene Expression Omnibus (GEO) and are accessible through GEO Series accession number GSE67905.

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2. Experimental design, materials and methods

2.1. Cell cultures

HeLa cells, purchased from American Type Culture Collection (ATCC; Manassas, VA, USA), were cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% FBS.

2.2. Transfection of siRNA oligonucleotides

We investigated the postmitotic effects of different mitotic aberrations [1], misaligned chromosomes by siCENP-E and monopolar spindles by siEg5 [2], siRNA oligonucleotides targeting CENP-E (M-003252-02), Eg5 (M-003317-01), and BubR1 (M-004101-02) were obtained from Dharmacon (SMART pools, Dharmacon, Lafayette, CO, USA). The siTrino negative control (B-Bridge International, Inc., Mountain View, CA, USA) was used as a non-silencing (NS) siRNA (siNS). Twenty-five nanomoles of pooled siRNA per gene were used for double knockdown (total siRNA concentration, 50 nM). siRNA transfection was performed as described previously [3]. Transfection of siRNA oligonucleotides was performed with Dharmafect (Dharmacon) in 6-well plates according to the manufacturer's specifications. Seventy-two hours after transfection, the cells were collected for RNA preparation for GeneChip microarray analysis.

2.3. GeneChip microarray analysis

To determine which signaling pathways contribute to the postmitotic effect of siCENP-E + siBubR1 compared with siEg5 +
siBubR1, we performed comprehensive gene expression analysis using microarray comparisons (Fig. 1).

Total RNAs were extracted using the RNeasy Miniprep kit (Qiagen, Valencia, CA, USA) according to the manufacturer’s protocol. Preparation of cDNAs and cRNAs, hybridization, and microarray scanning were performed according to the manufacturer’s protocols (Affymetrix Inc., CA, USA). Biotinylated cRNAs were hybridized to Affymetrix Human Genome U133 Plus 2.0 Array. Microarray Analysis Suite 5.0 (MAS5; Affymetrix) was used to quantify microarray signals, and the intensities were normalized to the median expression level by setting the median intensity to 1.0 using the GeneSpring software package (Agilent Technology, Santa Clara, CA, USA). Differentially expressed genes were identified with a fold change of >2.0. Probe sets with absent call in all samples for comparison were filtered out. In addition, intensity filtering was applied, with the criterion set to 0.5. The microarray data have been deposited in NCBI’s Gene Expression Omnibus (GEO) and are accessible through GEO Series accession number GSE67905.

3. Discussion

In this study, we acquired microarray gene expression profiles for siBubR1 + siCENP-E-treated, siBubR1 + siEg5-treated, and siBubR1 -treated cells. These expression data would be valuable for understanding the postmitotic effects of aneuploidy as well as polyploidy.

Conflict of interest

Yusuke Nakayama and Akihiro Ohashi are employees of Takeda Pharmaceutical Company, Ltd.

Acknowledgments

This research was supported by Takeda Pharmaceutical Company, Ltd.

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