Genomics Data 6 (2015) 182–183

Contents lists available at ScienceDirect

Genomics Data

journal homepage: http://www.journals.elsevier.com/genomics-data/

Data in Brief

Expression data from primary culture human myometrial cells

Kaiyu Lei *, Suren R. Sooranna, Mark R. Johnson

Imperial College London, UK

ARTICLE INFO

Article history:
Received 7 September 2015
Received in revised form 9 September 2015
Accepted 11 September 2015
Available online 12 September 2015

Keywords:
Myometrium
Pregnancy
Inflammation
P4
IL-1β

ABSTRACT

Inflammation plays a central role in many human diseases. Human parturition also resembles an inflammatory reaction, where progesterone (P4) and progesterone receptors (PRs) have already been demonstrated to suppress contraction-associated gene expression. In our previous studies, we have found that the progesterone actions, including progesterone-induced gene expression and progesterone's anti-inflammatory effect, are mediated by PR, GR or both. In this study, we used microarrays (GSE68171) to find P4 and IL-1β responsive genes and IL-1β responsive genes which were repressed by P4. These data may provide a broader view of gene networks and cellular functions regulated by P4 and IL-1β in human myometrial cells. These data will also help us understand the role of PR and GR in human parturition.

Specifications	
Organism/cell line/tissue	Human primary uterine smooth muscle cells
Sex	Female
Sequencer or array type	Affymetrix GeneChip® Scanner 3000
Data format	Raw
Experimental factors	Normal term not in labour samples
Experimental features	Primary cultures of human myometrial cells were grown from myometrial biopsies obtained at the time of elective caesarean section. Cells were exposed to different stimuli, IL-1β (5 ng/mL) and P4 (10 μM), either alone or in combination for 6 h, and then total RNA were extracted from each culture. Three comparisons were carried out including: 1. V vs. P4; 2. V vs. IL-1β; 3. IL-1β vs. IL-1β + P4.
Consent	All specimens were obtained after fully informed, written patient consent. The Riverside Ethics committee approved the study.
Sample source location	London, UK

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE68171 [1].

2. Experimental design, materials and methods

Primary human myometrial cells were isolated using a mixture of collagenases {1 mg/mL of collagenase 1 A and 1 mg/ml of collagenase XI (Sigma)} and cultured in DMEM medium containing phenol red 7.5% foetal calf serum, L-glutamine and 100 mU/mL penicillin and 100 μg/mL streptomycin in an atmosphere of 5% CO2: 95% air at 37 °C [2]. Cells were exposed to IL-1β, P4 either alone or in combination; ethanol was used as the vehicle control for 6 h. Total RNA was extracted and purified from myometrial cells grown in 6-well culture plates using RNAeasy mini kit (Qiagen). cDNA generated from 2 μg of total RNA using the GeneChip® Expression 3′-Amplification One-Cycle cDNA Synthesis Kit, in conjunction with the GeneChip® Eukaryotic PolyA RNA Control Kit (Affymetrix, Inc.). The cDNA was cleaned up using the GeneChip® Sample Cleanup Module and subsequently processed to generate biotin-labelled cRNA using the GeneChip® Expression 3′-amplification IVT Labelling Kit (Affymetrix, Inc.). 25 μg of labelled cRNA was fragmented using 5× fragmentation buffer and Rnase-free water at 94 °C for 35 min. 15 μg of the fragmented, biotin-labelled cRNA was made up in a hybridization cocktail and hybridised to the HgU133 Plus 2.0 array at 45 °C for 16 h. Following hybridization the arrays were washed and stained using the Affymetrix Fluidics Station 450. GeneChips were scanned using the Affymetrix GeneChip® Scanner 3000. All steps of the process were quality controlled by measuring yield (μg), concentration (μg/L) and 260:280 ratios *via* spectrophotometry using the Nanodrop ND-1000 and sample integrity using the Agilent 2100 bioanalyser (Agilent Technologies, Inc.). After general array quality control and data export, the data were normalised using Robust Multichip Average and imported into Partek Genomic Suite. Array data were then identified for any potential outliers and overall

* Corresponding author.

http://dx.doi.org/10.1016/j.gdata.2015.09.008

grouping/separation using Principal Component Analysis. The gene lists were generated by a sequential filtering approach based on the fold-change (normalisation to the control group) and the confidence (fold-change p value). The less-stringent gene list resulted from the fold-change greater than 1.5 by comparing the treatment group to the control group. The stringent gene list was obtained by further filtering with fold-change $p < 0.05$.

Acknowledgments and grant support

This work was supported by grants from Action Medical Research, Beneficentia Stiftung and the Chelsea and Westminster Health Charity, Borne. It was also supported by the National Institute for Health Research (NIHR) Biomedical Research Centre. The views expressed are those of the author(s) and not necessarily those of the NHS, the NIHR or the Department of Health. J.J.B. is supported by the Biomedical Research Unit, a joint initiative between University Hospitals Coventry and Warwickshire and the University of Warwick.

References

[1] K. Lei, E.X. Georgiou, L. Chen, A. Yulia, S.R. Sooranna, J.J. Brosens, P.R. Bennett, M.R. Johnson, Progesterone and the repression of myometrial inflammation: the roles of MKP-1 and the AP-1 system. Mol. Endocrinol. (2015) (me20151122).

[2] A.A. Mosher, K.J. Rainey, S.S. Bolstad, S.J. Lye, B.F. Mitchell, D.M. Olson, S.L. Wood, D.M. Slater, Development and validation of primary human myometrial cell culture models to study pregnancy and labour. BMC Pregnancy Childbirth 13 (Suppl. 1) (2013) S7.