Gene Expression Analysis of the IPEC-J2 Cell Line: A Simple Model for the Inflammation-Sensitive Preterm Intestine

The IPEC-J2 cell line was studied as a simple model for investigating responses of the newborn intestinal epithelium to diets. Especially, the small intestine of immature newborns is sensitive to diet-induced inflammation. We investigated gene expression of epithelial- and immune response-related genes in IPEC-J2 cells stimulated for 2 h with milk formula (CELL-FORM), colostrum (CELL-COLOS), or growth medium (CELL-CONTR) and in distal small intestinal tissue samples from preterm pigs fed milk formula (PIG-FORM) or colostrum (PIG-COLOS). High throughput quantitative PCR analysis of 48 genes revealed the expression of 22 genes in IPEC-J2 cells and 31 genes in intestinal samples. Principal component analysis (PCA) discriminated the gene expression profile of IPEC-J2 cells from that of intestinal samples. The expression profile of intestinal tissue was separated by PCA into 2 groups according to diet, whereas no diet-dependent grouping was seen for IPEC-J2 cells. Expression differences between PIG-FORM and PIG-COLOS were found for DEFB1, CXCL10, IL1RN, and ALPI, while IL8 was upregulated in CELL-FORM compared with CELL-CONTR. These differences, between IPEC-J2 cells and intestinal tissue from preterm pigs, both used as models for the newborn intestine, underline that caution must be exercised prior to analysis and interpretation of diet-induced effects on gene expression.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
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Number of pages: 7
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: ISRN Genomics
Volume: 2013
Article number: 980651
ISSN (Print): 2314-4637

Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
Original language: English
Electronic versions:
Ann Cathrine F. Støy.pdf
DOIs: 10.1155/2013/980651

Bibliographical note
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Source: dtu
Source-ID: u::7940
Research output: Research - peer-review › Journal article – Annual report year: 2013