

Toll-like receptor 1 as a possible target in non-alcoholic fatty liver disease

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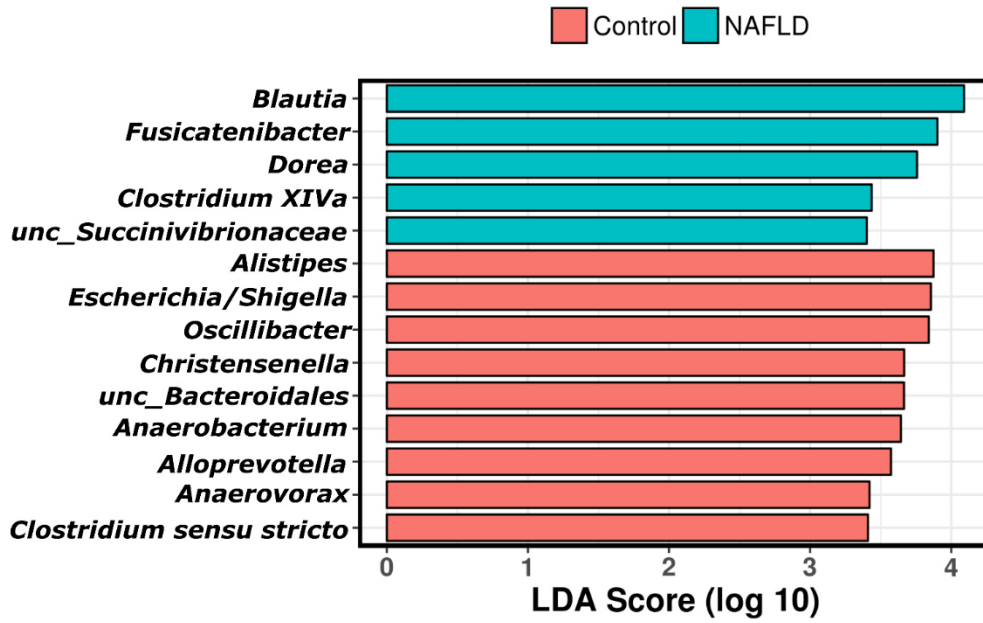


Figure S1. Histogram of the Linear Discriminant Analysis score (LDA) (log 10) computes for features with differential abundances of bacterial communities in NAFLD patients and controls. NAFLD, patients with non-alcoholic fatty liver disease; unc, unclassified.

Table S1. Expression of markers of Tlr signaling cascade in NAFLD patients and controls.

	C	NAFLD
<i>MYD88</i> mRNA expression (% of control)	100 ± 14.5	117.1 ± 12.7
<i>TIRAP</i> mRNA expression (% of control)	100 ± 15.5	171.8 ± 39.2
<i>IRF3</i> mRNA expression (% of control)	100 ± 14.3	119.9 ± 22.1

Data are shown as means ± SEM, n=10 controls, n=31 NAFLD patients. C, healthy controls; IRF3, interferon regulatory factor 3; MYD88, myeloid differentiation response 88; NAFLD, patients with non-alcoholic fatty liver disease; TIRAP, TIR domain containing adaptor protein.

Table S2. Pearson correlation between the bacterial taxa and expression of *TLR1*.

Genera	Correlation Coefficient	<i>P</i> value
o_Clostridiales	-0.081	0.72
g_Streptococcus	-0.121	0.59
g_Ruminococcus2	0.323	0.14
g_Ruminococcus	-0.439*	0.04
g_Roseburia	-0.006	0.98
g_Romboutsia	-0.041	0.86
g_Parabacteroides	0.057	0.80
g_Oscillibacter	-0.160	0.48
g_Lactobacillus	0.144	0.52
g_Intestinibacter	-0.192	0.39
g_Holdemanella	0.573*	0.01
g_Gemmiger	-0.419*	0.05
g_Fusicatenibacter	-0.014	0.95
g_Faecalibacterium	-0.090	0.69
g_Escherichia/Shigella	-0.239	0.28
g_Dorea	0.138	0.54
g_Dialister	-0.337	0.13
g_Coproccoccus	-0.154	0.49
g_Collinsella	-0.031	0.89
g_Clostridium.XVIII	-0.081	0.72
g_Clostridium.IV	-0.060	0.79
g_Catenibacterium	0.210	0.35
g_Blautia	-0.120	0.59
g_Bifidobacterium	-0.119	0.60
g_Barnesiella	-0.165	0.46
g_Bacteroides	-0.148	0.51

g_Anaerostipes	-0.162	0.47
g_Alistipes	-0.051	0.82
f_Ruminococcaceae	-0.314	0.15
f_Lachnospiraceae	-0.137	0.54
f_Coriobacteriaceae	-0.001	0.99

n=7 controls, n=16 NAFLD patients, * $p \leq 0.05$. Letters before the name represents the taxonomical level, g=genus, f=family, o=order.

Table S3. Primer sequences used for real-time PCR.

	Forward (5' - 3')	Reverse (5' - 3')
Human sequences		
18S	gggcccgaagcgttacttt	cgccgggtccaagaattcac
IRF3	gaggtgacagccttctaccg	tgctcacgtagctcatcac
MYD88	gcacatgggcacatacagac	gacatggttaggctccctca
TIRAP	agcccaagaagaggcccaac	tggcacacgcagacgtgata
TLR1	agggtcagctggactcaga	taattttggatgggcaaagc
TLR2	attgtgccattgctctttc	ctgcccttgagataccatt
TLR3	agccttcaacgactgatgct	ttccagagccgtgctaagt
TLR4	tgagcagtcgtgctgtatc	cagggcttttctgagtcgtc
TLR5	gagcccctacaagggaaaac	tgctgatggcattgctaaag
TLR6	caaggccctccaataactca	cattgcaaggaagagggtta
TLR7	aaatgtcacagccgtccctac	ttatttttacacggcgaca
TLR8	tccttcagtcgtcaatgctg	cgttggggaacttctgta
TLR9	aaatggcctttgactcatgg	acagcagctacaggaagga
TLR10	actttgccaccacaatctc	cccagaaaagcccacattta
Murine sequences		
18S	gtaaccggtgaacccatt	ccatccaatcggtagtagcg
F4/80	tggtgcctccctgactttc	caaggatccctgccctgcact
Tlr1	cgctggaccagagtttgt	cgcaccaggaaggtcagtt
Tnfa	cagccaaccaggcagcgttct	cctgccacaagcaggaatga

IRF3, interferon regulatory factor 3; MYD88, myeloid differentiation primary response 88; TIRAP, TIR domain containing adaptor protein; TLR, toll-like receptor; Tnf, tumor necrosis factor.