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Centro de Ciências Biológicas e da Saúde
Programa de Pós-Graduação em Ciências da Saúde
Mestrado em Ciências da Saúde

**Atividade antimicrobiana *in vitro* e potencial probiótico de *Bifidobacterium*
e *Lactobacillus* contra espécies de *Clostridium***

CINARA REGINA ARAGÃO VIEIRA MONTEIRO

São Luís

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Dissertação apresentada ao Programa de Pós-Graduação em Ciências da Saúde da Universidade Federal do Maranhão – UFMA, como requisito para obtenção do título de Mestre em Ciências da Saúde.

Orientador: Prof.º Dr. Valério Monteiro Neto

Co-orientadora: Prof.^a Dra. Maria Rosa Quaresma Bonfim

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Aprovada em / /

BANCA EXAMINADORA

Prof.º Dr. Valério Monteiro Neto (Orientador)
Universidade Federal do Maranhão

Prof.º Dr. Afonso Gomes Abreu Junior
Universidade Federal do Maranhão

Prof.^a Dra. Cristina de Andrade Monteiro
Universidade Ceuma

Prof.^a Dra. Lucilene Amorim Silva
Universidade Federal do Maranhão

“A única maneira de fazer um excelente trabalho é amar o que você faz. Se você ainda não encontrou, continue procurando. Não se acomode. Assim como tudo que importa para o coração, você saberá quando encontrar. ”

Steve Jobs

Dedico
Aos meus amores Rodrigo e
Giovanna

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LISTA DE SIGLAS E ABREVIATURAS

ATCC	American Type Culture Collection
CPE	<i>Clostridium perfringens</i> enterotoxin
DNA	Ácido Desoxiribonucléico
EN	Enterocolite Necrosante
IgA	Imunoglobulina tipo A
INCQS	Instituto Nacional de Controle de Qualidade em Saúde
MRS	Man-Rogosa-Stuart
NCIMB	National Collection of Industrial, Food and Marine Bacteria
PMC	Colite Pseudomembranosa
RCM	Reinforced Clostridial Medium
TcdA	Toxina <i>Clostridium Difficile</i> tipo A
TcdB	Toxina <i>Clostridium Difficile</i> tipo B
TGI	Trato Gastrointestinal
UFC	Unidades Formadoras de Colônias
DII	Doença Inflamatória Intestinal
DAA	Diarreia Associada a Antibiótico
H₂	Hidrogênio
CO₂	Dióxido de Oxigênio

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RESUMO

Espécies de *Clostridium*, principalmente *C. butyricum*, *C. difficile* e *C. perfringens*, são agentes de doenças infecciosas resultantes de disbiose intestinal. Em muitos casos, a recorrência pode ocorrer após antibioticoterapia, indicando a necessidade de novas opções terapêuticas que atuem sobre os patógenos e também restaurem a microbiota. Neste trabalho, investigou-se a atividade antimicrobiana *in vitro* e o potencial probiótico de cepas clínicas e de referência de *Bifidobacterium* e *Lactobacillus* contra espécies patogênicas de *Clostridium*. A atividade antimicrobiana foi avaliada pelo ensaio de difusão em sobrecamadas e pela inibição da produção de gás. Em seguida, o potencial probiótico das cepas selecionadas foi avaliado pela análise da capacidade de coagregação, propriedades de adesão às células eucarióticas e mucina, tolerância ao pH ácido e sais biliares, e pela determinação do perfil de susceptibilidade aos antibióticos. *Lactobacillus plantarum* ATCC 8014 foi a cepa mais promissora baseada em sua atividade inibitória contra *Clostridium* spp. Além disso, esta cepa preencheu os critérios para ser considerada um probiótico com base na sua capacidade de coagregação, propriedades de adesão e tolerância a condições adversas de pH e sais de ácidos biliares. No geral, os resultados indicam que, entre as linhagens estudadas, *L. plantarum* ATCC 8014 apresenta potencial probiótico para o controle de infecções pelas espécies de *Clostridium* estudadas e deve ser melhor avaliado em estudos animais.

Palavras-chave: Probióticos; *Lactobacillus plantarum*; *Clostridium*; Disbiose; Atividade antimicrobiana.

ABSTRACT

Clostridium species, mainly *C. butyricum*, *C. difficile*, and *C. perfringens*, are agents of infectious disease resulting from intestinal dysbiosis. In many cases, recurrence can occur after antibiotics, indicating the need for novel therapeutic options that act on the pathogens and also restore the microbiota. Herein, the *in vitro* antimicrobial activity and probiotic potential of clinical and reference strains of *Bifidobacterium* and *Lactobacillus* were investigated against pathogenic species of *Clostridium*. The antimicrobial activity was evaluated by the agar spot test and inhibition of gas production. Then, the probiotic potential of selected strains was assessed by analyzing their coaggregation ability, adhesive properties to host cells and mucin, tolerance to acidic pH and bile salts, and antimicrobial susceptibility profiles. *Lactobacillus plantarum* ATCC 8014 was the most promising strain based on its inhibitory activity against *Clostridium* spp. In addition, this strain met criteria to be considered a probiotic based on its coaggregation ability, adhesive properties, and tolerance to harsh conditions of pH and bile acid salts. Overall, the results indicate that among the studied strains, *L. plantarum* ATCC 8014 presents probiotic potential for controlling infections by the *Clostridium* species studied and should be further evaluated in *in vivo* animal studies.

Keywords: probiotics; *Lactobacillus plantarum*; *Clostridium*; dysbiosis; antimicrobial activity

1. INTRODUÇÃO

A microbiota de determinados sítios anatômicos do corpo humano, tais como a pele, trato respiratório superior, cavidade oral, trato gênito-urinário e trato gastrointestinal, apresentam uma grande diversidade de microrganismos que desempenham papéis importantes à saúde e ao metabolismo do ser humano. Estima-se que o número total de microrganismos da microbiota humana seja tão elevado que supera o número de células eucarióticas do organismo. Desses sítios anatômicos, a microbiota intestinal é incomparavelmente a que representa a maior diversidade de filos ou taxos, particularmente no cólon (KAMADA et al., 2013).

Adicionando ainda mais a essa complexidade, há também um elevado grau de variação interindividual no conteúdo de espécies bacterianas, o que significa que não há espécies microbianas "básicas" que estejam presentes em todos os seres humanos. Embora exista um grande grau de variação no conteúdo de espécies de microbiota intestinal entre indivíduos, há uma série de características consistentes que caracterizam a microbiota na saúde, a composição das espécies dentro dos hospedeiros individuais parece ser bastante estável durante períodos de tempo prolongados, mas a abundância relativa de algumas espécies constituintes parece variar constantemente em resposta a fatores como mudanças na dieta do hospedeiro (JIMÉNEZ et al., 2008).

Outra característica predominante da microbiota associada à saúde é que as bactérias anaeróbias obrigatórias superam em grande parte as espécies anaeróbias facultativas. De um modo geral, a grande maioria da microbiota intestinal pertence aos filos dos Bacteroidetes e Firmicutes, embora os membros do filo de Actinobacterias, como Bifidobactérias e Proteobactérias também possam estar relacionados (DONALDSON et al., 2015).

A microbiota intestinal é descrita como altamente benéfica à saúde do hospedeiro. Por outro lado, ela é também a fonte de compostos potencialmente danosos e de patógenos oportunistas. Desta forma, a saúde do hospedeiro está intimamente ligada ao seu equilíbrio balanceado. Em contraste, o termo "disbiose" refere-se a situações em que a composição microbiana e as atividades são deslocadas do seu estado normal e benéfico para outro que é mais deletério para a saúde do hospedeiro. De fato, numerosos distúrbios, tanto intestinais quanto sistêmicos, tem sido ligados à disbiose intestinal, incluindo-se diarreia associada a antibióticos, enterocolite necrosante, colite pseudomembranosa, doença de Crohn, entre outras

(CHAMBRUN et al., 2008; KAUR et al., 2011; PROSBERG et al., 2016; McFARLAND et al., 2016; PAMMI et al., 2017).

Entretanto, ainda não há uma clara compreensão de todos os aspectos etiológicos envolvidos na patogênese dessas doenças, existem evidências que apontam para o envolvimento de algumas espécies de *Clostridium*, entre outros patógenos oportunistas. Das espécies comumente relatadas, destacam-se *Clostridium butyricum*, *Clostridium difficile* e *Clostridium perfringens* (SOMMER; BACKHED, 2013; CASSIR et al., 2016).

Dado os papéis potencialmente importantes que a microbiota pode desempenhar na manutenção da homeostase ou na etiologia de várias doenças, a manipulação terapêutica da comunidade microbiana intestinal é um objetivo desejável. De um modo geral, isso pode ser alcançado com várias abordagens diferentes, como pela(o): 1) estimulação de respostas imunes do hospedeiro, 2) uso de drogas que atenuam especificamente atividades deletérias ou metabólitos da microbiota, 3) eliminação de espécies bacterianas através de antibióticos e 4) inoculação de espécies benéficas. Esta última estratégia é obtida pela ingestão de microrganismos designados de probióticos e aparenta ser a mais racional, considerando que a pressão seletiva a ser exercida afetaria menos o conjunto de bactérias que compõem a microbiota. As principais bactérias ditas como probióticas pertencem aos gêneros *Bifidobacterium* e *Lactobacillus* (EMAMI et al., 2009; TLASKALOVA-HOGENOVA et al., 2011; HILL et al., 2014; KUMAR; KUMAR, 2015).

As evidências atuais quanto a eficácia dos probióticos é variada, porém, é confundida pelo fato de que os regimes de tratamento em diferentes estudos são altamente heterogêneos, com diferentes espécies ou linhagens, dosagens, durações de tratamento e métodos de administração empregados. Além disso, dados clínicos recentes sugerem que probióticos específicos podem ser opções efetivas de tratamento para distúrbios relacionados a determinados casos de disbiose intestinal, tais como na prevenção de enterocolite necrosante em lactentes e na prevenção de diarreia associada aos antibióticos.

Apesar das evidências em pacientes, ainda não há comprovação *in vitro* da atividade antagonica contra os patógenos frequentemente envolvidos nessas síndromes clínicas. Portanto, este estudo teve por objetivo realizar seleção *in vitro* de linhagens de referência e de isolados clínicos de espécies de *Bifidobacterium* e *Lactobacillus* com atividade inibitória do crescimento de *Clostridium butyricum*, *Clostridium difficile* e *Clostridium perfringens*.

