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The complex microbial population residing in the human gastrointestinal tract consists of commensal, potential pathogenic and beneficial species, which are probably perceived differently by the host and consequently could be expected to trigger specific transcriptional responses. In this study, a comparative analysis of the global in vitro transcriptional response of human intestinal epithelial cells to Lactobacillus acidophilus NCFMTM, L. salivarius Ls-33, Bifidobacterium animalis subsp. lactis 420 and enterohaemorrhagic Escherichia coli O157:H7 (EHEC) was conducted. Of particular note, L. salivarius Ls-33 DCE-induced changes were overall more similar to those of B. lactis 420 than to L. acidophilus NCFMTM, which was consistent with previously observed in vivo immunomodulation properties. In gene ontology and pathway analyses, both specific and unspecific changes were observed. Common to all was the regulation of apoptosis and adipogenesis, and lipid metabolism related regulation by the probiotics. Specific changes, such as regulation of cell-cell adhesion by B. lactis 420, superoxide metabolism by L. salivarius Ls-33 and regulation of MAPK pathway by L. acidophilus NCFMTM, were noted. Furthermore, fundamental differences were observed between the pathogenic and probiotic treatments in the Toll-like receptor pathway, especially for adapter molecules with a lowered level of transcriptional activation of MyD88, TRIF, IRAK1 and TRAF6 by probiotics compared to EHEC. Results provided insights into the relationship between probiotics and human intestinal epithelial cells, notably with regard to strain-specific responses, and highlighted the differences between transcriptional responses to pathogenic and probiotic bacteria.

Keywords: Epithelial cells, Microarray, Probiotics, Escherichia coli, Cell line models