UNIVERSIDADE ESTADUAL DE MONTES CLAROS

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Avaliação dos Efeitos da Angiotensina-(1-7) Sobre o Tecido Adiposo, Inflamação e Microbiota Intestinal, e o Impacto do Uso de Probiotico na Expressão do Sistema Renina Angiotensina

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RESUMO

O tecido adiposo foi recentemente reconhecido como um importante órgão endócrino e metabólico responsável pela síntese de adipocinas que controlam o metabolismo, a homeostase corporal, e a inflamação. Evidências recentes sugerem o importante papel da Angiotensina-(1-7) no tratamento da obesidade e de distúrbios metabólicos devido a seu papel anti-inflamatório e por ser o principal contraregulador do eixo da Ang II do SRA. Além disso, é importante considerar outros reguladores metabólicos importantes, como a microbiota intestinal e sua modulação por meio de probioticos. Neste contexto, a presente tese como objetivo avaliar os efeitos da Ang-(1-7) sobre o tecido adiposo, inflamação e microbiota intestinal, e o impacto do uso de probiotico na expressão do sistema renina angiotensina. Para isso foram produzidos três produtos. No produto 1 realizamos uma revisão da literatura científica a cerca dos achados relacionados ao eixo ECA2/Ang-(1-7)/MasR com foco no seu papel na regulação da secreção de adipocinas e dos processos relacionados à inflamação aguda e crônica. É importante ressaltar o papel endócrino do tecido adiposo na síntese de adipocinas, modulando sua secreção e regulando diversos processos associados à inflamação aguda e crônica, além de sua relevância na homeostase do organismo. As vias moleculares envolvidas nos mecanismos de ação das adipocinas criaram a necessidade de novos estudos visando investigar intervenções terapêuticas, bem como novas ferramentas para esclarecer os mecanismos desconhecidos. A interação e relevância da Ang- (1-7) na expressão e inflamação das adipocinas foram discutidas em obesidade, diabetes tipo 2, doenças cardiovasculares, distúrbios renais e hepáticos, entre outros. Nesta perspectiva, concluímos que a inflamação pode ser modulada pelas adipocinas e Ang- (1-7) em diferentes órgãos e pode ser um alvo importante para o tratamento e a prevenção de respostas inflamatórias. No produto 2 avaliarmos os efeitos da administração oral com Ang-(1-7) sobre a microbiota intestinal em camundongos obesos. Camundongos Swiss machos foram divididos em quatro grupos: obesos e não-obesos / tratados e não tratados com ANG-(1-7). Foi observada uma diminuição significativa na glicemia de jejum, colesterol total, triglicérides e níveis de LDL e aumento de HDL em animais tratados com ANG-(1-7). A análise histológica mostrou redução da altura das vilosidades intestinais em camundongos tratados com ANG- (1-7). Adicionalmente, houve um aumento da abundância de Bacteroidetes e uma redução de Firmicutes (razão Bacteroidetes/Firmicutes aumentada) e Enterobacter cloacae foram observados no grupo HFD+ANG- (1-7). A expressão de RNAm intestinal do receptor TLR4 foi reduzida no grupo HFD+ANG- (1-7). Finalmente, a expressão intestinal do B0AT1 foi aumentada em animais obesos tratados com ANG-(1-7), mostrando um possível mecanismo associado à captação de triptofano. Os resultados do presente estudo sugerem, pela primeira vez, interação entre SRA e modulação da microbiota intestinal. Por fim, no produto 3 avaliamos o efeito da suplementação com Bifidobacterium longum nos parâmetros metabólicos e na expressão do sistema renina-angiotensina em camundongos obesos. Camundongos Swiis machos foram divididos em quatro grupos: obesos e não-obesos / tratados e não tratados com B. longum. Após quatro semanas de tratamento, os camundongos obesos que receberam o B. longum apresentaram diminuição significativa do peso corporal, da adiposidade, melhora na tolerância a glicose, redução dos níveis séricos de glicemia e colesterol total. Além disso, análises histológicas demonstraram redução do acúmulo de triglicérides hepático também no

grupo obeso tratado. Análises de mRNA mostraram aumento significativo na expressão da enzima-conversora de angiotensina 2 ECA2 e do RMAS nos camundongos obesos que receberam o *B. longum*. Nossos dados sugerem pela primeira vez a modulação do SRA pela cepa *B. longum*.

Palavras-chave: tecido adiposo; obesidade; enzima Conversora de Angiotensina 2; *Firmicutes; Bacteroidetes*; inflamação; intestino.

ABSTRACT

Adipose tissue has recently been recognized as an important endocrine and metabolic organ responsible for the synthesis of adipokines that control metabolism, body homeostasis, and inflammation. Recent evidence suggests the important role of Angiotensin- (1-7) in the treatment of obesity and metabolic disorders due to its anti-inflammatory action and for being the main counter-regulator of the AngII axis of the renin-angiotensin system (RAS). Also, it is important to consider other important metabolic regulators, such as the intestinal microbiota and its modulation using probiotics. In this context, the present thesis aims to evaluate the effects of Ang- (1-7) on adipose tissue, inflammation, and intestinal microbiota, as well as the impact of probiotic use on the expression of the RAS. For this, three products were produced.Regarding product 1, we conducted a review on the findings related to the ECA2/Ang-(1-7)/MasR axis focusing on its role in the regulation of adipokine secretion and processes related to acute and chronic inflammation. It is important to emphasize the endocrine role of adipose tissue in the synthesis of adipokines, modulating their secretion and regulating various processes associated with acute and chronic inflammation, as well as their relevance in the body's homeostasis. The importance of molecular pathways involved in the mechanisms of action of adipokines has created the need for new studies aimed at investigating therapeutic interventions, as well as new tools to clarify the unknown mechanisms. The interaction and relevance of Ang- (1-7) in the expression and inflammation of adipokines have been discussed in regards to obesity, type 2 diabetes, cardiovascular diseases, renal and hepatic disorders, among others. In this perspective, we conclude that inflammation can be modulated by adipokines and Ang- (1-7) in different organs and they may be important targets for the treatment and prevention of inflammatory responses. In relation to product 2, we evaluated the effects of oral administration with Ang- (1-7) on the intestinal microbiota of obese mice. Male Swiss mice were divided into four groups: obese and non-obese/treated and not treated with ANG- (1-7). A significant decrease in fasting glycemia, total cholesterol, triglycerides, and LDL levels, and an increase in HDL in animals treated with ANG- (1-7) were observed. Histological analysis showed a reduction of intestinal villus height in ANG-(1-7)treated mice. In addition, an increase in the abundance of *Bacteroidetes* and a reduction in*Firmicutes* (increased Bacteroidetes/Firmicutes ratio) and Enterobacter cloacae were observed in the HFD + ANG- (1-7) group. Intestinal mRNA expression of the TLR4 receptor was reduced in the HFD + ANG- (1-7) group. Finally, intestinal expression of BOAT1 was increased in obese animals treated with ANG- (1-7), showing a possible mechanism associated with tryptophan uptake. The results of the present study suggest, for the first time, an interaction between RAS and the modulation of the intestinal microbiota. Finally, concerning product 3, we evaluated the effect of Bifidobacterium longum supplementation on metabolic parameters and the expression of the renin-angiotensin system in obese mice. Male Swiis mice were divided into four groups: obese and non-obese/treated and not treated with B. longum. After four weeks of treatment, obese mice that received B. longum showed a significant decrease in body weight, adiposity, serum glycemia levels, and total cholesterol, as well as an improvement in glucose tolerance. Furthermore, histological analyses demonstrated a reduction in the accumulation of hepatic

triglycerides in the obese-treated group. Analyses of mRNA showed a significant increase in the

expression of angiotensin-converting enzyme 2 ECA2 and RMAS in the obese mice that received *B. longum*. Our data suggest for the first time the modulation of RAS by the *B. longum*strain.

Keywords: adipose tissue; obesity; angiotensin-converting enzyme 2; *Firmicutes*; *Bacteroidetes*; inflammation; intestine.

LISTA DE ABREVIATURAS E SIGLAS

AGT	Angiotensinogênio
ANG A	Angiotensina A
Ang I	Angiotensina I
Ang II	Angiotensina II
Ang-(1–7)	Angiotensina (1–7)
Ang-(1-9)	Angiotensina-(1-9)
AT1	Receptor da Angiotensina II Tipo 1
AT2	Receptor da Angiotensina II Tipo 2
B. longum	Bifidobacterium longum
CD-14	Cluster de diferenciação
CLG	Camundongo Livre de Germes
COX-2	Ciclo-oxigenase-2
DH	Dieta Hiperlipídica
ECA	Enzima Conversora da Angiotensina
ECA2	Enzima Conversora da Angiotensina
FAO	Organização das Nações Unidas para Alimentação e Agricultura
GRAS	Geralmente Reconhecido como Seguro
IL-1 β	Interleucina 1 Beta
IL-6	Interleucina 6
IL-6	Interleucina-6
LPS	Lipopolissacarídeos
IMC	Índice de Massa Corporal
Mas-KO	Camundongo Knoukout para o receptor Mas
MCP-1	Proteína De Quimioatração De Monócitos
METAHIT	Metagenoma do trato Gastrointestinal Humano
MrgD	Receptor D acoplado a proteína D relacionado com Mas
NOD-1 NF-KB	Proteína contendo domínio de oligomerização de ligação a nucleotídeo 1 Fator Nuclear Kappa B
OMS	Organização Mundial da Saúde
PAI-1	Inibidor do Ativador De Plasminogênio Tipo 1

РМН	Projeto Microbioma Humano
SRA	Sistema renina-angiotensina
TGF-β	Fator de crescimento transformador Beta
TGI	Trato Gastrointestinal
TNF-α	Fator de Necrose Tumoral Alfa
TRL4	Receptores do Tipo Tool 4

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1. INTRODUÇÃO

Obesidade

A Organização Mundial da Saúde (OMS) define a obesidade como uma condição de acúmulo anormal ou excessivo de gordura no tecido adiposo (1). A obesidade se tornou um problema de saúde mundial, sendo considerada uma pandemia. Estudos demonstram que, no ano de 2015 esta condição afetou cerca de 107,7 milhões de crianças e 603,7 milhões de adultos (2). Ainda segundo a OMS, em 2016, 39% dos adultos (com idade igual ou maior que 18 anos) apresentavam sobrepeso e 13% obesidade. Em números absolutos, mais de 1,5 bilhões de adultos apresenta sobrepeso e obesidade (3). Estima-se que em 2025, 18% dos homens e 21% das mulheres serão obesos (4). Ainda segundo a OMS, em 2030, a obesidade acometerá cerca de 20% da população adulta do mundo (5).

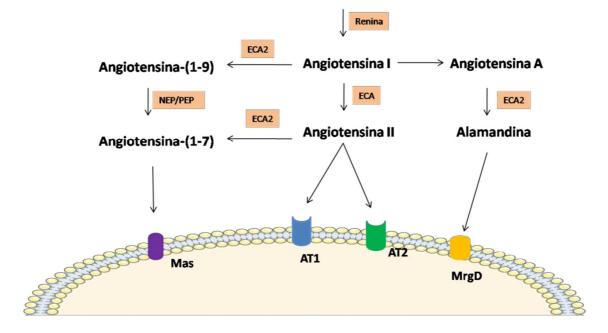
A obesidade pode ser classificada de acordo com o índice de massa corporal (IMC), calculado pelo peso em quilogramas dividido pela altura ao quadrado em metros. Segundo as diretrizes da OMS, um indivíduo obeso é aquele que possui um IMC $\geq 30 \text{ kg/m}^2$. O excesso de peso é classificado como IMC 25,0 a < 30 kg/m², o peso normal varia de um IMC de 18,5 a < 25 kg/m² e um IMC abaixo de 18,5 kg/m² é considerado abaixo do peso (6, 7).

A etiologia da obesidade é complexa e multifatorial, causada principalmente pelo desequilíbrio entre o consumo e gasto energético (8), e em menor proporção por fatores genéticos e ambientais (9). O aumento da prevalência da obesidade contribui fortemente para múltiplas doenças cardio-metabólicas, como diabetes tipo 2, dislipidemia, doença arterial coronariana, acidente vascular encefálico, hipertensão arterial e vários tipos de câncer (10- 12).

A obesidade é considera uma doença crônica que compromete a qualidade dos indivíduos acometidos (13), além de aumentar de maneira significativa os gastos públicos (14). Além disso, a etiologia da obesidade ainda não foi totalmente esclarecida, o que torna necessária a realização de novos estudos que possam elucidar os mecanismos moleculares adjacentes ao desenvolvimento desta doença. Neste contexto, a angiotensina-(1-7) se destaca, uma vez que, vários estudos já descreveram seu papel na redução da obesidade e das doenças metabólicas por ela desencadeadas (15, 16).

Sistema Renina-angiotensina (SRA)

O Sistema Renina-Angiotensina (SRA) é uma cascata enzimática que se inicia com a produção de angiotensinogênio (AGT), que é clivado pela enzima renina em angiotensina I (Ang I). Em seguida, a enzima conversora de angiotensina (ECA) transforma a Ang I no octapeptídeo Ang II, que é o produto final ativo mais descrito do SRA, atuando através de dois isotipos de receptores Ang II, o Receptor de Angiotensina tipo I (AT1) e o Receptor de Angiotensina tipo II (AT2) (17). Altos níveis de Ang II estão associados a vários distúrbios metabólicos (18). Em contrapartida, a enzima conversora de angiotensina 2 (ECA2) reduz os níveis de Ang II, transformando-a em Ang-(1-7), que também pode ser produzido a partir da Ang I, através da angiotensina- (1-9) (Ang-1–9) pela ação das endopeptidases: prolil- endopeptidase e endopeptidase neutra. A Ang-(1-7) atua através do receptor Mas exercendo efeitos antagônicos a Ang II, e a ativação do eixo ECA2/Ang-(1-7)/Mas melhora doenças metabólicas e crônicas (19). Além disso, a Ang-(1-7) pode sofrer descarboxilação formando a alamandina, que também pode ser formada a partir da hidrólise da angiotensina A (Ang A) por ação da ECA2 (20). A Alamandina age através do seu receptor (MrgD), e exerce efeitos similares a Ang-(1-7) (Figura 1) (21).



Angiotensinogênio

Figura 1: Visão geral do sistema renina-angiotensina (SRA). ECA, enzima conversora de angiotensina; ECA2, enzima conversora de angiotensina 2; AT1, receptor de angiotensina tipo 1; AT2, receptor de angiotensina tipo 2; Mas, Receptor Mas; MrgD, receptor D acoplado a proteína D relacionado com Mas, NEP, endopeptidase neutra; e PEP, prolil endopeptidase. Fonte: Adaptado de Qaradakhi, T., Apostolopoulos, V., Zulli, A., 2016 (21).

A maioria dos efeitos fisiológicos da Ang II são mediados pelos receptores AT1. A ligação da Ang II a esse receptor leva à inflamação, vasoconstrição, maior risco cardiovascular, aumento do estresse oxidativo e de fatores proliferativos, ativação do sistema nervoso, aumento da absorção de sódio, entre outros efeitos. Entretanto, os receptores AT2 embora encontrados em vários tecidos no período fetal, têm sua abundância diminuída após o nascimento. A ativação desses receptores está principalmente ligada a consequências antagônicas as dos receptores AT1, como vasodilatação, antiproliferação celular, melhora da função cardíaca e diminuição da absorção de sódio renal (22, 23).

A Ang-(1-7) é um heptapeptídeo com efeitos sistêmicos e locais significativos (24). A Ang- (1-7) é considerada o principal componente contrarregulatório do eixo Ang II/ECA/AT1 do SRA, atuando através do receptor Mas, que promove várias ações importantes, incluindo vasodilatação, redução do estresse oxidativo, efeitos antitrombóticos e melhora do metabolismo glicídico e lipídico (25).

As primeira evidências do papel metabólico da Ang-(1-7) e do seus receptor Mas vieram de ensaios com camundongos FVB/N com deficiência do receptor Mas (Mas-KO). Os Mas-KO apresentaram uma condição semelhante a síndrome metabólica, com hiperglicemia, intolerância à glicose, diminuição da sensibilidade à insulina e da captação de glicose via insulina em adipócitos, e diminuição do GLUT-4 no tecido adiposo branco. A deleção do receptor Mas também apresentaram dislipidemia, aumento da massa gorda, da expressão de insulina e leptina, e dos triglicerídeos musculares, além de, aumento da expressão do fator de crescimento transformador beta (TGF- β) e de AGT no tecido adiposo (26). Outros achados mostraram que a deleção do receptor Mas causa hipertensão arterial e disfunção endotelial (27). Além disso, a deficiência da ECA2 agrava a tolerância à glicose e a insensibilidade à insulina induzida por dieta (28).

Outros estudos revelaram que concentrações circulantes aumentadas de angiotensina (1-7), como resultado de expressão trangênica ou infusão crônica, melhora a hiperinsulinemia, a resistência à insulina e as respostas inflamatórias no tecido adiposo de ratos (29-31), e aumenta a sensibilidade à insulina e a tolerância à glicose em ratos com níveis normal de glicêmia (32). De maneira semelhante, o tratamento oral crônico com Ang-(1-7) diminui os níveis de glicemia, melhora a sensibilidade à insulina e previne a hiperinsulinemia em ratos diabéticos (31). Além dos efeitos metabólicos citados, é importante ressaltar que a ang- (1–7) tem um grande potencial

anti-inflamatório reduzindo as principais moléculas envolvidas nas doenças inflamatórias agudas e crônicas.

Tecido adiposo, adipocinas, Ang-(1-7) e inflamação

O tecido adiposo branco foi considerado por muitos anos um tecido cuja as principais funções eram reserva energética, na forma de triacilgliceróis, fornecimento de energia em um estado de jejum prolongado, proteção mecânica de órgãos e o isolamento térmico (33, 34). Entretanto, sabe-se hoje que o tecido adiposo é um importante órgão metabólico com função endócrino, responsável pela síntese e secreção de mais de 600 moléculas bioativas denominadas adipocinas (34).

As adipocinas estão envolvidas em vários processos metabólicos importantes, como regulação do apetite e saciedade, metabolismo energético, armazenamento de gordura, sensibilidade e secreção da insulina, regulação da pressão arterial, função endotelial, inflamação e homeostase (35, 36). Além disso, as adipocinas atuam em diferentes órgãos-alvo, como fígado, cérebro, músculo, coração, vasos, sistema imunológico e outros (35, 37-40).

Entre as principais adipocinas destaca-se a adiponectina, apelina, leptina, resistina, interleucina-1 β (IL-1 β), interleucina-6 (IL-6), fator de necrose tumoral-alfa (TNF α), proteína quimiotática de monócitos-1 (MCP-1), omentina, inibidor do ativador de plasminogênio tipo 1 (PAI-1), e os componentes do sistema renina-angiotensina, como o AGT, a AngII, ECA, ECA2, e Ang-(1-7) (34-36, 41).

No tecido adiposo, as adipocinas regulam as funções e o metabolismo dos adipócitos, a adipogênese e o recrutamento de células imunes (36, 37, 42). Assim como as adipocinas, o SRA também exerce efeitos importantes sob o tecido adiposo. Estudos experimentais em roedores e humanos ligaram a obesidade à ativação do eixo ECA/Ang II/AT1 (34, 43). O tecido adiposo expressa todos os componentes do SRA, e na obesidade torna-se o principal sítio produtor de AGT e Ang II (44). Por outro lado, o eixo Ang- (1-7)/MAS apresenta efeitos essenciais no armazenamento de gordura, captação de glicose e principalmente na regulação da produção de adipocinas (19, 45, 46), que por sua vez modulam a inflamação local e sistêmica (30, 31, 47).

Estudos em modelo experimental demonstraram que a administração oral de Ang- (1-7) foi capaz de prevenir a obesidade e a inflamação hepática através do bloqueio da via Resistina/Receptor tipo Toll 4/ Fator-Kappa Nuclear *Beta* (resistina / TLR4 / NF-k β) em ratos (48), e reduzir a inflamação hepática induzida por dieta hipercalórica, através da redução da expressão das citocinas proinflamatórias Fator de Necrose Tumoral *Alfa* (TNF- α) e interleucina- 6 (IL-6) (48). Além disso, o aumento de Ang-(1-7) por meio de expressão transgênica em ratos exerce um efeito protetor contra a inflamação induzido pela obesidade, diminuindo a expressão da ciclo-oxigenase-2 (COX-2) e Interleucina-1- *Beta* (IL-1 β) na gordura abdominal (31).

Microbiota intestinal e obesidade

Nos seres humanos, a microbiota intestinal é um complexo e dinâmico ecossistema que tem evoluído com seu hospedeiro (49). As comunidades microbianas em nosso intestino funcionam como um órgão com função metabólica, imunológica e endócrina (50). Atualmente, estima-se que o trato gastrointestinal (TGI) humano abriga aproximadamente 10¹⁴ micro-organismos, dez vezes mais do que o número de células no corpo humano, com 500-1000 espécies bacterianas distintas (51, 52). Estudos do Projeto Microbioma Humano (PMH) e do Metagenoma do trato Gastrointestinal Humano (*MetaHIT*) revelaram que a microbiota humana pode codificar pelo menos 10 milhões de genes [19], ou seja, 100 vezes mais genes do que o genoma humano (51).

A microbiota intestinal desempenha funções que o corpo humano sozinho não é capaz de realizar, resultando em uma relação simbiótica. Essa estreita relação é permite a manutenção de um TG intestinal normal, modulando processos como absorção de nutrientes a partir de alimentos ingeridos, motilidade e integridade da barreira intestinal, regulação do metabolismo do hospedeiro, principalmente o metabolismo glicídico e lipídico, e inflamação (53-55). Por exemplo, a microbiota fermenta componentes dos alimentos que não são digeridos pelo organismo, sintetiza proteínas e outros nutrientes essenciais, metaboliza toxinas alimentares e substâncias cancerígenas, assegura a maturação do sistema imunológico, afeta o crescimento e diferenciação de eritrócitos, regula a angiogênese intestinal, e protege contra patógenos entéricos (53).

Em geral, a microbiota intestinal é dominada por bactérias anaeróbicas pertencentes a três filos:

Bacteroidetes, *Firmicutes* e *Actinobacteria* (56-58). Geralmente, os *Firmicutes* e *Bacteroidetes* são mais abundantes, seguidos por *Proteobacteria* e *Actinobacteria*, e em menos quantidade, *Verrucomicrobia e Fusobacteria* (57).

A microbiota intestinal tem despertado o interesse da comunidade científica devido a sua relação direta com a saude humana. Desequilíbrios em sua composição (isto é, disbiose) têm sido associados a desordens imunológicas, suscetibilidade a infecções intestinais e, mais recentemente a várias doenças não-intestinais como doenças cardiovasculares, hepáticas, obesidade e diabetes (59-62). Uma vasta gama de estudos em modelos animais e em humanosrelataram a existência de uma relação direta entre a microbiota intestinal, a obesidade e seus distúrbios metabólicos associados (63-67). As primeiras evidências científicas sobre o papel da microbiota intestinal na regulação do peso corporal vieram de estudos conduzidos em camundongos livres de germes (CLG) (68).

Posteriormente, Backher et al. (69) descreveram um ganho total de 47% de massa gorda em camundongos selvagens quando comparados a CLG, mesmo quando estes apresentaram um maior consumo calórico. Além disso, quando o intestino de CLG foi colonizado por microbiota do ceco de camundongos selvagens, os camundongos CLG apresentaram um ganho de peso corporal de 60% (69). Também foi relatado que CLG alimentados com dieta ocidental rica em carboidratos ganharam menos peso que os camundongos selvagens, e não apresentaram alterações no metabolismo glicídico (70).

Estudos metagenômicos mostraram uma relação direta entre distúrbios metabólicos associados a obesidade e a disbiose intestinal (71, 72). Em camundongos e humanos, a diversidade microbiana e a proporção dos filos *Firmicutes* e *Bacteroidetes* estão associadas ao desenvolvimento da obesidade (72, 73). Esse achado foi corroborado por estudos realizados em camundongos ob/ob, modelo animal de diabetes tipo II, que apresentou uma menor razão *Bacteroidetes/Firmicutes* em relação ao tipo selvagem (74, 75). O aumento na abundância dos *Firmicutes* parece está associada alteração glicêmica com o aumento da captação de energia devido ao aumento do número de enzimas envolvidas na digestão do amido, sacarose e galactose (76). Ainda, CLG que receberam a microbiota intestinal de camundongos ob/ob tornaram-se obesos (77). Além disso, humanos obesos submetidos a restrição calórica apresentaram um aumento significativo na população de *Bacteroidetes*, demonstrando a relação direta desse filo com a perda de peso e com o fenótipo magro (71).

A dieta influência diretamente no desenvolvimento de disbiose intestinal, o consumo de uma dieta hiperlipídica (DH) aumenta a proporção de bactérias Gram-negativas no intestino (78), o que contribui para as doenças infecciosas e metabólicas (79). O aumento dessa classe de bactérias culmina em maior absorção de lipopolissacarídeos (LPS), principal componente da parede celular de micro-organismos Gram-negativos, que se acumula na circulação causando endotoxemia metabólica (80). A endotoxemia metabólica é caracterizada por um estado inflamatório crônico desencadeado pelo reconhecimento dos LPS microbianos e translocação bacteriana por interação com o receptor do tipo Toll 4(TLR4), Proteína contendo domínio de oligomerização de ligação a nucleotídeo 1(NOD-1), cluster de diferenciação 14 (CD-14), ativando a via do Fator Nuclear do tipo kappa beta(NF- κ B) (80). Recentemente foi descrito que a DH altera a composição da microbiota intestinal, entretanto, para o desenvolvimento da obesidade, a presença de endotoxemia metabólica é obrigatória (81). Em camundongos, a endotoxemia causa aumento do peso corporal, hiperinsulinemia, e hiperglicemia (80).

Fei e Zhao (82) demonstraram que o transplante da bactéria *Enterobacter cloacae* B29 produtorada de endotoxina de indivíduo com obesidade mórbida para CLG foi associado à indução da obesidade, resistência insulínica com aumento concomitante dos níveis circulantes de endotoxina. Além disso, patógenos como *Bacteroides, Clostridium, Escherichia coli, Vibrio* e *Fusarium* podem produzir toxinas que induzem dano celular através da interrupção das interações entre as proteínas intracelulares aumentando a permeabilidade celular e, eventualmente, induzindo a morte celular (83). Como tal, o aumento dos níveis de bactérias produtoras de endotoxina prejudica o equilíbrio metabólico do hospedeiro (82).

A microbiota intestinal contribui para a obesidade induzida por dieta, controlando o processo de β -oxidação de ácidos graxos e armazenamento de triglicerídeos (69) e promovendo a captação de energia em uma dieta rica em carboidratos (70). Além disso, tem sido demonstrado que o consumo de dieta hiperlipídica e a composição da microbiota intestinal estão relacionados a mudanças na morfologia das vilosidades intestinais (84). Contudo, os dados referentes à microbiota intestinal e o SRA são escassos na literatura, e a interação entre a ang- (1-7) e a microbiota intestinal ainda não foi elucidada.

Estudos realizados em modelos animais já revelaram a expressão de marcadores do SRA no intestino (85-87). Componentes de RAS, como os receptores AT1, AT2 e ECA, foram encontrados na borda do epitélio do jejuno e íleo de ratos, onde o fluxo de fluidos e eletrólitos é regulado (88). O fato do jejuno de ratos expressar AGT, que é o precursor da Ang II e outras angiotensinas bioativas, indica que o enterócitos são capazes de sintetizar Ang II (88). Recentemente, evidências da associação do SRA e da microbiota intestinal via modulação do ECA2 foram descritas (89-91). Níveis aumentados de ECA2 foram detectados no trato gastrintestinal humano e, posteriormente, foi identificada a coletrina, um homólogo da ECA2, com atividade não catalítica (92).

A ECA2 é essencial para a expressão intestinal do principal transportador de aminoácidos neutros (B0AT1), um importante transportador de triptofano (Trp) (90). Níveis aumentados de Trp foram associados com o aumento da produção de peptídeos antimicrobianos, que são importantes moduladores da microbiota intestinal. A deficiência de transporte de Trp leva à secreção aberrante desses peptídeos antimicrobianos e consequente proliferação de cepas microbianas prejudiciais, conferindo suscetibilidade à inflamação intestinal (89).

Além disso, recentemente, Borges et al. (93) demonstraram que ratos pré-tratados com A779 (agonista do receptor Mas) e camundongos Mas-KO expostos a Ang- (1-7) apresentaram deficiência na absorção de Trp. Esses achados sugerem que a Ang- (1-7) estimula a absorção do triptofano através do receptor Mas, e esse efeito está diretamente associado ao aumento da expressão e atividade da ECA2. Apesar das evidências descritas, estudos sobre o efeito da Ang- (1-7) na microbiota intestinal são ausentes na literatura.

Probióticos

A OMS e a Organização das Nações Unidas para Alimentação e Agricultura (FAO) definem probioticos como micro-organismos vivos que quando administrados em quantidades adequadas, conferem benefícios a saude do hospedeiro (94). Os efeito benéficos mediados pelos probioticos se devem a sua capacidade de modular a microbiota intestinal, deslocando o

equilíbrio microbiano para o lado positivo (95), e melhorando a imunidade da mucosa (96-98).

Entre os probióticos mais bem estudados estão às cepas bacterianas produtoras de ácido lático pertencentes aos gêneros *Bifidobacterium e Lactobacillus*, que têm um registro de segurança estabelecido e receberam o *status* GRAS (geralmente reconhecido como seguro) pela FAO (99), Atualmente, essas estirpes microbianas são amplamente utilizadas e estão incluídos em muitos alimentos funcionais e suplementos dietéticos (100-102).

Estudos revelaram que a administração de *Bifidobacterium* spp., inclusive do *B. longum*, reduz o peso corporal, melhora a tolerância à glicose e a resistência a insulina, protege da obesidade induzida por dieta mantendo a homeostase energética, reduzindo os níveis séricos de colesterol e triglicérides (103-106). Além disso, um ensaio clínico controlado duplo-cego randomizado demonstrou que os probióticos poderiam prevenir a produção de endotoxina e melhorar o metabolismo energético em indivíduos obesos (107).

2 OBJETIVOS

Objetivo geral

 Avaliar os Efeitos da Angiotensina-(1-7) Sobre o Tecido Adiposo, Inflamação e Microbiota Intestinal, e o Impacto do Uso de Probiotico na Expressão do Sistema Renina Angiotensina.

Objetivos específicos

- Realizar uma revisão da literatura científica a cerca dos achados relacionados ao eixo ECA2/ Ang-(1-7)/Mas com foco no seu papel na regulação da secreção de adipocinas e dos processos relacionados à inflamação aguda e crônica.
- Avaliar o efeito da angiotensina(1-7) sobre a microbiota intestinal de camundongos obesos.
- Avaliar o efeito da suplementação com *Bifidobacterium longum* no metabolismo e na expressão do sistema renina angiotensina hepático de camundongos obesos.

3 PRODUTOS

Produto 1: *Angiotensin-(1-7), Adipokines and Inflammation*, formatado segundo as normas para publicação do periódico <u>Metabolism Clinical and Experimental.</u> *Status:* publicado.

Produto 2: *Angiotensin-(1-7) Modulates Intestinal Microbiota Improving Metabolic Profile,* formatado segundo as normas para publicação do periódico <u>Cellular Microbiology</u>. *Status*: enviado para publicação.

Produto 3: *Bifidobacterium longum s*upplementation improves metabolic parameters and alters the expression of the renin-angiotensin system in obese mice, formatado segundo as normas para publicação do periódico <u>Life Sciences</u>. *Status*: enviado para publicação.

Produto 1

Angiotensin-(1-7), Adipokines and Inflammation

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Abstract

Nowadays the adipose tissue is recognized as one of the most critical endocrine organs releasing many adipokines that regulate metabolism, inflammation and body homeostasis. There are several described adipokines, including the renin-angiotensin system (RAS) components that are especially activated in some diseases with increased production of angiotensin II and several pro-inflammatory hormones. On the other hand, RAS also expresses angiotensin-(1–7), which is now recognized as the main peptide on counteracting Ang II effects. New studies have shown that increased activation of ACE2/Ang-(1–7)/MasR arm can revert and prevent local and systemic dysfunctions improving lipid profile and insulin resistance by modulating insulin actions, and reducing inflammation. In this context, the present review shows the interaction and relevance of Ang-(1–7) effects on regulating adipokines, and as one adipokine itself, modulating body homeostasis, with emphasis on its anti-inflammatory properties, especially in the context of metabolic disorders with focus on obesity and type 2 diabetes mellitus pandemic.

Keywords: Adipose tissue Angiotensin converting enzyme 2 (ACE2) Renin-angiotensin system Metabolism Mas receptor.

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1. Introduction

The angiotensin-(1–7) (Ang-(1–7)) is an heptapeptide with significant systemic and local effects, produced in the renin-angiotensin system (RAS) hormonal cascade, with pronounced effects counteracting the angiotensin II (Ang II) actions [1], especially considering

Ang II overproduction and high signaling present in several diseases, such as hypertension, diabetes, obesity, renal disorders and liver steatosis [2].

The RAS hormonal cascade initiates with the angiotensinogen (AGT) production, which is cleaved by the renin into angiotensin I (Ang I). Sequentially, the angiotensin converting enzyme (ACE) transforms the Ang I into the octapeptide Ang II, which is the most described active end product of the RAS, acting through two isotypes of Ang II receptors (AT1R and AT2R) [3]. High levels of Ang II produce AT1 hyperactivity and several metabolic disorders [4]. On the other hand, the angiotensin converting enzyme homolog 2 (ACE2) reduces Ang II levels by transforming it in Ang-(1–7), which also can be produced from Ang I passing through angiotensin-(1–9) (Ang-(1–9)) by the action of endopeptidases: prolyl-endopeptidase and neutral endopeptidase. The main described Ang-(1–7) effects are associated with Mas receptor activation, and the ACE2/Ang-(1–7)/Mas arm high activation has been effective in improving metabolic and chronic diseases [5]. Additionally, it is worth mentioning that Ang-(1–7) may be alternatively clived into alamandine that acts via its receptor MrgD, exerting similar actions to Ang-(1–7) [6].

The angiotensin II type I receptors modulate most of the Ang II physiological and pathophysiological effects. The Ang II binding to this receptor leads to vasoconstriction, inflammation, oxidative stress, proliferative factors augmentation, cardiovascular effects, nervous system activation, increased sodium absorption, among other effects. The Ang II type 2 receptors on the other hand, although found in several tissues in the fetal period, has its abundance decreased after birth. These receptors activation are mostly linked to beneficial consequences, including vasodilation, anti-proliferation (fibroblasts, endothelial cells and myocytes), cardiac function improvement and decreased sodium absorption in the proximal tubule [7,8].

The renin-angiotensin system activation is an important defense mechanism against hypovolemic hypotension, commonly observed during bleeding or salt privation. Aldosterone when bound to the mineralocorticoid receptor in epithelial cells of the renal collecting duct recruits sodium channels from the cytosol to the surface of the renal epithelial cells, thereby promoting increased sodium reabsorption, tubular potassium excretion and plasma volume expansion [9]. The aldosterone receptors are expressed in several tissues other than renal;

which when disturbed lead to vascular impairments. The aldosterone augments the Ang II actions, inducing vascular remodeling and inflammation, as well as the stimulation of mineralocorticoid receptors in the heart, kidneys, and brain. Moreover, the circulating aldosterone induces cardiac fibrosis and increased sympathetic activity [10].