2. REFERENCIAL TEÓRICO

2.1 Desenvolvimento da microbiota intestinal

A microbiota intestinal desempenha papel importante na vida humana, funcionando como barreira epitelial protetora do contra microrganismos patogênicos, auxiliando nas reações metabólicas, modulação de respostas imunes inatas e adaptativas do hospedeiro (SEKIROV; FINLAY, 2009; LITTMAN; PAMER, 2011; MATAMOROS et al., 2013; PEREZ-LOPEZ et al., 2016).

O desenvolvimento da microbiota inicia-se desde a vida intrauterina evoluindo seu amadurecimento e atingindo o estado adulto por volta dos 3 anos de idade, durante esse período é influenciado pela microbiota de adultos que convivem no mesmo ambiente familiar (PALMER et al., 2007; MATAMOROS et al., 2013).

Acreditava-se que o ambiente intrauterino e o recém-nascido eram estéreis até o parto, porém estudos do líquido amniótico e placenta maternos (DIGIULIO et al., 2008; SATOKARI et al., 2009; COLLADO et al., 2016) e do mecônio infantil (MADAN et al., 2012; COLLADO et al., 2016) revelaram a presença de microrganismos, sugerindo transferência microbiana. Considera-se assim que a via hematogênica corresponde a principal interface para translocação de bactérias intestinais da mãe para o feto (JIMÉNEZ et al., 2008).

Fatores externos à gravidez também podem influenciar no desenvolvimento da microbiota, tais como: uso de drogas, doenças, estresse, exposição a metais pesados, dieta e tratamentos com probióticos e antibióticos durante a gestação (BAILEY et al., 2004; LAHTINEN et al., 2009; MATAMOROS et al., 2013).

O tipo de parto apresenta influência direta na colonização intestinal inicial. Estudos demonstram que neonatos nascidos de parto vaginal sofrem maior influência da microbiota da genitália feminina e apresentam maior diversidade bacteriana quando comparadas com crianças nascidas de parto cesariano que sofrem maior influência da pele materna (DOMINGUEZ-BELLO et al., 2010; RUTAYISIRE et al., 2016).

O leite materno proporciona uma variedade de bactérias comensais e mutualísticas, com predomínio de *Staphylococcus spp*, *Streptococcus spp*, bactérias do ácido lático e

Bifidobacterium spp. A microbiota intestinal materna atinge as glândulas mamárias e colonizam o lactente durante o período de lactação, contribuindo também na maturação das respostas imunológicas (FERNÁNDEZ et al., 2012). Os principais fatores que influenciam no desenvolvimento da microbiota estão resumidos na Figura 1.

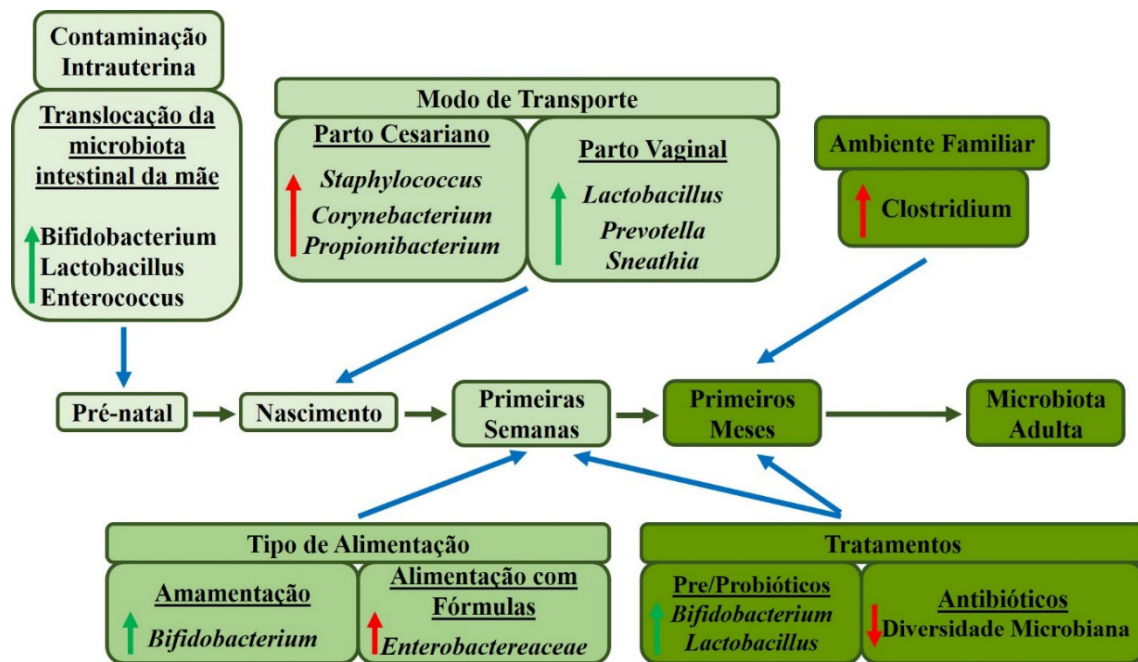


Figura 1: Fatores associados ao desenvolvimento da microbiota intestinal infantil (Fonte: MATAMOROS et al., 2013; modificado).

Inicialmente, a microbiota intestinal infantil é predominantemente colonizada por bactérias anaeróbias facultativas, como *Escherichia coli* e outros membros da família Enterobacteriaceae (JIMÉNEZ et al., 2008). Com a redução do suprimento de oxigênio por essas bactérias, o intestino torna-se um ambiente propício para o crescimento de microrganismos anaeróbios estritos como *Bacteroides spp*, *Bifidobacterium spp* e *Clostridium spp*. Essa baixa diversidade e complexidade bacterianas que caracterizam essa fase altera-se gradualmente até aproximadamente os 3 anos (MATAMOROS et al., 2013). Desses gêneros, as espécies de *Bifidobacterium* são os microrganismos dominantes na microbiota nesse período (TURRONI et al., 2012).

A composição biogeográfica na microbiota intestinal compreende as regiões específicas do trato gastrointestinal (TGI) no qual as características químicas e fisiológicas

interferem diretamente na formação microbiana em diferentes locais, definindo, desta forma, a microbiota específica para cada região (Figura 2) (DONALDSON et al., 2015).

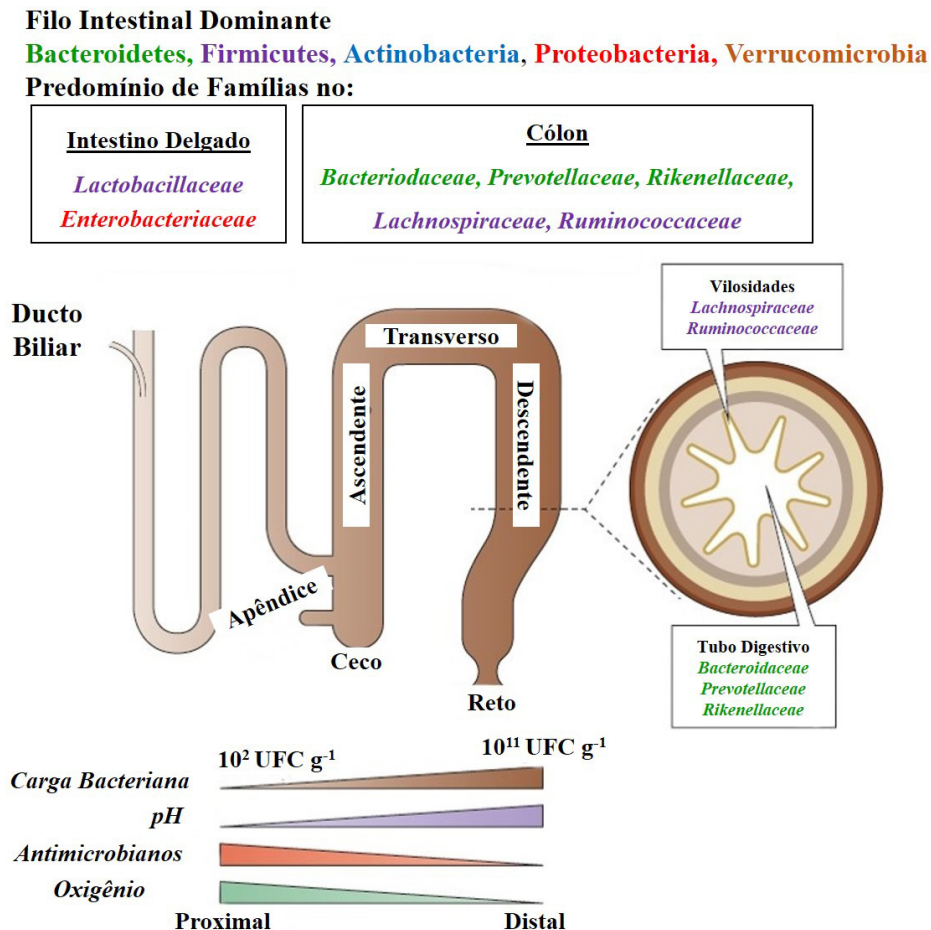


Figura 2: Composição da microbiota intestinal por região do trato gastrointestinal (Fonte: DONALDSON et al., 2015; modificado).

2.2 Probióticos e equilíbrio do ecossistema intestinal

Entre os microrganismos que compõem a microbiota intestinal existem espécies que atuam em uma relação de comensalismo, sem promover um benefício direto ao hospedeiro. Contudo, outros exercem ação mutualística, influenciando positivamente no metabolismo, na nutrição, no sistema imune e, até mesmo, apresentando atividade antimicrobiana. Esse aspecto tem sido evidenciado em estudos *in vitro* e *in vivo* que demonstraram que o ecossistema

bacteriano intestinal normal é extremamente eficaz em oposição a microrganismos patogênicos e oportunistas (EMAMI et al., 2009; TLASKALOVA-HOGENOVA et al., 2011).

Os microrganismos que exercem ações positivas à saúde do ser humano têm sido designados de probióticos. Segundo a Organização das Nações Unidas para Agricultura e Alimentação e a Organização Mundial de Saúde, probióticos são microrganismos vivos que, quando administrados em quantidades adequadas, conferem benefícios à saúde do hospedeiro (FAO/WHO, 2001). Os benefícios alcançados pelos probióticos possuem ação abrangente (Figura 3) (HILL et al., 2014). Assim, destacam-se a diminuição da diarreia em um menor tempo e consequentemente do tempo de hospitalização (VANDENPLAS, 2016), melhora da resposta imune nos diversos quadros alérgicos (DEL GIUDICE et al., 2017; DENNIS-WALL et al., 2017), prevenção do câncer do TGI (KAHOULI et al., 2017; SABER et al., 2017) e no controle dos níveis glicêmicos em pacientes diabéticos (HU et al., 2017; WANG et al., 2017).

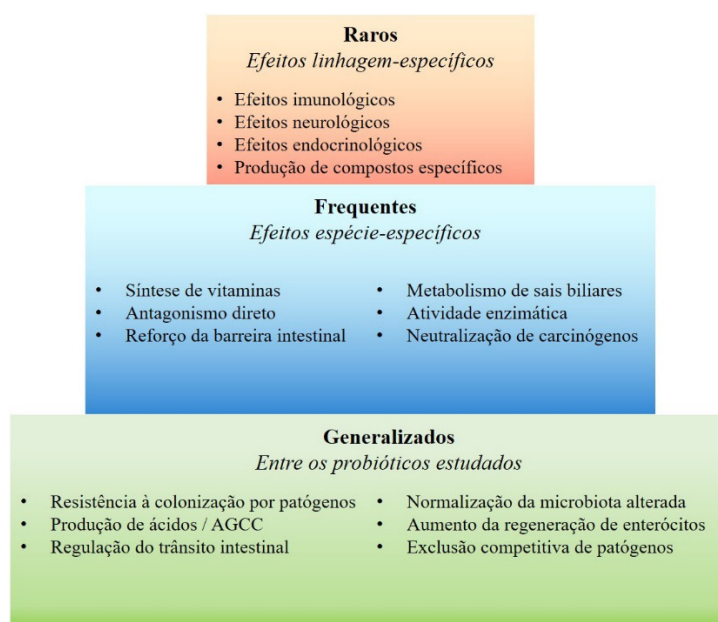


Figura 3: Benefícios dos probióticos (Fonte: HILL et al., 2014, modificado).

Várias linhagens têm sido definidas como probióticos, principalmente algumas pertencentes às espécies dos gêneros *Bifidobacterium*, *Lactobacillus*, *Saccharomyces*, *Streptococcus*, *Escherichia*, *Lactococcus* e *Enterococcus*, sendo estes dois últimos em menor escala (DE VRESE, SCHREZENMEIR, 2008; HILL et al., 2014; KUMAR; KUMAR, 2015).

Lactobacillus são microrganismos anaeróbios facultativos ou estritos, Gram-positivos, catalase negativa, não formadores de esporos, encontrados na microbiota normal humana de diferentes sítios anatômicos, incluindo o intestino (ZOETENDAL et al., 2006; KUMAR; KUMAR, 2015). Enquanto que, *Bifidobacterium* são bactérias Gram-positivas e anaeróbias estritas que também estão presentes normalmente no TGI de seres humanos e de animais, e não formam esporos (REUTER, 2001; TURRONI et al., 2011).

Evidências oriundas de experimentos com modelos animais reforçam os efeitos benéficos dos probióticos para a saúde humana. Estudos com *Lactobacillus casei* demonstram uma redução na permeabilidade intestinal em um modelo animal de colite aguda (ZAKOSTELSKA et al., 2011). Em ensaios com ratos, tratados com *Bifidobacterium lactis*, foi observado que há melhora do peristaltismo dos animais em comparação ao grupo controle (MATSUMOTO et al., 2012). Além disso, a administração de *L. reuteri* é capaz de promover diminuição na expressão de marcadores pró-inflamatórios em ratos recém-nascidos com enterocolite necrosante (EN) (LIU et al., 2012).

Após a comprovação científica das propriedades benéficas ao hospedeiro, vários produtos passaram a oferecer a suplementação dessas estirpes em sua formulação, incluindo iogurtes, leite fermentado e não-fermentado, queijo, sucos, *smoothies*, barras de cereais, dentre outras fórmulas infantis (CHAMPAGNE et al., 2005). Adicionalmente, os probióticos são comercializados como suplementos dietéticos e medicamentos (FOLIGNÉ et al., 2013; PASSARIELLO et al., 2014) (Figura 4).



Figura 4: Formas de consumo probiótico (Fonte: HILL et al., 2014, modificado).

Portanto, é razoável supor que a administração de probióticos poderia ser uma alternativa válida para o controle de infecções do TGI em todas as fases de desenvolvimento, em particular nos casos decorrentes de desequilíbrio da microbiota, inclusive em neonatos prematuros. Principalmente porque o intestino prematuro é mais susceptível a inflamações e lesões devido à permeabilidade aumentada, diminuição do peristaltismo aumentando o risco de

translocação bacteriana, alteração na produção do muco e diminuição da secreção de IgA. O uso de probióticos, isolados ou em combinação, poderiam modificar tais alterações (FROST, CAPLAN, 2013).

2.3 *Clostridium* e disbiose intestinal

A estabilidade da homeostase intestinal pode ser influenciada por vários fatores que incluem o pH intestinal, a fisiologia do hospedeiro, as interações entre os microrganismos, uso de antibióticos, funcionamento intestinal e resposta do sistema imunológico. O desequilíbrio em algum desses fatores propiciam a colonização de patógenos, levando ao desenvolvimento da disbiose (Figura 5) (BÄCKHED et al., 2005; THOMPSON-CHAGOYÁN et al., 2007; CONLON; BIRD, 2014).

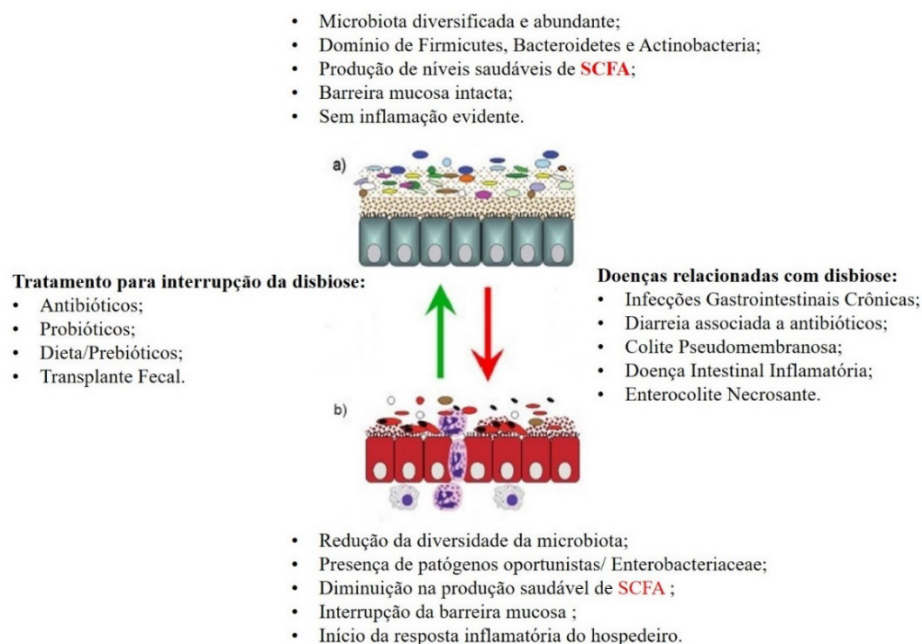


Figura 5: Correlação entre disbiose e homeostase intestinal (Fonte: WALKER; LAWLEY, 2013; modificado).

O termo disbiose intestinal, que surgiu da teoria da toxemia intestinal, refere-se a mudanças qualitativas e quantitativas da microbiota intestinal, incluindo distribuição bacteriana local e atividade metabólica. A dieta, estilo de vida e o uso de antibióticos podem alterar a

microbiota intestinal normal, tornando o ambiente propício à colonização e proliferação de enteropatógenos potenciais, os quais produzem metabólitos tóxicos (HAWRELAK; MYERS, 2004).

Um desequilíbrio na microbiota intestinal pode causar ou contribuir para o estabelecimento de doenças infecciosas e inflamatórias, como doença inflamatória intestinal (DII) (CHAMBRUN et al., 2008; KAUR et al., 2011; PROSBERG et al., 2016), diarreia associada a antibióticos (DAA) (McFARLAND et al., 2016), síndrome do intestino irritável (BENNET et al., 2015) e enterocolite necrosante (EN) (PAMMI et al., 2017). Além disso, há crescentes evidências revisadas na literatura sobre a associação de disbiose com outras doenças de natureza não-infecciosa, incluindo diabetes tipo 2 (SIRCANA et al., 2018), asma (DURACK et al., 2016), doença hepática gordurosa não alcoólica (BOURSIER et al., 2016), câncer colorretal (TILG et al., 2018), condições neurológicas (TREMLET et al., 2017) e doenças cardiovasculares (LEZUTEKONG et al., 2018).

O tratamento da disbiose têm evoluído ao longo dos tempos e, geralmente, é baseada em: 1) antibioticoterapia, 2) transplante ou bacterioterapia fecal e 3) uso de prebióticos e probióticos, além da adequação da dieta. Contudo, o nível considerável da resistência bacteriana aos antibióticos tem feito com que a terapia seja cada vez mais prolongada e por uso de múltiplos antibióticos, o que altera ainda mais a microbiota. Por outro lado, a bacterioterapia fecal, ou seja, a substituição da microbiota intestinal alterada a partir de um doador saudável, tem resultado em boa evolução clínica dos pacientes, porém estudos são necessários para elucidação dos mecanismos de ação envolvidos, do perfil microbiano adequado, bem como da resposta imune do hospedeiro para o controle do processo infeccioso (KELLY et al., 2012; WALKER; LAWLEY, 2013).

Dentro desse contexto, o uso de probióticos têm demonstrado ser uma conduta mais racional, associada ou não à terapia com antibióticos, para a abordagem dos pacientes com disbiose intestinal; contribuindo para uma microbiota saudável (WALKER; LAWLEY, 2013; HILL et al., 2014). Além do que, não haveria a mesma pressão seletiva sobre as bactérias da microbiota, exercida pela antibioticoterapia, proporcionando mais desequilíbrio no ecossistema intestinal.

Entre as bactérias do filo Firmicutes está o gênero *Clostridium* que é constituído por bacilos Gram-positivos, anaeróbios estritos, capazes de formar esporos em situações

desfavoráveis para seu crescimento e metabolismo, podendo assim sobreviver por um tempo prolongado no organismo do hospedeiro ou no meio ambiente (CASSIR et al., 2016).

Espécies do gênero *Clostridium* são encontradas na microbiota comensal do intestino de animais e humanos, onde vivem como saprófitas, porém em determinadas situações que resultam em desequilíbrio da microbiota, algumas espécies multiplicam-se excessivamente e passam a exercer ação enteropatogênica com grande repercussão para a saúde humana, tais como: *Clostridium butyricum*, *Clostridium difficile* e *Clostridium perfringens* (SOMMER; BACKHED, 2013).

C. butyricum é um microrganismo que fermenta uma variedade de substratos, principalmente carboidratos, produzindo diferentes tipos de ácidos orgânicos de cadeia curta, bem como gás hidrogênio (H₂) e dióxido de carbono (CO₂), como resultado do seu processo metabólico (KAO et al., 2014). Existe controvérsia com relação a sua patogenicidade, pois algumas linhagens de *C. butyricum* são utilizadas como probiótico, enquanto outras estão implicadas em condições patológicas, tais como botulismo e enterocolite necrosante (EN) em neonatos prematuros. Os dados da literatura sugerem que a capacidade de causar doença está relacionada não somente à produção de toxinas histolíticas, enterotoxigênicas e neurotoxinas, como também pela habilidade de sobreviver em condições ambientais adversas pelo processo de esporulação e de multiplicação rápida (HOWARD et al., 1977, FENICIA et al., 2007; MOROWITZ et al., 2010, CASSIR et al., 2015; CASSIR et al., 2016).

A segunda espécie, *C. difficile*, também é encontrada no trato gastrointestinal (TGI), mas em um número mais reduzido de indivíduos. A bactéria possui disseminação pela via fecal-oral, principalmente pelas mãos da equipe multidisciplinar hospitalar e por outros pacientes infectados. A patogênese da infecção é caracterizada por doença gastrointestinal adquirida pós-antibioticoterapia, principalmente em pacientes internados. A síndrome clínica pode variar de uma diarreia autolimitada até uma colite pseudomembranosa (PMC) grave e letal, particularmente em crianças e idosos com hospitalização recente ou residentes em asilos (SURAWICZ et al., 2013; CREWS et al., 2014).

O tratamento com antibióticos altera a microbiota normal, favorecendo o crescimento desse microrganismo, o qual é altamente resistente a antimicrobianos e produtor de duas toxinas de natureza protéica: toxina A do *C. difficile* (TcdA) e toxina B do *C. difficile* (TcdB) (SANDORA et al., 2011; KIM et al., 2012; SAMMOS et al., 2013; ABT et al., 2016). Os flagelos existentes nesse patógeno proporciona a ligação com as células epiteliais intestinais, favorecendo assim a ação das exotoxinas que causam inflamação intestinal e diarreia (PRUITT;

LACY, 2012; STEVENSON et al., 2015; ABT et al., 2016; ANJUWON-FOSTER; TAMAYO, 2017).

A terceira espécie, *C. perfringens*, também está associada a uma desordem intestinal, apesar de poder ser encontrada normalmente no TGI de animais e humanos. Adicionalmente, possui como habitat natural o solo e pode contaminar alimentos, pois os esporos termorresistentes sobrevivem ao cozimento e germinam posteriormente. Possuem um crescimento rápido, formando colônias espalhadas e grande potencial patogênico devido à ação de enterotoxinas que atuam como superantígenos. Até o momento, 13 toxinas já foram descritas para a espécie, contudo as dos tipos A a E são consideradas letais (Tabela 1) (PETIT et al., 1999; BRYNESTAD; GRANUM, 2002; UZAL et al., 2014).

Tabela 1: Principais doenças associadas com *Clostridium perfringens* em animais e humanos (Fonte: UZAL et al., 2014, modificada)

Tipos de <i>Clostridium perfringens</i>	Toxinas Produzidas	Doenças mais significantes
A	CPA	Gangrena Gasosa em humanos e animais
	CPA, CPE	Intoxicação alimentar e não alimentar
	CPA, NetB	Enterite Necrótica em animais
B	CPA, CPB, ETX	Enterite Necrohemorrágica em animais
C	CPA, CPB	Enterite Necrótica Humana, Enterite Necrótica Neonatal em animais
D	CPA, ETX	Enterotoxemia em animais
E	CPE, ITX	Doenças gastrointestinal em animais

*CPA = Alpha; CPB = Beta; ETX = Epsilon; ITX = Iota; CPE = Enterotoxina

A enterotoxina CPE (de *C. perfringens* enterotoxin) é o principal fator de virulência do *C. perfringens* tipo A e corresponde à segunda causa mais comum de intoxicação alimentar e doença gastrointestinal humana no mundo e terceira nos EUA, sendo responsável por 5 a 15% dos casos de diarreia associada a antibioticoterapia, juntamente com o *C. difficile*. A intoxicação alimentar normalmente é autolimitada durando cerca de 24h. Contudo, a bactéria pode causar também infecções invasivas graves que resultam em necrose tecidual que requerem antibioticoterapia e, muitas vezes, debridamento e amputação de um membro (BRYNESTAD; GRANUM, 2002; MCCLANE; CHAKRABARTI, 2004; UZAL et al., 2014).

3. OBJETIVOS

3.1. Geral:

Investigar a ação antimicrobiana de espécies de *Lactobacillus* e *Bifidobacterium* como potenciais probióticos contra espécies de *Clostridium*.

3.2. Específicos:

- Realizar triagem de linhagens de *Bifidobacterium* e *Lactobacillus* capazes de inibir o crescimento de espécies patogênicas de *Clostridium*;
- Caracterizar o potencial probióticos da espécie com maior atividade antimicrobiana através da capacidade de coagregação, adesão à mucina, e tolerância ao pH e sais biliares;
- Determinar o perfil de susceptibilidade aos antibióticos da espécie selecionada.

4. RESULTADOS

4.1 CAPÍTULO 1: *In vitro* antimicrobial activity and probiotic potential of *Bifidobacterium* and *Lactobacillus* against pathogenic species of *Clostridium*

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In vitro antimicrobial activity and probiotic potential of *Bifidobacterium* and *Lactobacillus* against pathogenic species of *Clostridium*

Cinara R. A. V. Monteiro ^{1,2}, Monique S. do Carmo ^{1,2}, Bruna O. Melo ², Matheus S. Alves ², Camilla I. dos Santos ², Sílvia G. Monteiro ^{2,3}, Maria Rosa Quaresma Bomfim ², Elizabeth S. Fernandes ², and Valério Monteiro-Neto ^{1,2*}

¹ Programa de Pós-graduação em Ciências da Saúde, Universidade Federal do Maranhão, Av. dos Portugueses, campus do Bacanga, São Luís, MA, Brazil; cinaraaragao@hotmail.com (C.R.A.V.M.);

² Programa de Pós-graduação, Universidade Ceuma, Rua dos Castanheiros No. 1, jardim Renascença II, São Luís, MA, Brazil; carmo.monique@outlook.com (M.S.C.); brunaoliv.96@gmail.com (B.O.M.); matheusjoc@hotmail.com (M.S.A.); camilla_itapary@hotmail.com (C.I.S.); silvio.monteiro@ceuma.br (S.G.M.); mrqbomfim@yahoo.com.br (M.R.Q.B.); elizabeth.soares@ceuma.br (E.S.F.)

³ Departamento de Biologia, Universidade Federal do Maranhão, Av. dos Portugueses, campus do Bacanga, São Luís, MA, Brazil;

* Correspondence: valerio.monteiro@ceuma.br; Tel.: +55-98-3214-4252

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Abstract: *Clostridium* species, mainly *C. butyricum*, *C. difficile*, and *C. perfringens*, are agents of infectious disease resulting from intestinal dysbiosis. In many cases, recurrence can occur after antibiotics, indicating the need for novel therapeutic options that act on the pathogens and also restore the microbiota. Herein, the *in vitro* antimicrobial activity and probiotic potential of clinical and reference strains of *Bifidobacterium* and *Lactobacillus* were investigated against pathogenic species of *Clostridium*. The antimicrobial activity was evaluated by the agar spot test and inhibition of gas production. Then, the probiotic potential of selected strains was assessed by analyzing their coaggregation ability, adhesive properties to host cells and mucin, tolerance to acidic pH and bile salts, and antimicrobial susceptibility profiles. *Lactobacillus plantarum* ATCC 8014 was the most promising strain based on its inhibitory activity against *Clostridium* spp. In addition, this strain met criteria to be considered a probiotic based on its coaggregation ability, adhesive properties, and tolerance to harsh conditions of pH and bile acid salts. Overall, the results indicate that among the studied strains, *L. plantarum* ATCC 8014 presents probiotic potential for controlling infections by the *Clostridium* species studied and should be further evaluated in *in vivo* animal studies.

Keywords: probiotics; *Lactobacillus plantarum*; *Clostridium*; dysbiosis; antimicrobial activity

1. Introduction

In humans, the normal intestinal microbiota consists of a large number and high diversity of commensal microorganisms (about 10^{13} to 10^{14}), mainly in the large intestine, where they establish a symbiotic relationship that influences the entire host organism [1–3]. Intestinal homeostasis is maintained through complex interactions between the host's immune system and the microbiota [4,5]. However, this mutualistic relationship can be disrupted by a variety of factors, such as changes in diet, use of antibiotics, and immunomodulatory drugs, among others, leading to changes in both bacterial function and diversity, a clinical condition called dysbiosis [6,7].

An imbalance in the intestinal microbiota may cause or contribute to the establishment of infectious and inflammatory diseases such as inflammatory bowel disease [8], antibiotic-associated

diarrhea (AAD) [9], irritable bowel syndrome [10] and necrotizing enterocolitis (NEC) [11]. In addition, there is growing evidence in the literature on the association of dysbiosis with other non-infectious diseases, including type 2 diabetes [12], asthma [13], non-alcoholic fatty liver disease [14], colorectal cancer [15], neurological conditions [16], and cardiovascular diseases [17].

In some infectious disorders of the intestinal tract resulting from dysbiosis, certain specific bacteria have been implicated as etiologic agents, especially potentially pathogenic *Clostridium* species. For example, *Clostridium difficile* is described as one of the leading causes of diarrhea and colitis associated with antibiotic use, with detection frequency ranging from 13% to 28% [9,18]. Mortality rates in patients with *C. difficile* infection may exceed 30%, especially in those individuals experiencing recurrence of infection within 6 months of initial treatment [19].

NEC is the most common and serious intestinal disorder among preterm infants and is diagnosed through radiological findings that include, among other manifestations, the presence of intestinal pneumatosis [20]. Its incidence may reach 12% in children that weigh less than 1 kg at birth [21] and mortality may range from 20 to 50% [22]. Risk factors for NEC include those that affect the normal microbiota, such as neonatal immaturity, enteral feeding, and intestinal colonization [23]. Its etiology is controversial however, and several causative organisms have been proposed, including viruses, *Staphylococcus* spp., various gram-negative bacilli, and *Clostridium* spp. [24]. Recent studies point to *Clostridium butyricum* as an important cause of NEC [25-27], although there are nontoxigenic strains that can be employed as probiotics [28].

Clostridium perfringens causes infection in both humans and animals [29]. In humans, like *C. difficile*, under conditions of intestinal microbiota imbalance, *C. perfringens* may similarly be involved in cases of AAD, although with a lower prevalence [9,30,31]. Depending on the toxigenic type, *C. perfringens* may also cause other disorders in the intestinal tract, such as food poisoning and necrotic enteritis, in addition to tissue infections accompanied by myonecrosis, such as gas gangrene due to trauma [29].

Antibiotic therapy is the first line of treatment for these infectious intestinal disorders. However, recurrence is frequent, particularly in cases of AAD, since the microbiota remains unbalanced due to the use of broad-spectrum antibiotics [9,19]. Alternative interventions have been employed, such as narrow-spectrum antibiotics, dietary changes, fecal transplantation, and probiotics, which may attenuate the clinical symptoms of dysbiosis, restore diversity of the intestinal microbiota, and improve host health [32-34].

Some studies have shown alleviation of AAD [35,36] and NEC [37,38] with probiotics. The efficacy of distinct probiotic strains, especially among species of *Bifidobacterium* and *Lactobacillus*, suggests that they may have common properties that could positively impact patient health in these infections [32,39]. However, the basis of these properties is not yet fully understood [39] and there are no compelling explanations for the effects of probiotics in AAD or NEC. Several plausible mechanisms have been investigated and may contribute to the observed health benefits, but in terms of translational research, this is an evident shortcoming that hinders the development of improved therapies.

Therefore, the objective of this study was to carry out an *in vitro* screening of clinical and reference strains of *Bifidobacterium* and *Lactobacillus* with antimicrobial activity against *C. butyricum*, *C. difficile*, and *C. perfringens*. The most promising strain was subjected to analysis of criteria for consideration as a potential probiotic, including its ability to adhere to eukaryotic cells and mucus and its tolerance to acidic pH and bile salts.

2. Materials and Methods

2.1 Bacterial strains and growth conditions

The following *Bifidobacterium* and *Lactobacillus* reference strains were studied: *Bifidobacterium longum* subsp. *longum* ATCC 15707, *Lactobacillus brevis* ATCC 367, *Lactobacillus delbrueckii* subsp. *delbrueckii* ATCC 9649, *Lactobacillus fermentum* ATCC 23271, *Lactobacillus paracasei* subsp. *paracasei* ATCC 335, *Lactobacillus plantarum* ATCC 8014, and *Lactobacillus rhamnosus* ATCC 9595, which were

obtained from the National Institute of Quality Control in Health (INCQS, FIOCRUZ, Rio de Janeiro, Brazil). *Lactobacillus rhamnosus* GG (LGG, ATCC 53103) was isolated from a commercial probiotic product (Floridral - Pharmaforce ApS, Copenhagen, Denmark) and used as a positive control. In addition, fecal isolates from newborn infants were evaluated and maintained in the Culture Collection Sector of Ceuma University, including *Bifidobacterium longum* 49.3, *Bifidobacterium animalis* subsp. *lactis* 56.1, *Bifidobacterium bifidum* 14.2, and *Lactobacillus fermentum* 54.2. All *Bifidobacterium* and *Lactobacillus* isolates were routinely cultured on agar or MRS broth (Man-Rogosa-Sharpe, Difco-BD, Detroit, MI, USA) with 0.25% L-cysteine and incubated at 37 °C for 24–48 h under anaerobic conditions. Cultures were stored in MRS broth with 20% glycerol at –80 °C.

C. butyricum ATCC 860, *C. difficile* ATCC 9689, and *C. perfringens* ATCC 12924 were obtained from INCQS (FIOCRUZ, Rio de Janeiro, Brazil). *Clostridium* strains were cultured in RCM (reinforced clostridial medium, Acumedia, Lansing, MI, USA) or thioglycolate medium (Acumedia) and incubated at 37 °C for 24–48 h in an anaerobic atmosphere. They were stored in RCM with 20% glycerol at –80 °C.

2.2 Antimicrobial activity screening

The ability of potential probiotics to inhibit *Clostridium* growth was evaluated in two distinct assays. All assays were performed in triplicate over three days.

2.2.1. Agar spot test

The agar spot test procedure was performed as described previously [40], with modifications. Briefly, in a Petri dish containing 10 mL of MRS agar, 5 µL of each probiotic culture was spotted onto one quadrant of the culture medium, followed by incubation at 37 °C for 24 h under anaerobic conditions. After incubation, 10 mL of thioglycolate agar was overlaid onto the MRS agar containing the growth of *Bifidobacterium* and *Lactobacillus* strains. After solidification of the culture medium at room temperature (25 – 28 °C), *Clostridium* spp. suspensions (McFarland standard No. 0.5, 1.5×10^8 colony-forming units per milliliter - CFU/mL) were spread with the aid of a swab. The plates were incubated at 37 °C for 24 h under anaerobic conditions. The formation of a clear halo around growth of the probiotics was indicative of antimicrobial activity. The diameter of the growth inhibition halo was measured and expressed in millimeters.

2.2.2 Inhibition of gas production

The ability of probiotics to inhibit the growth of *Clostridium* strains was also evaluated by assessing the inhibition of gas production due to the fermentative action of the pathogens, as described previously [41,42], with some modifications. Briefly, the assay was performed by inoculating 1 µL ($\sim 10^7$ UFC) of *Clostridium* culture into the upper third of the RCM agar layer (supplemented with 1.5 g/100 mL bacteriological agar), composed of 3 mL per tube. Subsequently, 3 mL of MRS containing 0.7 g% bacteriological agar was melted, cooled to 50 °C, and inoculated with 30 µL ($\sim 10^8$ UFC) of each probiotic culture. The contents were homogenized by vortexing and immediately poured over the RCM agar layer in tubes inoculated with the *Clostridium* strains. RCM agar with *Clostridium* and MRS agar without inoculated probiotics were used as negative controls. The tubes were incubated under anaerobic conditions at 37 °C for 24 h. The assays were performed in triplicate, with and without buffering of the MRS medium with K_2HPO_4 and KH_2PO_4 (100 mM) to verify whether or not the inhibition was due to acid production by the probiotics. A positive assay for antimicrobial activity was characterized by the absence of gas production, that is, when bubbles were not formed inside the culture media or medium breakage did not occur.

2.3 Coaggregation test

After cultivation of the probiotic strains and *Clostridium* species, aliquots of 1 mL of each culture were washed twice with phosphate-buffered saline (PBS, pH 7.2), centrifuged at $5,000 \times g$ for 15 min, and resuspended in PBS. The optical density of each suspension was adjusted ($OD_{620 \text{ nm}} = 0.1$), and 500- μL aliquots of the probiotic suspensions were mixed with 500 μL of each pathogen suspension in 24-well plates (Nunc, Roskilde, Denmark) and incubated at 37°C for 4 h under constant stirring (100 rpm) on an orbital shaker. Plates were observed for macroscopically visible clumps and under inverted microscopy [43]. Glass slides were also prepared with 5 μL of each suspension and evaluated under the microscope for visualization of bacterial coaggregates after Gram staining. *L. fermentum* ATCC 23271 was used as a positive control in this assay, since high coaggregation scores were previously demonstrated [44]. Control assays were performed with individual bacterial samples to assess their ability to autoaggregate.

2.4 Mucin binding assay

The ability of selected probiotic strains to bind to mucin was evaluated essentially as described by Tallon et al. [45]. A volume of 100 μL of a 10 mg/mL mucin solution in PBS (pH 7.2) was added to the wells of polystyrene microtiter plates (Nunc) and incubated overnight at 4°C . The wells were washed twice with 200 μL PBS and saturated with a 2% (w/v) bovine serum albumin (BSA) solution (Sigma-Aldrich, St. Louis, MO, USA) for 4 h at 4°C . Finally, the wells were washed twice with 200 μL PBS. At least four replicates were used to estimate the adhesion of a given strain. Probiotic cultures in MRS broth were washed three times in PBS, and the final suspension was standardized by spectrophotometry ($OD_{600 \text{ nm}} = 0.1$). Aliquots of 100 μL of the bacterial suspension were added to each well, and the microplates were incubated at 37°C for 1 h. After this, the wells were washed 12 times with 1 mL PBS to remove non-adherent bacteria. The wells were treated with 200 μL of 0.5% Triton X-100 (Sigma-Aldrich), and the plates were then incubated for 2 h at room temperature under orbital shaking to release the adhered bacteria. Then, the wells were scraped with a sterile tip, and the number of bacteria with binding ability to mucin was estimated by serial decimal dilutions in PBS and plating on MRS agar, followed by incubation at 37°C for 24 h under anaerobic conditions. *L. fermentum* ATCC 23271 was used as a positive control [44].

2.5 Adhesion to eukaryotic cells

Adhesion to HeLa was evaluated according to the method of Carmo et al [44]. A 300- μL aliquot of each potential probiotic cultured in MRS broth was washed three times with PBS (pH 7.4, Sigma-Aldrich), and the bacterial pellet was resuspended in 300 μL Dulbecco's modified Eagle's medium (DMEM, Sigma-Aldrich). Monolayers of HeLa cells grown in 24-well microplates (Nunc) containing DMEM supplemented with 10% fetal bovine serum (Gibco, Gaithersburg, MD, USA), with or without glass coverslips, were inoculated with 50 μL ($\sim 2.3 \times 10^7$ CFU) of bacterial suspension and incubated at 37°C under 5% CO_2 for 3 h. Then, each well was washed three times with PBS to remove non-adherent bacteria. For quantification of the adherent bacteria, the HeLa cell monolayers in the wells without coverslips were treated with 1 mL of 0.1% Triton X-100 (Sigma-Aldrich) for 5 min and scraped with the aid of a tip. Thereafter, serial decimal dilutions were spread on MRS agar plates and incubated at 37°C for 24 h. The total number of bacteria adhered to the cells was expressed as CFU per milliliter. Visualization of bacterial adherence to eukaryotic cells was performed after fixation with methanol (Amresco, Gyea, Australia) and staining with May-Grunwald and Giemsa (Amresco). Gram staining was also used to better visualize gram-positive *Lactobacillus* adhered to the cells. The coverslips were then mounted on glass slides and visualized by light microscopy under a $100\times$ oil immersion objective.

2.6 Tolerance to acidic pH and bile salts

Tolerance of selected bacteria to acidic pH (2 and 4) and bile salts (0.5% and 1%, Oxgall, Sigma-Aldrich) was evaluated as previously described, with minor modifications [46]. Briefly, 900 µL MRS, adjusted to pH 2 or 4 or non-adjusted (control) or supplemented with 0, 0.5, or 1.0% (w/v) Oxgall (Sigma-Aldrich), was inoculated with 100 µL of a 24-h culture, which had been previously washed three times with PBS and resuspended in the same volume of MRS broth. After incubation at 37 °C for 3 h under anaerobic conditions, the percentage of viable bacteria relative to that in the control was determined by plate counting on MRS agar.

2.7 Antibiotic susceptibility testing

Antibiotic susceptibility of probiotics was determined by a modification of the agar overlay diffusion method, as previously described [47]. Commercial discs (Oxoid) containing different antibiotics, including ciprofloxacin (5 µg), clindamycin (2 µg), chloramphenicol (30 µg), erythromycin (15 µg), gentamicin (10 µg), penicillin (10 µg), rifampicin (5 µg), co-trimoxazole (25 µg), vancomycin (30 µg), and tetracycline (30 µg), were placed on MRS agar plates inoculated with *Lactobacillus* (10⁸ CFU/mL). The plates were incubated anaerobically at 37 °C for 24 h. Antibiotic susceptibility was evaluated based on the diameter (in millimeters) of the growth inhibition zone around the discs [47]. The reference strain *Staphylococcus aureus* ATCC 25923 was used for quality control of antibiotic discs and tested in Mueller-Hinton agar, as recommended [48].

2.8 Statistical analyses

Statistical analyses were performed using NCSS 11 Statistical Software (2016; NCSS, Kaysville, UT, USA). Adherence to eukaryotic cells and to mucin was expressed as log CFU/mL (± SD). Tolerance to acidic pH and to bile salts was compared to growth in standard MRS medium. The Shapiro-Wilk test was carried out and confirmed that all variables were normally distributed. Thus, all comparisons were carried out by the Student *t*-test. Statistical significance was established at *p* < 0.05. All assays were performed in three independent experiments conducted on three different days.

3. Results

3.1. Selection of strains with antimicrobial activity against *Clostridium* spp.

The antimicrobial effects of potential probiotics, as determined by the agar spot test, are shown in Table 1. Eleven strains (91.7%) were able to inhibit *C. butyricum*, whereas *C. difficile* and *C. perfringens* were inhibited by 9 (75%) strains each. The diameter of the inhibition zone varied among the clinical and reference probiotic strains. Of the 12 species tested, 8 (66.7%) exhibited antimicrobial activity against all three *Clostridium* species. The largest inhibition zones were produced by *L. plantarum* ATCC 8014, mainly against *C. butyricum* (17 mm). Only *B. animalis* 56.1 showed no inhibitory activity against any *Clostridium* species in this assay.

Table 1. Inhibitory activity of *Bifidobacterium* and *Lactobacillus* against *Clostridium* spp. based on the agar spot test.

Potential probiotics	Diameter of inhibition zones (mm \pm SD) of:		
	<i>C. butyricum</i>	<i>C. difficile</i>	<i>C. perfringens</i>
<i>B. animalis</i> 56.1	0	0	0
<i>B. bifidum</i> 14.2	12 (1.6)	12 (0.4)	11 (1.7)
<i>B. longum</i> ATCC 15707	11 (0.4)	12 (0.2)	11 (1.4)
<i>B. longum</i> 49.3	12 (0.4)	11 (0.0)	10 (0.7)
<i>L. brevis</i> ATCC 367	9 (0.4)	0	0
<i>L. delbrueckii</i> ATCC 9649	10 (1.5)	11 (0.7)	12 (2.4)
<i>L. fermentum</i> ATCC 23271	10 (1.1)	10 (0.5)	10 (0.6)
<i>L. fermentum</i> 54.2	13 (0.7)	9 (0.4)	10 (0.0)
<i>L. paracasei</i> ATCC 335	11 (0.5)	12 (0.3)	11 (0.4)
<i>L. plantarum</i> ATCC 8014	17 (0.8)	13 (1.1)	13 (0.6)
<i>L. rhamnosus</i> ATCC 9595	11 (0.0)	0	0
<i>L. rhamnosus</i> GG ATCC 53103	10 (0.9)	0	0

To assess whether or not the inhibitory activity on *Clostridium* spp. was due to acid produced by the probiotics, a test was conducted to evaluate the inhibition of gas production by *C. butyricum* ATCC 860 in culture medium. This test was carried out in MRS medium with and without phosphate buffer. *C. butyricum* ATCC 860 was selected because this strain usually produces a large amount of gas resulting from its fermentative activity in thioglycolate medium or RCM. In the presence of buffer, the strains *L. brevis* ATCC 367, *L. delbrueckii* ATCC 9649, *L. paracasei* ATCC 335, *L. plantarum* ATCC 8014, *L. rhamnosus* ATCC 9595, *B. animalis* 56.1, and *B. longum* ATCC 15707 inhibited gas production by *Clostridium* spp., whereas the other strains did not (Figure 1). Among the strains that inhibited gas production in the absence of the phosphate buffer, only *B. bifidum* 14.2 gave a negative result when the assay was carried out in the of presence phosphate buffer in the MRS medium (Table 2).

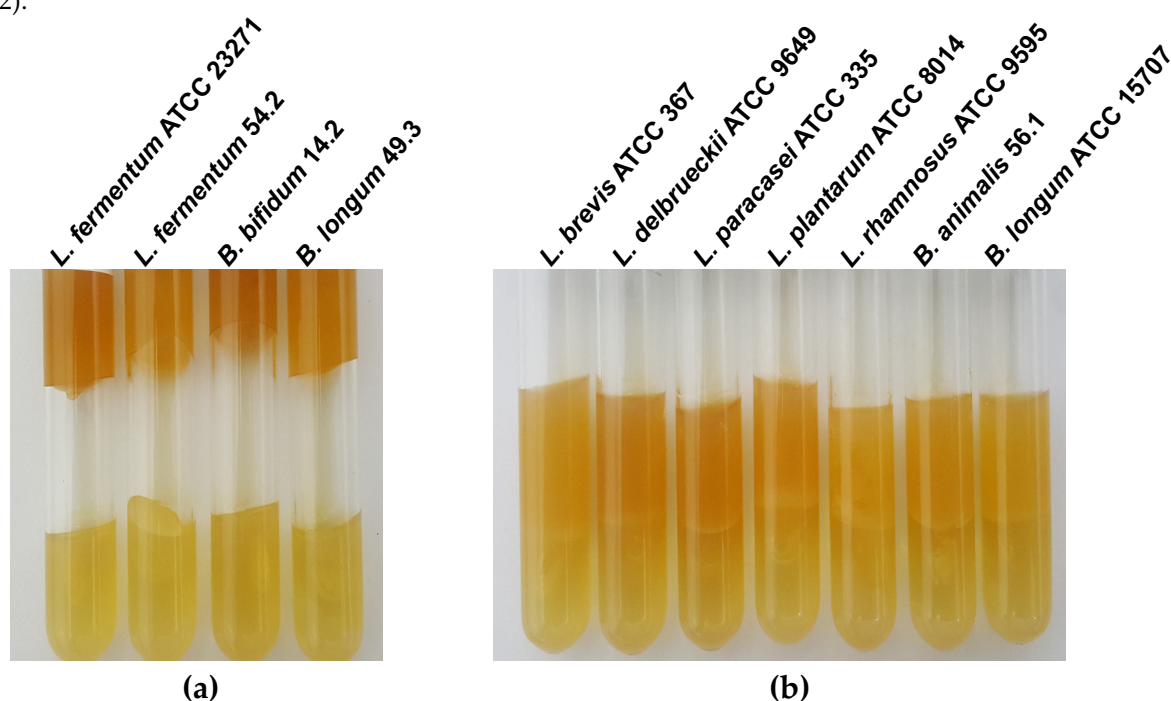


Figure 1. Inhibition of gas production. The lower layer corresponds to the RCM agar inoculated with *Clostridium butyricum* ATCC 860, and the upper layer is MRS medium with 0.7% agar and 100 mM phosphate buffer inoculated with *Bifidobacterium* and *Lactobacillus* strains; cultures were incubated at 37 °C for 24 h under anaerobic conditions. (a) Gas production by *C. butyricum* in buffered MRS medium, indicating the absence of inhibitory activity of *Lactobacillus* and *Bifidobacterium* strains; (b) Inhibitory activity of five *Lactobacillus* and two *Bifidobacterium* strains on gas production by *Clostridium butyricum*.

Table 2. Inhibition of gas production by *C. butyricum* induced by probiotics grown in MRS medium with and without phosphate buffer.

Strains	Without buffer	With buffer
<i>B. animalis</i> 56.1	+	+
<i>B. bifidum</i> 14.2	+	–
<i>B. longum</i> ATCC 15707	+	+
<i>B. longum</i> 49.3	–	–
<i>L. brevis</i> ATCC 367	+	+
<i>L. delbrueckii</i> ATCC 9649	+	+
<i>L. fermentum</i> ATCC 23271	–	–
<i>L. fermentum</i> 54.2	–	–
<i>L. paracasei</i> ATCC 335	+	+
<i>L. plantarum</i> ATCC 8014	+	+
<i>L. rhamnosus</i> ATCC 9595	+	+

3.2. *L. plantarum* ATCC 8014 presents probiotic potential

L. plantarum ATCC 8014, the strain with the highest antimicrobial activity in the agar spot test for the three *Clostridium* strains, was selected for further analysis and characterization as a potential probiotic. In terms of its coaggregation capacity, we observed that *L. plantarum* ATCC 8014 interacted clearly with the pathogens, forming bacterial aggregates with the three species of *Clostridium* (Figure 2).

Investigation of the adhesion properties of *L. plantarum* ATCC 8014 revealed its ability to interact with eukaryotic cells, as demonstrated in the assay with HeLa cells (Figure 3). In fact, adherence values for *L. plantarum* ATCC 8014 were higher than those observed for *L. fermentum* ATCC 23271 (Table 3, $P = 0.0037$). In contrast, *L. fermentum* ATCC 23271 exhibited a greater ability to bind mucin than *L. plantarum* ATCC 8014 (Table 3, $P < 0.0001$).

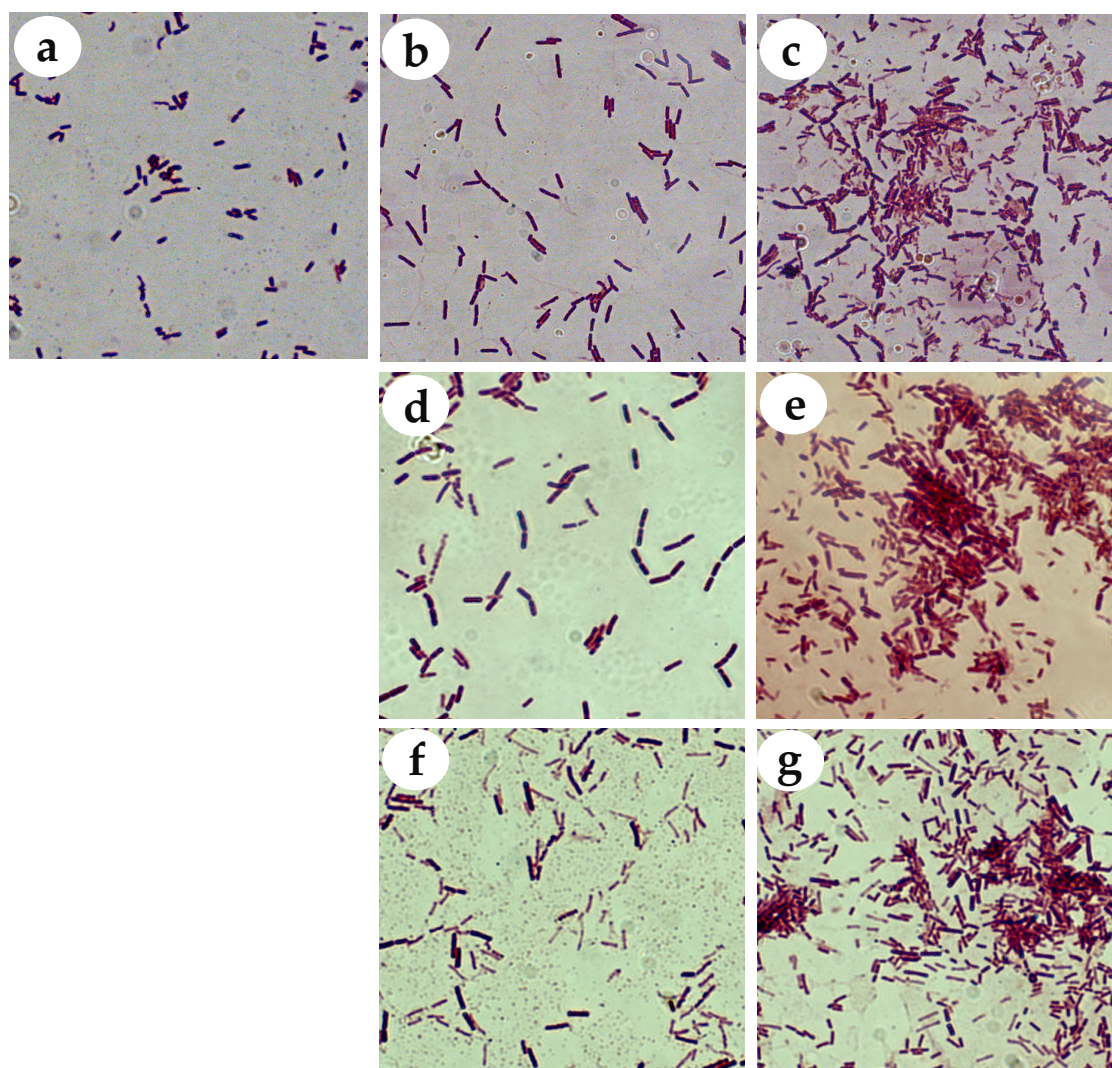


Figure 2. Coaggregation of *L. plantarum* ATCC 8014 with the three species of *Clostridium*. (a) *L. plantarum*; (b) *C. butyricum*; (c) Coaggregation of *L. plantarum* and *C. butyricum*; (d) *C. difficile*; (e) Coaggregation of *L. plantarum* and *C. difficile*; (f) *C. perfringens*; (g) Coaggregation of *L. plantarum* and *C. perfringens*.

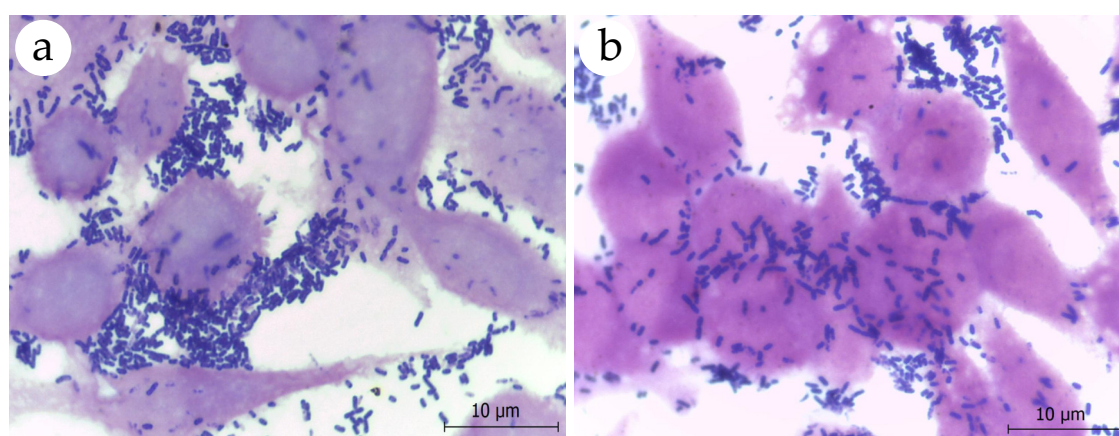


Figure 3. Adhesion assay of (a) *L. plantarum* ATCC 8014 and (b) *L. fermentum* ATCC 23271 to HeLa cells after inoculation of approximately 10^7 CFU of bacterial suspensions. Cell monolayers were Gram-stained.

Table 3. Adherence properties of *L. plantarum* ATCC 8014 to eukaryotic cells and to mucin in comparison with the control

Assays ¹	<i>L. plantarum</i> ATCC 8014	<i>L. fermentum</i> ATCC 23271	<i>p</i> Value ²
Cell adhesion	7.602 (±0.135)	7.349 (±0.053)	0.0037
Mucin binding	5.057 (±0.062)	5.370 (±0.031)	< 0.0001

¹ Data are expressed as mean log₁₀ CFU/mL (standard deviations) of triplicate experiments performed on three independent days. ² Comparative analysis was performed by Student's *t*-test (*p* < 0.05).

L. plantarum ATCC 8014 exhibited growth at pH 2 and 4 after 180 min of exposure, with growth values of 70.3% and 97.8%, respectively, relative to that observed in standard MRS medium (Table 4). Assays performed at bile salt concentrations of 0.5% and 1.0% resulted in growth values of 110.8% and 90.1%, respectively, relative to that observed in standard medium. No differences were observed relative to the growth of *L. fermentum* strain ATCC 23271 (Table 4).

Table 4. Survival of *L. plantarum* ATCC 8014 and *L. fermentum* ATCC 23271 in the presence of acidic pH and bile salts

Conditions	% Survival (± SD) ¹		<i>p</i> value ²
	<i>L. plantarum</i>	<i>L. fermentum</i>	
pH 2.0	70.3 (± 4.46)	64.7 (± 6.49)	0.1155
pH 4.0	97.8 (± 5.67)	106.2 (± 9.36)	0.7606
Bile salts 0.5%	110.8 (12.04)	112.7 (± 8.79)	0.0912
Bile salts 1.0%	90.1 (± 3.77)	92.6 (± 3.07)	0.2419

¹ Data represent survival percentage of microorganisms after 180 min of exposure to distinct conditions in comparison to bacterial growth of each under standard conditions. ² Comparative analysis was performed by the Student's *t*-test (*p* < 0.05).

The antibiotic susceptibility profile of *L. plantarum* ATCC 8014 was evaluated using the overlay diffusion method. *L. plantarum* ATCC 8014 showed resistance to ciprofloxacin and vancomycin, and sensitivity to all other antibiotics tested (Table 5).

Table 5. Antimicrobial susceptibility of *L. plantarum* ATCC 8014 according to agar overlay diffusion

Results	Antibiotics
Susceptible	Clindamycin Chloramphenicol Erythromycin Gentamicin Penicillin Rifampicin Tetracycline
Moderately susceptible	Co-trimoxazole
Resistant	Ciprofloxacin Vancomycin

4. Discussion

Some probiotic strains have been successfully used in clinical studies for the treatment or prevention of DAA [35,36] and EN [37,38]. However, their mechanisms of action remain unclear. It can be argued that this is not important, since the positive effects of probiotic interventions are generally observed with some reliability. However, controversial findings on AAD and NEC interventions have been reported in the literature, as a positive effect does not always occur when used in cases of dysbiosis [49]. A better understanding of the relevant "central probiotic properties" that contribute to their inhibitory effects on major etiological agents of these clinical syndromes could therefore aid in the design of a more rational strategy for selecting and producing more effective probiotics [32].

In this study, we showed that different clinical and reference species present different levels of antimicrobial efficacy against *C. butyricum*, *C. difficile*, and *C. perfringens*. Evaluation of the antimicrobial activity of 12 potential probiotic bacteria, including four species of *Bifidobacterium* and eight species of *Lactobacillus*, indicated that *L. plantarum* strain ATCC 8014 exhibited the greatest capacity of inhibiting the growth of the three reference strains of *Clostridium*, based on the activity detected using screening methods. In addition to *L. plantarum* ATCC 8014, other species showed inhibitory activity against one or all *Clostridium* strains. However, their antimicrobial activities were evidenced with lower zones of inhibition or were variable in comparison to the inhibition test of gas production. This variability in performance has previously been reported and suggests that more than one method should be used to assess the antimicrobial activity of probiotics, given that the conditions of each methodology may interfere with the results [50].

Various species of *Lactobacillus* are able to produce compounds with antimicrobial activities, including organic (acetic and lactic) acids, low-molecular-weight compounds, antifungal peptides, and antibacterial peptides (bacteriocins) [51,52]. It appears however that the inhibition of *Clostridium* growth exhibited by the probiotic strains was not the result of the overproduction of acids, since the addition of buffer to the MRS media did not affect the inhibitory activity of the majority of these species. Furthermore, some species of *Clostridium* exhibit intense fermentative activity, resulting in the production of large quantities of organic acids, including acetic, lactic, formic, butyric, and propionic acid, among other substances; thus, they would likely already be habituated to these and would survive acidic pH conditions [52,53].

Therefore, it is most likely that other molecules produced by the probiotics are involved in the inhibition of *Clostridium* strains. Recently, it has been demonstrated that *Lactobacillus* metabolites

isolated from vaginal smears exerted *in vitro* bacteriostatic effects against *C. perfringens* in adult vaginal swabs [54]. This activity has been associated to the production of protein compounds such as bacteriocins, which are produced by several species of probiotics and have bactericidal or bacteriostatic actions. Bacteriocins may increase the permeability of the inner membrane of bacteria, thus contributing to their rupture and interfering with bacterial cell wall synthesis, resulting in pore formation by binding to the peptidoglycan precursor lipid [55]. Lacticin 3147, for example, produced by *Lactococcus lactis*, forms selective pores in the cell walls of some pathogenic gram-positive bacteria, including *C. difficile*, resulting in its death [56].

The nature of the compound(s) produced by *L. plantarum* ATCC 8014 and its potential bactericidal or bacteriostatic actions are not yet known. However, even if such compounds have bacteriostatic action or are capable of inducing only sporulation, such action could be relevant to controlling the clinical manifestation of infections caused by *Clostridium*, neutralizing the metabolic activity of the pathogen and, consequently, the production of toxins and other virulence factors involved. In addition, bacteriocins have a more targeted inhibitory action against gram-positive bacteria [50,52].

Several criteria are used to define microorganisms as probiotics, including the ability to: 1) coaggregate with microbial pathogens; 2) adhere to eukaryotic cells and mucus; and 3) tolerate conditions of acidic pH and bile salts, among other properties [57,58]. *L. plantarum* ATCC 8014 fulfilled these criteria to be considered a potential probiotic, as it tolerated acidic pH and bile salts under the conditions tested, coaggregated with *Clostridium* spp., and exhibited adhesive properties suggesting its capacity for *in vivo* colonization. Although it demonstrated lower mucin binding than the *L. fermentum* strain ATCC 23271, the results of the binding assay were still high.

A worrying issue in the selection of probiotics is the potential transmissibility of drug resistance exhibited by probiotic bacteria to be used in foods or supplements, especially if the microorganism in question carries plasmids [59,60]. In this study, *L. plantarum* ATCC 8014 showed resistance to ciprofloxacin and vancomycin. However, despite having plasmids [61], resistance to these antibiotics is considered intrinsic and non-transmissible in this species [62,63].

Ingestion of non-pathogenic bacterial species, such as probiotics, may contribute to important protective functions by reducing paracellular permeability, providing an innate defense against pathogens and a physical impediment in the form of the mucosal layer, which may help protect against infection, prevent inflammation, and maintain mucosal integrity. In addition, there is a large panel of probiotic strains that are currently in use. However, in most cases, probiotic action has been shown to be species-specific or even strain-specific [32,64 70,65,66]. Thus, the possibility of a potential probiotic with proven antimicrobial action against multiple pathogenic species of *Clostridium*, which are commonly associated with pathologies resulting from an imbalance in the microbiota, represents a significant advance for the reduction of morbidity and mortality rates arising from these clinical syndromes. In addition to being a more rational therapeutic approach, use of a probiotic would not have a negative impact on the intestinal microbiota and would not exert pressure for the selection of resistant bacteria, as with conventional antibiotic therapy [67].

5. Conclusion

Our findings allow us to conclude that *L. plantarum* strain ATCC 8014 has probiotic potential, with antimicrobial activity against *C. butyricum* ATCC 860, *C. difficile* ATCC 9689, and *C. perfringens* ATCC 12924. Additionally, this microorganism fulfills essential criteria for status as 'generally recognized as safe' (GRAS). However, *in vivo* studies are needed for a better assessment of its efficacy and safety.

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
ANEXOS

ANEXO 1 – Normas da revista *NUTRIENTS* para publicação de artigo

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Nutrition
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Nutrients — Instructions for Authors

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Manuscript Submission Overview

Types of Publications

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Manuscripts submitted to *Nutrients* should neither been published before nor be under consideration for publication in another journal. The main article types are as follows:

- **Articles:** Original research manuscripts. The journal considers all original research manuscripts provided that the work reports scientifically sound experiments and provides a substantial amount of new information. Authors should not unnecessarily divide their work into several related manuscripts, although Short *Communications* of preliminary, but significant, results will be considered. Quality and impact of the study will be considered during peer review.
- **Reviews:** These provide concise and precise updates on the latest progress made in a given area of research. Systematic reviews should follow the PRISMA guidelines. (https://www.mdpi.com/editorial_process#standards)
- **Case reports:** Case reports present detailed information on the symptoms, signs, diagnosis, treatment (including all types of interventions), and outcomes of an individual patient. Case reports usually describe new or uncommon conditions that serve to enhance medical care or highlight diagnostic approaches.

Submission Process

Manuscripts for *Nutrients* should be submitted online at susy.mdpi.com (<https://susy.mdpi.com>). The submitting author, who is generally the corresponding author, is responsible for the manuscript during the submission and peer-review process. The submitting author must ensure that all eligible co-authors have been included in the author list (read the [criteria to qualify for authorship](#)) and that they have all read and approved the submitted version of the manuscript. To submit your manuscript, register and log in to the [submission website](https://susy.mdpi.com) (<https://susy.mdpi.com>). Once you have registered, [click here to go to the submission form for *Nutrients*](https://www.mdpi.com/user/manuscripts/upload/?journal=nutrients) (<https://www.mdpi.com/user/manuscripts/upload/?journal=nutrients>). All co-authors can see the manuscript details in the submission system, if they register and log in using the e-mail address provided during manuscript submission.

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Manuscript Preparation

General Considerations

- **Research manuscripts** should comprise:
 - Front matter: Title, Author list, Affiliations, Abstract, Keywords
 - Research manuscript sections: Introduction, Materials and Methods, Results, Discussion, Conclusions (optional).
 - Back matter: Supplementary Materials, Acknowledgments, Author Contributions, Conflicts of Interest, References.
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- **Keywords:** Three to ten pertinent keywords need to be added after the abstract. We recommend that the keywords are specific to the article, yet reasonably common within the subject discipline.

Research Manuscript Sections

- **Introduction:** The introduction should briefly place the study in a broad context and highlight why it is important. It should define the purpose of the work and its significance, including specific hypotheses being tested. The current state of the research field should be reviewed carefully and key publications cited. Please highlight controversial and diverging hypotheses when necessary. Finally, briefly mention the main aim of the work and highlight the main conclusions. Keep the introduction comprehensible to scientists working outside the topic of the paper.
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Back Matter

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- All Figures, Schemes and Tables should be inserted into the main text close to their first citation and must be numbered following their number of appearance (Figure 1, Scheme I, Figure 2, Scheme II, Table 1, etc.).
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- All table columns should have an explanatory heading. To facilitate the copy-editing of larger tables, smaller fonts may be used, but no less than 8 pt. in size. Authors should use the Table option of Microsoft Word to create tables.
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Additional data and files can be uploaded as "Supplementary Files" during the manuscript submission process. The supplementary files will also be available to the referees as part of the peer-review process. Any file format is acceptable, however we recommend that common, non-proprietary formats are used where possible.

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Restrictions on data availability should be noted during submission and in the manuscript. "Data not shown" should be avoided: authors are encouraged to publish all observations related to the submitted manuscript as Supplementary Material. "Unpublished data" intended for publication in a manuscript that is either planned, "in preparation" or "submitted" but not yet accepted, should be cited in the text and a reference should be added in the References section. "Personal Communication" should also be cited in the text and reference added in the References section. (see also the MDPI reference list and citations style guide).

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Data may be deposited with specialized service providers or institutional/subject repositories, preferably those that use the DataCite mechanism. Large data sets and files greater than 60 MB must be deposited in this way. For a list of other repositories specialized in scientific and experimental data, please consult databib.org or re3data.org. The data repository name, link to the data set (URL) and accession number, doi or handle number of the data set must be provided in the paper. The journal *Data* (<https://www.mdpi.com/journal/data>) also accepts submissions of data set papers.

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New sequence information must be deposited to the appropriate database prior to submission of the manuscript. Accession numbers provided by the database should be included in the submitted manuscript. Manuscripts will not be published until the accession number is provided.

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Research and Publication Ethics

Research Ethics

Research Involving Human Subjects

When reporting on research that involves human subjects, human material, human tissues, or human data, authors must declare that the investigations were carried out following the rules of the Declaration of Helsinki of 1975 (<https://www.wma.net/what-we-do/medical-ethics/declaration-of-helsinki/> (<https://www.wma.net/what-we-do/medical-ethics/declaration-of-helsinki/>)), revised in 2013. According to point 23 of this declaration, an approval from an ethics committee should have been obtained before undertaking the research. At a minimum, a statement including the project identification code, date of approval and name of the ethics committee or institutional review board should be cited in the Methods Section of the article. Data relating to individual participants must be described in detail, but private information identifying participants need not be included unless the identifiable materials are of relevance to the research (for example, photographs of participants' faces that show a particular symptom). Editors reserve the right to reject any submission that does not meet these requirements.

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- Reduction in number of animals used, and
- Refinement of experimental conditions and procedures to minimize the harm to animals.

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1. Home Office. Animals (Scientific Procedures) Act 1986. Code of Practice for the Housing and Care of Animals Used in Scientific Procedures. Available online: <http://www.official-documents.gov.uk/document/hc8889/hc01/0107/0107.pdf> (<http://www.official-documents.gov.uk/document/hc8889/hc01/0107/0107.pdf>).

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Methods sections for submissions reporting on research with cell lines should state the origin of any cell lines. For established cell lines the provenance should be stated and references must also be given to either a published paper or to a commercial source. If previously unpublished *de novo* cell lines were used, including those gifted from another

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An example of Ethical Statements:

The HCT116 cell line was obtained from XXXX. The MLH1⁺ cell line was provided by XXXXX, Ltd. The DLD-1 cell line was obtained from Dr. XXXX. The DR-GFP and SA-GFP reporter plasmids were obtained from Dr. XXX and the Rad51K133A expression vector was obtained from Dr. XXXX.

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1. Wager, E.; Kleinert, S. Responsible research publication: international standards for authors. A position statement developed at the 2nd World Conference on Research Integrity, Singapore, July 22-24, 2010. In *Promoting Research Integrity in a Global Environment*; Mayer, T., Steneck, N., eds.; Imperial College Press / World Scientific Publishing: Singapore; Chapter 50, pp. 309-16.

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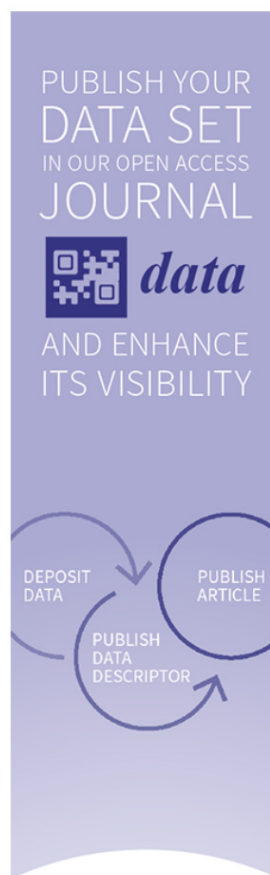
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E-mails: cinaraaragao@hotmail.com, carmo.monique@outlook.com, brunaoliv.96@gmail.com, matheusjoc@hotmail.com, camilla_itapary@hotmail.com, silvio.monteiro@ceuma.br, mrqbomfim@yahoo.com.br, elizabeth.fernandes@ceuma.br, valerio.monteiro@ceuma.br

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