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(54) Benævnelse: **BIFIDOBACTERIUM LONGUM TIL BEHANDLING AF FEDME OG ASSOCIEREDE METABOLSKE SYGDOMME**

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DESCRIPTION

Introduction

[0001] The invention relates to a strain of *Bifidobacterium longum.*

[0002] Obesity is one of the most serious public health challenges of the 21st century. Globally, approximately 13% of adults are obese with a further 39% considered overweight (WHO, 2015). Obesity is a multifactorial disorder which is the result of a long-term imbalance between energy intake and expenditure and is influenced by genetic and environmental factors. Obesity is characterized by insulin resistance and a chronic low-grade inflammation (Gregor and Hotamisligil, 2011, Kahn *et al.,* 2006). The intimate interplay between the immune system, metabolism, and gut microbiota may play an important role in controlling obesity and metabolic homeostasis. Obesity increases the risk of developing and exacerbating a cluster of chronic metabolic disorders such as type 2 diabetes (T2DM), non-alcoholic fatty liver disease (NAFLD), hypertension, atherosclerosis, dyslipidemia and cardiovascular disease (Guh *et al.,* 2009) with the prevalence of metabolic comorbidities increasing in-line with increasing BMI (Gupta *et al.,* 2015). Obesity also increases the risk of developing serious and potentially life-threatening diseases such as allergy & asthma, osteoarthritis, gallbladder disease and Non-alcoholic steatohepatitis (NASH), a condition in which fat builds up in the liver and major cause of cirrhosis of the liver.

[0003] Metabolic syndrome, an increasingly common condition, refers to the combination of obesity, hyperlipidemia (high triglycerides), hypertension (high blood pressure) and glucose intolerance (high blood sugar) and low HDL cholesterol. These risk factors assist in identifying subjects at high risk of developing type2 diabetes (T2D) and cardio-vascular disease.

[0004] Non-alcoholic fatty liver disease (NAFLD) is a very common disorder and refers to a group of conditions where there is accumulation of excess fat in the liver of people who drink little or no alcohol.

[0005] The more severe form of NAFLD is called non-alcoholic steatohepatitis (NASH). NASH causes the liver to swell and become damaged. NASH tends to develop in people who are overweight or obese, or have diabetes, high cholesterol or high triglycerides.

[0006] A large body of clinical and experimental data shows that increased flux of free fatty acids from increased visceral adipose tissue can lead to NAFLD related with insulin resistance. Thus, individuals with obesity, insulin resistance, and dyslipidemia are at the greatest risk of developing NAFLD.

[0007] Since the observation that germ-free mice were found to be leaner than their conventionally-raised counterparts (Backhed *et al.,* 2004) the contribution of the gut microbiota

to the development of obesity is increasingly being investigated (Backhed *et al.,* 2007, Cani *et al.,* 2008b, Ridaura *et al.,* 2013, Vrieze *et al.,* 2012) . The contribution of the gut microbiota to obesity is multifactorial and involves issues such as enhanced energy harvest and fat storage (Turnbaugh *et al.,* 2006) altered metabolic pathways (Kotzampassi *et al.,* 2014, Turnbaugh *et al.,* 2009) and bacterial translocation leading to chronic low-grade inflammation (Cani *et al.,* 2007, Cani *et al.,* 2008a). The manipulation of gut microbiota by probiotics is therefore a potential therapeutic tool to help ameliorate obesity and improve metabolic health. Lactobacillus strains are commonly used as probiotics and have a body of evidence that supports heath benefit effects in vivo in a strain specific manner (Aronsson *et al.,* 2010, Lee *et al.,* 2006, Naito *et al.,* 2011).

[0008] The mechanism of action of these strains are not well characterised. One group of molecules that are of interest are bacterial exopolysaccharides (EPS). EPS's are high-molecular-weight polymers that are composed of sugar residues and are secreted by bacteria into the surrounding environment. Exopolysaccharide (EPS)-producing bacteria have been shown to have immunomodulatory effects (Fanning *et al.,* 2012, Hidalgo-Cantabrana *et al.,* 2014, Vinderola *et al.,* 2006, Volman *et al.,* 2008, Jones *et al.,* 2014). Many lactic acid bacteria (LAB) have the ability to synthesize EPS. However, EPS are heterogeneous molecules and differ in composition, charge and molecular structure which may account for the strain-specific bioactivity observed (Adams *et al.,* 2008, Bland *et al.,* 2004, Hidalgo-Cantabrana *et al.,* 2012, Kankainen *et al.,* 2009).

[0009] The chronic low-grade inflammation associated with obesity and metabolic disorders (Gregor and Hotamisligil, 2011) is one risk factor that could be targeted for manipulation by administration of probiotics to favourably influence the development of obesity. We have previously shown that another lactic acid bacterium, *B. longum* NCIMB41003, has anti-inflammatory effects. This bacterium has a substantial EPS coat. The EPS material also has an anti-inflammatory effect as described in WO2010055499A.

[0010] WO2011/058535 describes *Bifidobacterium longum* strain NCIMB 41676.

[0011] Di Gioia Diana et al: "Bifidobacteria: their impact on gut microbiota composition and their applications as probiotics in infants", Applied Mircobiology and Biotechnology, Springer, DE, vol. 98, no. 2, 28 November 2013 (2013-11-28), pages 563-577, XP035328401 is a review of Bifidobacteria.

[0012] Michele Malaguarnera et al: "Bifidobacterium longum with Fructo-Oligosaccharides in Patients with Non Alcoholic Steatohepatitis", Digestive Diseases and Sciences, Kluwer Academic Publishers-Plenum Publishers, NE, vol. 57, no. 2, 8 September 2011 (2011-09-08), pages 545-553, XP035005634 presents a study of a *Bifidobacterium longum* plus FOS which is reported to reduce NASH activity and serum ALT levels.

[0013] US2013/261071A1 describes an isolated exopolysaccharide from *Bifidobacterium* strain NCIMB 41003.

Statements of Invention

[0014] The invention provides the deposited strain NCIMB 41715. A strain of *Bifidobacterium longum* AH1362 deposited with the NCIMB under accession number NCIMB 41715.

[0015] According to one aspect the invention provides a composition for use in the prevention or treatment of obesity and obesity-related Metabolic Syndrome comprising an effective amount of the strain. The strain produces a polysaccharide and increases energy excretion. The strain was isolated from a faecal sample from a placebo-fed healthy adult volunteer.

[0016] The isolated strain of the invention may be used for reducing body fat accumulation in a subject. The strain may be used for blocking weight gain or reducing weight. The strain may be used for the treatment, prevention, or alleviation of a condition resulting from excessive body fat accumulation.

[0017] The invention also provides a method for preventing or treating obesity, comprising administering a composition comprising a strain deposited with the NCIMB under accession number NCIMB 41715 to a subject in need of preventing or treating obesity.

[0018] The invention further provides a method for preventing or treating obesity-related metabolic syndrome, comprising administering a composition comprising a strain of deposited with the NCIMB under accession number NCIMB 41715 to a subject in need of preventing or treating obesity- related metabolic syndrome.

[0019] The invention also provides a method for preventing or treating Non-alcoholic fatty liver disease (NAFLD), comprising administering a composition comprising a strain of *Bifidobacterium longum* AH1362 deposited with the NCIMB under accession number NCIMB 41715 to a subject in need of preventing or treating Non-alcoholic fatty liver disease (NAFLD).

[0020] The strain may be in the form of viable cells. The strain may be in the form of non-viable cells. The general use of probiotic bacteria is in the form of viable cells. However, use can also be extended to non-viable cells such as killed cultures, mixtures of viable and non-viable cultures or compositions containing beneficial factors expressed by the probiotic bacteria. This could include thermally killed micro-organisms or micro-organisms killed by exposure to altered pH or subjection to pressure or gamma irradiation. With non-viable cells product preparation is simpler, cells may be incorporated easily into pharmaceuticals and storage requirements are much less limited than viable cells. *Lactobacillus casei* YIT 9018 offers an example of the effective use of heat killed cells as a method for the treatment and/or prevention of tumour growth as described in US Patent No. US4347240.

[0021] The invention also provides a formulation which comprises a strain as described herein. The formulation may further comprise a probiotic material. The formulation may further

comprise a prebiotic material. The formulation may further comprise a carrier. The carrier may be an ingestible carrier may a pharmaceutically acceptable carrier such as a capsule, tablet or powder. The ingestible carrier may be a food product such as acidified milk, yoghurt, frozen yoghurt, milk powder, milk concentrate, cheese spreads, dressings or beverages. Some examples include a fermented food product such as a fermented milk product. The formulation may further comprise a protein and/or peptide, in particular proteins and/or peptides that are rich in glutamine/glutamate, a lipid, a carbohydrate, a vitamin, mineral and/or trace element.

The *Bifidobacterium* strain may be present in an amount of more than 10^6 cfu per gram of the formulation. The formulation may further comprise an adjuvant. The formulation may further comprise a bacterial component. The formulation may further comprise a drug entity. The formulation may further comprise a biological compound. In all cases the formulation comprises a strain as described herein and may include a carrier or other agent. Such a carrier or other agent in some cases do not occur in nature. The formulation may in some cases be used for immunisation and vaccination protocols.

[0022] The invention also provides a freeze-dried composition comprising a strain of the invention or a formulation of the invention.

[0023] The invention also provides a strain or a formulation as described herein for use in foodstuffs.

[0024] The invention also provides a strain or a formulation as described herein for use as a medicament.

[0025] The invention also provides a strain or a formulation as described herein for use in the prophylaxis and/or treatment of obesity and related illnesses.

[0026] The invention also provides a strain or a formulation as described herein for use in the prophylaxis and/or treatment of non-alcoholic fatty liver disease (NAFLD).

[0027] Strains as described herein may be used in the preparation of a panel of biotherapeutic agents for modifying the levels of IL-10.

[0028] The invention also provides a strain or a formulation as described herein for use in the prophylaxis and/or treatment of obesity related inflammation.

[0029] The invention also provides a strain or a formulation as described herein for use in the prophylaxis and/or treatment of obesity related metabolic dysregulation.

[0030] It will be appreciated that the specific strain of the invention may be administered to animals (including humans) in an orally ingestible form in a conventional preparation such as capsules, microcapsules, tablets, granules, powder, troches, pills, suppositories, suspensions and syrups. Suitable formulations may be prepared by methods commonly employed using conventional organic and inorganic additives. The amount of active ingredient in the medical

composition may be at a level that will exercise the desired therapeutic effect.

[0031] The formulation may also include a bacterial component, a drug entity or a biological compound.

[0032] In addition, a vaccine comprising the strains of the invention may be prepared using any suitable known method and may include a pharmaceutically acceptable carrier or adjuvant.

[0033] The invention also includes mutants and variants derived from the strain of the invention, whilst still having the activity of the deposited strain. The mutants and variants include a strain whose genetic and/or phenotypic properties are altered compared to the parent strain. A naturally occurring variant includes the spontaneous alterations of targeted properties selectively isolated. Deliberate alteration of parent strain properties is accomplished by conventional (*in vitro*) genetic manipulation technologies, such as gene disruption, conjugative transfer, etc. Genetic modification includes introduction of exogenous and/or endogenous DNA sequences into the genome of a strain, for example by insertion into the genome of the bacterial strain by vectors, including plasmid DNA, or bacteriophages.

[0034] Natural or induced mutations include at least single base alterations such as deletion, insertion, transversion or other DNA modifications which may result in alteration of the amino acid sequence encoded by the DNA sequence.

[0035] The terms mutant, variant and genetically modified mutant also include a strain that has undergone genetic alterations that accumulate in a genome at a rate which is consistent in nature for all micro-organisms and/or genetic alterations which occur through spontaneous mutation and/or acquisition of genes and/or loss of genes which is not achieved by deliberate (*in vitro*) manipulation of the genome but is achieved through the natural selection of variants and/or mutants that provide a selective advantage to support the survival of the bacterium when exposed to environmental pressures such as antibiotics. A mutant can be created by the deliberate (*in vitro*) insertion of specific genes into the genome which do not fundamentally alter the biochemical functionality of the organism but whose products can be used for identification or selection of the bacterium, for example antibiotic resistance.

[0036] A person skilled in the art would appreciate that mutant or variant strains of can be identified by DNA sequence homology analysis with the parent strain. Strains of having a close sequence identity with the parent strain without demonstrable phenotypic or measurable functional differences are considered to be mutant or variant strains. A strain with a sequence identity (homology) of 99.5% or more with the parent DNA sequence may be considered to be a mutant or variant. Sequence homology may be determined using on-line homology algorithm "BLAST" program, publicly available at http://www.ncbi.nlm.nih,gov/BLAST/.

[0037] Mutants of the parent strain also include derived strains having at least 95.5% sequence homology to the 16s - 23s intergenic spacer polynucleotide sequence of the parent strain. These mutants may further comprise DNA mutations in other DNA sequences in the

bacterial genome.

Brief Description of the Figures

[0038] The invention will be more clearly understood from the following description of some embodiments thereof, given by way of example only, with reference to the accompanying figures, in which:

Fig. 1 shows Strain bulkiness of *B. longum* NCIMB 41715, and *B. longum* NCIMB 41003 as measured by EPS fluffy pellet height;

Fig. 2 is a bar chart of % adhesion to hexadecane of *B. longum* NCIMB 41715, and *B. longum* NCIMB 41003;

Fig. 3 is a chart of IL-10 induction in the PBMC cytokine induction assay following 48 h stimulation with the EPS +ve *B. longum* NCIMB 41003 and a low EPS producing *Lactobacillus* strain. There is an enhanced induction of the anti-inflammatory cytokine IL-10 following stimulation with the EPS + ve *B. longum* NCIMB 41003 relative to the EPS low *Lactobacillus* strain;

Fig. 4 is a chart of TNF-α induction in the PBMC cytokine induction assay following 48 h stimulation with *B. longum* NCIMB 41003 and a low EPS producing *Lactobacillus* strain. There is a decreased induction of the pro-inflammatory cytokine TNF-α induction following stimulation with the EPS + ve *B. longum* NCIMB 41003 relative to the EPS low *Lactobacillus* strain;

Fig. 5 is a chart of IL-10 induction in the PBMC cytokine induction assay following 48 h stimulation with *B. longum* NCIMB 41003 and *B. longum* NCIMB 41715. Both strains induce, in a dose responsive manner, similar levels of the anti-inflammatory cytokine IL-10;

Fig. 6 is a chart of TNF-α induction in the PBMC cytokine induction assay following 48 h stimulation with *B. longum* NCIMB 41003 and *B. longum* NCIMB 41715. *B. longum* NCIMB 41715 induce similar levels of TNF-α relative to *B. longum* NCIMB 41003;

Fig. 7 shows that when compared to the high-fat diet (HFD) control group, *B. longum* NCIMB 41715 showed a significant reduction of fat mass gain by week 16 while *B. longum* NCIMB 41003 had no significant effect;

Fig. 8 illustrates the effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on fat pad weight. *B. longum* NCIMB 41715 had a significant reduction in fat pad weights (subcutaneous fat and epipidymal fat) while *B. longum* NCIMB 41003 had no significant effect;

Fig. 9 illustrates the effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on hepatic total cholesterol and triglycerides. *B. longum* NCIMB 41715 but not *B. longum* NCIMB 41003 reduced hepatic total cholesterol and triglycerides in DIO mice;

Fig. 10 illustrates the effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on

plasma total cholesterol;

Fig. 11 illustrates the effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on plasma LDL- cholesterol;

Fig. 12 illustrates the effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on plasma VLDL- cholesterol;

Fig. 13 illustrates the effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on terminal blood glucose;

Fig. 14 shows the cumulative food intake per mouse following *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 administration relative to the high-fat diet (HFD) control group in the DIO mouse model; and

Fig. 15 presents the estimation of % cumulative energy excretion following *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 administration relative to the high-fat diet (HFD) control group in the DIO mouse model.

Detailed description of the invention

[0039] A deposit of *Bifidobacterium longum* AH1362 was made at the National Collections of Industrial and Marine Bacteria Limited (NCIMB) Ferguson Building, Craibstone Estate, Bucksburn, Aberdeen, AB21 9YA, Scotland, UK on May 6, 2010 and accorded the accession number NCIMB 41715.

[0040] This specification also makes reference by way of comparison to the strain *Bifidobacterium longum* 35624 which is deposited at the National Collections of Industrial and Marine Bacteria Limited (NCIMB) Ferguson Building, Craibstone Estate, Bucksburn, Aberdeen, AB21 9YA, Scotland, UK on January 13, 1999 under accession number NCIMB 41003.

Examples

[0041] The following examples further describe and demonstrate embodiments within the scope of the invention. The examples are given solely for the purpose of illustration and are not to be construed as limitations of the present invention, as many variations thereof are possible without departing from the spirit and scope of the invention.

[0042] We have found that a novel EPS-producing Bifidobacterium strain (*B. longum* AH1362) attenuated markers associated with obesity and associated metabolic disorders. *B. longum* AH1362 administration was associated with alteration of gut microbiota, decreased fat storage

and decreased hepatic triglyceride and hepatic total cholesterol levels and increased fat excretion. Surprisingly, administration of *B. longum* NCIMB 41003 did not have the same effect.

Example 1 - Identity of *B. longum* NCIMB 41715 was confirmed by BLAST analysis of the intergenic spacer (IGS) region.

Method

[0043] 16s-23s intergenic spacer (IGS) sequencing was performed to identify *B. longum* NCIMB 41715. Briefly, total DNA was isolated from the strains using 100 µl of Extraction Solution and 25 µl of Tissue Preparation solution (Sigma-Aldrich, XNAT2 Kit). The samples were incubated for 5 minutes at room temperature followed by 2 h at 95 °C and then 100 µl of Neutralization Solution (Sigma-Aldrich, XNAT2 kit) was added. DNA solution was quantified using a Nanodrop spectrophotometer and stored at 4°C. PCR was performed using the IGS primers. The primer pairs used for identification of the both strain were IGS R 5'-CTGGTGCCAAGGCATCCA-3' and IGS L 5'-GCTGGATCACCTCCTTTCT-3'. The cycling conditions were 94°C for 4 min (1 cycle), 94°C for 45 sec, 53°C for 45 sec, 72°C for 45 sec (28 cycles). The PCR reaction contained 2 µl (100 ng) of DNA, PCR mix (Sigma-Aldrich, Red Taq), 0.025 nM IGS L and R primer (MWG Biotech, Germany). The PCR reactions were performed on an Eppendorf thermocycler. The PCR products were run alongside a molecular weight marker (100 bp Ladder, Roche) on a 2 % agarose EtBr stained gel in TAE, to determine the IGS profile. PCR products of Bifidobacterium (single band) were purified using the Promega Wizard PCR purification kit. PCR products of Lactobacillus yield 3 bands. The band present at approx. 280 bp (lowest band) was excised, purified using the GenElute Agarose Spin Column (Sigma-Aldrich) and re-sequenced as above and the PCR product was purified using the Promega Wizard PCR purification kit. The purified PCR products were sequenced at Beckman Coulter Genomics (UK) using the primer sequences (above) for the intergenic spacer region. Sequence data was then searched against the NCBI nucleotide database to determine the identity of the strain by nucleotide homology. The resultant DNA sequence data was subjected to the NCBI standard nucleotide-to-nucleotide homology BLAST search engine (http://www.ncbi.nlm.nih.gov/BLAST/) to identify the nearest match to the sequence.

Results

[0044]
Table 1: Blast results of the intergenic spacer (IGS) region of *B. longum* NCIMB 41715.

Sample	Accession no	Closest Match on NCBI BLAST 07/12/15	Identities	% Match	bp
NCIMB 41715	gb(CP010453.1)	Bifidobacterium longum strain BG7, complete genome	480/484	99%	495
	emb(LN824140.1)	Bifidobacterium longum subsp, infantis genome assembly			

Table 2: Sequence of the intergenic spacer (IGS) region of *B. longum* NCIMB 41715.

IGS sequence of *B. longum* NCIMB 41715 (495 nt)	TGCTGGGATCACCTCCTTTCTACGGAGAATTCAGTCGGATGTTCGT CCGACGGTGTGCGCCCCGCGCGTCGCATGGTGCG ATGGCGGCGGGGTTGCTGGTGTGGAAGACGTCGTTGGCTTTGCCC TGCCGGTCGTGCGGTGGGTGCGGGGTGGTATGGAT GCGCTTTTGGGCTCCCGGATCGCCACCCCAGGCTTTTTGCCTGGCG CGATTCGATGCCCGTCGTGCCTGGGGGCCGGCCG
	TGTGCCGGCGCGATGGCGTGGCGGTGCGTGGTGGCTTGAGAACT GGATAGTGGACGCGAGCAAAACAAGGGTTTTTGAAT CTTTGTTTTGCTGTTGATTTCGAATCGAACTCTATTGTTCGTTTCGA TCGTTTTGTGATCATTTTTAGTGTGATGATTTG TCGTCTGGGAATTTGCTAGAGGAATACTTGCGGCCATGCACTTCGT GGTGTGTGTTGCTTGCAAGGGCGTATGGTGGAGG CCTTCGACCACCAGA

Example 2 - EPS Fluffy Pellet Test (Strain Bulkiness)

Method

[0045] Each strain was fermented in a broth. The particulate collected after centrifugation was washed and subsequently freeze dried.

[0046] The freeze-dried powder, adjusted for total cell number (2 x 10E10), was re-suspended in 10 ml PBS and centrifuged at 4000rpm/10mins/4°C.

Results

[0047] **Figure 1:** Strain bulkiness of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 as

measured by EPS fluffy pellet height.

[0048] *B. longum* NCIMB 41003 produced a 0.9 cm fluffy pellet while. *B. longum* NCIMB 41715 produced a 2.5 cm fluffy pellet

Conclusion

[0049] *B. longum* NCIMB 41003 is known to be a high EPS producer. The EPS fluffy pellet test, and the resulting pellet height, confirms that *B. longum* NCIMB 41715 produces EPS, and produces more EPS than *B. longum* NCIMB 41003.

Example 3 - Microbial adhesion to hexadecane (MATH) assay

[0050] Hydrophobicity is the physical property of a molecule whereby it repels water. Hydrophobic materials are used for oil removal from water, the management of oil spills, and chemical separation processes to remove non-polar substances from polar compounds. Hydrophobicity of a bacterial cell depends on the composition of its cell surface with respect to the proteins, peptides and polysaccharides present. The ability of a probiotic strain to adhere to the intestinal mucosa helps the bacterial cell to establish itself during gastrointestinal transit providing it with a competitive advantage in the intestine. Hydrophobicity of a strain is one factor contributing to adhesive ability. The determination of bacterial adhesion to hexadecane as an indication of the strains ability to adhere to intestinal epithelial cells is a valid qualitative approach (Kiely & Olson, 2000).

Method

[0051] The ability of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 to adhere to hexadecane as a measure of their hydrophobicity was determined using the microbial adhesion to hexadecane (MATH) test. Adhesion to hexadecane was measured according to the method of Rosenberg *et al,* 1980 with some modifications (Crow and Gopal, 1995; Bellon-Fontaine *et al,* 1996). Bacteria were harvested in the stationary phase by centrifugation at 5000g for 15min, washed twice with PBS, and re-suspended in 0.1 mol/l KNO_3 (pH 6.2) to an OD_{600} of 0.8. The absorbance of the cell suspension was measured at 600nm (A0). 2ml of hexadecane (Sigma Aldrich) was added to 2ml of cell suspension. After 10min pre-incubation at room temperature, the two-phase system was mixed by vortexing for 2mins. The aqueous phase was removed after 20min of incubation at room temperature, and its absorbance at 600nm (A1) was measured. The % of bacterial adhesion to hexadecane was calculated as (1-A1/A0) x 100, where A0 and A1 are the absorbance before and after extraction with the solvents, respectively. Experiments were done in triplicate with cells coming from independent cultures.

Results

[0052] **Figure 2:** % adhesion of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 to hexadecane as a measure of their hydrophobicity.

Conclusion

[0053] *B. longum* NCIMB 41715 (58.3%) showed a higher affinity for hexadecane, indicating that it had greater hydrophobicity,, in comparison to *B. longum* NCIMB 41003 (28.6%).

Example 4 - PBMC Anti-inflammatory profiles

[0054] The anti-inflammatory profile of *B. longum* NCIMB 41715, *B. longum* NCIMB 41003 and a low EPS producing *Lactobacillus* strain were examined by assessing the induction of the anti-inflammatory cytokine IL-10 and the pro-inflammatory cytokine TNF-α in the peripheral blood mononuclear cell (PBMC) cytokine induction assay.

Method

Peripheral blood mononuclear cell (PBMC) cytokine induction assay

[0055] Blood was obtained from three healthy volunteers under approval of the Clinical Research Ethics Committee of the Cork Teaching Hospitals. Subjects were all and had abstained from probiotic, antibiotic or anti-inflammatory medication usage for one month or longer prior to blood donation. PBMCs were extracted from whole blood by density gradient separation using histopaque (Sigma-Aldrich), a hydrophilic polysaccharide that separates layers of blood, with a 'buffy coat' forming under a layer of plasma which contains the PBMCs. For each strain, 100 mg of freeze-dried powder was weighed out and re-suspended in sterile Dulbecos PBS (Sigma-Aldrich). The bacterial cells were washed twice by centrifugation (4000rpm/10min/4°C/Brake 0) and re-suspended in sterile PBS. Direct microscopic counts were performed and the cell preparations were diluted to the appropriate concentrations to give a ratio of 100:1; 50:1; 25:1 total bacteria: PBMC cells. Technical replicates were performed in triplicate. PBMCs were then incubated at a concentration of 2×10^5 cells/ml for 48 h at 37°C (in the presence of penicillin and streptomycin (Sigma-Aldrich)) with control media, or with increasing concentrations of the bacterial strains: 1×10^6 cells/ml (25: 1 Bacterial:PBMC), 1×10^7 cells/ml (50:1 Bacteria:PBMC) and 2×10^7 cells/mL (100:1 Bacteria:PBMC). Supernatants

were assayed for the anti-inflammatory cytokine IL-10 and the pro-inflammatory cytokine TNF-α which were measured using the MesoScale Discovery (MSD) multiplex platform tissue culture kits (Meso Scale Diagnostics, Maryland, USA). *B. longum* NCIMB 41003, which has previously been shown to have anti-inflammatory activity (Groeger *et al.,* 2013) was used as a positive control to validate the accuracy of the assay.

Results

[0056] Figure 3: IL-10 induction in the PBMC cytokine induction assay following 48 h stimulation with the EPS +ve *B. longum* NCIMB 41003 and a low EPS producing *Lactobacillus* strain.

[0057] There is an enhanced induction of the anti-inflammatory cytokine IL-10 following stimulation with the EPS + ve *B. longum* NCIMB 41003 relative to the EPS low *Lactobacillus* strain.

[0058] Figure 4: TNF-α induction in the PBMC cytokine induction assay following 48 h stimulation with *B. longum* NCIMB 41003 and a low EPS producing *Lactobacillus* strain. There is a decreased induction of the pro-inflammatory cytokine TNF-α induction following stimulation with the EPS + ve *B. longum* NCIMB 41003 relative to the EPS low *Lactobacillus* strain.

[0059] Figure 5: IL-10 induction in the PBMC cytokine induction assay following 48 h stimulation with *B. longum* NCIMB 41003 and *B. longum* NCIMB 41715. Both strains induce, in a dose responsive manner, similar levels of the anti-inflammatory cytokine IL-10.

[0060] Figure 6: TNF-α induction in the PBMC cytokine induction assay following 48 h stimulation with *B. longum* NCIMB 41003 and *B. longum* NCIMB 41715. *B. longum* NCIMB 41715 induce similar levels of TNF-α relative to *B. longum* NCIMB 41003.

Conclusion

[0061] *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003, which are EPS-rich, induce similar anti-inflammatory immune profiles in a PBMC cytokine induction assay. The low-EPS producing strain produces a very different immune profile.

Example 5 - Effect of administration of *B. longum* NCIMB 41715, *B. longum* NCIMB 41003 and an EPS low *Lactobacillus* strain on metabolic outcomes in the diet-induced obesity (DIO) mouse model

Method

Animals

[0062] 7-week-old male C57BL/6JRccHsd mice (Harlan Laboratories, Netherlands) (72 mice, n=12 per group), randomized based on body weight, were maintained in a controlled environment with 22±3°C temperature, 50±20% humidity, a light/dark cycle of 12 h each and 15-20 fresh air changes per hour. Mice were housed group wise (4 mice per cage) and autoclaved corncob was used as bedding material. Mice were received at 5 weeks of age and were quarantined for one week followed by acclimatization for one week prior to commencement of study. From Day 0 mice were fed, *ad libitum,* and mice in each cage were provided with 50ml of plain sterile drinking water (groups 1 and 2; Table 1) or drinking water containing freeze-dried probiotic (1 x 10^9cfu/dose/day) via polycarbonate bottles fitted with stainless steel sipper tubes (groups 3, 4, 5 and 6; Table 1). Treatment continued for 16 weeks.

Experimental Design

[0063] Day 0 onwards, group 1 was fed with low fat diet (LFD) D12450 (10% kcal% fat, gamma irradiated; Research Diets Inc, USA) and the other five groups (groups 2 to 6) were fed with high fat diet (HFD) D12451 (45% kcal% fat, gamma irradiated; Research Diets Inc) for a period of 16 weeks. HFD feeding induced insulin resistance and obesity in animals which was characterized by increase in body weight and fasting blood glucose values. Group 1 and 2 were provided with plain sterile drinking water while groups 3, 4, 5 and 6 were provided with drinking water containing 1 x 10^9cfu/dose/day of the appropriate probiotic (Table 1). General health observation was performed on a daily basis at the same time of the day. This included alertness, hair texture, cage movement and presence of any discharge from nose, eyes, mouth and ears. Pre-measured feed was kept in each cage and the left-over feed was measured and recorded on every third day to access the amount of food consumed by the mice. Water consumption of the animals was measured on a daily basis starting from the first dosing day. Mice in each cage (n=4) were provided with 50 mL of water daily. The remaining water in each cage was measured every 24 h.

Weights and tissue sampling

[0064] Body weights were recorded individually for all animals at receipt, day of randomization, prior to treatment, and once in three days thereafter. The percent change in bodyweight was calculated according to the formula (TT-TC)/TC * 100 where TT is the test day treated and TC is the test day control. Mice were subjected to Echo Magnetic Resonance Imaging (MRI) using an Echo MRI (EchoMRI-700™) on day -1 and 28, 56, 84 and 112 to assess body fat and lean

mass composition. The animal was placed in a plastic holder without sedation or anaesthesia. Fat is measured as the mass of all the fat molecules in the body. Lean is a muscle tissue mass equivalent of all the body parts containing water. Contribution to "free water" comes mostly from the bladder. Total water includes both the free water and the water contained in lean mass, which is the entire water content of the body. Plastic holders were sanitized between animals from different groups to avoid cross-contamination. Aseptic technique was followed while handling animals from different groups. At the end of week 16, the animals were sacrificed by CO_2 asphyxiation. Liver, skeletal muscle, visceral fat (epididymal, renal and mesenteric), subcutaneous fat, spleen, caecum, brown adipose fat, brain and intestine were collected, weighed and stored at -80°C for future biochemical and genetic analysis.

Metabolic markers

[0065] Blood samples were collected at morning 9 am by the tail nipping method on day 0, 30, 60, 90 and 112 for random blood glucose measurements (total 5 samplings were done), starting/including the first dosing day. Blood glucose analysis was done by Johnson and Johnson glucometer (One touch Ultra 2). Aseptic technique was followed while handling animals from different groups. At the end of 16 weeks, mice were fasted for 6 h and blood was collected by the tail nipping method (non-anesthetic mode of blood collection) for blood glucose estimation. Blood was collected by retro-orbital puncture method under light isoflurane anesthesia and plasma was separated which was used for estimating total cholesterol (TC), triglycerides (TG), high-density lipoprotein (HDL) cholesterol, low-density lipoprotein (LDL) cholesterol and non-esterified fatty acids (NEFA) by fully automated random access clinical chemistry analyzer (EM-360, Erba Mannheim, Germany). Plasma VLDL levels were obtained by the calculation method: (VLDL=Triglycerides (mg/dl)/5). For hepatic TC and TG estimation, liver was homogenized in isopropanol (1ml/50mg tissue) and incubated at 4°C for 1 h. The samples were centrifuged at 4°C for 5 min at 2,500 rpm. Cholesterol and triglyceride concentrations in the supernatants were measured by a fully automated random access clinical chemistry analyzer (EM-360, Erba Mannheim).

Energy excretion estimation

[0066] Two faecal pellets were collected from each mouse at Weeks 6, 10 and 15 and analyzed for their gross calorific value by bomb calorimetry. For bomb calorimetry analysis, the samples were weighed and oven-dried at 60°C for 48 h. The energy content of the faeces was assessed with a Parr 6100 calorimeter using an 1109 semi-micro bomb (Parr Instruments & Co., Moline, Illinois, USA). The calorimeter energy equivalent factor was determined using benzoic acid standards and each sample (100 mg) was analysed in triplicate. Cumulative energy excretion of probiotic fed mice over the course of the study was estimated as a percentage relative to energy excreted by mice from the high-fat diet control group.

Statistical analysis

[0067] Statistical analysis was performed using unpaired t-test for differences between two groups. One-way analysis of variance (ANOVA), followed by Tukey's multiple comparison test was used when more than two groups were assessed. Data were analyzed using GraphPad Prism version 5.00 for Windows (GraphPad Software). The results were considered statistically significant when $p < 0.05$.

Table 5: Experimental groups and associated diet and treatment regimens. LFD= Low fat diet control; HFD= high-fat diet control.

Groups	Number of mice/group	Diet regimen	Treatment regimen
Group 1 (LFD control)	12	10% fat kcal	Plain sterile drinking water, daily
Group 2 (HFD control)	12	45% fat kcal	Plain sterile drinking water, daily
Group 4 (HFD + EPS low *Lactobacillus* strain)	12	45% fat kcal	1 x 10^9 cfu/dose/day in drinking water, daily
Group 5 (HFD + *B. longum* NCIMB 41715)	12	45% fat kcal	1 x 10^9 cfu/dose/day in drinking water, daily
Group 6 (HFD + *B. longum* NCIMB 41003)	12	45% fat kcal	1 x 10^9 cfu/dose/day in drinking water, daily

Results

[0068] Figure 7: When compared to the high-fat diet (HFD) control group, *B. longum* NCIMB 41715 showed a significant reduction of fat mass gain by week 16 while *B. longum* NCIMB 41003 had no significant effect.

[0069] Figure 8: Effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on fat pad weight. *B. longum* NCIMB 41715 had a significant reduction in fat pad weights (subcutaneous fat and epipidymal fat) while *B. longum* NCIMB 41003 had no significant effect.

[0070] Figure 9: Effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on hepatic total cholesterol and triglycerides. *B. longum* NCIMB 41715 but not *B. longum* NCIMB 41003 reduced hepatic total cholesterol and triglycerides in DIO mice.

[0071] Figure 10: Effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on plasma total cholesterol.

[0072] Figure 11: Effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on plasma LDL-cholesterol.

[0073] Figure 12: Effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on plasma VLDL-cholesterol.

[0074] Figure 13: Effect of *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 on terminal blood glucose.

[0075] Figure 14: Cumulative food intake per mouse following *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 administration relative to the high-fat diet (HFD) control group in the DIO mouse model.

[0076] Figure 15: Estimation of % cumulative energy excretion following *B. longum* NCIMB 41715 and *B. longum* NCIMB 41003 administration relative to the high-fat diet (HFD) control group in the DIO mouse model.

[0077] The low EPS producing *Lactobacillus* strain did not have any significant effect in this model.

<u>Conclusion</u>

[0078] *B. longum* NCIMB 41715 administration led to a significant reduction in fat mass by week sixteen for both strains. This was accompanied by a statistically significant reduction in subcutaneous fat and epididymal fat for *B. longum* NCIMB 41715. *B. longum* NCIMB 41715 administration led to a significant reduction in hepatic total cholesterol and triglyceride levels when compared to the HFD control group. Furthermore, a significant improvement on total cholesterol, LDL-cholesterol and VLDL-cholesterol was also observed with administration of *B. longum* NCIMB 41715 when compared to the HFD control group. Despite no significant difference in cumulative food intake over the course of the study, we observed an increase in % energy excretion for *B. longum* NCIMB 41715, suggesting that the administration of the hydrophobic *B. longum* NCIMB 41715 strain may reduce the amount of energy extracted from ingested food which could be responsible for the improvements in metabolic outcomes observed in this DIO mouse model.

Prebiotics

[0079] The introduction of probiotic organisms is accomplished by the ingestion of the micro-organism in a suitable carrier. It would be advantageous to provide a medium that would promote the growth of the strain in the large bowel. The addition of one or more oligosaccharides, polysaccharides, or other prebiotics enhances the growth of lactic acid bacteria in the gastrointestinal tract. Prebiotics refers to any non-viable food component that is specifically fermented in the colon by indigenous bacteria thought to be of positive value, e.g. bifidobacteria, lactobacilli. Types of prebiotics may include those that contain fructose, xylose,

soya, galactose, glucose and mannose. The combined administration of a probiotic strain with one or more prebiotic compounds may enhance the growth of the administered probiotic *in vivo* resulting in a more pronounced health benefit, and is termed synbiotic.

Other active ingredients

[0080] It will be appreciated that the strain may be administered prophylactically or as a method of treatment either on its own or with other probiotic and/or prebiotic materials as described above. In addition, the strain may be used as part of a prophylactic or treatment regime using other active materials such as those used for treating inflammation or other disorders especially those with an immunological involvement. Such combinations may be administered in a single formulation or as separate formulations administered at the same or different times and using the same or different routes of administration.

Formulations

[0081] One or more of the strains of the invention may be administered to animals (including humans) in an orally ingestible form in a conventional preparation such as capsules, microcapsules, tablets, granules, powder, troches, pills, suppositories, suspensions and syrups. Suitable formulations may be prepared by methods commonly employed using conventional organic and inorganic additives. The amount of active ingredient in the medical composition may be at a level that will exercise the desired therapeutic effect.

[0082] The formulation may also include a bacterial component, a drug entity or a biological compound.

[0083] In addition, a vaccine comprising one or more of the strains of the invention may be prepared using any suitable known method and may include a pharmaceutically acceptable carrier or adjuvant.

[0084] The strains of the invention may be formulated to facilitate controlled release such as a delayed release of the strain. For example, the formulation may be adapted to release the strain at a particular location in the gastrointestinal tract such as the small intestine or in the colon. To achieve such a controlled release the strain may be formulated in a capsule which has a coating which is adapted to release the strain at a particular location. A range of coatings are available to facilitate such controlled release. One such family of coatings are those available under the Trade Mark Eudragit.

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1

Patentkrav

1. Stamme af *Bifidobacterium longum* AH1362 deponeret hos NCIMB under til-gangsnummer NCIMB 41715.

5 **2.** Stammen ifølge krav 1 i form af levedygtige celler.

3. Stammen ifølge krav 1 i form af ikke-levedygtige celler.

4. Formulering der omfatter en stamme ifølge et hvilket som helst af kravene 1
10 til 3.

5. Formuleringen ifølge krav 4 der yderligere omfatter et probiotisk materiale el-ler et præbiotisk materiale.

15 **6.** Formulering ifølge krav 4 eller 5 der yderligere omfatter en indtagelig bærer, hvilken indtagelig bærer kan være en farmaceutisk acceptabel bærer, såsom en kapsel, en tablet eller et pulver, hvilken indtagelig bærer kan være et fødevare-produkt, såsom syrnet mælk, yoghurt, frosset yoghurt, mælkepulver, mælke-koncentrat, smøreoste, dressinger eller drikkevarer.
20

7. Formulering ifølge et hvilket som helst af kravene 4 til 6 der yderligere omfat-ter et protein og/eller peptid, især proteiner og/eller peptider der er rige på glutamin/glutamat, en lipid, et carbohydrat, et vitamin, et mineral og/eller et sporelement.
25

8. Formulering ifølge et hvilket som helst af kravene 4 til 7, hvor stammen er til stede i en mængde på mere end 10^6 cfu pr. gram formulering.

9. Formulering ifølge et hvilket som helst af kravene 4 til 8 der yderligere omfat-
30 ter en adjuvans og/eller en lægemiddelenhed.

2

10. Frysetørret sammensætning der omfatter en stamme ifølge et hvilket som helst af kravene 1 til 3 eller en formulering ifølge et hvilket som helst af kravene 4 til 9.

5 **11.** Fødevare der omfatter en stamme ifølge et hvilket som helst af kravene 1 til 3, en formulering ifølge et hvilket som helst af kravene 4 til 9 eller en sammensætning ifølge krav 10.

12. Medikament der omfatter en stamme ifølge et hvilket som helst af kravene 1 til 3, eller en formulering ifølge et hvilket som helst af kravene 4 til 9 eller en sammensætning ifølge krav 10.

13. Kapsel der omfatter en stamme ifølge et hvilket som helst af kravene 1 til 3, en formulering ifølge et hvilket som helst af kravene 4 til 9 eller en sammensæt-15 ning ifølge krav 10, hvilken kapsel kan tilpasses til kontrolleret frigivelse i mave-tarmkanalen.

14. Stamme ifølge et hvilket som helst af kravene 1 til 3 eller en formulering ifølge et hvilket som helst af kravene 4 til 9 eller en sammensætning ifølge krav 20 10 til anvendelse i forebyggelse eller behandling af fedme eller fedme-relateret metabolisk syndrom.

15. Stamme ifølge et hvilket som helst af kravene 1 til 3 eller en formulering ifølge et hvilket som helst af kravene 4 til 9 eller en sammensætning ifølge krav 25 10 til anvendelse i forebyggelse eller behandling af ikke-alkoholisk fedtlever-sygdom (NAFLD).
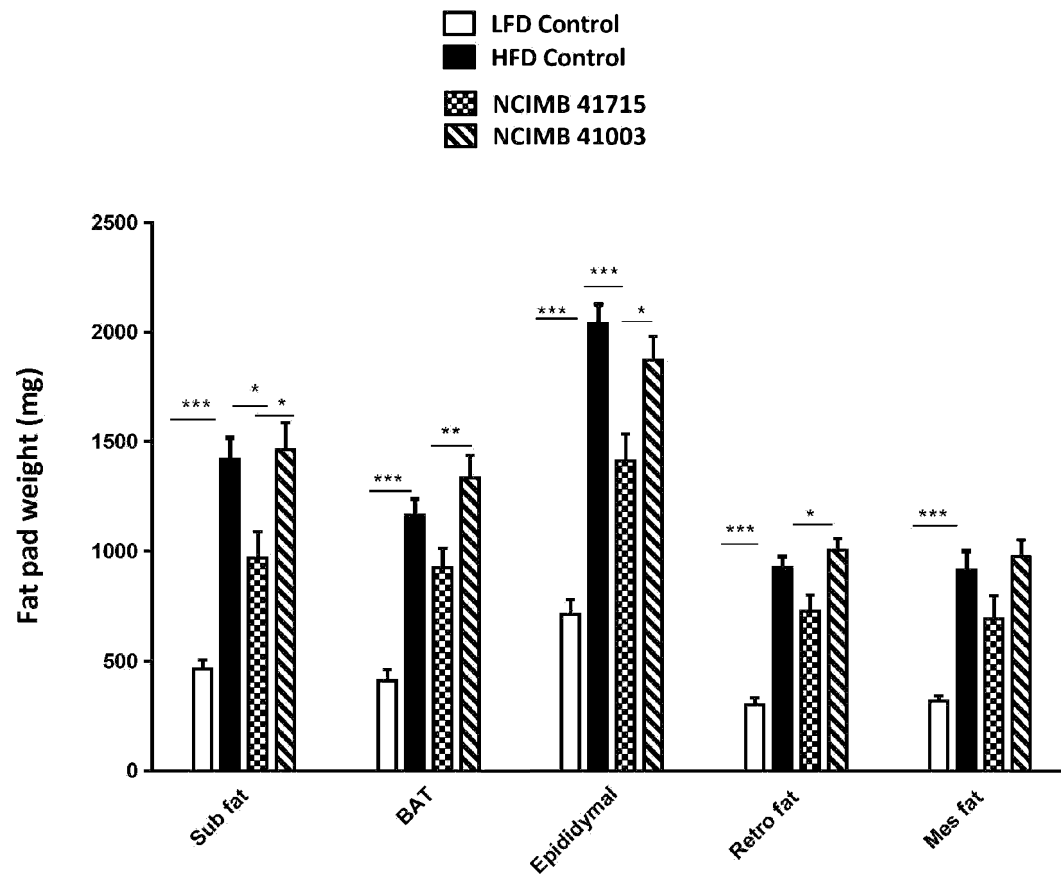
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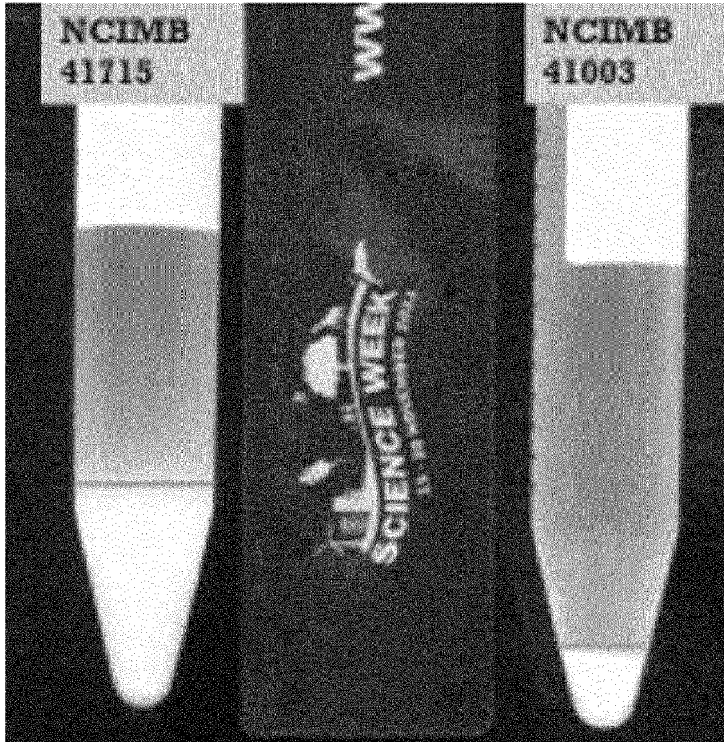
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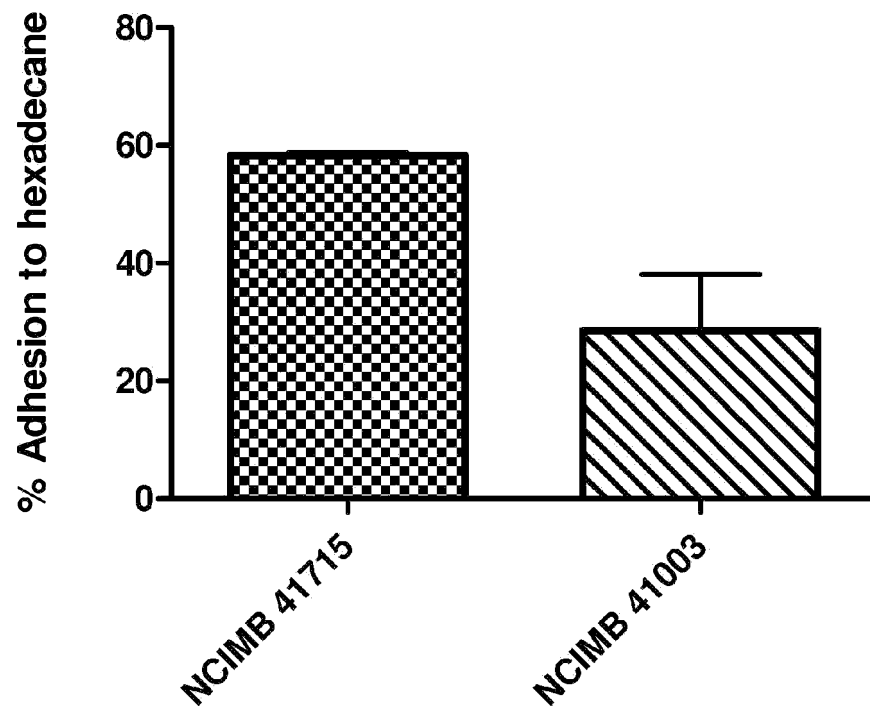
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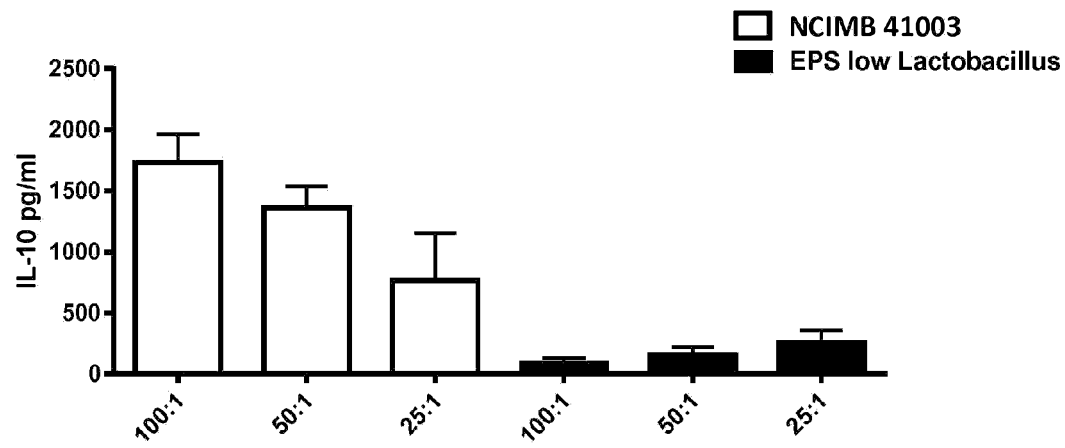
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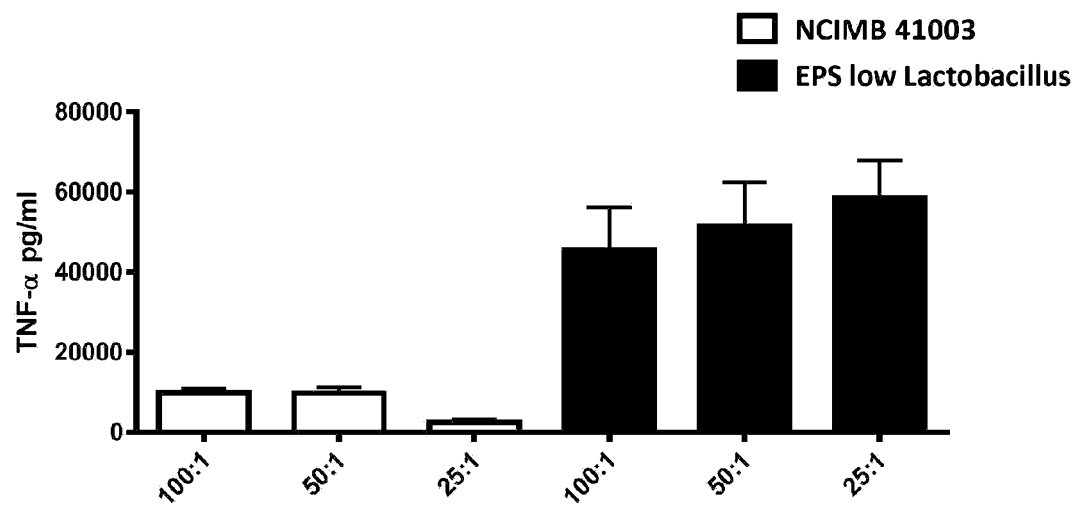
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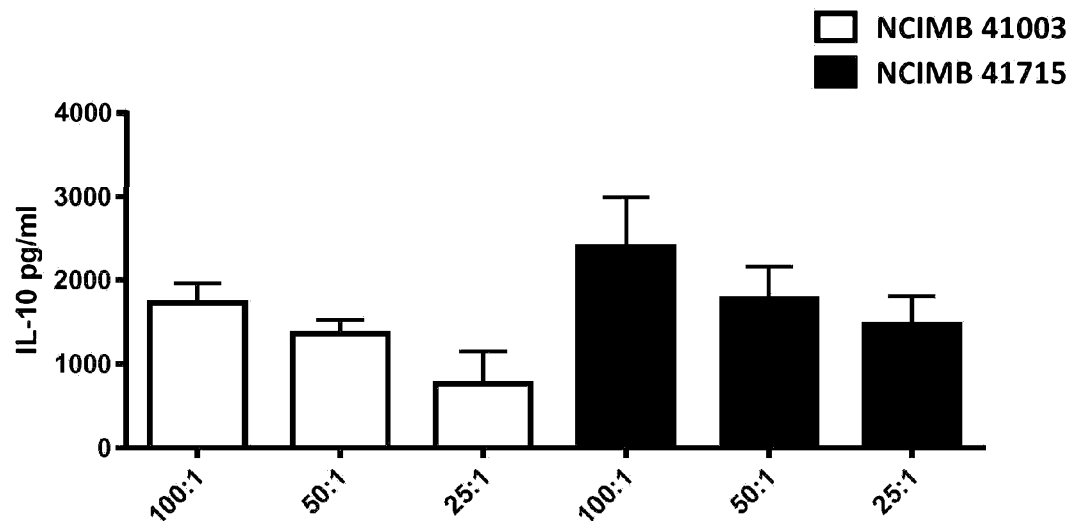
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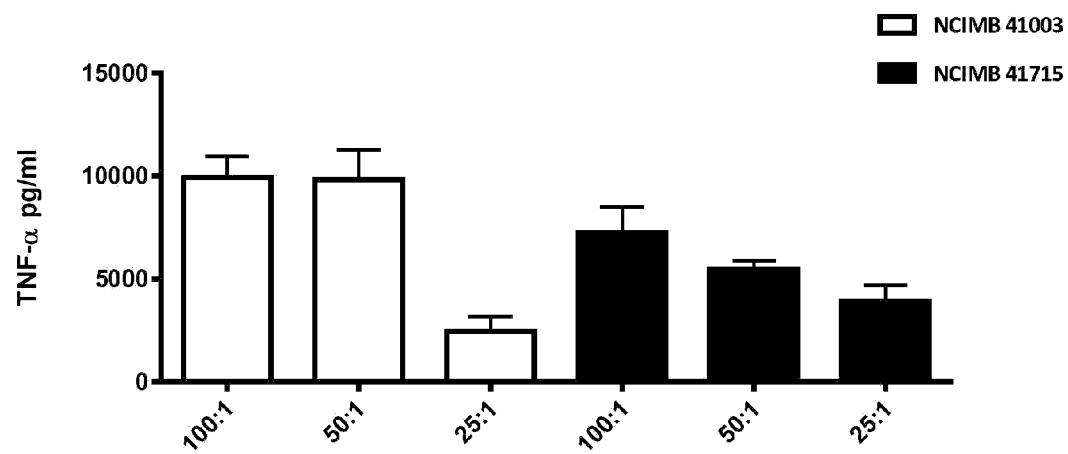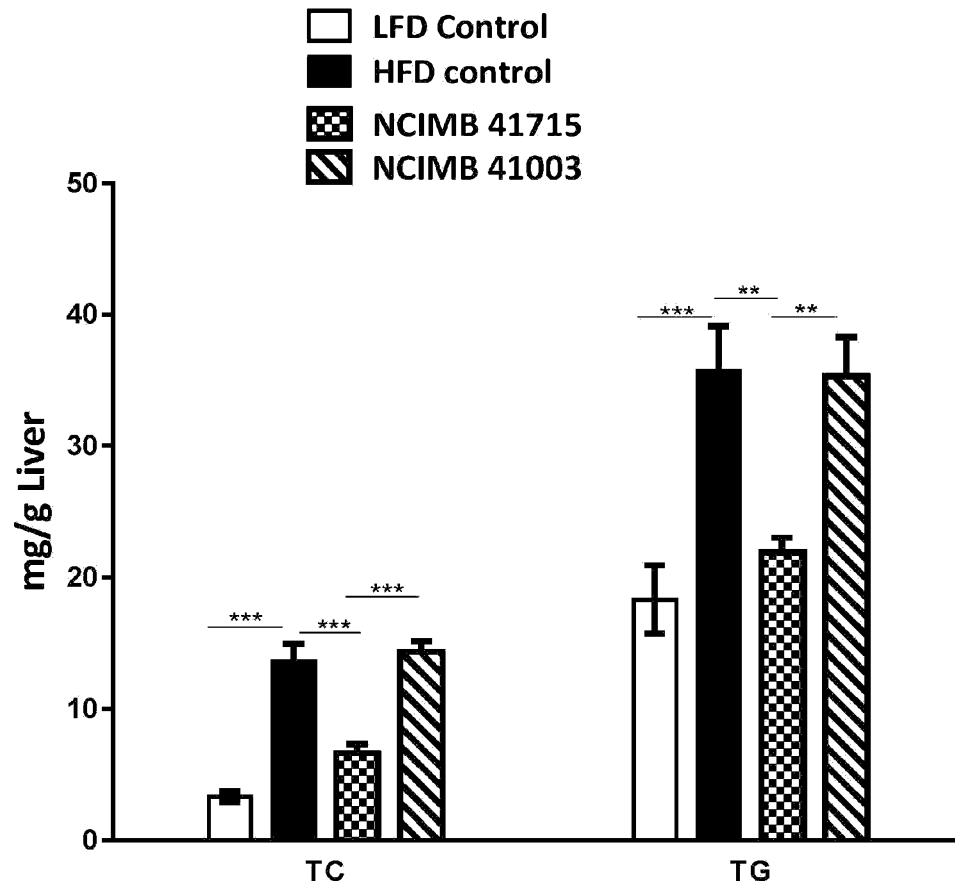

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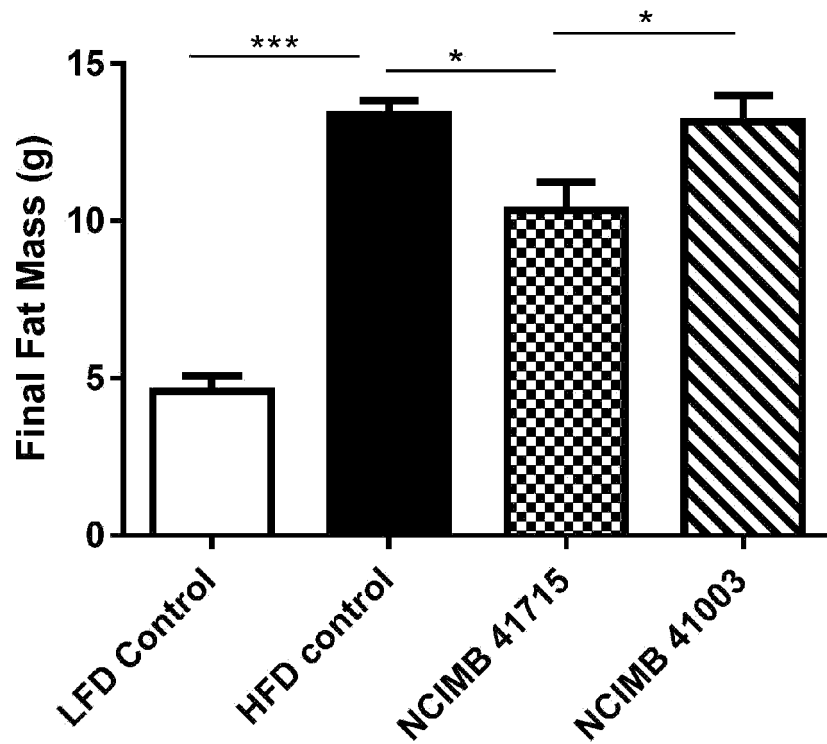
1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)

*** p<0.001. ** p<0.01, * p<0.05.

Fig. 7
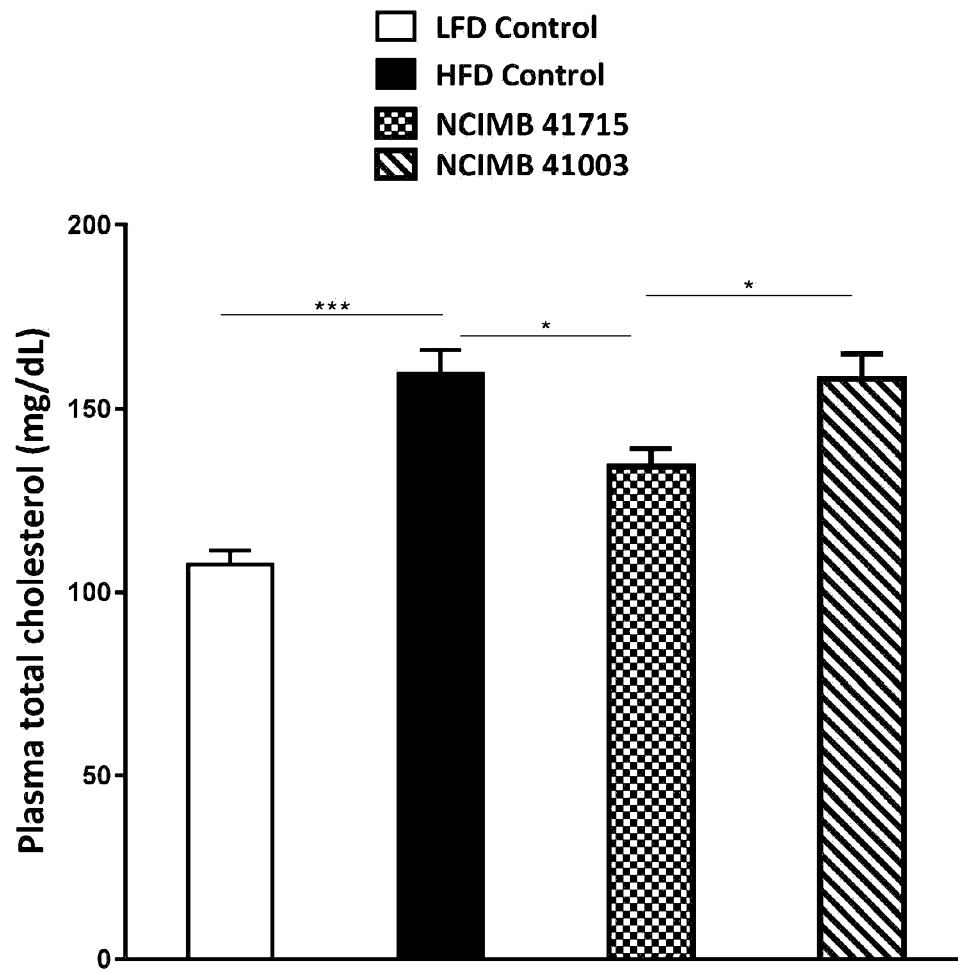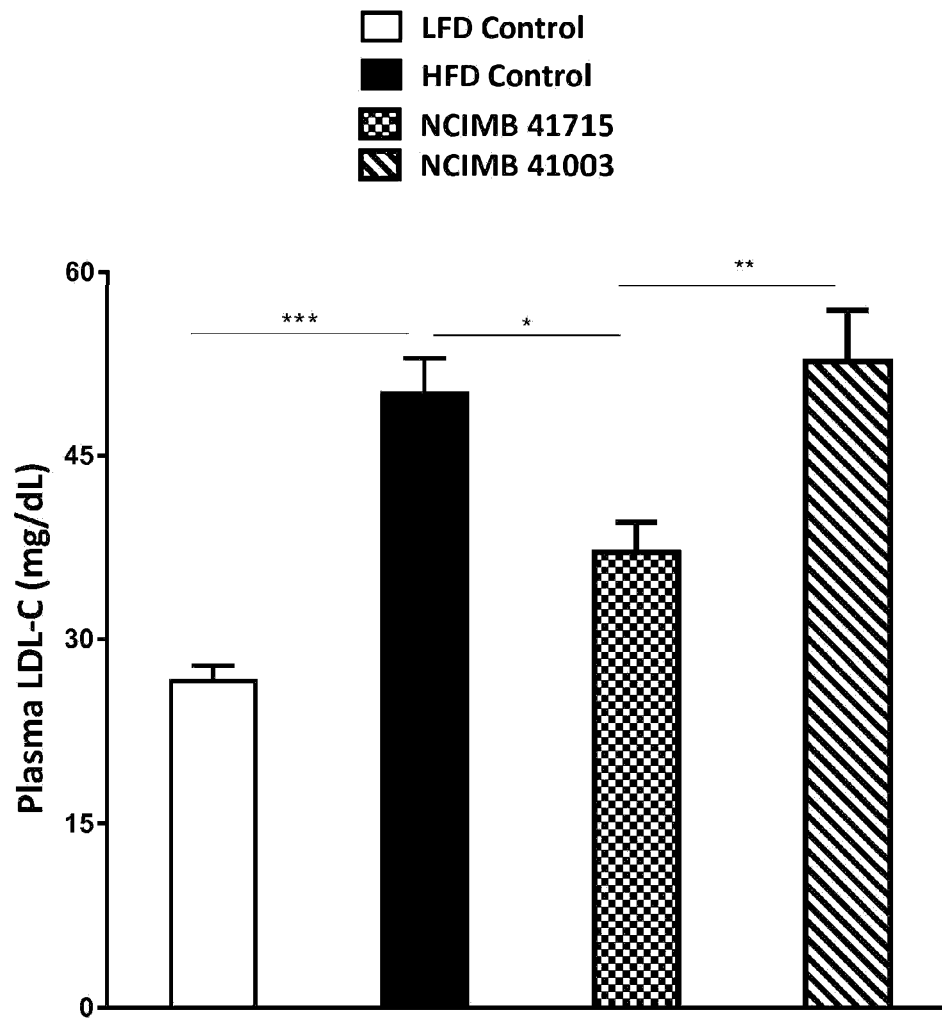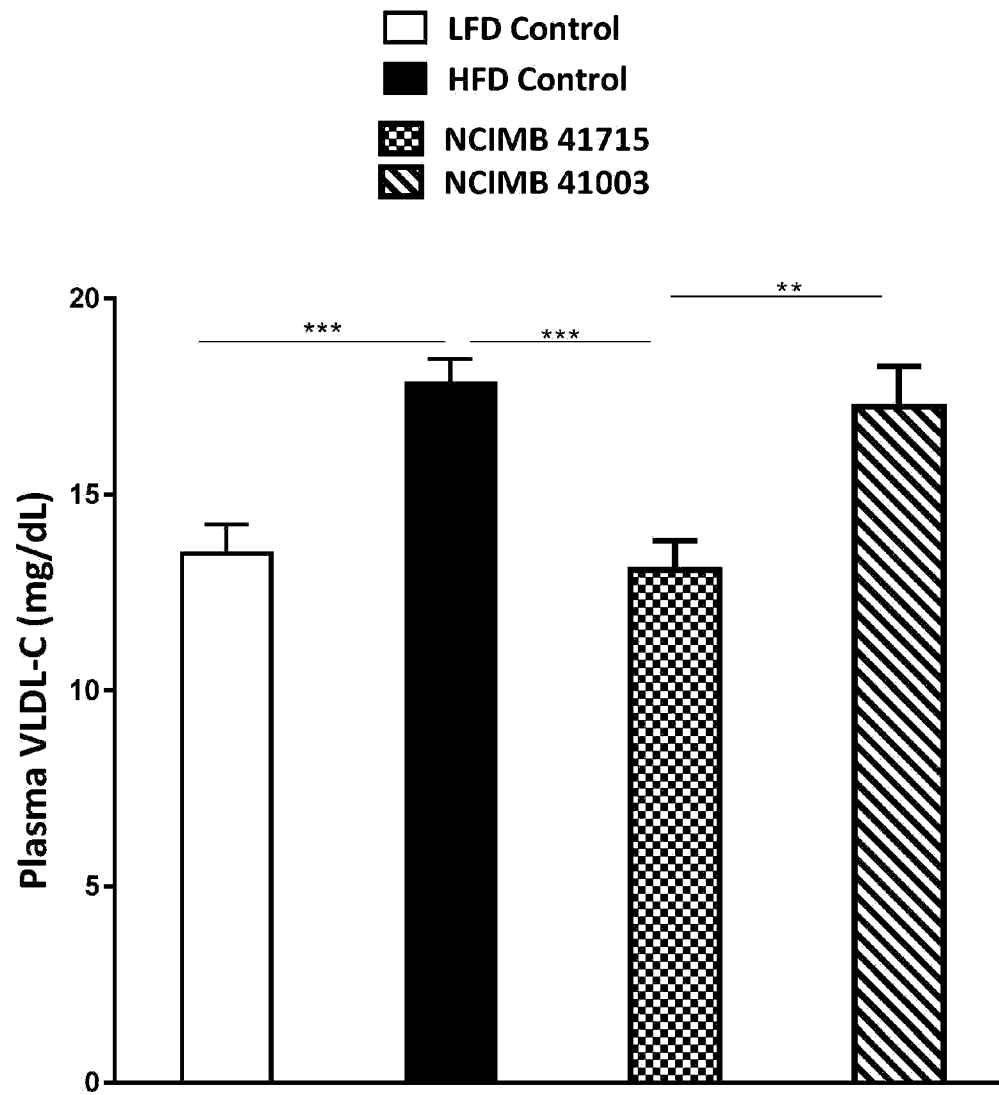
1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)

*** p<0.001. ** p<0.01, * p<0.05.

Fig. 8
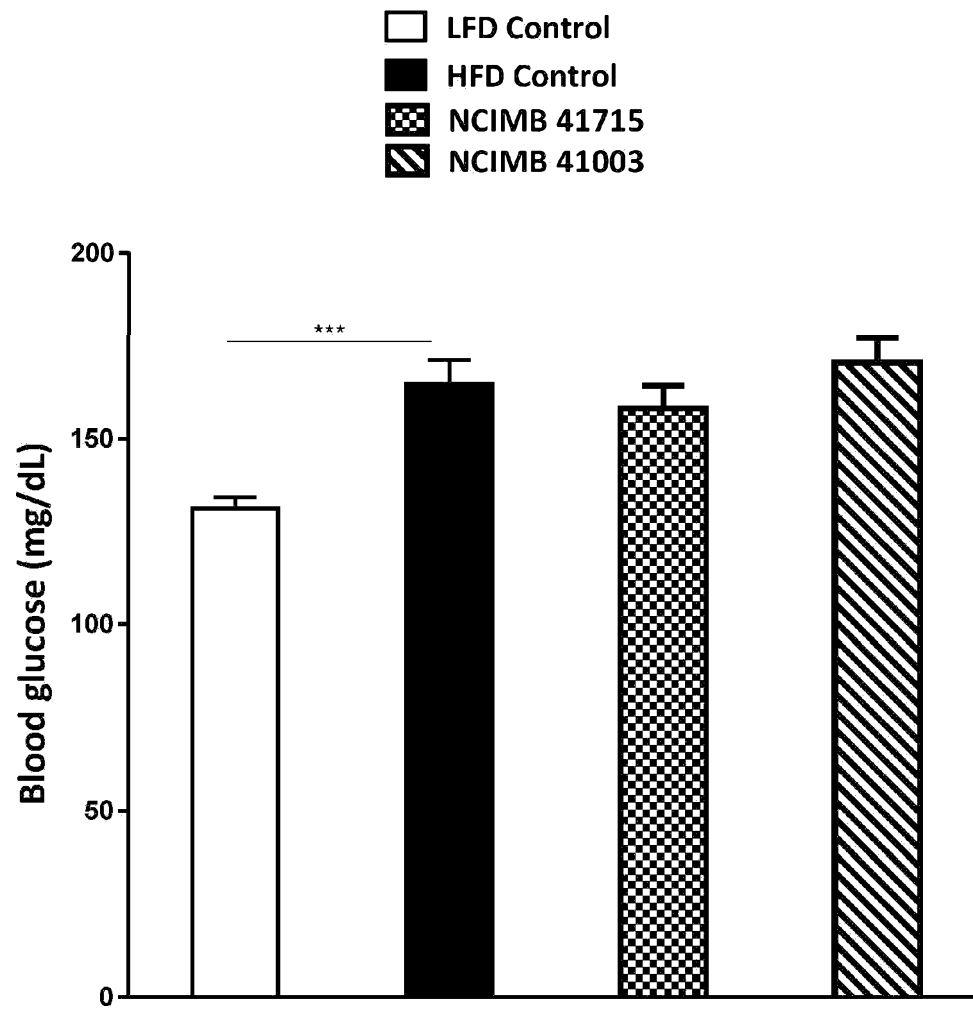
1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)
   *** p<0.001. ** p<0.01, * p<0.05

Fig. 9

1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)
   *** p<0.001. ** p<0.01, * p<0.05.

Fig. 10

1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)
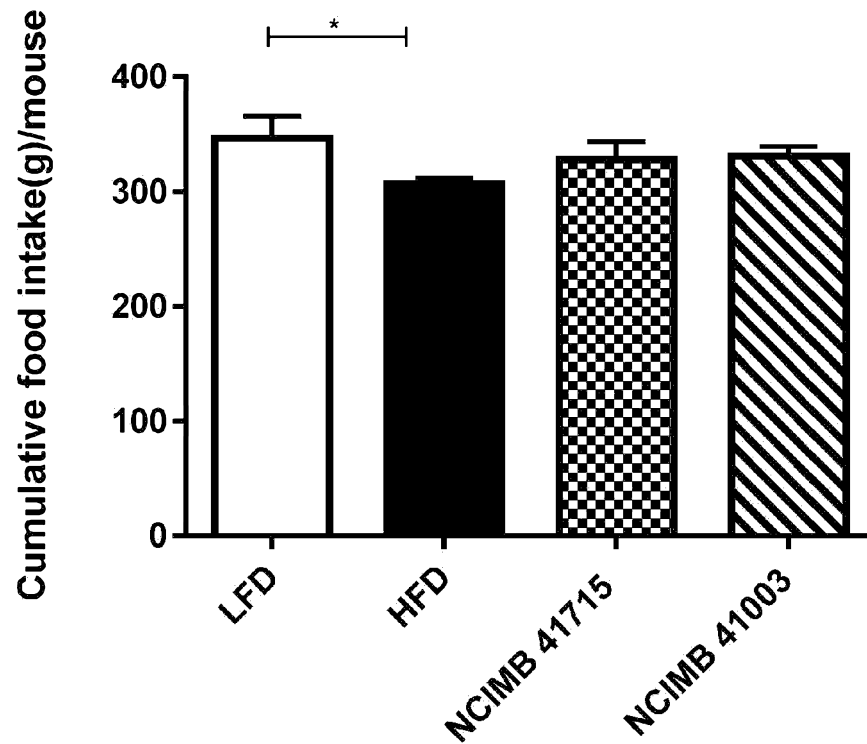*** p<0.001. ** p<0.01, * p<0.05.

Fig. 11

1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)
   *** p<0.001. ** p<0.01, * p<0.05.

Fig. 12

1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)
    *** p<0.001. ** p<0.01, * p<0.05.

Fig. 13

1) Unpaired student t-test (Lean versus DIO)
2) One-way ANOVA followed by Tukeys multiple comparison test (DIO versus all strains)
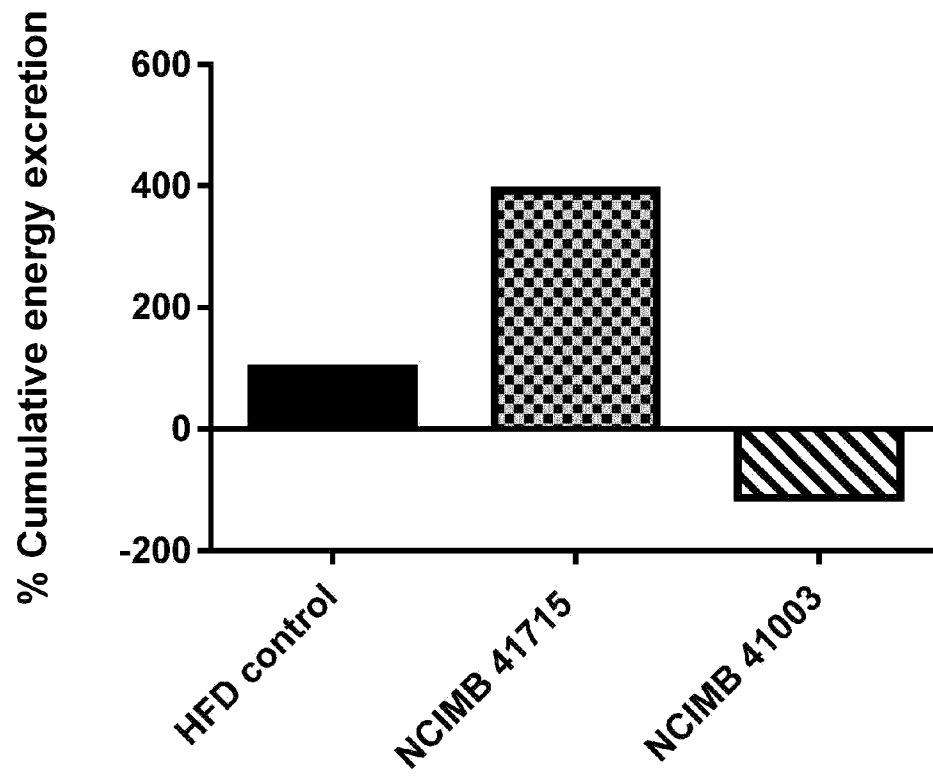   *** $p < 0.001$. ** $p < 0.01$, * $p < 0.05$.

Fig. 14

Fig. 15