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Lactobacillus paracasei and *Lactobacillus plantarum* Strains Downregulate Proinflammatory Genes in an *Ex Vivo* System of Cultured Human Colonic Mucosa

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Online Resource 6: Functional annotations analysis – group comparison

The following tables are complementary data to Table 3 and are enumerating all significant annotation terms (FDR<0.05).

Table a: Significant annotations terms (FDR<0.05) corresponding to up- and downregulated genes in the PMA/IO stimulated group (Inflamed) compared to the Control group.

Category	Annotation term	Significance (FDR)	Molecules
upregulated genes:			
BP:	immune response	2.49E-07	15
	immune system process	3.58E-06	16
	positive regulation of immune system process	1.59E-03	7
	regulation of lymphocyte proliferation	2.16E-03	5
	regulation of leukocyte proliferation	2.26E-03	5
	regulation of mononuclear cell proliferation	2.26E-03	5
	regulation of leukocyte activation	2.77E-03	6
	regulation of immune system process	3.09E-03	8
	regulation of cell activation	3.54E-03	6
	regulation of immune effector process	4.60E-03	5
	positive regulation of protein secretion	4.64E-03	4
	positive regulation of leukocyte activation	5.53E-03	5
	positive regulation of cell activation	6.58E-03	5
	regulation of homeostatic process	7.28E-03	5
	regulation of multicellular organismal process	9.34E-03	11
	regulation of response to stimulus	9.63E-03	8
	regulation of activated T cell proliferation	1.00E-02	3
	regulation of lymphocyte apoptosis	1.00E-02	3
	regulation of lymphocyte mediated immunity	1.05E-02	4

	regulation of adaptive immune response based on	1.10E-02	4
	positive regulation of lymphocyte proliferation	1.10E-02	4
	regulation of immune response	1.14E-02	6
	positive regulation of leukocyte proliferation	1.16E-02	4
	regulation of adaptive immune response	1.16E-02	4
	positive regulation of mononuclear cell proliferation	1.16E-02	4
	regulation of protein secretion	1.29E-02	4
	negative regulation of cell proliferation	1.47E-02	7
	regulation of leukocyte mediated immunity	1.49E-02	4
	regulation of T cell proliferation	1.56E-02	4
	regulation of defense response	1.70E-02	5
	response to stimulus	1.82E-02	22
	regulation of lymphocyte activation	1.92E-02	5
	positive regulation of protein transport	1.95E-02	4
	regulation of interleukin-12 production	2.04E-02	3
	regulation of response to stress	2.67E-02	6
	regulation of cytokine production	3.98E-02	5
	regulation of immunoglobulin mediated immune	4.04E-02	3
	positive regulation of cell killing	4.04E-02	3
	regulation of B cell mediated immunity	4.04E-02	3
	regulation of immunoglobulin production	4.72E-02	3
	regulation of cell proliferation	4.74E-02	9
MF:	Cytokine activity	4.5E-03	6
KEGG:	Cytokine-cytokine receptor interaction	1.1E-05	9
downregulated genes:			
BP:	response to wounding	7.68E-03	7
	wound healing	7.82E-03	5
	regulation of localization	1.60E-02	7
	regulation of transport	2.24E-02	6
	response to external stimulus	2.50E-02	8
MF:	Heparin binding	1.3E-02	4
	Glycosaminoglycan binding	3.2E-02	4
	Pattern binding	4.2E-02	4
	Polysaccharide binding	4.2E-02	4

The analysis is based on the default parameters in D.A.V.I.D. and uses FDR correction for multiple testing. BP: biological process; CC: cellular component; MF: molecular function; KEGG: KEGG pathway.

Table b: Significant annotations terms (FDR<0.05) corresponding to up- and downregulated genes in the iLP group compared to the PMA/IO stimulated (Inflamed) group.

Category	Annotation term	Significance (FDR)	Molecules
upregulated genes:			
BP, CC, MF, KEGG:	None significant		
downregulated genes:			
BP:	immune response	3.64E-04	13
	taxis	8.45E-04	7
	chemotaxis	8.45E-04	7
	response to external stimulus	1.28E-03	14
	immune system process	3.10E-03	14
	response to chemical stimulus	1.03E-02	15
	locomotory behavior	1.53E-02	7
	regulation of lymphocyte apoptosis	1.75E-02	3
	regulation of cell proliferation	2.26E-02	11
	response to wounding	2.43E-02	9
	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2.46E-02	4
	regulation of adaptive immune response	2.59E-02	4
	locomotion	3.21E-02	8
CC:	Extracellular space	1.7E-04	13
	Extracellular region part	1.1E-03	14
MF:	cytokine activity	2.28E-05	9
	chemokine activity	5.70E-04	5
	chemokine receptor binding	7.33E-04	5
	G-protein-coupled receptor binding	1.45E-03	6
	receptor binding	4.38E-03	13
KEGG:	Cytokine-cytokine receptor interaction	2.7E-06	11

The analysis is based on the default parameters in D.A.V.I.D. and uses FDR correction for multiple testing. BP: biological process; CC: cellular component; MF: molecular function; KEGG: KEGG pathway.

Table c: Significant annotations terms (FDR<0.05) corresponding to up- and downregulated genes in iLP(A^-) group compared to the PMA/IO stimulated (Inflamed) group.

Category	Annotation term	Significance (FDR)	Molecules
upregulated genes:			
BP, CC, MF, KEGG:	None significant		
downregulated genes:			
BP:	immune response	2.82E-08	17
	immune system process	7.85E-07	18
	response to external stimulus	9.67E-06	16
	response to wounding	3.09E-04	11
	response to stimulus	3.69E-04	28
	positive regulation of immune system process	3.93E-04	8
	chemotaxis	4.04E-04	7
	taxis	4.04E-04	7
	regulation of leukocyte activation	4.97E-04	7
	regulation of immune effector process	5.34E-04	6
	regulation of cell activation	6.68E-04	7
	positive regulation of leukocyte activation	6.74E-04	6
	regulation of response to stimulus	6.97E-04	10
	regulation of lymphocyte mediated immunity	7.14E-04	5
	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	7.68E-04	5
	regulation of adaptive immune response	8.25E-04	5
	positive regulation of cell activation	8.40E-04	6
	regulation of leukocyte mediated immunity	1.16E-03	5
	regulation of immune system process	1.18E-03	9
	regulation of secretion	1.48E-03	7
	regulation of cell proliferation	1.76E-03	12
	regulation of cell killing	2.29E-03	4
	regulation of programmed cell death	2.32E-03	12
	regulation of cell death	2.39E-03	12
	regulation of immune response	2.74E-03	7
	regulation of lymphocyte activation	3.27E-03	6
	positive regulation of biological process	3.32E-03	19
	positive regulation of cellular process	3.35E-03	18
	regulation of lymphocyte proliferation	3.83E-03	5
	regulation of leukocyte proliferation	4.01E-03	5
	regulation of mononuclear cell proliferation	4.01E-03	5
	regulation of cellular localization	4.52E-03	7
	negative regulation of cell proliferation	5.29E-03	8
	positive regulation of lymphocyte activation	6.94E-03	5
	positive regulation of protein secretion	7.17E-03	4
	regulation of response to stress	7.68E-03	7
	locomotory behavior	7.68E-03	7
	regulation of apoptosis	9.53E-03	11

	positive regulation of secretion	1.08E-02	5
	positive regulation of cell proliferation	1.19E-02	8
	regulation of homeostatic process	1.27E-02	5
	regulation of lymphocyte apoptosis	1.35E-02	3
	regulation of activated T cell proliferation	1.35E-02	3
	regulation of T cell activation	1.40E-02	5
	locomotion	1.51E-02	8
	positive regulation of lymphocyte proliferation	1.69E-02	4
	positive regulation of mononuclear cell proliferation	1.79E-02	4
	positive regulation of leukocyte proliferation	1.79E-02	4
	inflammatory response	1.86E-02	7
	regulation of protein secretion	1.98E-02	4
	regulation of transcription, DNA-dependent	2.15E-02	16
	cell-cell signaling	2.29E-02	9
	positive regulation of cell differentiation	2.35E-02	6
	regulation of T cell proliferation	2.39E-02	4
	behavior	2.45E-02	8
	regulation of localization	2.54E-02	9
	defense response	2.67E-02	9
	regulation of RNA metabolic process	2.69E-02	16
	positive regulation of transcription, DNA-dependent	2.69E-02	8
	positive regulation of RNA metabolic process	2.82E-02	8
	regulation of defense response	2.92E-02	5
	positive regulation of protein transport	2.98E-02	4
	regulation of multicellular organismal process	3.03E-02	11
	response to chemical stimulus	3.10E-02	13
	positive regulation of transcription from RNA polymerase II promoter	3.61E-02	7
	response to stress	3.83E-02	15
	positive regulation of T cell activation	4.25E-02	4
CC:	Extracellular space	1.3E-6	15
	Extracellular region part	2.1E-6	17
	Extracellular region	1.6E-2	21
MF:	cytokine activity	7.39E-07	10
	receptor binding	3.58E-04	14
	chemokine activity	3.80E-04	5
	chemokine receptor binding	4.89E-04	5
	G-protein-coupled receptor binding	8.94E-04	6
KEGG:	Cytokine-cytokine receptor interaction	7.3E-10	14
	Jak-STAT signaling pathway	5.8E-06	9

The analysis is based on the default parameters in D.A.V.I.D. and uses FDR correction for multiple testing. BP: biological process; CC: cellular component; MF: molecular function; KEGG: KEGG pathway.

Table d: Significant annotations terms (FDR<0.05) corresponding to up- and downregulated genes in the iBL23 group compared to the PMA/IO stimulated (Inflamed) group.

Category	Annotation term	Significance (FDR)	Molecules
upregulated genes:			
BP, CC, MF, KEGG:	None significant		
downregulated genes:			
BP:	immune response	5.78E-05	13
	immune system process	4.82E-04	14
	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	1.49E-02	4
	regulation of adaptive immune response	1.57E-02	4
	response to external stimulus	1.83E-02	11
	regulation of cell proliferation	2.44E-02	10
	taxis	3.74E-02	5
	chemotaxis	3.74E-02	5
	regulation of leukocyte activation	4.27E-02	5
	regulation of lymphocyte proliferation	4.80E-02	4
	regulation of immunoglobulin mediated immune response	4.92E-02	3
	regulation of B cell mediated immunity	4.92E-02	3
	regulation of leukocyte proliferation	4.96E-02	4
	regulation of mononuclear cell proliferation	4.96E-02	4
CC:	Extracellular space	1.3E-03	11
	Extracellular region part	4.8E-03	12
	Extracellular region	1.2E-02	17
MF:	cytokine activity	6.00E-06	9
	receptor binding	3.64E-03	12
	chemokine activity	7.76E-03	4
	G-protein-coupled receptor binding	8.80E-03	5
	chemokine receptor binding	9.34E-03	4
KEGG	Cytokine-cytokine receptor interaction	1.6E-06	11
	Jak-STAT signaling pathway	7.2E-03	6

The analysis is based on the default parameters in D.A.V.I.D. and uses FDR correction for multiple testing. BP: biological process; CC: cellular component; MF: molecular function; KEGG: KEGG pathway.