The RAS upregulation in the central nervous system is characterized by an increased renin

activity and high aldosterone levels [11]. Moreover, it was also reported in the literature that in patients with visceral obesity, this hormone levels are normalized following weight loss [12]. In contrast, the renin-angiotensin aldosterone system blockage with ACE inhibitors and AT1R blockers is one of the most used approaches in the treatment of hypertension, congestive heart failure and coronary artery disease [13]. Studies suggest that the mineralocorticoids receptors in adipocytes promote the expression of inflammatory adipokines and facilitate the aldosterone pro-adipogenic effect. These receptors inhibition in experimental studies lead to decreased levels of proinflammatory factors in the adipose tissue and increased adiponectin expression in the heart and adipose tissue [14]. In summary, the increased amount of visceral adipose tissue induces the production of aldosterone and other hormones, which facilitates the appearance of chronic inflammation in the adipose tissue and consequent adipokines overexpression.

The Mas receptor (MasR) signaling activated by the Ang-(1–7) has several pathways, however, the most described via includes phosphatidylinositol-4,5-bisphosphate 3-kinase/protein kinase B (PI3K/ AKT) or forkhead box protein O1 (FOXO1) [15]. Another crucial signaling effect involves the direct activation of insulin receptor and insulin receptor substrate (IRS) [16,17]. Particularly in the adipose tissue, Ang-(1–7)/MasR axis presents essential effects modulating fat storage, glucose uptake and especially adipokines production regulation [5,18,19], which in turn alter local and systemic inflammation [20–22].

Several studies have shown that Ang-(1–7) exerts inhibitory effects on inflammation and cellular growth mechanisms [23,24]. Ang-(1–7) reduces key molecules signaling pathways thought to be relevant for acute and chronic inflammatory associated diseases. Excess or stressed adipose tissue may work as a systemic pump secreting pro-inflammatory adipokines and reducing the anti-inflammatory hormones [25]. In normal physiology the systemic AGT is mostly produced by the liver, however, in some diseases or hormonal disorders (such as obesity), the white adipose tissue assumes a pivotal role on AGT production, abnormally increasing the Ang II locally and also augmenting circulatory levels [26,27].

Here, we review findings related to the ACE2/Ang-(1-7)/Mas axis function with focus on the role on regulating adipokines secretion and modifying processes associated with acute and chronic inflammation. As most of the studies that involve the Ang-(1-7) signaling pathways were performed under an experimental context with animal models, we opted to discuss the human studies and their clinical importance at the end of each topic.

Adipokines, angiotensin-(1–7) and adipose tissue

The adipose tissue has long being recognized for its role in body energetic demands

supply in a prolonged fasting state, calories storage, body temperature control, and organs mechanical protection [28,29]. Recently, the adipose tissue was defined as an important endocrine organ, responsible for the synthesis and secretion of more than 600 bioactive molecules named adipokines [29]. In mammals there are two main types of adipose tissue, the white adipose tissue (WAT) and brown adipose tissue (BAT). These organs develop opposing roles, as while the WAT acts as by storing energy in the form of lipids, the BAT is responsible for the heat generation via energy consumption. Experimental studies with mice demonstrated that the BAT aids in the protection against the development of obesity and metabolic diseases via activation of thermogenesis [30].

The adipokines are involved in the satiety and appetite regulation, energetic metabolism, fat storage, insulin secretion and sensitivity, arterial pressure, endothelial function and homeostasis [31,32]. At the systemic level, the adipokines act in different target organs, such as liver, brain, muscle, heart, vessels, immunological system and others [31,33–36].

The leptin and adiponectin levels might be used to distinguish the WAT and BAT, as the WAT expresses large amounts of these adipokines, while in BAT these molecules are little expressed, especially when the thermogenesis is active [37]. Similar to the WAT, the BAT also produces bioactive molecules called batokines [38,39]. These molecules may have different and/or opposing actions to the WAT adipokines, and act in different targets (e.g., central nervous system) in the control of energy expenditure. Experimental studies showed that several molecules synthetized by the BAT have already been described to exert autocrine, paracrine and endocrine actions, and the main examples are: Triiodothyronine, prostaglandins, angiotensinogen, interleukin- 1α , insulinlike growth factor I, Interleukin-6, vascular endothelial growth factorA, fibroblast growth factor-2, nitric oxide, and fibroblast growth factor-21 [40–47].

Additionally, studies have reported a different type of adipocytes called beige. These adipocytes are brown-like cells (UCP+), but localized in the WAT [48, 49]. These cells are originated from the browning process, which is responsible for the dynamic conversion of white adipocytes into brown-like adipocytes due to the exposure to physiological, pharmacological or hormonal stimuli [50,51]. The white adipocytes browning is generally induced by the exposure to cold and physical exercise [50,52]. However, this process does not completely transform nor transdifferentiate white adipocytes into brown adipocytes; white adipocytes become only a phenotype resembling a brown adipocyte, which is also called a beige adipocyte [53,54]. The WAT browning exerts regulatory effects on the metabolism, such as increased energy expenditure, weight loss, insulin sensitivity and improved glucose tolerance, and although being performed on a rodent model, open perspectives as a potential target in the

prevention and treatment of metabolic diseases, such as diabetes and obesity [55]

Among the main adipokines it is possible to highlight the adiponectin (involved in insulin sensitivity regulation, antidiabetogenic, antiatherosclerotic and anti-inflammatory effects), apelin (insulin secretion inhibition), leptin (appetite and satiety control, energy intake, locomotor activity, energy expenditure, fertility, among others), resistin (related to obesity, insulin resistance and inflammation), proinflammatory adipokines (e.g., interleukin- 1 β (IL-1 β), interleukin-6 (IL-6), tumor necrosis factor- α (TNF α), monocyte chemoattractant protein-1 (MCP-1), among others), and omentin (anti-inflammatory) [29,31,32].

In the adipose tissue, the adipokines modulate adipocyte functions and metabolism, adipogenesis and immune cells recruitment [32,33,56]. With local action we may cite bone morphogenic protein-4 (BMP-4) that regulates adipogenic cell precursors differentiation, bone morphogenic protein-7 (BMP-7) that stimulates the brown adipose tissue, regulates energy intake, and increases energy expenditure. Ghrelin inhibits BMP-4, BMP-7, and vascular endothelial growth factor (VEGF) that stimulate angiogenesis in the adipose tissue [29,31,32].

As well as the adipokines, the RAS was also described as a critical metabolic regulator. Experimental studies with rodents and humans, linked obesity with the ACE/Ang II/AT1 RAS axis activation [57,58]. The adipose tissue expresses all RAS components, and it is involved in the obesity effects and development due to its increased size, AGT and Ang II production [57]. On the other hand, animal studies evidenced that the RAS counterregulatory axis (ACE2/Ang-(1–7)/Mas) is capable of improving the lipid and glucose metabolism via decreased body adiposity, and directly at molecular signaling levels [27,59]. Mas receptor deficiency in mice was associated with a worse metabolic profile, with lower glucose tolerance, dyslipidemia, hypertension, increased leptin expression, decreased glucose uptake by adipocytes and increased adipose tissue size [27]. In the same way, transgenic rats with

Ang-(1–7) overexpression presented improved metabolic efficiency, increased glucose tolerance and insulin sensitivity and higher glucose uptake via insulin [60]. It was also observed lipid parameters improvements with decreased triglycerides and cholesterol, as well as decreased abdominal fat mass in studies performed with rats [60,61].

It has been demonstrated that during adipogenesis, the apelin expression is increased in mice cell lines [62,63]. Some other in vitro studies showed that RAS blockage (Ang II/ACE) improves apelin expression and secretion in adipocytes from mice, which leads to reduced ROS and lipid accumulation in the adipocytes differentiation process [63]. AT1R blockage and consequent AT2R increase reduces TNF α expression and increases apelin expression in the

mice white adipose tissue [63, 64], suggesting an essential AT2R role in the browning regulation. In humans, apelin seems to induce white adipocyte browning, inhibiting AT1 via its interaction with the apelin receptor (APJ receptor) in vitro [65].

It is important to point that the adipokines may have an indirect effect on the RAS via modulation of insulin levels and lipid profile, thus evidencing an indirect relationship among these molecules. Nickenig and colleagues reported that insulin may upregulate AT1 via posttranscriptional mechanisms, thus linking hyperinsulinemia, hypertension and atherosclerosis [66]. The authors argue that the insulin influence on the RAS, more specifically on the AT1 receptor, takes place via tyrosine phosphorylation and MAP kinase- dependent intracellular pathways. Moreover, the lipid profile has also been associated with the RAS modulation (AT1 upregulation and increased AngII synthesis) [67]. The lipids influence on the AT1 expression and Ang II production, in contrast with the aforementioned insulin effects, seem to be via mRNA stabilization, and increased chymase system activity. As we know and will discuss throughout this review, the adipokines have an important influence on the glycemic and lipid profiles, and this influence may thus explain their relationship with the RAS modulation (Fig. 1).

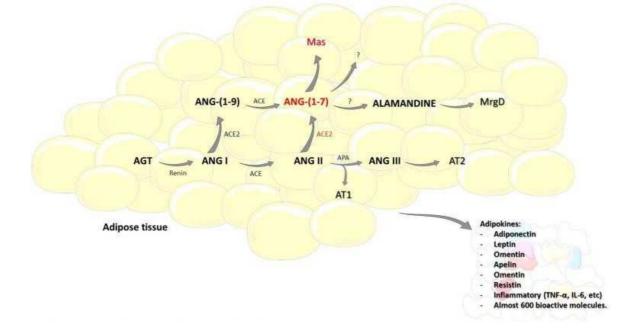


Fig. 1. Renin-angiotensin system and adipose tissue. AGT: angiotensinogen; ANG I: angiotensin I; ANG-(1–9): angiotensin 1–9; ANG-(1–7): angiotensin (1–7); ANG II: angiotensin II; ANG III: angiotensin III; Mas: Mas receptor; AT1: AT1 receptor; AT2: AT2 receptor; ACE: angiotensin-converting enzyme; ACE2: angiotensin-converting enzyme 2; APA: aminopeptidase A; MrgD: Mas-related G-protein coupled receptor D; TNF- α : Tumor necrosis factor alpha; IL-6: Interleukin 6.

The interaction between proinflammatory adipokines and RAS is also described in the literature. A study performed with adipose tissue samples from malnourished and obese mice and also confirmed in humans showed that the inflammatory state is shared between these two nutritional states and that the renin-angiotensin system modulates both profiles [68]. Interestingly, it has been reported in the literature that a possible strong influencer of the adipocytes expression/secretion profile is the muscle. The muscle is recognized as another important endocrine organ in our organism and expresses several important molecules, collectively called myokines, which counterbalance the adipokines released by the adipose tissue [69–71]. In this sense, the muscle influence might be also modulating the RAS expression in the adipose tissue.

1.2 Adipokines, Ang-(1–7) and inflammation

In the last years, Ang-(1–7) has been studied for its antiinflammatory properties in several disorders. Considering metabolic diseases, such as obesity and type 2 diabetes, it was evidenced that increased circulating Ang-(1–7) exerts a protective effect against the inflammatory process induced by obesity by decreasing ciclo-oxigenase2 (COX-2) and IL-1 β expression in transgenic rats' abdominal fat [20]. Additionally, it was shown in another study that oral administration of Ang-(1–7) is capable of preventing obesity and liver inflammation via resistin/toll like receptor 4/Nuclear Factor-kappa β (Resistin/TLR4/NFk β) pathway blockage in rats [72], and reduces diet-induced hepatic inflammation by decreasing TNF- α and IL-6 expression [72]. Interestingly, another possible mechanism by which Ang-(1–7) exerts its beneficial effects in inflammatory conditions associated to metabolic disorders in mice, is via Sirtuin 1 (SIRT1), a NAD-dependent deacetylase already described to be involved on improving several metabolic diseases [73].

Interestingly, Ang-(1–7) also ameliorates epicardial adipose tissue (EAT) inflammation induced by obesity. ACE2 knockout obese mice showed increased interferon gamma (IFN-y) expression in EAT, along with predominant CD11c+/F4/80+ Mf macrophage profile, while treatment with Ang-(1–7) reverted this inflammatory profile, mainly by decreasing TNF- α and IL-6 expression [74]. These findings are noticeable considering that epicardial fat is a current study target aiming to understand the association between obesity, metabolic diseases, and atherosclerosis.

In cardiovascular diseases, especially considering vascular inflammation, Ang-(1-7) diminished macrophage infiltration, MCP-1, IL-6, TNF- α , NFK β , vascular cell adhesion protein

1 (VCAM-1), reactive oxygen species (ROS) levels, apoptosis and increased nitric oxide release, thus reducing atherosclerosis risks [75]. Furthermore, Ang-(1–7) was capable of resolving endothelial cell inflammation in vivo, thus preventing early atherosclerosis via decreased MCP-1, VCAM-1, IL-6 and atherosclerotic plaque inhibition in human cell lines and knockout APOE mice, both in vitro [76].

The Ang-(1–7) anti-inflammatory effects were also confirmed in rat pancreatic acinar cell lines, where this peptide attenuated caerulein (an acute pancreatitis inducer) induced inflammation by downregulating TLR4/NFK β pathway [77]. In macrophage cell culture, Ang-(1–7) was capable of preventing proto-oncogene tyrosine-protein kinase Src activation, which are proteins necessary to the inflammatory response induced by lipopolysaccharide (LPS) [78].

In humans studies, endothelial cells culture, Ang II induced inflammation was prevented by Ang-(1–7) via reduced lectin-like oxidized low-density lipoprotein (LDL) receptor-1 (LOX-1) expression, a novel scavenger receptor for oxidized LDL (oxLDL), a potent inflammatory activator [79]. In uropathies, which are also characterized by an inflammatory profile, Ang-(1– 7) shown to be a protective compensatory molecule reducing inflammatory processes by decreasing macrophage infiltration and apoptosis [80]. The

renoprotective role of Ang-(1–7) is mostly discussed and reported by several studies showing neutrophil influx, and downregulation of chemokine (C-X-C motif) ligand 1 (CXCL), IL-6, TNF- α , endothelin 1 (ET-1), IL-1 β and MCP-1.

These studies illustrate and confirm the Ang-(1–7) beneficial antiinflammatory effects in several inflammatory conditions, which are associated with adipokines disruption, such as obesity, type 2 diabetes, cardiovascular diseases, renal and hepatic disorders, among others (Fig. 2).

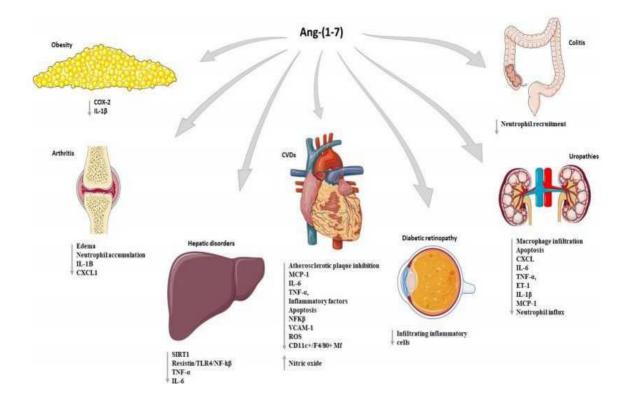


Fig. 2. Ang-(1–7) effects on inflammation. CVDs: cardiovascular diseases; ROS, reactive oxygen species; TNF- α : tumor necrosis factor alpha; IL-6: interleukin 6; IL-1 β : interleukin-1 β ; CXCL1: chemokine (C-X-C motif) ligand 1; SIRT1: Sirtuin 1; TLR4: Toll-like receptor 4; NF- $\kappa\beta$: factor nuclear kappa β ; MCP-1: monocyte chemoattractant protein-1; VCAM-1: vascular cell adhesion molecule 1; ET-1: endothelin 1.

Angiotensin (1–7) and adipokines in different organs

The adipokines produced and released by the adipose tissue mediate the communication network between this tissue and other organs [35]. Modifications in the adipose tissue homeostasis alter the adipokines secretion to a pattern that induces metabolic dysfunctions [33, 34]. Angiotensin-(1–7) presents biological and pharmacological properties that are beneficial in the metabolic dysfunctions resolution [81], being relevant to explore the adipokines effects in different metabolic organs, highlighting Ang-(1–7) as a therapeutic tool.

Adiponectin

The adipokines released by the adipose tissue affect several biological processes involved in hepatic function, including angiogenesis, vasodilation, inflammation, and deposition of extracellular matrix proteins, thus modulating hepatic fibrogenesis [82]. In the liver, decreased adiponectin levels may predispose to steatosis and advanced hepatic lesion [82,83]. This adipokine acts by reducing the hepatic stellate cells activation, proliferation, and survivor [76]. Recent studies have evaluated adiponectin analog actions since it is not viable to

increase circulating adiponectin levels in humans. These agents attenuate hepatic fibrosis in animal models [84], and have potential to become new anti-fibrotic therapeutic drugs [85].

Taking into consideration the Ang-(1–7) employment for therapeutic purposes, a study from Tang et al. evidenced the Ang-(1–7) therapeutic role in preventing non-alcoholic fatty liver disease (NAFLD) in mice via an adiponectin-independent mechanism, which may be partially attributed to the mitogen activated protein kinases (MAPK) hepatic pathway. The study suggests that Ang-(1–7) treatment may stimulate AMPK α 2 expression and 5' AMPactivated protein kinase (AMPK) phosphorylation, which eventually triggered signaling cascades, being still necessary for further clarification [86]. The RAS positive regulation in hepatic diseases via AT1R/AT2R is directly associated with a pro-fibrotic process, findings evidenced in rat models [87–90]. In a cirrhotic mouse model, increased ACE2 expression inhibited hepatic fibrosis via increased Ang-(1–7), while ACE2 blocking exacerbated the fibrotic process, shedding light to the ACE2 therapeutic potential in the treatment of chronic hepatic fibrosis animal model where AVE 0991 (Ang-(1–7) agonist) reduced ACE, 1A1 collagen and α -actin expression and hydroxyproline levels, an important collagen component, which all together ameliorates fibrosis [92].

In the mice pancreas, adiponectin stimulates insulin secretion in vivo, and hypoadiponectinemia causes β cells dysfunction [93]. Consistent with these findings, mice without adiponectin exhibited dietinduced hepatic insulin resistance. Adiponectin exerts beneficial effects via activation of its two receptors: adiponectin receptor 1 (AdipoR1) and adiponectin receptor 2 (AdipoR2) [93,94].

The liver is also an important target in human studies, where hepatic stellate cells isolated from humans cirrhotic liver were shown to overexpress renin, ACE, and Ang II [95]. Increased hepatic stellate cells proliferation and extracellular matrix production via signaling pathways mediated by MAPK, phosphoinositol/Ca2+, and ROS generation are promoted by AT1R/ACE/Ang II axis activation [96–98].

Additionally, the cardiovascular system is another important investigation target in human studies. It is discussed that adiponectin might be involved in the chronic cardiac insufficiency (CCI) pathogenesis. A study performed by Kreth et al., characterized the adiponectin and its receptors expression in CCI to evaluate the impact of microRNAs in the cardiac adiponectin system. In CCI, AdipoR1 cardiac expression was four-fold increased, while the AdipoR2 increase was two times lower, showing the adiponectin association with its

receptors in the heart and that the microRNA-150 targeting might be a strategy to restore the cardioprotective adiponectin effects [99].

Leptin

Establishing the association between leptin and Ang-(1-7), a study performed by Uchiyama et al., investigated the perirenal visceral adipose tissue and visceral perirenal adipocyte isolated from Wistar male rats. The authors observed that Ang-(1-7) increased leptin secretion and expression, while alamandine decreased the leptin secretion and expression in the adipose tissue and serum [100]. Few studies are presenting the relation between leptin and Ang-(1-7), and among them, Schuchardet et al. demonstrated the Ang-(1-7)

7) potential in regulating rats food intake and body weight. Ang-(1–7) also contributes to weight loss following AT1R blockage, since transgenic rats remained leptin responsible even with a chocolate and cookie diet. It is also suggested that Ang-(1–7) agonists might be pharmacological candidates in the obesity treatment and a new tool to treat metabolic disorders [101].

Mas double deficiency in ApoE-KO (DKO) mice leads to a lipodystrophy similar state, with increased hepatic lipid content and increased alanine aminotransferase levels. It was also observed increased cholesterol, triglycerides, and fasting glucose levels and decreased HDL and leptin levels [102].

Hamrick showed that leptin treatment in vivo increases myogenic genes expression in mice primary myoblasts. Leptin may centrally reduce medullar adipogenesis via its receptors in the hypothalamus, as well as directly through their receptors on bone marrow stem cells. Thus, aging seems to significantly alter the crosstalk mediated by leptin among organs and tissues [103].

The renal dysfunction in the chronic renal disease context is associated with high leptin levels, that also in NAFLD causes activation of renal mesangial cells and tubular inflammation via a NOX2 dependent pathway that positively regulates the pro-inflammatory miR21 molecule, findings from a mice model [104,105]. The Ang-(1–7)/MasR axis in the mice kidneys have vasodilatory, antiproliferative, antidiuretic and antinatriuretic activities [106,107].

In the heart, Carmo et al. recently determined that neuronal-SOCS3 deficiency in mice is a potential negative regulator of the leptin signaling pathway that amplifies the chronic leptin effects on food intake, energy expenditure, glucose and arterial pressure, protecting against the adverse cardiometabolic effects in obesity [108]. Oral administration of alamandine generated antihypertensive and antifibrotic effects in rats [109]. Furthermore, its subcutaneous application also exerted antihypertensive effects, with improved cardiac hypertrophy and left ventricle function. Alamandine may exert its beneficial effects via the protein kinase A (PKA) signaling pathway modulation [110]. Interestingly, Wang et al. showed in rats that leptin is also produced by the skeletal muscle, and the leptin receptors are abundant in skeletal muscle and mesenchymal stem cells derived from bone (stroma), thus confirming this adipokine effects on the muscle cells [111].

The leptin influence on the human cardiovascular system and adipose metabolism has also been investigated and the main findings evidence a positive leptin effect produced by the pericardial adipose tissue and blood vessels [112]. An interesting study performed by Oral et al. showed that leptin administration in nine women with lipodystrophy and leptin serum levels below 4 ng/mL, significantly improved lipodystrophy besides insulin resistance [113].

Resistin

It was shown that Ang-(1–7) oral treatment improved the obese rats' metabolic profile (improved body weight, abdominal fat mass, insulin plasma levels, and circulating lipid levels) via decreased resistin, TLR4, ACE and increased ACE2 expression in the liver [72]. Santos and colleagues showed that Ang-(1–7) decreases MAPK phosphorylation, reducing IL-6 and TNF- α expression via resistin/TLR4/NF-kβ-pathway down-regulation in rats [72].

Resistin levels are increased in obesity. In a study performed in highfat-fed mice, the resistin levels normalization by antisense oligonucleotides reverses hepatic insulin resistance [114,115]. These proteins supposedly contribute to the visceral adiposity deleterious metabolic effects. Increased insulin secretion was observed in mice MasKO pancreatic islets treated with A776 (Mas antagonist) and stimulated with Ang- (1–7), although the insulin expression was not altered, indicating a smaller Ang-(1–7) not exclusively by Mas-dependent pathways [116].

Translational studies that investigated the resistin role in humans reported interesting findings. First, resistin expression was shown to be increased in fibrotic liver. In hepatic stellate cells, resistin seems to increase MCP-1 and interleukin-8 (IL-8) expression [117], besides contributing to the lipids uncontrolled uptake. The hepatic low-density lipoprotein receptor (LDL) negative regulation and de novo lipogenesis stimulation in hepatic cells are triggered by resistin and may augment dyslipidemia and hepatic steatosis [118].

In the pancreatic islets on the other hand, the literature regarding the resistin expression is scarce [119]. However, Alexandra et al. showed the resistin expression in human pancreatic islets via qRT-PCR and immunohistochemistry shedding new light on the resistin potential role in the pancreas [119].

Second, regarding the relationship between inflammation and the adipokines, Hollebeke

et al. studied the abdominal muscular density and area with inflammatory mediators associated with adiposity and resistin. The results showed that the muscular area was not associated with any inflammatory mediators studied, including resistin. It was yet not verified that higher densities of several muscle groups in the abdomen are significantly associated to lower IL-6 and resistin levels, independent from the muscle area in these groups [120].

Lastly, in the cardiovascular system, resistin levels are associated with coronary artery disease and heart failure severity. Turgay et al. evaluated if there is a relation between resistin levels and final diastolic pressure in the left ventricle and observed no correlation between resistin levels and left ventricular-end diastolic pressure, coronary artery disease severity, echocardiographic diastolic dysfunction parameters and constraint induced movement therapy. More studies are necessary to evaluate the resistin efficacy for clinical use [121].

Omentin

The association between omentin and Ang-(1–7) is still unknown in the literature, becoming a potential target for new studies. Omentin is an anti-inflammatory protein and improves insulin sensitivity [122]. If the omentin directly regulates the hepatic cells, biological function is still not clear in the literature. Unbalanced nitric oxide levels contribute to splanchnic vasodilation and hepatic vasoconstriction and consequently portal hypertension [123]. Although several mechanisms influence the vasodilation process, the RAS is one of the most studied over the years, and it is discussed that the ACE/Ang II/AT1 axis has been intimately associated with cardiovascular dysfunctions and metabolic disturbances [124].

Sit et al. evaluated the inflammatory response effects on serum omentin levels in acute and chronic pancreatitis and found that omentin levels elevation in rats at the early stage of pancreatitis was due to omentin's anti-inflammatory effects [125]. Castro et al. showed that both adipose tissue metabolism and adipokine secretion might be affected in diabetic rats, but omentin was no different between the groups [126].

The omentin role in human studies are more focused on metabolic diseases, where it was evidenced decreased omentin levels in type 1 and 2 diabetes mellitus, correlating with insulin resistance [127,128], which might be explained by the strong relationship between arterial pressure and insulin plasma concentration in hypertensive individuals with obesity, acting not only in the sympathetic nervous system, but also in renal function and arterial walls, leading to increased arterial pressure [129].

Moreover, Zorlu et al. compared serum omentin and obestatin levels in type 2 diabetic patients with normoalbuminuria and macroalbuminuria and observed that higher obestatin

serum levels were associated with macroalbuminuria, whereas serum omentin levels were similar between groups suggesting that obestatin may play a role in the underlying pathogenic mechanisms leading to diabetic nephropathy [130].

In the cardiovascular context, Fernándes-Trasancos et al. evaluated the omentin effects on the epicardial adipose tissue and vascular cells. This study showed that omentin treatment increased adiponectin levels induced by adipogenesis and reduced TNF- α levels in mature adipocytes. Omentin improved insulin activity in EAT and subcutaneous adipose tissue explants from patients with cardiovascular disease and decreased smooth muscle cells migration [131]. It is observed in the literature that omentin positively associates with adiponectin [129], which may justify the inflammation attenuation in the epicardial adipose tissue via ACE/Ang-(1–7)/Mas that reduces obesity-induced cardiac dysfunction by increasing adiponectin levels.

Apelin

Recently, Sabry et al. assessed the apelin treatment effects on diabetes mellitus type 2 induced by obesity and the possible interaction between the apelin/APJ and the renin-angiotensin system. The study showed that apelin-13 administration in rats resulted in improved insulin resistance, dyslipidemia, inflammation, oxidative stress, reduced AT1 gene expression and increased ACE2 expression in the adipose tissue, evidencing that the apelin beneficial effects are NO/ACE2/Ang-(1–7) dependent [132].

A review showed that apelin is the second catalytic substrate for ACE2 and acts as an inotropic and cardiovascular protective peptide. Chen et al. showed that microRNAs, linked to ACE2/apelin modulation, exhibit beneficial effects in the cardiovascular system and hypertension. The crosstalk between ACE2, the apelin system and microRNAs provides an important hypertension mechanist view [133]. Another review of the literature evidenced that the Apelin/APJ system is mainly expressed in vascular smooth muscle cells (VSMC). The study by Luo et al. was the first to demonstrate that the apelin/APJ system increases the VSMC proliferation by the extracellular signal–regulated kinase 1 (ERK1)/2-cyclin D1 signal pathway, thus being a promising target for the management of the vascular disease management [134]. The apelin effects on the cerebral arteries are unknown. Mughal, Sun and, O'Rourke, have demonstrated that apelin reduces the cerebral arteries nitric oxide-induced relaxation by inhibiting the calcium-activated high conductance K channels activation [135].

Recently, it was showed that the apelin/APJ system develops a critical role in kidney disease [136]. Guo et al. verified in mice that this system induces podocyte dysfunction in diabetic nephropathy via endoplasmic reticulum stress induced by decreased proteasome

activity in podocytes [137]. In this sense, the apelin-APJ system, in animal models, develops diverse roles in renal disease and might be a potential target in the renal disease treatment [138].

The inflammation develops an essential role in pancreatitis, and thus, Hans et al. showed that apelin inhibited the positive regulation of TNF- α , MIP-1 α/β and IL-1 β in mice with chronic pancreatitis, thus evidencing that apelin is involved in the inflammatory mediator's modulation in pancreatitis in this animal model [139].

The human studies involving the investigation of the apelin role on the other hand, are mainly focused on metabolism. It was reported that the physical exercise beneficial metabolic effects might be mediated by myokines. In this sense, Besse-Patim et al. studied the physical training effects and apelin expression in the human skeletal muscle. It was observed that physical training increases apelin expression in an obese individual via exercise-induced signaling pathways, thus being considered a new myokine with autocrine and paracrine actions. The physical activity beneficial effects on reducing arterial pressure in hypertensive individuals are linked, at least in part, to an increased apelin/APJ system expression. [140].

Interestingly, in vitro experiments with human cells evidenced that the angiotensinconverting enzyme 2 (ACE2) is a counterproductive regulator of the renin-angiotensin system (RAS), catalyzing the conversion of Ang II to Ang-(1–7). The apelin is a second catalytic substrate for ACE2 and functions as an inotropic peptide and cardioprotective [141].

Although an antagonistic relationship has been proposed between RAS and apelin, this functional interaction remains uncertain. In this perspective, we may conclude that adipokines, produced by the adipose tissue, have paracrine and autocrine actions that thus exert an effect in several organs and consequently different physiological and pathophysiological conditions (Fig. 3). These observations and evidence highlight the adipokines importance as molecular targets to be modulated in metabolic diseases treatment and prevention.

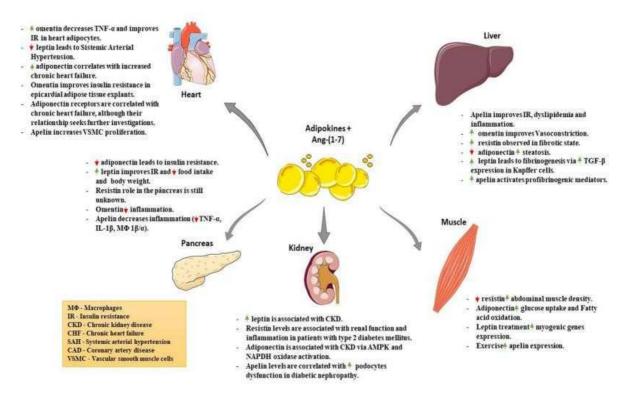


Fig. 3. Ang- (1–7) effects on adipokines: Ang-(1–7) has a protective effect despite the relationship between omentin and Ang-(1–7) being unknown. In the liver, the decrease of Adiponectin and increase of the other adipokines contribute to deleterious effects. In the pancreas there is an opposite effect to the liver and little is known about the effects of resistin. In the muscle, the decrease in resistin leads to an increase in abdominal muscle density and the increase in other adipokines has beneficial effects. Little is known about the impact of omentin on muscle. In the kidneys, the rise in adipokines contributes to the adverse effects. In the heart and blood vessels, the apelin/APJ system increases the proliferation of vascular smooth muscle cells while the other adipokines do not have favorable effects.

2. Adipokines and clinical implications

According to the Global report on diabetes from the World Health Organization, the diabetes prevalence almost quadrupled since 1980, reaching 422 million adults, which is in great part, due to the increased overweight/obesity (considered the main diabetes type 2 risk factor) prevalence. Type 2 diabetes mellitus may lead to macro and microvascular complications, and in 2012, was the direct death cause of 1.5 million people [142]. This growing prevalence and mortality generate social and economic implications in the health systems globally. It is necessary to find therapeutic targets aimed to set not only type 2 diabetes mellitus treatments but also risk factors attenuation [143]. In this context, deepening the knowledge of the adipokines endocrine effects in different target organs, their signaling pathways and links with RAS may contribute to developing new drugs, aiming at the diseases associated with broad-spectrum obesity therapy.

In obesity and type 2 diabetes mellitus, insulin resistance affects the perivascular adipose tissue endocrine function, altering vasoconstrictor and vasodilator molecules secretion and increasing the oxygen reactive species production. A study demonstrated that plasma adipokines or their receptors expression might improve insulin sensitivity and reduce cardiometabolic diseases morbimortality. In this perspective, the adipokines may constitute potential therapeutic targets for obesity and type 2 diabetes mellitus [144,145]. A study investigated the association between adipokines, anthropometric measures and biochemical parameters in type 2 diabetes mellitus, demonstrating that central obesity is correlated with adipokines synthesis unbalance, reinforcing their importance in type 2 diabetes mellitus [146]. Besides that, adipokines may be considered clinical biomarkers for the diagnosis and early interventions in pre-diabetic and T2DM patients [147].

Although several studies point to physiological and pathophysiological Ang-(1–7) properties in type 2 diabetes mellitus progression, its protective effects against hyperglycemia damage are still not completely elucidated. A clinical study also showed that intra-arterial infusion of Ang-(1–7) in obese patients exerted favorable effects by stimulating insulin-triggered vasodilation and inhibiting endothelin-1 vasoconstriction, which are comorbidities associated with obesity and insulin/glucose impaired metabolism [148].

Interestingly, a phase II, open-label pilot study reported that ACE2 infusion in patients with pulmonary arterial hypertension improved pulmonary hemodynamics and reduced oxidative stress and inflammation [149]. This study exemplifies the clinical application of RAS modulation in ameliorating disorders, such as hypertension. Recombinant ACE2 infusion in healthy individuals was also evaluated. The treatment was well tolerated and lead to significant changes in the RAS peptides concentrations [150].

Studies performed with animal models demonstrated that adiponectin exerts a fundamental role in obesity-associated diseases pathophysiology. Acting through its receptors (AdipoR1 and AdipoR2), it exerts direct effects on the liver, skeletal muscles, and vasculature (metabolic tissues), improving insulin sensitivity, lipid profile and producing anti-atherogenic and anti-inflammatory effects [151–154].

Leptin regulates energy homeostasis by inhibiting hunger (anorexigenic) and by increasing energy expenditure in over food conditions and increased fatty acid uptake. Leptin receptors are distributed in peripheral tissues, but the central nervous system is considered the main ingestion regulation site, which occurs via neurotensin (neurotransmitter). Recent findings demonstrated a positive association between circulating leptin and neurotensin, broadening the leptin-neurotensin peripheral and central mechanisms understanding, with new therapeutic

approaches perspectives [155].

Resistin was primarily known as a hormone secreted by adipocytes, but it is mainly expressed and secreted by macrophages. Increased resistin levels are associated with insulin resistance, endothelial dysfunction, and smooth muscle cells proliferation, promoting type 2 diabetes mellitus and mediating atherosclerosis pathogenesis [156].

Hepatic biopsies have shown that resistin plays an important role in the hepatic insulin resistance pathogenesis, aggravating NAFLD, being the most significant expression in patients with T2DM and dyslipidemia [157].

Apelin exerts significant effects on glycaemic and lipid metabolism, and it is mainly expressed and released by adipocytes. The apelin injection stimulated glucose uptake by the adipose tissue in mice and human [158,159]. Additionally, exogenous apelin administration in patients with central obesity resulted in insulin-stimulated vasodilation, thus showing the apelin effects on hemodynamic alterations associated with insulin impaired function conditions such as obesity [160].

Recently, ghrelin has been associated with several significant effects, besides its contribution as an orexigenic hormone, acting in the systemic metabolism. The ghrelin agonism may offer a therapeutic possibility for diabetic gastroparesis and anorexia, and its receptor antagonism may be used in the treatment of obesity and to improve glycaemic metabolism and type 2 diabetes mellitus [161,162].

3. Concluding remarks

In summary, it is important to highlight the adipose tissue endocrine significance on synthesizing adipokines, modulating its secretion and regulating several processes associated with acute and chronic inflammation, besides its relevance in whole body homeostasis. In the present review, we evidenced the main adipokines participation and their interaction with inflammation and the ACE2/Ang-(1-7)/MasR RAS axis. The molecular pathways involved in the adipokines action mechanisms raised the need for new studies aiming to investigate therapeutic interventions, as well as new tools to clarify the unknown mechanisms. The Ang-(1-7) interaction and relevance on the adipokines expression and inflammation were discussed in obesity, type 2 diabetes, cardiovascular diseases, renal and hepatic disorders, among others. In this perspective, we concluded that inflammation may be modulated by adipokines and Ang-(1-7) in different organs and might be an important target for the treatment and prevention of inflammatory responses.

Conflicts of interest

The authors declare no conflicts of interest.

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Produto 2

Angiotensin-(1-7) Modulates Intestinal Microbiota Improving Metabolic Profile

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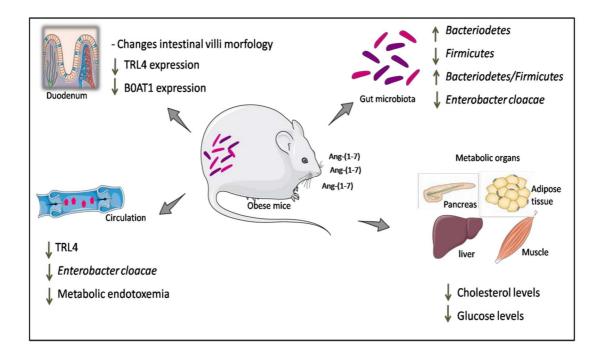
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small intestine.

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Abbreviations: ACE, Angiotensin-converting enzyme; ACE2, Angiotensin-converting enzyme 2; AGT, Angiotensinogen; ANG-(1-7), Angiotensin-(1-7); ANGII, Angiotensin II; AT₁, Type 1 Angiotensin II receptor; AT₂, Type 2 Angiontensin II receptor; B0AT1, Neutral amino acid transporter; CD-14, Cluster of differentiation 14; GAPDH, Glyceraldehyde 3-phosphate dehydrogenase; gDNA, Genomic DNA; GF, Germ- free; GLP-1, Glucagon-like peptide-1; HDL, High-density lipoprotein; HFD, High-fat diet; HPβCD, Hydroxypropyl-β-cyclodextrin; KO, Knockout; LDL, Low-density lipoprotein; LPS, Lipopolysaccharides; MAP3K7, Mitogenactivated protein kinase kinase kinase 7; Mas, Mas Receptor; MYD88, Myeloid differentiation primary response gene 88; NF-KB, Factor nuclear kappa B; NOD1, Nucleotide-binding oligomerization domain-containing protein 1, qPCR, Real time-PCR; SCFAs, Short-chain fatty acids; SEM, Standard error; ST, Standard; TIS, Interactions total score; TRAF6, TNF receptor-associated factor 6; TRL4, Toll-like receptor 4; TRP, Tryptophan; UBE2N, Ubiquitin-Conjugating Enzyme E2 N; WNL, Weighted number of links; WT, Wild-type.

Graphical Abstract



Abstract

The renin-angiotensin system (RAS) and especially angiotensin-(1-7) [ANG-(1-7)] were recognized as essential agents on modulating energy homeostasis and body weight. Moreover, the gut microbiota also received attention when recent studies showed its ability to reverse obesity and metabolic disorders. Therefore, the present study aimed to evaluate the ANG-(1-7) oral administration effects on intestinal microbiota in obese mice. Mice were divided into 4 groups: obese and non-obese/ treated and non-treated with ANG-(1-7). Was observed a significant decrease in the fasting plasma glucose, total cholesterol, triglycerides, and LDL levels and increased HDL in animals treated with ANG-(1-7). The histological analysis showed intestinal villi height reduction in mice treated with ANG-(1-7). Additionally, increased *Bacteroidetes* and decreased *Firmicutes* (increased *Bacteroidetes/Firmicutes* ratio) and *Enterobacter cloacae* populations were observed in the HFD+ANG-(1-7) group. Finally, the intestinal expression of Neutral Amino Acid Transporter (B0AT1) was increased in animals treated with ANG-(1-7), showing a possible mechanism associated with tryptophan uptake. The results of the

present study suggest, for the first time, interaction between RAS and intestinal microbiota modulation.

1. Introduction

Obesity has become a pandemic and a severe public health problem. Compared to the 1980's, there was an increase of more than twice the number of obese individuals, and estimates indicate that by 2030, 57.8%, about 3.3 billion people, will be overweight or obese (Kelly, Yang, Chen, Reynolds, & He, 2008). The increase in the prevalence of obesity is directly related to metabolic alterations, characterized by arterial hypertension, dyslipidemia, hyperglycemia and hyperinsulinemia (Alberti, Zimmet, & Shaw, 2006).

Obesity is associated with several metabolic disarrangements, including an altered expression of the renin-angiotensin system (RAS), a hormonal cascade composed by several important bioactive peptides that modulates the whole-body metabolism (Santos et al., 2013; Santos et al., 2008; Santos et al., 2012). The ANG-(1-7)/ACE2/Mas axis counterbalance the ANGII/ACE/AT1 arm harmful effects (Santos et al., 2010), which when overexpressed induces significant glycemic and lipid alterations, besides the vascular damage (Santos et al., 2010; Santos et al., 2012). Santos et al. (Santos et al., 2012) described an improved lipid and glycemic profile in transgenic rats with increased circulating ANG- (1-7). Furthermore, the Mas receptor suppression in FVB/N mice induced harmful metabolic alterations in glycemic and lipid metabolism, promoting fat mass gain and a metabolic syndrome-like state (Santos et al., 2008). These findings point to the RAS as an important therapeutic target for the treatment of obesity-associated disorders.

Another important player in whole-body metabolism and obesity is the intestinal microbiota that modulates energy homeostasis and body weight (Tremaroli & Backhed, 2012). In mice and humans, the microbial diversity and the *Firmicutes* and *Bacteroidetes* phylum proportion are associated with obesity development (Ley et al., 2005; Ley, Turnbaugh, Klein, & Gordon, 2006). The intestinal microbiota contributes to diet-induced obesity by controlling the fatty acid β -oxidation process and triglycerides storage (Backhed et al., 2004) and promoting energy uptake in a high- carbohydrate diet (Backhed, Manchester, Semenkovich, & Gordon, 2007). Germ-free (GF) mice that received microbiota from *wild-type* (WT) donors presented increased adiposity and glycemic and lipid metabolism alterations

(Backhed et al., 2004). Subsequently, Riduara et al. (Ridaura et al., 2013) showed that microbiota transplant from the obese to the lean twin mice was not capable of inducing obesity, evidencing the protective effects of the lean individual's microbiota.

Data regarding intestinal microbiota and RAS are scarce in the literature, and the interaction between ANG-(1-7) and intestinal microbiota was not yet elucidated. Some authors suggested a possible interaction between the beneficial RAS axis (ACE2/ANG-(1-7)/Mas) and the intestinal microbiota via ACE2 modulation (J. M. O. Andrade, de Farias Lelis, Mafra, & Cota, 2017; Hashimoto et al., 2012).. Hashimoto et al. (Hashimoto et al., 2012) revealed that ACE2 deficiency in mice resulted in highly increased susceptibility to intestinal inflammation, and suggested that an altered intestinal microbiota composition and increased susceptibility to colitis may be driven by the RAS via ACE2 modulation. Furthermore, ACE2 exerts an essential role in the intestinal tryptophan transport, modulating the activity of the main neutral aminoacids transporter, BOAT1, localized in the located on the edge of the small intestine brush (Cole-Jeffrey, Liu, Katovich, Raizada, & Shenoy, 2015). ACE2- KO mice presented reduced serum neutral aminoacids levels and a deficient uptake of tryptophan (Trp). ACE2 deficiency was also correlated with decreased antimicrobial peptides levels and consequent altered intestinal microbiota ecology, which is restored after tryptophan administration (Hashimoto et al., 2012).

In this perspective, the present study aimed to evaluate the ANG-(1-7) effects on the intestinal microbiota of mice. To achieve that goal, we assessed the ANG-(1-7) oral administration effects on obese mice microbiota and associated metabolic morphologic parameters and performed bioinformatics analysis to explore the possible links between the RAS and intestinal microbiota.

2. Methods

Drug

In order to guarantee the oral absorption and effect of ANG-(1-7) through the gastrointestinal tract, the peptide was formulated using [hydroxypropyl- β -cyclodextrin/ANG-(1-7)- HP β CD/ANG-(1-7)], which consist on an ANG-(1-7) molecule included in acyclic oligosaccharides (cyclodextrin) (Lula et al., 2007). HP β CD/ANG-(1-7) was donated by the National Institute of Science and

Technology - INCT-NanoBiofar (UFMG/Brazil). The daily dose (concentration of 100 μg/kg) was based on a previous study (J. M. Andrade et al., 2014), and ANG- (1-7) was mixed in the animal's diet.

Animals and Diets

The experiment was conducted with 32 male Swiss (four weeks old) divided into 4 groups (n=8 each) and fed the following experimental diets, respectively, for 4 weeks: Standard Diet *ad libitum* ST+HP β CD (ST), ST+ANG-(1–7)/HP β CD (ST+ANG-(1-7)), High-fat diet+HP β CD (HFD), and HFD + ANG-(1–7)/HP β CD(HFD+ANG-(1–7)). Obesity was induced by HFD (24.55% of carbohydrate, 14.47% of protein, and 60.98% fat, presenting a total of 5.28 kcal/g of diet). The control group was fed ST (50.30% of carbohydrate, 41.90% of protein, and 7.80% of fat with a total of 2.18 kcal/g of diet) (Haslam & James, 2005; Rocha & Libby, 2009). All experimental procedures were approved by the Ethics Committee of the State University of Montes Claros and were conducted by following the regulations described in the Committee's Guiding Principles Manual (Protocol number 103/2016).

Measurements of Body Weight, Food Intake, and Tissue Collection

The body weight and food intake were measured three times a week during all experimental procedure. Overnight fasted mice were killed by decapitation and samples of blood, adipose tissues (epididymal, mesenteric and retroperitoneal) and duodenum were collected, weighed, immediately frozen in liquid nitrogen and stored at -80°C for subsequent analysis.

Determination of Blood Measurements

Serum was obtained after centrifugation(3200 rpm for 10 minutes at 4°C). Glucose, total cholesterol, triglycerides and high-density lipoprotein (HDL) were assayed using enzymatic kits (Wiener®, Argentina). Measurements were made on a Wiener BT-3000 plus ChemistryAnalyzer (Wiener®, Argentina). Low-density lipoprotein (LDL) was calculated based on the Friedewald formula (Friedewald, 1972).

Histology Staining

Duodenum samples were fixed in 10% neutral-buffered formalin at 4°C overnight, dehydrated through a graded alcohol series, xylene, and paraffin, and then embedded in paraffin. Sections of 5µm were prepared for Hematoxylin & Eosin staining. The slides were analyzed in an FSX100 Inverted Microscope (São Paulo, Brazil).On each slide, the length of the intestinal villi was evaluated (measured from the base of the intestinal villi to the lamina muscularis mucosa)(Navarrete, Vasquez, & Del Sol, 2015) using the Image J software (Wayne Rasb and, National Institutes of Health, Bethesda, MD).

Gut Microbiota Analyzes

Stool samples collected from the mice large intestine immediately after the sacrifice were used. The samples were stored and frozen at -80°C for subsequent analyses. Genomic DNA (gDNA) was extracted from 50mg of each sample, by silica particles, following washing for impurities removal and resuspension in Tris-EDTA. The gDNA amplification was performed by Real Time-PCT (qPCR) following the method described by Lee (2014), sequences of primers described in Table 1. Relative comparative CT method was applied to compare DNA concentrations between groups, using the $2-\Delta\Delta$ CT equation (Livak & Schmittgen, 2001).

Primer target	Primer name	Primer sequences (5'-3')	Reference
Total bacteria	341F 543R	CCTACGGGAGGCAGCAG ATTACCGCGGTGCTGG	Lee et al., 2014 [1].
Bacteriodetes	Bact934F Bact1060R	GGA RCA TGT GGT TTA ATT CGA TGA T AGC TGA CGA CAA CCA TGC AG	Lee et al., 2014 [1].
Firmicutes	Firm934F Firm1060R	GGA GYA TGT GGT TTA ATT CGA AGC A AGC TGA CGA CAA CCA TGC AC	Lee et al., 2014 [1].
Lactobacillus spp.	F R	AGCAGTAGGGAATCTTCCA CACCGCTACACATGGAG	Lee et al., 2014 [1].
Enterobacter clocae	F R	CGAGAGCCTGUTGCTG GAT TGGCTGACCCAAT	Anbazhagan et al., 2010 [2].
TRL-4	F R	TGGCTGGTTTACACATCCATCGGT TGGCACCATTGAAGCTGAGGTCTA	Qin et al., 2015 [3].
B0AT1	SLC6A19F SLC6A19 R	TTC ACA TCT GTG TAT GCG GCC A AGT GGC ATT GCA CCA CTG TT	Yangzom et al., 2015 [4].

Table 1. Specific mice primers used in this study.

Reverse transcription and qRT-PCR

Total RNA from the duodenum was prepared using TRIzol reagent (Invitrogen Corp.®, San Diego, California, USA), treated with DNAse and reverse transcribed with M-MLV (Invitrogen

Corp.®). The endogenous glyceraldehyde 3-phosphate dehydrogenase (GAPDH), Toll-Like Receptor 4 (TRL-4) and Neutral Amino Acid transporter (B0AT1) were amplified using specific primers and SYBR green reagent (Applied Biosystems®, USA) in a plus-one platform (Applied Biosystems®). Relative comparative CT method was applied to compare gene expression levels between groups, using the $2-\Delta\Delta$ CT equation (Livak & Schmittgen, 2001).

Bioinformatics analysis

The bioinformatics was performed as previously described (Santos, 2016). The critical genes involved in the RAS modulation of the intestinal microbiota were identified through a search on the Gene Cards database. The keywords were "renin-angiotensin system" and "microbiota" and "liver". The word "liver" was chosen as one of the key-words because of its important role as a metabolic organ and accessory organ of the intestine. A list composed by potential "gene candidates" that are associated with the keywords chosen was retrieved. Following that, the gene list was expanded in the web-available software STRING (version 9.1), mapping the interaction network among the protein- coding genes. Direct and indirect gene interactions were considered with a high confidence degree (over 0.9, interval 0-0.99); the number of clusters was obtained when mathematical convergence was achieved, and the leader genes were identified. Topological analyses were performed in the Cytoscape software.

Statistical Analysis

All data were transferred to GraphPad Prism software (Version 5.0®, San Diego, California, USA) and analyzed with 95% confidence (p<0.05). Data are expressed as the mean \pm SEM. The statistical significance of differences in mean values between mice groups was assessed by One-Way ANOVA followed by Tukey post-test, and Student t-test. Differences among various classes based on the weighted number of links (WNL) versus the global connectivity Interactions Total Score (TIS) were assessed by the Kruskal-Wallis test. Statistical significance was set at p<0.05.

3. Results

Body Weight, Food Intake, and Tissue Collection

First, we assessed the body and fat weight. Differences in body weight were not observed between the HFD and HFD+ANG-(1-7) groups (HFD, 59.35 g \pm 1.93; HFD+ANG-(1-7), 56.30 g \pm 0.61). As expected, the ST and ST+ANG-(1-7) groups adiposity (sum of the adipose tissues: epididymal,

mesenteric and retroperitoneal) was significantly smaller as compared to the HFD groups (ST, 0.023 g/BW±0.004; ST+ANG-(1-7), 0.023 g/BW±0.002; HFD, 0.041 g/BW±0.008; HFD+ANG-

(1-7), 0.043 g/BW±0.008), and no differences were observed between HFD and HFD+ANG-(1-7). Also, differences in food intake (ST, 0.1987 g \pm 0,008; ST+ANG-(1-7), 0,191 g \pm 0.007; HFD, 0,107g \pm 0.006, HFD+ANG-(1-7), 0,109 g \pm 0.009) and energy intake (ST, 0.441 Kcal \pm 0.017; ST+ANG-(1-7), 0.400Kcal \pm 0.021; HFD, 0.561 Kcal \pm 0.043, HFD+ANG-(1-7), 0.601 Kcal \pm 0.061) were not found between the animals treated with similar diets.

HFD+ANG-(1-7) mice exhibited significantly decreased glucose levels (HFD, 155.7 mg/dl±3.93 vs. HFD+ANG-(1-7), 108.0mg/dl±5.05) as compared to the HFD group (Figure 1A). Total cholesterol (HFD, 147.5 mg/dl±12.52; HFD+ANG-(1-7), 95.20±1.37) and triglyceride (HFD,128.3 mg/dl±9.30 versus HFD+ANG-(1-7), 79 mg/dl±13.46) levels were also decreased in the HFD-ANG-(1-7) treated group (Figure 1B and 1C). The serum HDL levels were increased in the animals treated with ANG-(1-7) as compared to HFD group (HFD, 55.33 mg/dl±5.55; HFD+ANG-(1- 7), 87.80 mg/dl±7.65(Figure 1D).Also, serum LDL levels were increased in the HFD group as compared to ST (ST, 14.15 mg/dl±2.945; HFD, 43.65 mg/dl±12.24), while the HFD+ANG-(1-7) group presented reduced levels of LDL as compared to HFD (HFD, 43.65 mg/dl±12.24; HFD+ANG- (1-7), 15.63 mg/dl±4.151) (Figure 1E).

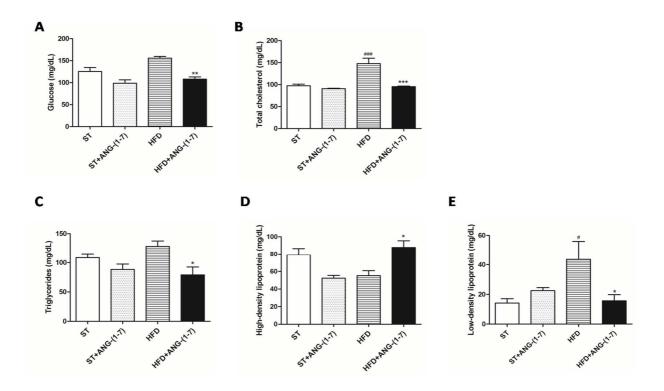


Figure 1. Oral treatment with angiotensin-(1-7) improves the plasmatic parameters of obese mice. A. Glucose levels **B.** Total cholesterol. **C**. Triglycerides. **D**. High-density lipoprotein. Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as [#]p< 0.05 ^{###}p<0.001 in comparison to the ST group, and *p<0.05, **p<0.01, ***p<0.001 in comparison to the HFD group (one-way ANOVA).

The duodenum histological analyses performed to examine the ANG-(1-7) effects in villi size evidenced a substantial decrease in the villus height in relation to HFD (HFD, 452.9 μ m±11.83; HFD+ANG-(1-7), 405.1 μ m±10.00) (Figure 2A and B).

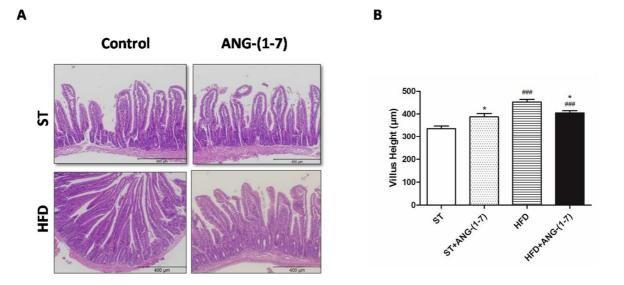


Figure 2. Angiotensin-(1-7) alters the height of intestinal villi. A. Duodenum villi Hematoxylin & Eosin (HE) staining. B. ImageJ analysis of villi Height and thickness. Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as *p<0.05 ***p<0.001 in comparison to the ST group, and *p< 0.05, **p< 0.01, ***p< 0.001 in comparison to the HFD group (one-way ANOVA).

The gut microbiota analyses evidenced that ANG-(1-7) modulates the microbial populations that colonize the intestine. The HFD+ANG-(1-7) on the other hand, displayed a slight increase *Bacteroidetes as* compared to HFD (HFD, 0,0420 \pm 0.004 vs. HFD+ANG-(1-7), 0,790 \pm 0.298) (Figure 3A). Additionally, the *Firmicutes* population was decreased in the ST + ANG-(1-7) (ST, 0.38 \pm 0.086 versus ST + ANG- (1-7), 0.03 \pm 0.033) and HFD + ANG- (1-7) (HFD, 2.35 \pm 0.36 versus HFD + ANG- (1-7), 1.10 \pm 0.40) groups (Figure 3B).The *Bacteroidetes/Firmicutes* ratio (Figure 3C) confirmed the significant *Bacteroidetes* increase and *Firmicutes* decrease in the treatment groups (HFD+ANG-(1-7) as compared to HFD (HFD, 0.167 \pm 0.003; HFD+ANG-(1-7), 0.743 \pm 0.172).

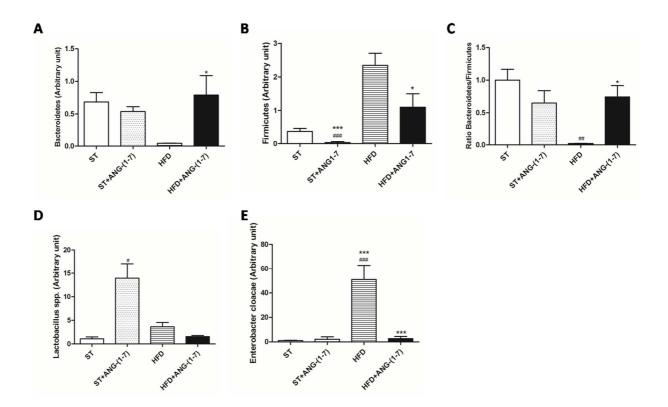


Figure 3. Angiotensin-(1-7) modulates the intestinal microbiota. A. *Bacteroidetes*. B. *Firmicutes*. C. Bacteroidetes/Firmicutes ratio. D. *Lactobacillus spp.* and E. *Enterobacter cloacae*. Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as [#]p < 0.05 ^{###}p<0.001 in comparison to the ST group, and *p<0.05, **p< 0.01, ***p< 0.001 in comparison to the HFD group (one-way ANOVA).

We also evaluated the ANG-(1-7) oral administration effects on *Lactobacillus* gDNA expression (Figure 3D), where a significant increase in the ST+ANG-(1-7) fed animals wasobserved (ST, 1,080 \pm 0.400; ST+ANG-(1-7), 13,92 \pm 3.138). Significant differences were not found between the HFD and HFD+ANG-(1-7) groups. As expected, the HFD group presented a significantly higher expression of *Enterobacter cloacae* in the HFD group(Figure 3E), and interestingly, the treatment with ANG-(1-7) was capable of decreasing this microbial population in the HFD+ANG-(1-7) treated animals (HFD, 50.98 \pm 11.62; HFD+ANG-(1-7), 2.65 \pm 1.72).

The Gene Cards and String data base analyses included four genes related to RAS and microbiota; all scored over 7.5. Figure 4A displays the interaction map obtained. The genes that showed a higher weighted number of links (WNL) and lower total interaction score (TIS) were considered leaders TRAF6 (TNF receptor-associated factor 6), TRL4 (Toll-like receptor 4), MAP3K7

(mitogen-activated protein kinase kinase kinase 7), MYD88 (Myeloid differentiation primary response gene 88) and *UBE2N* (Ubiquitin-Conjugating Enzyme E2 N) (Fig. 4B).

To confirm the main bioinformatic findings, we assessed the TRL4 expression by qRT-PCR in our study. Differences between ST versus ST+ANG-(1-7) were not found (ST, 1.00 ± 0.0 ; ST+ANG-(1-7), 0.41 ± 0.027). The HFD group, on the other hand, presented a significantly higher expression as compared to HFD+ANG-(1-7) group (HFD, 10.18 ± 2.73 and HFD+ANG-(1-7), $1.37\pm.070$) (Figure 4C). To establish a link between the ANG-(1-7) effects on microbiota and inflammation, we evaluated the B0AT1 intestinal expression, which is an essential mediator of the microbiota effects. We observed that ingestion of HFD with ANG-(1-7) promoted a significant increase of B0AT1 in duodenal enterocytes (HFD, 0.05 ± 0.03 ; HFD+ANG-(1-7), 0.18 ± 0.03) (Fig. 4D).

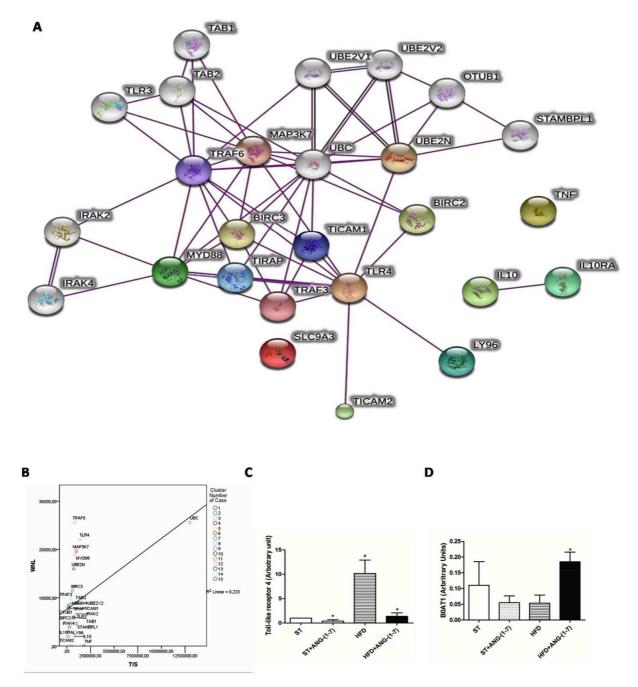


Figure 4. Bioinformatics and RT-PCR analyzes demonstrated that the renin-angiotensin system and the intestinal microbiota regulate inflammation via TRL4, and increases intestinal expression of B0AT1 mRNA in obese mice. A. STRING network B. Diagram showing condition- related connectivities (WNL, weighted number of links) versus the global connectivities (TIS Interactions Total Score). The leader genes and clusters. TRAF6 (TNF receptor-associated factor 6), TRL-4 (Toll-like receptor 4), MAP3K7 (mitogen-activated protein kinase 7), MYD88 (Myeloid differentiation primary response gene 88) and UBE2N (Ubiquitin-Conjugating Enzyme E2 N) genes presented higher WNL and lowered TIS. The results of the Kruskal-Wallis test. Statistical significance was set at a p-value. Statistical significance was set at a p-value <0.05. C. Duodenum TRL4 mRNA expression performed by qRT-PCR analyses. D. Duodenum B0AT1 mRNA expression performed by qRT-PCR analyses. Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as #p<0.05 in comparison to the ST group, and *p< 0.05 in comparison to the HFD group (one-way ANOVA) and Student's t-test.

4. Discussion

The present study reported for the first time that the oral administration of ANG-(1-7) modulated the intestinal villi size and improved glucose and lipid metabolic parameters along with other metabolic homeostasis critical regulators. Furthermore, previous studies have already demonstrated beneficial ANG-(1-7) chronic (long-term treatments) effects on reducing body weight and fat mass (Oliveira Andrade et al., 2014; Santos et al., 2013).

The fasting glucose, total cholesterol, and triglyceride levels reduction and the high HDL levels observed in obese treated animals might be strongly related to the RAS expression markers regulation. Mas receptor deficiency in FVB/N (Mas-KO) mice leads to severe glucose and lipid metabolism changes, inducing a condition similar to the metabolic syndrome, displaying increased fasting glucose levels, glucose intolerance, reduced insulin sensitivity, dyslipidemia, and angiotensinogen increased expression(Santos et al., 2008). On the other hand, a transgenic rat model with increased chronic ANG-(1-7) plasma levels evidenced increased glucose tolerance, improved insulin sensitivity and consequently, increased glucose uptake. Decreased cholesterol and triglyceride levels were also detected, as well as decreased abdominal fat mass associated with unaltered food intake. These alterations were accompanied by reduced angiotensinogen levels in the adipose tissue (Santos et al., 2010).

HFD fed animals presented increased intestinal villi height (Navarrete et al., 2015; Soares, Beraldi, Ferreira, Bazotte, & Buttow, 2015), which suggest associated digestibility adaptations (Santoro et al., 2003) and the HFD consistency (Pluske, Hampson, & Williams, 1997), or increased food retention in the duodenum or proximal jejunum caused by a decrease in intestinal motility (Fu et al., 2014). Petit et al. (Petit et al., 2007) and Wit et al. (de Wit et al., 2008) suggested that such variances are associated with increased cell proliferation, and consequent intestinal mass increase via

Ki-67 (cell nuclear proliferation marker) increased expression in enterocytes and cell cycle regulation via apoptosis. The ANG-(1-7) seems to modulate the mechanisms involved in intestinal villi morphology alterations induced by high-fat diets.

In addition to diet, the intestinal microbiota also contributes to changes in the villi and intestinal

crypts morphology. Sharma et al. (Sharma, Schumacher, Ronaasen, & Coates, 1995) demonstrated that rats transplanted with lean human microbiota displayed reduced villi and intestinal crypts as compared to non-transplanted rats. Other studies showed that germ-free mice presented a reduced total intestinal area (Gordon & Bruckner-Kardoss, 1961) and villi thickness (Reinhardt et al., 2012) due to reduced cell regeneration (Banasaz, Norin, Holma, & Midtvedt, 2002), and extended cell cycles (Alam, Midtvedt, & Uribe, 1994).

The intestinal microbiota comprises approximately 100-500 species, predominating the *Firmicutes* and *Bacteroidetes* phyla, but also presenting other phyla such as *Actinobacteria*, *Proteobacteria*, *Verrumicrobia*, *Fusobacteria* and *Cyanobacteria* (Qin et al., 2010; "Structure, function and diversity of the healthy human microbiome," 2012). The intestinal microbiome exerts a vital role in energetic metabolism, where individuals with obesity and insulin resistance are also accompanied by intestinal dysbiosis (Karlsson, Tremaroli, Nielsen, & Backhed, 2013; Ley et al., 2006). Ley et al. (Ley et al., 2006) described several microbial groups that may contribute to obesity development. Metagenomic studies show that the *Firmicutes* proportion is bigger in obese humans and animals as compared to lean controls (Kien, Schmitz-Brown, Solley, Sun, & Frankel, 2006; Turnbaugh et al., 2006). Studies performed in ob/ob mice demonstrated that this strain has a smaller *Bacteroidetes/Firmicutes* ratio as compared to WT animals (Fleissner et al., 2010; Villanueva-Millan, Perez-Matute, & Oteo, 2015).

Moreover, *Firmicutes*-rich ob/ob mice appear to present glycemic alterations, with increased energy harvesting due to an increased number of enzymes involved in the starch, sucrose and galactose digestion (Arora & Sharma, 2011). A low proportion of *Bacteroidetes/Firmicutes* was associated with increased lipopolysaccharides (LPS) release in the circulation, contributing to the low- grade systemic chronic inflammation observed in obesity (Caricilli et al., 2011). Germ-free animals that received intestinal microbiota from ob/ob mice become obese, confirming the association between microbiota and obesity (Alang & Kelly, 2015; Turnbaugh et al., 2006).Obese individuals submitted to calorie restriction had a significant increase in the *Bacteroidetes* population, suggesting this phyla importance on weight loss and lean phenotype (Karlsson et al., 2013).

In our study, describing for the first time the modulation of the intestinal microbiota via ANG-(1-7), it was observed that ANG- (1-7) attenuated the increase in *Firmicutes* and increased the *Bacteroidetes / Firmicutes* ratio, which may be directly related to the metabolic efficiency improvement. The *Bacteroidetes* and intestinal microbiota diversity expansion are also associated with short-chain fatty acids (SCFAs) that induce Glucagon-like peptide-1 (GLP-1) release by intestinal L cells, improving insulin sensitivity and diabetes (Drucker & Nauck, 2006).

The *Lactobacillus* spp. the population was increased in the ST+ANG-(1-7) fed animals. *Lactobacillus* strains that produce SCFAs, especially the conjugated linoleic acid (Lee et al., 2006),promoted body weight loss and decreased adiposity, improved glucose tolerance modulating the leptin expression and fatty acid synthetase. Other studies suggest that *Lactobacillus* improve the lipid profile via fatty acids oxidation (Kim, Park, Kim, Kim, & Hyun, 2013)or lipoprotein lipase inhibition (Aronsson et al., 2010). *Lactobacillus* strains solidify the junctions between epithelial cells, resulting in reduced epithelial permeability, improving the intestinal barrier integrity and facilitating tissue repair after injury (Cario, Gerken, & Podolsky, 2007).

Increased gram-negative bacteria population was found in the intestine from obese individuals, leading to increased LPS absorption that when accumulated in the circulation causes "metabolic endotoxemia." Endotoxemia in murine models is associated with metabolic alterations similar to those induced by HFD, such as body weight gain, hyperinsulinemia, and hyperglycemia(Cani et al., 2007). It was recently described that HFD alters the intestinal microbiota composition, however, for the obesity development, the presence of metabolic endotoxemia is mandatory (de La Serre et al., 2010).

The ANG-(1-7) decreased the *Enterobacter cloacae* B29 population in HFD fed animals. This bacteria strain was described as an endotoxin producer, inducing obesity and insulin resistance in germ-free mice that received this isolated strain from individuals with obesity degree III. Energy balance alterations in metabolic disease are associated with circulating endotoxins. Although the mechanism by which the ANG-(1-7) promotes the *Enterobactercloacae* B29 decrement in the obese microbiota were still not described, the metabolic endotoxemia reduction might be a therapeutic target

in the metabolic syndrome treatment (de La Serre et al., 2010; Fei & Zhao, 2013).

The intestinal metabolic endotoxemia is characterized by a chronic inflammation state

unleashed by microbial LPS recognition, and bacteria translocation via intestinal receptors (NOD1, CD-14, and TLR-4) (Amar et al., 2011). The bacteria antigen interaction and its receptors activate NF- KB and AP-1, transcription factors responsible for increasing the proinflammatory cytokine transcription. The binding of LPS to TRL-4 is mediated by the CD14 pattern recognition receptor, which also mediates MyD88-dependent TNF α expression, inducing TRIF-mediated IFN expression (Gioannini et al., 2004; Kagan & Medzhitov, 2006). Interestingly, in CD-14 KO animals, HFD or LPS administration did not induce metabolic alterations or metabolic endotoxemia, demonstrating the TRL4 role on body weight regulation and glucose tolerance (Cani et al., 2007).

This association was confirmed by bioinformatics and TLR4 expression analyses, which demonstrated a possible interaction among intestinal microbiota, RASand signaling inflammatory pathways (TRAF6, TRL-4, and Myd88). Santos et al. (Santos et al., 2013)shown that HFD+ANG-(1-7) fed rats presented decreased hepatic inflammation via decreased TRL4 and ACE expression, and increased ACE2 expression.

RAS components such as ACE, AT1 and AT2 receptors, and angiotensinogen were found in the border of rats jejunal and ileum epithelium, where the fluids and electrolytes flux is regulated (Wong, Debnam, & Leung, 2007). The fact that the rat jejunum expresses angiotensinogen, which is a precursor of Ang II and other bioactive angiotensins, indicates that enterocytes are capable of synthesizing Ang II (Wong et al., 2007). Recently, evidence of the RAS and intestinal microbiota association via ACE2 modulation have been published (J. M. O. Andrade et al., 2017; Camargo et al., 2009; Cole-Jeffrey et al., 2015). Increased ACE2 levels were detected in the human gastrointestinal tract, and posteriorly, collectrin,an ACE2 homolog, was identified, suggesting a non-catalytic ACE2 activity (Zhang et al., 2001). ACE2 is essential for B0AT1 intestinal expression, an important tryptophan (Trp) transporter (Camargo et al., 2009). Hashimoto et al. (Hashimoto et al., 2012)

demonstrated that ACE2 deficiency results in increased intestinal inflammatory susceptibility and germ-free mice transplanted with ACE2 KO mice acquired colitis.

Borges et al. (Borges et al., 2017) demonstrated that rats pre-treated with A779 (Mas antagonist), and Mas-KO mice exposed to ANG-(1-7) presented a deficiency in Trp absorption. These

findings suggest that the ANG-(1-7) stimulates the tryptophan absorption via the Mas receptor, and this effect was directly associated with an increased ACE2 expression and activity.

A possible mechanism by which angiotensin-(1-7) modulates the intestinal microbiota. It was already described that ANG-(1-7) administration improves tryptophan transportation in the intestinal mucosa (Borges et al., 2017) via BOAT1 (Hashimoto et al., 2012). In our study, BOAT1 expression was increased in ANG-(1-7) treated animals, suggesting a possible interaction between ANG-(1-7) and BOAT1. Previous studies describe that increased Trp levels were associated with increased antimicrobial peptides production, modulating the intestinal microbiota. Trp transport deficiency leads to aberrant secretion of antimicrobial peptides and consequent proliferation of malefic microbial strains, thus conferring intestinal susceptibility to inflammation (Hashimoto et al., 2012).

We have shown that the oral administration of ANG-(1-7) has altered the glucose and lipid levels and intestinal villi morphology, possibly via intestinal microbiota, promoting the proliferation of beneficial microbial classes and reducing metabolic endotoxemia triggered by *Enterobacter cloacae*, and TLR4 intestinal expression. The results of the present study suggest, for the first time, the interaction between RAS and intestinal microbiota. B0AT1 appears to be one of the mediators, since uptake of Trp may play an important role in intestinal microbiota modulation mediated by ANG- (1-7) (Borges et al., 2017). It is worth mentioning that there are many questions to be addressed in future studies such as: How does ANG-(1-7) interact with B0AT1? Is there a direct correlation between ANG-(1-7) and the synthesis of specific microbial metabolites that alter the host metabolism? In conclusion, the present study describes a significant ANG-(1-7) effect, a major RAS component, on the obese mice intestinal microbiota.

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Author contributions

RA.S.S, S.H.S.S, A.S.M, J.R.O. and D.F.L. contributed to the design of the study, acquisition of the data, and analysis and interpretation of the data. J.M.O.A., D.F.L., S.H.S.S. and I.V.B. contributed

to drafting the article and revising it critically for important intellectual content, and A.M.B.P., A.L.S.G.

and B.M.A.C. contributed to the final approval of the version to be submitted. All authors read and

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Conflict(s) of Interest/Disclosure(s)

The authors declare that they have no competing interest/ disclosure(s).

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Produto 3

Title: Bifidobacterium longum supplementation improves metabolic parameters and alters the expression of the renin-angiotensin system in obese mice.

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Abbreviations: ACE, Angiotensin-converting enzyme; ACE2, Angiotensin-converting enzyme 2; AGT, Angiotensinogen; ANG-(1-7), Angiotensin-(1-7); ANGII, Angiotensin II; AT₁, Type 1 Angiotensin II receptor; AT₂, Type 2 Angiontensin II receptor; *B. longum*, *Bifidobacterium longum*; CNS, Central Nervous System; FAO, Food and Agriculture Organization; GAPDH, Glyceraldehyde 3-phosphate dehydrogenase; GLP-1, Glucagon-like peptide-1; GPR43, short chain fatty acid receptor; GLUT-4, *glucose* transporter type 4; HDL, High-density lipoprotein; HFD, High-fat diet; IKK- β , IkB kinase beta; LPS, Lipopolysaccharides; Mas, Mas Receptor; NF-KB, Factor nuclear kappa B; NKT, Natural Killer Cells; RT-PCR, Real time-PCR; PYY, peptide YY; SCFAs, Short-chain fatty acids; SCFAs, short chain fatty acid; SEM, Standard error; ST, Standard; TNF- α , Tumor Necrosis Factor alfa; TRL4, Toll-like receptor 4; WHO, World Health Organization.

Abstract

The beneficial effects mediated by probiotics are due to their ability to modulate the intestinal microbiota. Recently, the important role of the microbiota in metabolic regulation has been described, and the use of probiotics has become increasingly common. However, the mechanisms involved in the control of obesity by *Bifidobacterium longum* and its effect on the renin-angiotensin system (RAS) have not yet been described. Thus, the objective of the present

study was to evaluate the effect of *Bifidobacterium longum* supplementation on metabolic parameters and RAS expression in obese mice. Methods: Mice were divided into four groups: obese and non-obese/treated and not treated with *Bifidobacterium longum*. Results: After four weeks of treatment, obese mice that received *B. longum* showed a significant decrease in body weight, adiposity, serum glycemia and total cholesterol levels, as well as an improvement in glucose tolerance. In addition, histological analyses demonstrated a reduction in the accumulation of hepatic triglycerides in the obese-treated group. Analyses of mRNA showed a significant increase in the expression of the angiotensin-converting enzyme 2 (ECA2) and the Mas receptor (MASR) in the obese mice that received *B. longum*. Conclusion: Our data suggest for the first time the modulation of RAS by the*B. longum* strain. These findings may contribute tobetter understand the metabolic effect mediated by probiotics. However, the mechanisms that involve the possible role of *B. longum* in the ECA2/Ang- (1-7)/MASS axis of the RAS activation in the liver need to be further investigated.

Introduction

Obesity has become a global health problem and is considered a pandemic (1). According to the World Health Organization (WHO), in 2030, this condition will affect about 20% of the world's adult population (2). The etiology of obesity is multifactorial, being caused mainly by the imbalance between energyconsumption and expenditure (3). Obesity is a chronic disease that contributes heavily to multiple cardio-metabolic diseases, such as type 2 diabetes, dyslipidemia, coronary artery disease, stroke, hypertension, and various types of cancer (4-6).

Recent evidence has shown that the intestinal microbiota plays an important role in metabolic regulation, functioning as an organ with metabolic, immunological, and endocrine function (7), performing essential functions that the human body alone is not able to perform, resulting in a symbiotic relationship. This close link is essential for the absorption of energy from ingested food, motility and integrity of the intestinal barrier, regulation of host metabolism, especially the metabolism of glucose, lipid, and inflammation (8-10).

The intestinal microbiota consists of three main phyla: *Bacteroidetes (Porphyromonas, Prevotella, Bacteroides), Firmicutes (Ruminococos,*

Clostridium,Lactobacillus, and *Eubacteria*), and *Actinobacteria* (*Bifidobacteria*) (11) with the majority of intestinal microbiota being represented by *Bifidobacterium* and *Bacteroides* (12). The World Health Organization (WHO) and the Food and Agriculture Organization of the United Nations (FAO) define probiotics as live microorganisms which, when administered in adequate amounts, confer benefits to the host's health (13). The beneficial effects mediated by probiotics are due to their ability to modulate the intestinal microbiota and the mucosal immune system (14-16). Among the most well-studied probiotics are lactic acid-producing bacterial strains belonging to the *Bifidobacterium* and *Lactobacillus* genera, which have an established safety record and have received

the GRAS status (generally recognized as safe) by the US Food and Drug Administration (17), and are widely used and included in many functional foods and dietary supplements (18-20). Studies have shown that the administration of *Bifidobacterium* spp., including *B. longum*, reduces body weight, improves glucose tolerance and insulin resistance, and protects from diet-induced obesity by maintaining energy homeostasis, as well as reducing serum cholesterol levels and triglycerides (21-23). Another important metabolic regulator is the renin-angiotensin system (RAS), an enzymatic cascade composed of two main axes: the ECA/AngII/AT1R axis, which is over-expressed in obesity conditions and exerts deleterious effects, and the ECA2/Ang-(1-7)/MASRaxis, which counter-regulates the AngII axis by improving metabolic efficiency (24-26).

Considering the aforementioned, we hypothesized that the supplementation of obese animals with probiotic *B. longum* can modulate the ECA2/Ang-(1-7)/MASR axis of the reninangiotensin system by improving the metabolic changes observed in obesity. Thus, the objective of the present study was to evaluate the effect of *Bifidobacterium longum* supplementation on metabolic parameters and the RAS expression in obese mice.

Materials and Methods Animals and Diets

The experiment was conducted with 32 four-week-old male Swiss mice divided into 4 groups (n=8 each) and fed, for 4 weeks, the following experimental diets, respectively: Standard Diet *ad libitum* (ST), Standard Diet *ad libitum* + *Bifidobacterium longum* (ST + *B. Longum*), High-fat diet (HFD), andHigh-fat diet+ *Bifidobacterium longum*(HFD + *B. longum*). The control group was fed an SD (50.30% carbohydrate, 41.90% protein, and 7.80% fat, totaling 2.18 kcal/g) (27, 28). Obesity was induced with an HFD (24.55% carbohydrate, 14.47% protein, and 60.98% fat, totaling 5.28 kcal/g), for eight weeks. The*B. longum*probiotic was administered by gavageat a dose of 50 billion bacteria/kg body wt⁻¹ daily (29). Animals in control groups received a saline solution. All experimental procedures were approved by

the Ethics Committee of the State University of Montes Claros and were conducted by following the regulations described in the Committee Guiding Principles Manual (Protocol number 103/2016).

Measurements of Body Weight, Food Intake, and Tissue Collection

The body weight, food intake, and energy intake were measured three times a week during all experimental procedures. Mice were fasted overnight and killed bydecapitation.Samples of blood, adipose tissues (epididymal, mesenteric, and retroperitoneal) and liver were collected, weighed, immediately frozen in liquid nitrogen, and stored at -80°C for subsequent analyses.

Histology Staining

Epididymal adipose tissue and liver samples were fixed in 10% neutral-buffered formalin at 4°C overnight, dehydrated by escalating grades of alcohol, xylene, and paraffin, and then embedded in paraffin. Sections of 5 µm were prepared for Hematoxylin & Eosin staining. The slides were analyzed in an FSX100 Inverted Microscope (Sao Paulo, Brazil). All samples were analyzed by densitometry, using the Image J software (Wayne Rasband, National Institutes of Health, Bethesda, MD).

Glucose tolerance and insulin sensitivity tests

For the glucose-tolerance test, D-glucose (2 mg/g body weight) was intraperitoneally injected into overnight fasted mice. Glucose levels from tail blood samples were monitored at 0, 15, 30, 60, and 120 minutes after injection. Insulin sensitivity tests were performed with the animals in the fed state, after intraperitoneal injection of insulin (0.75 U/kg body weight), and tail blood samples were taken at the time points 0, 15, 30, and 60 minutes after injection for the measurement of blood glucose levels.

Determination of Blood Measurements

Serum was obtained after centrifugation (3200 rpm for 10 minutes at 4°C). Glucose, total cholesterol, triglycerides, and high-density lipoprotein (HDL) were assessed using enzymatic kits (Wiener®, Argentina). Measurements were performed on a Wiener BT-3000 plus ChemistryAnalyzer (Wiener®, Argentina).

Reverse transcription and qRT-PCR

Total RNA extracted from the liver was prepared using TRIzol reagent (Invitrogen Corp.®, San Diego, California, USA), treated with DNAse and reverse transcribed with M-MLV (Invitrogen Corp.®). The endogenous glyceraldehyde 3-phosphate dehydrogenase (GAPDH), Angiotensin-converting enzyme (ACE), Angiotensin-converting enzyme 2 (ACE2), and Mas receptor (MASR) were assessed using specific primers and SYBR green reagent (AppliedBiosystems®, USA) in a plus-one platform (Applied Biosystems®). Relative comparative CT method was applied to compare gene expression levels between groups, using the $2-\Delta\Delta$ CT equation (30), sequences of primers described in Table 1.

Primer target	Primer name	Primer sequences (5'-3')
ACE	F	CTC CTG GGA CTT CTA CAAC
	R	CTC CAT GTT CAC AGA GGT ACA CT
ACE2	F	GGA TAC CTA CCC TTC CTA CAT CAG C
	R	CAT CCC CAC ATA TCA CCA AGCA
MASR.	F	ACT GCC GGG CGG TCA TCA TC
	R	GGT GGA GAA AAG CAA GGA GA

Table 1 – Specific mouse primers used in this study.

Statistical Analysis

All data were analyzed with GraphPad Prism software (Version 5.0®, San Diego, California, USA), at a 95% confidence (p<0.05). Data are expressed as the mean \pm SEM. The statistical significance between mice groups was assessed by One-Way ANOVA followed by Tukey post-test, and Student t-test. Statistical significance was set at p<0.05.

RESULTS

Food intake, energy intake, body weight, tissue weight, and adiposity

The analyses of food consumption (ST, 0.193 ± 0.010 ; ST+*B.longum*; 0.180 ± 0.009 ; HFD, 0.106 ± 0.007 ; HFD+*B. Longum*, 0.110 ± 0.007) and energy consumption (ST, 0.442 ± 0.014 ; ST+*B.longum*; 0.404 ± 0.011 ; HFD, 0.495 ± 0.032 ; HFD+*B. Longum*, 0.5491 ± 0.032) showed no statistically significant differences between the mice fed the same type of diet (**Fig. 1a and 1b**). In the analysis of area under the body weight curve, a statistically significant reduction was observed in the probiotic treated group (HFD + B.

Longum) when compared to the HFD group (HFD, 5758 ± 189.3 ; HFD + *B. Longum*, 4942 ± 125.4) (Fig. 1c).

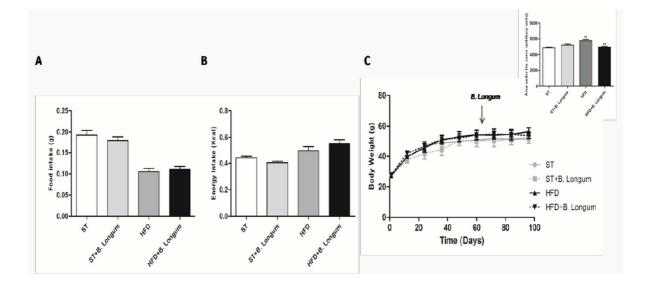


Figure 1. *B. logum* reduces body weight of mice with obesity induced by the hyperlipid diet. Food intake (a), energy intake (b), daily body weight and area under the curve (c). Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as $^{*}p<0.05$ $^{##}p<0.01$ $^{###}p<0.001$ in comparison to the ST group, and $^{*}p<0.05$, $^{**}p<0.01$, $^{***}p<0.001$ in comparison to the HFD group (one-way ANOVA).

The weight of the epididymal adipose tissue ((HFD, 0.029 ± 0.007 ; HFD+*B*. *Longum*, 0.017 ± 0.003), retroperitoneal (HFD, 0.01075 ± 0.001 ; HFD+*B*. *Longum*, 0.005 ± 0.001), mesenteric (HFD, 0.007 ± 0.002 ; HFD+*B*. *Longum*, 0.005 ± 0.001) and adiposity (HFD, 0.047 ± 0.005 ; HFD+*B*. *Longum*, 0.028 ± 0.004) were reduced in obese mice treated with *B*. *longum* (Fig 2a-d).

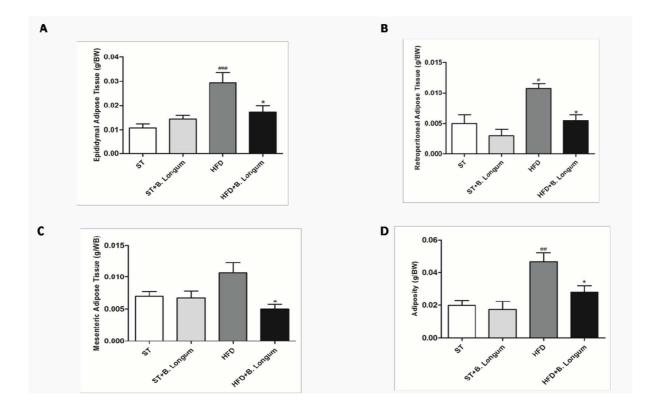


Figure 2. *B. longum* supplementation reduces adiposity of mice with obesity induced by HFD. Epididymal adipose tissue weight (a), retroperitoneal adipose tissue weight (b), mesenteric adipose tissue weight (c), adiposity (d). Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as [#]p< 0.05 ^{##} p< 0.01 ^{###}p<0.001 in comparison to the ST group, and *p<0.05, **p<0.01, ***p<0.001 in comparison to the HFD group (one-way ANOVA).

Tolerance test, insulin sensitivity, and biochemical analyses

The area analysisunder the curve of the glucose tolerance test showed that obese animals treated with *B. longum* presented significantly reduced levels of glucose when compared to their respective control (HFD, 40543 \pm 5215 vs. HFD +*B. Longum*, 26178 \pm 2882) (**Fig. 3a**). However, no differences were found between the groups in the insulin resistance test (4B)(ST, 6428 \pm 183.0 vs. ST+*B. Longum*, 6928 \pm 384.2; HFD, 6885 \pm 195.2 vs. HFD+*B. Longum*, 6635 \pm 351.0) (**Fig. 3b**). In comparison to the HFD group, the mice fed the HFD + *B. Longum*, presented reduced levels of fasting glycemia (HFD, 143.8 mg/dL \pm 12.24 vs. HFD + *B. Longum*, 77.00 mg/dL \pm 13.8) (**Fig. 3c**) and total cholesterol (HFD, 156.7 mg/dL \pm 23.73 vs. HFD + *B. Longum*, 105.7 mg/dL \pm 5.78) (**Fig. 3d**). However, the levels of triglycerides(ST,111.8 mg/dL \pm 6.275 vs. ST+ *B. Longum*, 80.80 mg/dL \pm 6.264; HFD, 134.7

mg/dL \pm 9.528 vs. HFD +*B*. *Longum*, 141,7 mg/dL \pm 27.28) (**Fig. 3e**) and (ST,60.53 mg/dL \pm 3.135 vs. ST+ *B*. *Longum*, 45.67 mg/dL \pm 2.038; HFD, 55.33 mg/dL \pm 5.549 vs. HFD +*B*. *Longum*, 55.63 mg/dL \pm 8.074) (**Fig. 3f**) did not differ statistically in comparison to their respective controls.

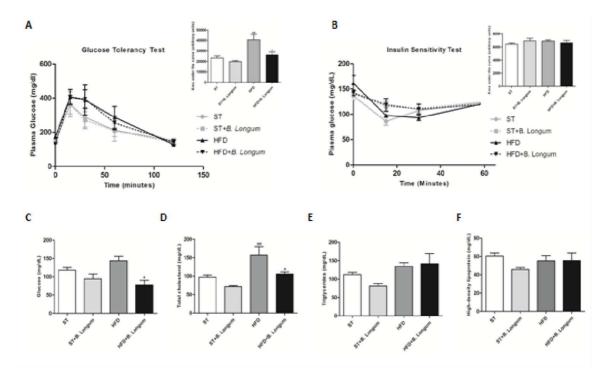
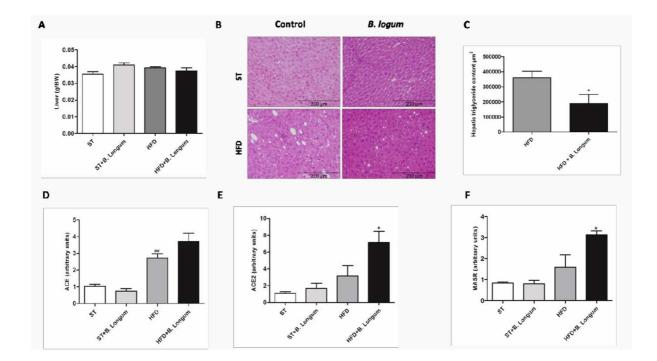


Figure 3. *B. longum* improves glucose tolerance and blood glucose and cholesterol levels in obese mice. Glucose tolerance teste and area under the curve (a), insulin sensitivity teste and area under the curve (b), glucose levels (c), total choresterol (d), triglycerides (e), and Highdensity lipoprotein (f). Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as [#]p< 0.05 ^{##} p< 0.01 ^{###}p<0.001 in comparison to the ST group, and *p<0.05, **p<0.01, ***p<0.001 in comparison to the HFD group (one- way ANOVA).

Liver weight, hematoxylin-eosin staining, and PCR analisys

No statistically significant differences were found regarding the liver weight of the mice (**Fig. 4a**). Hepatic triglyceride decreased in the group of obese animals that received *B. longum* when compared to the obese control (HFD, 359865 \pm 43636; HFD+ *B. longum*, 190024 \pm 60260) (**Fig 4b-c**).

Quantitative real-time PCR (qRT-PCR) analysis showed increased expression of ACE2 (HFD, 3.143 ± 1.244 vs. HFD +*B. Longum*, 7.158 ± 1.315) and MASR (HFD, 1.597 ± 0.584 vs. HFD +*B. Longum*, 3.137 ± 0.186) in the group fed the HFD+*B. Longum* versus control HFD mice. No significant differences in the ACE (HFD, 2.171 ± 0.2619 vs. HFD +*B*.



Longum, 3.708 ± 0.510) expression were observed between groups and their respective controls (**Fig 4d-f**).

Figure 4. *B. longum* reduces the deposition of hepatic fat and modulates the expression of the axis ACE2/Ang-(1-7)/MasR of the rennin-angiotensin system. Liver weigh (a), hepatic Hematoxylin & Eosin (HE) staining (b), ImageJ analysis of hepatic triglycerides content (c), hepatic angiotensin-converting enzyme (ACE) mRNA expression (d), hepatic angiotensin-converting enzyme 2 (ACE2) mRNA expression (e), and Mas receptor (MASR) mRNA expression (f). Data are presented as means \pm SEM. Statistically significant differences between the groups are indicated as [#]p<0.05 ^{###}p<0.001 in comparison to the HFD group (one-way ANOVA). HE ImagJ analysis was performed using Student's t-test).

Discussion

Experimental and clinical studies have shown that supplementation with probiotics exerts different metabolic effects and that these effects are strain-dependent (31, 32). There are several mechanisms by which bacterial strains perform their functions (33-35). Here, we demonstrate for the first time that probiotic supplementation with *Bifidobacterium longum* alters the expression of the RAS and the metabolism of obese mice.

Our results demonstrated an anti-obesity effect of the *B. longum* strain in obese mice. Chen et al. (36) also reported that the administration of *B. longum* improved the metabolic profile of mice fed a hyperlipidic diet, reducing body weight, adipocyte size, leptin levels, and increasing adiponectin levels. Leptin is an adipokine that acts as a global messenger of the central nervous system (CNS), controlling food intake, energy expenditure, satiety, and appetite (37). Obesity and metabolic syndrome are characterized by a resistance to leptin due to the increase in adipokine levels (38). On the other hand, adiponectin regulates insulin sensitivity and exerts antidiabetogenic, anti-atherosclerotic, and anti-inflammatory effects, with an enhancement of metabolic efficiency when their levels are increased (39-41).

Improvement in glucose tolerance and reduction in serum glucose and total cholesterol levels of obese animals that received *B. longum* corroborate with the results of other studies (36, 42-44), and may be directly associated with particularities of the interaction of this microorganism with the intestinal microbiota of the host (17). As described previously, *Bifidobacterium* belongs to the *Bacteroidetes* phylum, and the increase in its abundance is directly related to the lean phenotype and metabolic improvement (8, 45). Microorganisms colonizing the intestinal microbiota have the ability to degrade polysaccharides and dietary fiber, producing short-chain fatty acids (SCFAs). In the intestine, SCFAs bind to the short-chain fatty acid receptor (GPR43) leading to secretion of anorexigenicpeptides, including glucagon-like peptide-1 (GLP-1) and YYpeptide (PYY), resulting in improved glucose tolerance and increased energy use (17).

Obesity is characterized by a low-grade inflammatory state (46-48) that causes increased intestinal permeability, allowing the diffusion of bacterial fragments, such as lipopolysaccharides (LPS), from the intestine to the bloodstream, resulting in metabolic endotoxemia. Individuals fed a high-fat diet have increased plasma levels of LPS (49, 50), which stimulate inflammation through interaction with TRL4 receptors (51, 52), leading to increased weight gain and fat mass, hepatic triglycerides accumulation, insulin resistance, type 2 diabetes, and atherosclerosis (44, 53). These changes were associated with a significant reduction in the population of *Lactobacillus* spp., *Bifidobacterium* spp., and *Bacteroides - Prevotella* spp in the intestine.

In addition, prebiotic fibers were added to the hyperlipid diet of rats and, as a result, an increased abundance of intestinal *Bifidobacteria* was observed, and consequently improved glucose tolerance, increased glucose-induced insulin secretion, normalized low-grade inflammation, and decreased endotoxemia and proinflammatory cytokines (44, 54-57). Studies in humans revealed that a lower *Bifidobacterium* abundance was found in overweight, obese or type 2 diabetic patients, whereas this abundance was higher in lean individuals(58). In addition, *B. longum* correlated negatively with serum levels of LPS, raising the possibility that this microorganism could be involved in the improvement of metabolic endotoxemia in human beings (58, 59).

Recent studies have shown that bacteria producing lactic acid, including *Bifidobacterium longum* (60), have hypocholesterolemic effects in rats and humans. Some possible mechanisms have been suggested such as (61-63): (1) fermentation products of lactic acid bacteria inhibit enzymes involved in the synthesis of cholesterol and thus reduce their production; (2) lactic acid bacteria facilitate the elimination of cholesterol in feces; (3) bacteria inhibit the absorption of cholesterol back into the body by binding to cholesterol; (4) bacteria interfere with the process of recycling bile salt (a metabolic product of cholesterol) and facilitate its elimination, which increases the demand for bile salt produced from cholesterol and therefore results in the consumption of body cholesterol; and (5) the assimilation of lactic acid.

Obese animals that received *B. longum* had a lower deposition of liver fat. Recently, Xu et al. demonstrated that *Bifidobacterium longum* supplementation attenuated the accumulation of hepatic fat in a model of non-alcoholic fatty liver disease (64). In addition, supplementation with VSL#3, a preparation composed of a mixture of four strains of *Lactobacillus (L. casei, L. plantarum, L. acidophilus, and L. delbrueckii subsp. bulgaricus)*, three strains of *Bifidobacterium (B. longum, B. breve,* and *B. infantis)*, and *Streptococcus thermophilus,* improved the fat-induced dietary hepatic steatosis and insulin resistance in mice by modulating hepatic natural killer T cells (NKT cells), suppressing the TNF- α /IKK- β signaling pathway, and reducing hepatic inflammatory signaling (65). It has also been suggested in some studies that *B. longum* can mitigate hepatic injuries caused by endotoxin-induced activation of macrophages (66, 67).

Increased hepatic ECA2 and MasR expression observed in obese animals treated with

B. longum describes for the first time a modulation of the ECA2/Ang- (1-7)/MasR axis by a probiotic strain. In addition, the metabolic improvement observed in treated animals is also associated with RAS, since the increased expression of ACE2 and the Mas receptor is directly related to the increase in Ang- (1-7) (68). The first study showing the metabolic potential of Ang-(1-7)/MasR was performed by Santos et al. (26), who demonstrated a worsening of metabolic efficiency, as wel as dyslipidemia, insulin resistance, and decreased expression of adiponectin and GLUT-4 in transgenic mice with Mas receptor suppression. Later, it was revealed that circulating Ang- (1-7) overexpression improved the metabolic profile by lowering lipids and reducing adipose tissue mass in TGR-L3292 rats (68).

Regarding hepatic homeostasis, an oral administration of Ang-(1-7) may decrease gluconeogenesis in the liver, improving glucose and lipid metabolism (69). In addition, in HFD-fed rats, inflammatory marker levels were decreased by regulation of the

resistin/TLR4/NF-KB pathway (68). Another remarkable finding was that obese mice treated with an oral formulation of Ang-(1-7) showed a significant reduction in levels of TNF- β and IL-6, as well as decreased markers related to adipogenesis, such as acetyl CoA carboxylase (ACC), PPAR-Y, and sterol-1c binding regulatory proteins (SREBP-1c) (70).

In summary, we showed that oral supplementation with *B. longum* improved the metabolic profile of mice with hyperlipidemic diet-induced obesity, decreasing body weight, adiposity, glucose tolerance, serum glucose, and total cholesterol levels. Analysis of hepatic tissue revealed that treated-obese mice had lower triglyceride deposition in the liver. Additionally, increased ECA2/Ang- (1-7)/MASR axis expression was observed in obese-treated animals. The results of the present study suggest, for the first time, the modulation of the RAS by the *B. longum*strain. These findings may contribute to better understand the metabolic effects mediated by probiotics. However, the mechanisms that involve the possible role of *B. longum* in the activation of the ECA2/Ang-(1-7)/MASR axis of the RAS in the liver need to be further investigated.

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Author contributions

RA.S.S, S.H.S.S, A.S.M, J.R.O. and D.F.L. contributed to the design of the study, acquisition of the data, and analysis and interpretation of the data. J.M.O.A., D.F.L., S.H.S.S. and I.V.B. contributed to drafting the article and revising it critically for important intellectual content, and A.M.B.P. and A.L.S.G. contributed to the final approval of the version to be submitted. All authors read and approved the final manuscript.

Conflict(s) of Interest/Disclosure(s)

The authors declare no competing interest/ disclosure(s).

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4 CONCLUSÕES

Conclui-se que a ang-(1-7) é um importante mediador negativo de processos inflamatórios agudos e crônicos, regulando a secreção e ação das adipocinas, e funcionando muitas vezes como uma adipocina, com ação em diferentes órgãos. Além disso, a administração oral de ANG- (1-7) melhora a hiperglicemia, dislipidemia e altera a morfologia das vilosidades intestinais, possivelmente através da modulação da microbiota intestinal, com consequente melhora da disbiose intestinal e da endotoxemia metabólica. Além disso, mostramos que a suplementação oral com o probiotico *B. longum* melhorou o perfil metabólico e diminuiu a deposição de triglicerídeos no fígado de camundongos com obesos. Adicionalmente, foi observado um aumento da expressão do eixo ECA2/Ang-(1-7)/MASR.

Em conjunto, esses achados sugerem para o promissor papel da ang-(1-7) e do probiótico *B longum* no tratamento dos distúrbios metabólicos associados à obesidade por meio da regulação da inflamação e da microbiota intestinal.

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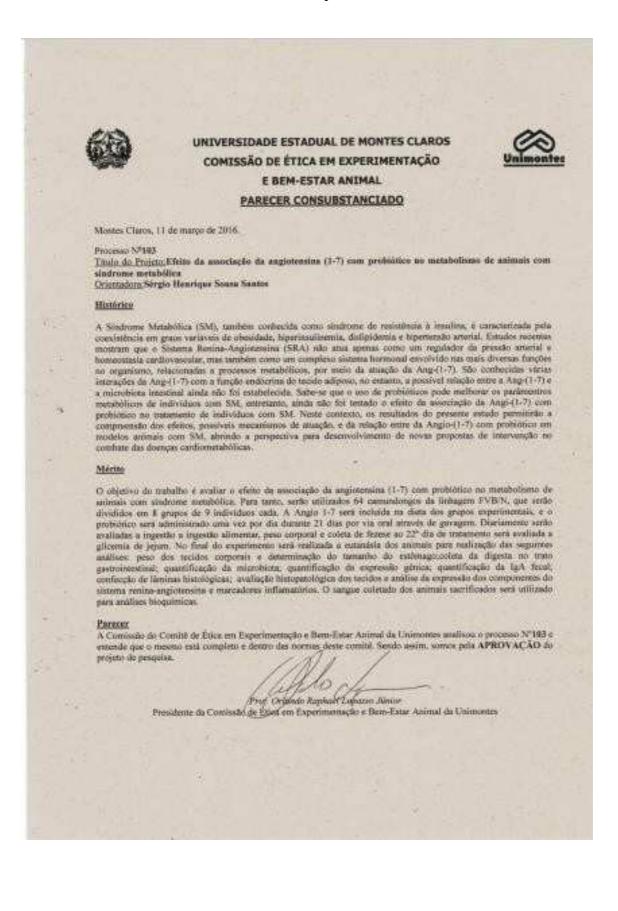
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ANEXOS

ANEXO A – Parecer do Comitê de Ética e Pesquisa



ANEXO B - Normas para publicação no periódico Cellular Microbiology

Author Guidelines

Cellular Microbiology is published monthly and is covered by Wiley Blackwell's *Accepted Articles* and *Early View* services.

Cellular Microbiology publishes outstanding original scientific contributions on the intersection of microbial and host cell biology. The focus is the host cell responses elicited by the interaction of micro-organisms. Equal emphasis is placed on responses to prokaryotic, viral and eukaryotic micro-organisms. In addition to mammalian systems, papers addressing other hosts such as plants and insects are strongly encouraged.

The Journal is a member of the Committee on Publication Ethics (COPE): http://www.publicationethics.org.uk

Editorial Policy

The scope of *Cellular Microbiology* includes the host cell responses and interactions elicited by prokaryotic, viral and eukaryotic microorganisms, including helminths, protozoa and fungi, that illuminate exploitation of host cell components, function and signalling pathways, and may include modulation or alteration of immune responses. Mechanistic insight obtained through robust biochemical, genetic, cellular, and bioimaging technologies are expected to support observational data. In addition to mammalian and plant systems, papers addressing other hosts such as invertebrate systems are encouraged. Because viruses are inherently dependent upon the host cell, virology-based submissions to *Cellular Microbiology* should advance knowledge of the interaction of viruses and host cells. In addition to the principal content of full length and short research papers, issues may include Editorials/Opinions, Microreviews and Technoreviews as regular features.

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Full length or shorter communications of original research will be published (Breaking Reports). Only complete reports will be published; notes or preliminary communications will not be considered.

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Cellular Microbiology now offers the opportunity to publish 'Breaking Reports'. Such submissions will be handled expeditiously through the review process. Breaking Reports are short-format papers that report a single, key message highlighting a ground-breaking advance. These reports should not exceed 5-6 printed pages of the journal (approximately 5,000 words) including a maximum of three display items and no more than 30 references. The report should be divided into sections as described for full articles.

Microreviews

In addition to primary research articles, short Microreviews are published in areas of particular interest and current importance in the field of *Cellular Microbiology*. The content of these reviews should appeal broadly to the readership and highlight both recent advances and areas that require additional research. Reviews should focus on cell biological themes rather than being organism specific and should include a broad range of microbial-host interactions.

Technoreviews

Short reviews dealing with technical advances that provide new approaches for examination of hostpathogen interactions are welcome. Technoreviews should provide an overview of the development and/or application of the methodology including its relative strengths, advantages and potential limitations.

Submission of Manuscripts

All manuscripts should be submitted online at **http://mc.manuscriptcentral.com/cell-micro**. Any articles submitted as hardcopy will be returned to the authors for re-submission. A user ID and password are required and can be obtained on the first use of the site. Any articles submitted as hardcopy will be returned to the authors for re-submission. Full instructions are provided.

Full help and support are provided by e-mail (support@scholarone.com), the web (http://mc.manuscriptcentral.com/cell-micro). If you cannot submit online please contact the Central Editorial Office:

Cellular Microbiology Central Editorial Office, Wiley-Blackwell 9600 Garsington Road Oxford OX4 2DQ UK Fax: +44 1865 714591 E-mail: cell-micro-editorial-office@wiley.com

Manuscripts will be directed by subject category to the appropriate Editor.

• Manuscripts addressing mechanisms of pathogenesis and bacterial-cellular interactions will be directed to either Sergio Grinstein, Feng Shao, or Thierry Soldati.

- Manuscripts concerning parasitology will be directed to Artur Scherf.
- Mycology manuscripts will be handled by Neil Gow.
- Virology manuscripts will be directed to Jacomine Krijnse Locker.
- