**ORIGINAL ARTICLE** 



# Comparative accounts of probiotic properties of spore and vegetative cells of *Bacillus clausii* UBBC07 and in silico analysis of probiotic function

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#### Abstract

In this study, the spores and vegetative cells of *B. clausii* were independently evaluated for probiotic properties such as acid, gastric juice, bile, and intestinal fluid tolerance, adhesion to solvents/mucin and zeta potential. In addition, in silico identification of genome features contributing to probiotic properties were investigated. The results showed that spores were highly stable at gastric acidity and capable to germinate and multiply under intestinal conditions as compared to vegetative cells. The higher hydrophobicity of spores, compared to vegetative cells, is advantageous for colonization and persistence in the intestine. Furthermore, the presence of  $F_0F_1$  ATP synthase, amino acid decarboxylase, bile acid symporter, mucin/collagen/fibronectin-binding proteins, heat/cold shock proteins, and universal stress proteins suggests that the strain is able to survive stress. In conclusion, the results demonstrate that *B. clausii* UBBC07 spores show significantly higher survival and adhesion in nivitro gastrointestinal conditions as compared to vegetative cells. Besides, this study provides a comparative analysis of the in vitro probiotic properties of spores and vegetative cells of *Bacillus clausii* UBBC07.

Keywords Bacillus clausii UBBC07 · Spores · Vegetative cells · Probiotics properties · Zeta potential

# Introduction

Probiotics are defined as live microorganisms that, when administered in adequate amounts, confer a health benefit on the host (Hill et al. 2014). To date, *Lactobacillus* and *Bifidobacteria* are the most investigated probiotic cultures as compared to *Bacillus* (Bhushan et al. 2019). As per the recommendations of health institutions of Canada and Italy, the use of  $1 \times 10^9$  colony forming units (cfu) of these bacteria were permitted per serving for nonstrain-specific claims (Hill et al. 2014). There are several probiotic products on the market, but only a few fulfill criteria of labelled concentration claims at the end of the shelf-life (Vecchione et al. 2018). Besides this, the ability of bacteria to tolerate gastric and intestinal conditions is imperative for the delivery of health benefits to the host (Bhushan et al. 2020). In

☐ J. J. Ahire jayesh@uniquebiotech.com; jjahire@gmail.com comparison to vegetative cells, spores are highly stable at various industrial, environmental, and gastro-intestinal conditions, thus ensuring the delivery of recommended probiotic dose to the gut (Patel et al. 2009; Ahire et al. 2020c).

Comparative probiotic properties of spores and vegetative cells of spore-formers have rarely been investigated (Bernardeau et al. 2017). Cenci et al. (2006) showed the ability of *Bacillus clausii* spores to germinate during gastrointestinal transit and the possibility for vegetative cells to survive in the intestinal tract. Patel et al. (2009) evaluated probiotic properties of a mixture of spores and vegetative cells of *B. megaterium*. Recently, Sharma et al. (2020) characterized the probiotic properties of the ambiguous biotype i.e. spores or vegetative cells of *Bacillus* spp., isolated from fermented food. Moreover, probiotic properties of spores or vegetative cells or mixture.

*Bacillus clausii* is a Gram-positive, aerobic, sporeforming, motile, rod-shaped, facultative alkaliphilic soil bacterium (Cenci et al. 2006). It is one of the human probiotics, which is able to survive gastrointestinal transit and colonize the gut even in the presence of antibiotics (Duc et al. 2004; Ianiro et al. 2018). Preclinical and clinical studies suggest that *B. clausii* probiotic is effective in



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the treatment of diarrhea, recurrent respiratory infections and acute gastroenteritis (Marseglia et al. 2007; Ianiro et al. 2018; Paparo et al. 2020). Currently tested strain, Bacillus clausii UBBC07 (MTCC 5472) is a non-toxic, spore-forming probiotic bacterium available on the Indian market since 2005 (Upadrasta et al. 2016; Lakshmi et al. 2017). A daily dose of 4 billion cfu of UBBC07 spores is recommended to alleviate diarrhea in children and adults (Sudha et al. 2013, 2019). Recently, B. clausii UBBC07 has been reported for the production of lantibiotic clausin and reduction of uremic toxins in acetaminophen-induced uremic rats (Patel et al. 2019; Ahire et al. 2020b). In this study, for the first time, we describe the comparative probiotic properties of spores and vegetative cells of Bacillus clausii UBBC07 and in silico identification of genome features contributing to probiotic properties.

## **Materials and methods**

#### Preparation of vegetative cells and spores

Bacillus clausii UBBC07 (MTCC 5472) was obtained from the Unique Biotech culture collection, Hyderabad, India. The strain was cultivated aerobically in BHI broth (HiMedia, India) at 37 °C for 24 h and purity confirmed by plating on BHI agar. A single colony was inoculated in 10 ml BHI broth and incubated for 24 h at 37 °C with shaking (180 rpm). Vegetative cells were harvested by centrifugation at  $11,000 \times g$  for 10 min at 4 °C (Sorvall Legend XTR, Thermo Scientific, USA) and washed twice with phosphate buffer saline (PBS, pH 7.3). The cell pellet obtained was resuspended in PBS and investigated for probiotic properties. Simultaneously, the strain was cultivated aerobically in BHI broth at 37 °C for 96 h to sporulate. Spores were harvested by centrifugation, washed twice with PBS, and heat-treated at 80 °C for 20 min to kill vegetative cells. The resultant spore suspension was evaluated for probiotic properties.

# Survival of spores and vegetative cells under in vitro GIT conditions

#### Acid tolerance

The 100  $\mu$ l of *B. clausii* UBBC07 vegetative cells and spore suspension was inoculated separately in 900  $\mu$ l PBS pH (1.0, 2.0 and 3.0) and incubated aerobically at 37 °C for 0, 1, 2 and 3 h (Ahire 2012). Survivability was determined by plating on BHI agar.



#### Synthetic gastric juice tolerance

Spores or vegetative cells of UBBC07 were diluted 1:10 in filter sterilized (0.2 µm cellulose acetate; Sartorius, Germany) synthetic gastric juice [g 1<sup>-1</sup>: pepsin ( $\geq$  3000 NFU mg<sup>-1</sup>), 0.0133; lysozyme ( $\geq$  40,000 U mg<sup>-1</sup>), 0.1; bile, 0.05; proteose peptone, 8.3; glucose, 3.5; KCl, 0.37; NaCl, 2.05; CaCl<sub>2</sub>, 0.11; KH<sub>2</sub>PO<sub>4</sub>, 0.6; pH 2.5] and incubated aerobically at 37 °C for 3 h (Pedersen et al. 2004). Survival was determined at 0, 30 and 180 min time intervals by plating appropriate dilutions on BHI agar plates.

#### **Bile salt tolerance**

The UBBC07 suspension (vegetative cells or spores) was inoculated 1:10 in BHI broth supplemented with 0.1, 0.3, 0.5, 1.0 and 2.0% (w/v) bile (HiMedia, India). The tubes were incubated aerobically at 37 °C for 24 h. Tolerance was evaluated by determining optical density at 600 nm (Ahire 2012).

### Intestinal fluid tolerance

The UBBC07 suspension (vegetative cells or spores) was diluted 1:10 in filter sterilized intestinal fluid [1 mg ml<sup>-1</sup> pancreatin (amylase 100 U mg<sup>-1</sup>; lipase 8 U mg<sup>-1</sup>; protease 100 U mg<sup>-1</sup>: Sisco Research Laboratory, India) prepared in 0.85% (w/v) NaCl supplemented with 0.3% bile (w/v); pH 8.0], and incubated aerobically at 37 °C for 6 h. Survivability was determined at 0 and 6 h by plating on BHI agar.

### **Microbial adhesion to solvents**

The cell pellet or spores obtained from *B. clausii* UBBC07 were washed twice with PBS (pH7.3) and dissolved in 50 ml 0.1 mol l<sup>-1</sup> KNO<sub>3</sub> (pH 6.2). Absorbance of suspensions was measured at 600 as A<sub>0</sub> using a UV–visible spectrophotometer (Thermo Scientific, USA). To every 3 ml of this suspension, 1 ml solvent (xylene, chloroform, and ethyl acetate) was added and left standing for 10 min at 37 °C. Thereafter, the two phases were mixed by vortexing for 2 min and incubated aerobically at 37 °C for 30 min. The aqueous phase was removed and the absorbance (600 nm) measured as A<sub>1</sub> (Ahire et al. 2013). The percentage of microbial adhesion was calculated as  $(A_0 - A_1/A_0) \times 100$ .

#### Adhesion to porcine mucin

The 6-well tissue culture plates (Thermo Scientific, Denmark) were coated at 4 °C for 24 h with 100  $\mu$ g ml<sup>-1</sup> of porcine stomach mucin (Sigma Aldrich, USA) dissolved in 0.05 mol l<sup>-1</sup> Na<sub>2</sub>CO<sub>3</sub> (pH 9.7). After incubation, the coating solution was discarded and each well was treated with 2 ml PBS containing 1% (w/v) Tween 20 for 1 h. Finally, each well was washed with PBS containing 0.05% (w/v) Tween 20 and inoculated with 2 ml vegetative cells and or spore solution (0.5 OD) prepared in PBS (0.05% (w/v) Tween 20; pH 7.3) buffer. The plates were incubated overnight at 4 °C (Pedersen et al. 2004). After incubation, wells were washed with PBS containing 0.05% (w/v) Tween 20 and visualized using an inverted microscope (CKX53, Olympus, Japan). Adhesion was quantitatively determined by staining the wells with 0.1% (w/v) crystal violet (Ahire et al. 2014). Experiments were performed in triplicate.

## **Determination of zeta potential**

The zeta potential of *B. clausii* UBBC07 (vegetative cells or spores) prepared in PBS (pH 7.3) was measured using the Zetasizer Nano-ZS (Malvern, UK). The DTS1070 capillary cell was used as per the procedure described by Ahire et al. (2020a).

# In silico identification of genome features contributing to probiotic properties

*Bacillus clausii* UBBC07 whole genome (GenBank accession no. LATY0000000) was investigated for the presence of genes or specific domains involved in acid tolerance, bile salt tolerance, adhesion to gut mucosa and environmental stress resistance as described by Khatri et al. (2019). The RAST (Rapid Annotation using Subsystem Technology; Brettin et al. 2015) and SEED (Overbeek et al. 2014) viewer comparative blast search tool was used along with NCBI standard protein BLAST.

# **Statistical analysis**

Statistical analyses were performed using GraphPad Prism (USA). The statistical differences among means were determined using Tukey's multiple comparison test and *t*-test. Data were presented as the mean and standard deviation. The *p*-value of less than 0.05 was considered significant.

# Results

# **Acid tolerance**

The exposure of spores (~7.48 log  $_{10}$  cfu ml<sup>-1</sup>) to pH 1–3 for 3 h did not show any significant (p > 0.05) loss in survival (pH 1: 95.93 ± 2.02; pH 2: 94.92 ± 2.31; pH 3: 94.91 ± 2.30; pH 7.3: 94.79 ± 2.31%) as compared control (pH 7.3) (Fig. 1). On the contrary, the exposure of ~9.87 log  $_{10}$  cfu ml<sup>-1</sup> vegetative cells to pH 1 and 2 significantly (p < 0.0001) reduced survivability within an hour, with

no vegetative cells surviving. At pH 3 the vegetative cells showed significant (p < 0.0001) reduction in survival up to 3 h (1 h: 88.02±1.80; 2 h: 55.62±0.75; 3 h: 38.80±0.70%) (Fig. 1). Similar results were recorded when cells were exposed to pH 7.3, however, the decreased in survivability (1 h: 97.07±0.30; 2 h: 95.57±0.75; 3 h: 91.1±5.56%) was less as compared to pH 3 (Fig. 1). The difference recorded in viability between 0 to 3 h were significant (p < 0.05).

# Synthetic stomach juice tolerance

In synthetic gastric juice, the spore count was deceased significantly (p < 0.01) from 0 (7.62  $\pm 0.06 \log_{10}$  cfu ml<sup>-1</sup>) to 180 min (7.30  $\pm 0.07 \log_{10}$  cfu ml<sup>-1</sup>) of incubation (Fig. 2a). The percentage survival was determined as 95.75  $\pm 1.00\%$ . Survival of vegetative cells were significantly (p < 0.0001) reduced to zero during the incubation (0 min: 9.7  $\pm 0.05$ ; 30 min: 8.2  $\pm 0.09$ ; 180 min: 0 log <sub>10</sub> cfu ml<sup>-1</sup>) in gastric juice (Fig. 2a).

# **Bile salt tolerance**

Increasing concentrations of bile salts showed no adverse effects on the survivability of spores (bile 0.1%:  $91.93 \pm 3.76$ ; 0.3%:  $100.24 \pm 3.05$ ; 0.5%:  $109.05 \pm 1.70$ ; 1.0%:  $112.95 \pm 5.13$ ). In addition, 2.0% bile salt levels enhanced growth ( $147.43 \pm 3.89\%$ ; p < 0.01) (Fig. 2b). Survivability of vegetative cells decreased (bile 0.3%:  $72.56 \pm 0.78$ ; 0.5%:  $51.80 \pm 2.30$ ; 1.0%:  $41.04 \pm 0.52$ ) significantly (p < 0.01) when bile salt concentration was increased from 0.1% (Fig. 2b). No significant (p > 0.05) changes in survivability was recorded at 0.1% bile as compared with the control.

# Intestinal fluid tolerance

In synthetic intestinal juice, the spore count increased significantly (p < 0.0001) from 0 (7.69 ± 0.08 log<sub>10</sub> cfu ml<sup>-1</sup>) to 360 min (8.51±0.07 log<sub>10</sub> cfu ml<sup>-1</sup>) of incubation (Fig. 3a). The survival was recorded as 110.66±0.94%. On the contrary, the vegetative cell counts decreased significantly (p < 0.0001) from 7.59±0.11 log<sub>10</sub> cfu ml<sup>-1</sup> (0 min) to 5.77±0.07 log<sub>10</sub> cfu ml<sup>-1</sup> (360 min) (Fig. 3a). Moreover, the vegetative cells showed 76.05±0.96% survivability.

# **Microbial adhesion to solvents**

*Bacillus clausii* UBBC07 spores had higher adhesion to chloroform (98.33 $\pm$ 0.57%) and ethyl acetate (94.66 $\pm$ 0.58%) as compared to xylene (65.66 $\pm$ 2.51%) (Fig. 3b). Whereas vegetative cells adhered greater to chloroform (50.33 $\pm$ 2.08%) as compared with xylene (22.66 $\pm$ 4.72%) and ethyl acetate (25.66 $\pm$ 4.16%) (Fig. 3b).





**Fig. 1** Acid tolerance of spores and vegetative cells of *Bacillus clausii* UBBC07. Panel **a** pH 1.0; **b** pH 2.0; **c** pH 3.0; **d** pH 7.3 (control). The primary *y*-axis indicates vegetative cell count and

secondary y-axis for spores. All data are represented as mean  $\pm$  SD. \*p < 0.05; \*\*\*\*p < 0.0001: significant difference compared to initial or 0 time point

### Adhesion to porcine mucin

Spores had significantly (p < 0.01) higher crystal violet optical density readings  $(0.084 \pm 0.004)$  as compared to vegetative cells  $(0.065 \pm 0.005)$ . Figure 4 describes the adhesion of spores and vegetative cells to mucin-coated wells.

#### **Determination of zeta potential**

Spores had significantly (p < 0.05) higher zeta potential  $(-28.3 \pm 1.04 \text{ mV}; 7.95 \pm 0.04 \log_{10} \text{ cfu ml}^{-1})$  as compared to vegetative cells  $(-23.4 \pm 2.23 \text{ mV}; 8.01 \pm 0.05 \log_{10} \text{ cfu ml}^{-1})$ .

# In silico identification of genome features contributing to probiotic properties

The in silico analysis of *B. clausii* UBBC07 genome revealed the presence of 10 domains for acid tolerance, three for bile tolerance, 11 for adhesion to gut mucosa, and 15 for environmental stress resistance (Table 1).



### Discussion

The ability of probiotics to reach the gut in sufficient numbers is imperative in order for cells to confer health benefits. As per recommendations, most probiotic products contain billions of cells and the benefits they confer is dependent on the strains ability to survive transit through the gut. There are several factors which contribute to the success of probiotic, such as the stability at various industrial processes and tolerance to the gastrointestinal tract stress (Ahire 2012). The use of spore probiotic is advantageous over the vegetative cells since spore's unique intrinsic makeup (dipicolinic acid, proteins, lipids, and carbohydrates) and extremely low permeability provides high tolerance to the stomach acidity, bile salt and intestinal conditions (Bernardeau et al. 2017). In this study, the Bacillus clausii UBBC07 spores demonstrated high resistance to acidic conditions (pH 1, 2, and 3) and synthetic gastric juice (pH 2.5) as compared to vegetative cells. These in vitro results suggests that spores are probably able to survive and deliver prerequisite quantities to the small intestine. Cenci et al. (2006) has shown that B. *clausii* spores tolerated pH 2 and vegetative cells  $pH \le 4$ . Recently, the in vitro investigation of B. clausii spore germination in the Simulator of Human Intestinal Microbial



**Fig.2 a** Synthetic gastric juice; **b** bile salt tolerance of spores and vegetative cells of *Bacillus clausii* UBBC07. The primary *y*-axis indicates optical density for vegetative cell and secondary *y*-axis for spores. All data are represented as mean  $\pm$  SD. \*\*p < 0.01; \*\*\*\*p < 0.0001: significant difference compared to initial or 0 time point for gastric juice and 0% concentration for bile

Ecosystem (SHIME) indicated the survival of spores and accompanied vegetative cells under SHIME-fed stomach simulations (Ahire et al. 2020b). Besides this, none of the studies evaluated the comparative probiotic properties of spore and vegetative cells.

Bile acid is the major component of bile, which acts as an emulsifier to facilitate the digestion of lipids and lipidsoluble-vitamins in the intestine. In higher concentrations, the bile acid is toxic to the bacterial cells by causing membrane damage, protein denaturation, and oxidative damage to the DNA (Prete et al. 2020). Therefore, the investigation of probiotic bacteria to survive bile acids is important to predict their persistence in the gut. In this study, the bile tolerance observed in UBBC07 spores was higher than the vegetative biotype, which is due to the intrinsic resistance of spores to the bile. However, the increased  $\log_{10}$  cfu ml<sup>-1</sup> from *B*. clausii spores at higher bile levels suggested bile-induced spore germination (Giel et al. 2010). The capabilities of B. clausii spores to germinate under fed and fasted in vitro intestinal-SHIME-conditions have recently been reported (Ahire et al. 2020b). Ghelardi et al. (2015) showed that the B. clausii spores germinate and undergoes multiplication



**Fig. 3 a** Intestinal fluid tolerance; **b** Adhesion to solvents of spores and vegetative cells of *Bacillus clausii* UBBC07. All data are represented as mean $\pm$ SD. \*\*\*\*p < 0.0001: significant difference compared to initial or 0 time point

under stimulated in vivo human intestinal environments. Moreover, bile tolerance is a strain-specific trait (Hyronimus et al. 2000).

The tolerance of probiotics to the intestinal fluid containing pancreatin and bile under alkaline conditions is a good model to estimate their survivability in the gut. In the present investigation, B. clausii spores replicated in simulated intestinal conditions as compared with vegetative cells. This finding indicates the germination and multiplication ability of B. clausii spores in the intestinal fluid. The 76% viability of vegetative cells to the intestinal fluid assures the persistence of the strain in the gut. Furthermore, it has been reported that B. clausii survival and persistence in alkaline conditions might be due to the alkaliphilic nature of this species (Nielsen et al. 1995; Vecchione et al. 2018). Overall, these results corroborate well with previous in-vitro and -vivo findings that B. clausii spores germinate and multiply in human intestinal conditions (Cenci et al. 2006; Ghelardi et al. 2015; Ahire et al. 2020b).

Like stomach and intestinal stress tolerance, the adhesion of probiotics is an important property for successful colonization in the gut. In the present study, we investigated the





Fig. 4 Representative image of adhesion of spores and vegetative cells of *Bacillus clausii* UBBC07 to mucin. Panel **a** Control; **b** Spores; **c** Vegetative cells after crystal violet strain

adhesion of spores and vegetative cells of *B. clausii* using adhesion to -solvents, -mucin and zeta potential. In adhesion to solvents, the adhesion to xylene is an indication of hydrophobic surface properties (Bellon-Fontaine et al. 1996). The high percent affinity of spores to xylene as compared with vegetative cells indicated higher surface hydrophobicity of spores. This may be due to the relative abundance of protein in the outer coat or exosporium of spore compared with peptidoglycan on the vegetative cell surface (Jindal and Anand 2018). High adhesion of spores to chloroform and ethyl acetate as compared with vegetative cells indicated the electron-donating and electron-accepting properties of biological surfaces (Bellon-Fontaine et al. 1996). The strong adhesion of spores to porcine mucin and significantly higher net negative zeta potential value over vegetative cells further confirmed the findings. Overall, these results show that spores are highly hydrophobic and more capable of adhering to gut epithelial lining as compared to vegetative cells.

In another investigation, we have analyzed the whole genome sequence of *B. clausii* UBBC07 to identify the genome features contributing to probiotic properties. The presence of F0F1 ATP synthase complex indicated the ability of bacteria to resist the acidic environment of the stomach by maintaining H<sup>+</sup> homeostasis (Cotter and Hill 2003; Azcarate-Peril et al. 2004; Khatri et al. 2019). The ornithine/lysine/arginine decarboxylase family proteins catalyze the decarboxylation of amino acids resulting in the alkalinization of the cytosol and generation of a proton motive force, which can be exploited for acid resistance and/or the production of ATP (Romano et al. 2013). The sodium bile acid symporter family proteins contribute to bile resistance and adaptation to the gut environment (Price et al. 2006). Besides this, the proteins detected for mucus, collagen, and fibronectin-binding along with sortase, flagellin, and triosephosphate isomerase ensures adhesion to the intestinal mucosal layer and persistence of bacteria to the intestine. Furthermore, B. clausii UBBC07 harbors proteins for universal-, oxidative-, hyperosmoticstress, heat resistance, cold and heat shock, Clp protease, and chaperonins (GroEL and GroES) for survival and growth under environmental stress. Overall, these results corroborate well with the previous reports on in silico analysis of proteins involved in probiotic properties of B. clausii Enterogermina<sup>®</sup> (Khatri et al. 2019).

In conclusion, *Bacillus clausii* UBBC07 spores demonstrated excellent gastro-intestinal resistance as compared with vegetative biotype. No loss in viability, good adhesion, and spore germination under simulated in vitro human intestinal conditions ensures the delivery of the recommended amount of probiotics to the gut. Moreover, in silico analysis revealed the presence of proteins involved in probiotic properties in *B. clausii* UBCC07 genome. Therefore, we recommend that spores of *B. clausii* UBBC07 be used to deliver probiotic to the human and or animal gut where they germinate and colonise to confer intended health benefits.



Table 1	Distribution of proteins	s involved in probiotic	properties in B. cla	ausii UBCC07 genome
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Acid tolerance     F0F1 ATP_synthase     KK185936     ATP synthase subunit A       KK185898     ATP synthase subunit C     KK185899     ATP synthase subunit B       KK185890     ATP synthase defti (OSCP) subunit     KK185901     ATP synthase subunit alpha       KK185901     ATP synthase subunit alpha     KK185902     ATP synthase subunit agamma       KK185902     ATP synthase subunit agamma     KK185903     ATP synthase subunit painon       KK185903     ATP synthase subunit cpsilon     KK185904     ATP synthase subunit cpsilon       Amino acid decarboxylase     KK185796     OrnLys/Arg decarboxylase       Bile tolerance     Sodium bile acid symporter     KK185526     Bile acid sodium symporter       KK186648     Sodium transporter     KK186648     Sodium transporter       KK186648     Sodium transporter     KK186648     Sodium transporter       KK186506     Sortase     KK187777     F0pA       Sortase     KK187560     Sortase     KK184941       Sortase     KK18754     Sortase     KK184941       Sortase     KK187574     Sortase     Flagellin_N       Flagellin     KK184853     Cp10     Chaperonins Grof5     KK18485	Category	Probiotic feature	Accession numbers	Identified-domain
KKI8589       ATP synthase subunit C         KKI8580       ATP synthase subunit B         KKI8500       ATP synthase subunit apha         KKI8500       ATP synthase subunit beta         KKI8500       Maginar/Sinderwalka         Bile acid symporter       KKI8502       Bile acid solum symporter         KKI8500       Solum tansporter       KKI8502       Solum bile acid solum symporter         KKI8500       Solum bile acid solum protein       *       Gran_os_anchor         Athesion to gut mucosa       Mucus binding protein       KKI87776       Solare         KKI8707       Sortase       KKI8777       Sortase         Figellin       KKI8777       Sortase       Solase         KKI84781	Acid tolerance	F0F1 ATP_synthase	KKI85936	ATP synthase subunit A
KKI8589       ATP synthase subunit B         KKI8500       ATP synthase subunit Jah0         KKI8501       ATP synthase subunit Jah0         KKI8502       ATP synthase subunit Jah0         KKI8503       ATP synthase subunit Jah0         KKI8504       ATP synthase subunit Jah0         KKI8505       Bile acid soum symporter         KKI8505       Bile acid Soum symporter         KKI8504       Solum bile acid Symporter         KKI8505       Bile acid Soum symporter         KKI8505       Solum bile acid family transporter         KKI8506       Gollagen binding protein         † Protoccin binding protein       †         KKI87200       Sortase         KKI87107       Solagelin_A         KKI8707       Sortase         KKI8707       Solagelin_A         KKI8707       Sortase         KKI8707       Sortase         KKI8707       Solagelin_A         KKI8707       Solagelin_A         KKI8707       Solagelin_A			KKI85898	ATP synthase subunit C
KK18500     ATP synthase delta (OSCP) subunit       KK18501     ATP synthase subunit apha       KK18500     ATP synthase subunit beta       KK18500     ATP synthase subunit beta       KK18500     ATP synthase subunit beta       KK18500     ATP synthase subunit pasilon       KK18501     ATP synthase subunit beta       KK18502     ATP synthase subunit pasilon       Bile tolerance     Sodium bile acid symporter       KK18502     Bile acid sodium symporter       KK18504     Sodium bile acid family transporter       KK18505     Sodium bile acid family transporter       KK18504     Sodium bile acid family transporter       KK18505     Sortase       Adhesion to gut mucosa     Mucus binding protein     *       Collagen binding protein     *     Collagen_bind       KK18770     FbpA     Sortase       KK187126     Sortase     KK1870       Sortase     KK18707     FbpA       KK18707     FbpA     FbpA       KK18707     FbgBellin_N     Sortase       KK18708     Sortase     Coll sock protein     KK18707       Fiosephosphate isomerase     KK187126<			KKI85899	ATP synthase subunit B
KK185001   ATP synthase subunit aghma     KK185002   ATP synthase subunit gamma     KK185003   ATP synthase subunit gamma     KK18504   ATP synthase subunit epsilon     KK18505   Arr synthase subunit epsilon     KK18505   Bita exit asodium symporter     Bitle tolerance   Sodium bile acid symporter     KK18505   Bita exit asodium symporter     KK18505   Bita exit asodium symporter     KK18505   Bita exit asodium symporter     KK18505   Gram_pos_anchor     Adhesion to gut mucosa   Mucus binding protein   *     Collagen binding protein   *   Collagen_bind     Fibronectin binding protein   *   Collagen_bind     Fibronectin binding protein   *   Sortase     KK18706   Sortase   Sortase     KK18707   FbpA   Sortase     Fibronectin binding protein   *   Sortase     KK18706   Sortase   Sortase     KK18707   Sortase   Sortase     Fibronectin binding protein   *   Sortase     KK18707   Sortase   Sortase     KK18707   Flagellin_C   Sortase     Coll aper binding protein   KK18707   Flagellin_C     KK18707   Flagellin_C			KKI85900	ATP synthase delta (OSCP) subunit
KKI8502       ATP synthase subunit gamma         KKI8503       ATP synthase subunit beta         KKI8504       ATP synthase subunit beta         KKI8506       OrrLys/Arg decarboxylase         KKI8506       OrrLys/Arg decarboxylase         Bile tolerance       Sodium bile acid symporter         KKI8506       Sodium transporter         KKI8507       Bile acid family transporter         KKI8506       Sodiam transporter         KKI8507       Sodiage binding protein         KKI8507       Sortase         Sortase       KKI87126         Sortase       Sortase         KKI8606       Sortase         Flagellin       KKI8707         Trasphosphate isomerase       KKI8707         KKI8708       Chaperonins GroEL         Chaperonins GroEL       KKI8708         Chaperonins GroEL       KKI84848         Cold sho			KKI85901	ATP synthase subunit alpha
KKI85903   ATP synthase subunit beta     KKI85504   ATP synthase subunit epsilon     KKI85504   ATP synthase subunit epsilon     KKI85536   Ora/Lys/Arg decarboxylase     KKI85536   Ora/Lys/Arg decarboxylase     KKI85536   Sodium transporter     KKI85546   Sodium bile acid symporter     KKI85546   Sodium bile acid family transporter     KKI86556   Sodium bile acid family transporter     KKI8657   Sodiam transporter     Collagen binding protein   *     Fibronectin binding protein   KKI8777     Fibronectin binding protein   KKI87176     Sortase   KKI87260     Sortase   Sortase     KKI8707   Sortase     KKI8717   Sortase     Fagellin   KKI87176     Fagellin   KKI87176     Sortase   KKI87176     Fagellin   KKI87176     Fagellin, N   Sortase     KKI87499   Flagellin, N     Cilaperonins GroEL   KKI8420     Cilaperonins GroEL   KKI8420     Cilaperonins GroEL   KKI8420     Cilaperonins GroEL   KKI8420     Cila shock protein   KKI8712     KKI8790   Cilaperonica GroE     KKI8740   Cilaperota			KKI85902	ATP synthase subunit gamma
KKI8504   Arrino acid decarboxylase   KKI85796   Orn/Lys/Arg decarboxylase     KKI85796   Orn/Lys/Arg decarboxylase     Bile tolerance   Sodium bile acid symporter   KKI8505   Bile acid sodium symporter     KKI85546   Sodium transporter     KKI85546   Sodium bile acid family transporter     KKI85546   Sodium bile acid family transporter     Adhesion to gut mucosa   Mucus binding protein   *   Collagen_bind     Fibronectin binding protein   *   Collagen_bind   Collagen_bind     Fibronectin binding protein   *   Sortase   Sortase     KKI87126   Sortase   Sortase   KKI8710   Sortase     KKI87540   Sortase   Sortase   KKI8710   Sortase     Flagellin   KKI8754   Sortase   Sortase     KKI8754   Sortase   KKI8710   Flagellin_C     Environmental stress resistance   Chaperonins GroEL   KKI84820   ClP_protease     KKI8778   ClP_protease   KKI8779   ClP_protease     KKI8779   ClP_protease   KKI8740   Sortase     Environmental stress resistance   KKI8402   ClP_protease   KKI8740     Clageronins GroEL   KKI84837   ClP_protease     KKI8797   ClP_protease <td< td=""><td></td><td>KKI85903</td><td>ATP synthase subunit beta</td></td<>			KKI85903	ATP synthase subunit beta
Amino acid decarboxylase       KKI85796       Orn/Lys/Arg decarboxylase         KKI84553       Arginine/lysine/ornithine decarboxylase         Bile tolerance       Sodium bile acid symporter       KKI85026       Bide acid sodium symporter         KKI85026       Sodium transporter       KKI85026       Sodium transporter         Adhesion to gut mucosa       Mucus binding protein       *       Gram_oos_anchor         Collagen binding protein       KKI87777       BpA       BpA         Sortase       KKI877260       Sortase       Sortase         KKI87260       Sortase       KKI87760       Sortase         Fagellin       KKI87770       Bpa       Bilm_O         KKI87260       Sortase       KKI87760       Sortase         Fagellin       KKI87770       Biagellin_C       Sortase         Fagellin       KKI87760       Sortase       Sortase         Fagellin       KKI87760       Sortase       Sortase         Fagellin       KKI87770       Biagellin_C       Sortase         Fagellin       KKI87760       Sortase       Sortase         Fagellin       KKI87760       Sortase       Sortase			KKI85904	ATP synthase subunit epsilon
Bile tolerance       Sodium bile acid symporter       KKI8553       Arginine/lysine/omithine decarboxylase         Bile tolerance       Sodium bile acid symporter       KKI8502       Bile acid sodium symporter         KKI8554       Sodium tansporter       KKI8502       Sodium tile acid family transporter         Adhesion to gut mucosa       Mucus binding protein       *       Collagen_binding       Collagen_binding         Fibronectin binding protein       *       Collagen_binding       Collagen_binding       Collagen_binding         Fibronectin binding protein       KKI8777       BpA       Sortase         Sortase       KKI8756       Sortase       Sortase         KKI8750       Sortase       KKI8750       Sortase         Fagellin       KKI87510       Bagellin_C       KKI87510       Bagellin_C         Toisephosphate isomerase       KKI87507       Hagellin_C       Sortase         Environmental stress resistance       Chaperonins GroEL       KKI87302       Cp10       Sortase         Cly protease       KKI8737       Cl_protease       Cl       Sortase       Sortase         Environmental stress resistance       Chaperonins GroEL       KKI84884       Cl_protease       Cl		Amino acid decarboxylase	KKI85796	Orn/Lys/Arg decarboxylase
Bile tolerance   Sodium bile acid symporter   KKI85025   Bile acid sodium symporter     KKI85546   Sodium transporter     KKI85546   Sodium bile acid family transporter     Adhesion to gut mucosa   Mucus binding protein   *   Gram_pos_anchor     Collagen binding protein   *   Collagen_bind     Fibronectin binding protein   *   Collagen_bind     Fibronectin binding protein   KKI87777   FbpA     Sortase   KKI87126   Sortase     KKI87404   Sortase   Sortase     KKI87404   Sortase   KKI8720     KKI87404   Sortase   Sortase     KKI87404   Sortase   KKI8720     Flagellin   KKI87404   Sortase     Triosephosphate isomerase   KKI87490   Flagellin_N     Environmental stress resistance   Chaperonins GroEL   KKI88100   Chp_protease     Clp protease   KKI87492   CLP_protease     KKI87492   CSD   CSD     Heat shock protein   KKI87492   CSD     KKI87492   CSD   Sortase     KKI87492   CSD   SO     Heat shock protein   KKI87492   CSD     KKI87492   CSD   SO     Heat resistance   KKI87492			KKI84553	Arginine/lysine/ornithine decarboxylase
KKI85546   Sodium transporter     KKI86848   Sodium bile acid family transporter     KKI86848   Sodium bile acid family transporter     Adhesion to gut mucosa   Mucus binding protein   *   Gram_pos_anchor     Collagen binding protein   *   Gram_pos_anchor     Fibronectin binding protein   KKI87777   FbpA     Sortase   KKI87777   FbpA     Sortase   KKI87260   Sortase     KKI87260   Sortase   KKI8764     Sortase   KKI87260   Sortase     KKI87260   Sortase   KKI8754     Sortase   KKI8754   Sortase     KKI8754   Sortase   KKI8767     Flagellin   KKI8777   Flagellin_N     Triosephosphate isomerase   KKI85107   Flagellin_N     Chaperonins GroEL   KKI84884   Cpn00_TCP1     Chaperonins GroES   KKI84784   CLP_protease     KKI87126   Cplotase   KKI87492   CSD <	Bile tolerance	Sodium bile acid symporter	KKI85025	Bile acid sodium symporter
Adhesion to gut mucosa   Mucus binding protein   *   Gran_pos_anchor     Collagen binding protein   †   Collagen_bind     Fibronectin binding protein   †   Collagen_bind     Fibronectin binding protein   KKI87777   FopA     Sortase   KKI87126   Sortase     Sortase   KKI87260   Sortase     KKI87260   Sortase   KKI87260     Sortase   KKI87260   Sortase     Flagellin   Sortase   KKI87499   Flagellin_N     Triosephosphate isomerase   KKI87499   Flagellin_N     Environmental stress resistance   Chaperonins GroEL   KKI84885   Cp10     Clp protease   KKI8787   CLP_protease     Cold shock protein   KKI84782   CspC     Heat shock protein   KKI84885   GrpE     Heat resistance   KKI84983   DnJ <td></td> <td>KKI85546</td> <td>Sodium transporter</td>			KKI85546	Sodium transporter
Adhesion to gut mucosa   Mucus binding protein   *   Gram_pos_anchor     Collagen binding protein   *   Collagen_bind     Fibronectin binding protein   KI87777   FbpA     Fibronectin binding protein   KK1877260   Sortase     Sortase   KK187260   Sortase     KK187260   Sortase   KK187260     Sortase   KK187260   Sortase     KK187260   Sortase   Sortase     KK184941   Sortase   Sortase     Flagellin   KK184754   Sortase     Flagellin   KK187379   Flagellin_C     Triosephosphate isomerase   KK185379   Flagellin_N     Environmental stress resistance   Chaperonins GroEL   KK18485   Cpn0_TCP1     Claperonins GroES   KK18485   CLP_protease     KK187787   CLP_protease   KK187379     Cold shock protein   KK18485   CLP_protease     KK187492   CSD   Claperonins GroEL   KK184787     Cold shock protein   KK184787   CLP_protease     KK187492   CSD   Claperonins GroEL   KK184787     Cold shock protein   KK184983   DnaJ     Heat shock protein   KK184983   DnaJ     Heat shock protein   KK184983   Dn			KKI86848	Sodium bile acid family transporter
Collagen binding protein†Collagen_bindFibronectin binding proteinKK187777FbpAFibronectin binding proteinKK187777FbpASortaseKK187126SortaseKK1872601SortaseKK1872601KK1847541SortaseKK184754FlagellinKK184754SortaseFlagellinKK185107Flagellin_NTriosephosphate isomeraseKK18379TIMEnvironmental stress resistanceChaperonins GroELKK184885Cpn00_TCP1Chaperonins GroESKK184885CLP_proteaseClip proteaseKK185387CLP_proteaseCold shock proteinKK185485CLP_proteaseCold shock proteinKK184482CspCHeat shock proteinKK184485GripEHeat resistanceKK184985DnalOxidative stressKK184983DnalOxidative stressKK184787UspKK18500Universal StressKK185106UspKK18708UreVen	Adhesion to gut mucosa	Mucus binding protein	*	Gram_pos_anchor
Fibronectin binding protein   KK18777   FbpA     Sortase   KK187126   Sortase     KK187260   Sortase     KK187260   Sortase     KK184911   Sortase     KK184914   Sortase     KK184754   Sortase     Flagellin   KK184754     KK184754   Sortase     Flagellin   KK184754     Sortase   KK184754     Plagellin_C   KK184754     Chaperonins GroEL   KK184754     Chaperonins GroES   KK18485     ClP_protease   CLP_protease     Clog shock protein   KK184754     KK18778   CLP_protease     Cold shock protein   KK184062     Cold shock protein   KK184062     Heat shock protein   KK184985     GryE   Hpypersomotic stress     KK18407   PMSR     Universal Stress   KK18477     Universal Stress   KK18477     Universal Stress   KK18477	-	Collagen binding protein	†	Collagen_bind
SortaseKK187126SortaseKK187260SortaseKK187260SortaseKK184941SortaseKK184941SortaseKK186106SortaseKK18754SortaseFlagellinKK18754Flagellin_CKK187499Triosephosphate isomeraseKK185107Flagellin_NTimosephosphate isomeraseChaperonins GroELKK18484Chaperonins GroESKK18485Clp proteaseKK184682Clp proteaseKK18779KK187787CLP_proteaseCld shock proteinKK187492KK187492CSDHeat shock proteinKK18485Heat resistanceKK184985GrpEHyperosmotic stressKK186288PMSRHyperosmotic stressKK186288PMSRUniversal StressKK188101UspKK18708Urp		Fibronectin binding protein	KKI87777	FbpA
KI87260     Sortase       KI84941     Sortase       KI86106     Sortase       KI86106     Sortase       KI84754     Sortase       Flagellin     KI85107     Flagellin_C       KI87499     Flagellin_N       Triosephosphate isomerase     KK185379     TIM       Chaperoning GroEL     KK184884     Cpn60_TCP1       Chaperoning GroES     KK184885     Cpn0       Clp protease     KK185377     CLP_protease       Clog shock protein     KK185387     CLP_protease       KK18778N     CLP_protease     KK18798       Cold shock protein     KK185462     SpC       Heat shock protein     KK184482     CspC       Heat shock protein     KK185463     Grup       Heat shock protein     KK184985     Grup       Heat shock protein     KK184983     DnaJ       Migneric stress     KK186288     PMSR       Migneric stress     KK186176     Usp       Migneric stress     KK186187     Usp       KK188047     Usp     Jand       KK18810     Usp     Jand		Sortase	KKI87126	Sortase
KI84941     Sortase       KI86106     Sortase       KI84754     Sortase       Flagellin     KK184754     Sortase       Triosephosphate isomerase     KK185107     Flagellin_N       Triosephosphate isomerase     KK184379     TIM       Environmental stress resistance     Chaperonins GroEL     KK184884     Cpn60_TCP1       Chaperonins GroES     KK184885     Cp100     Cl2protease       Cl2 protease     KK184850     CL2-protease       KK18787     CL2-protease     CL2       KK187878     CL2-protease     KK187492       Heat shock protein     KK184482     CsD       Heat resistance     KK18493     JnaJ       Heat resistance     KK184983     JnaJ       Mider verses     KK186288     PMSR       Mider verses     KK18770     Usp       Mider verses     KK18770     Usp       KK187008     Usp     Stress			KKI87260	Sortase
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Universal Stress KK184787 Usp KK185810 Usp KK187408 Usp			KKI88047	PMSR
KK185810 Usp KK187408 Usp		Universal Stress	KKI84787	Usp
			KKI85810	Usp
<b>KKI07400</b> USP			KKI87408	Usp

\*Located on LATY01000009 with locus tag WZ76\_RS06065 †Located on LATY01000017 with locus tag WZ76\_RS12025

Author contributions JJA contributed to the study conception, design, acquisition and analysis of data, drafting and critically revising the manuscript. MSK carried out the material preparation and data collection. RSM contributed to the study conception and review. All authors approved the final submitted manuscript.

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**Data availability** The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation, to any qualified researcher.

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#### **Compliance with ethical standards**

**Conflict of interest** JJA, MSK and RSM are employed by Unique Biotech Limited, India, which is a manufacturer of probiotics. This does not alter our adherence to journal policies on sharing data and materials.

**Ethics approval** The research conducted for this article did not involve studies on humans or animals.

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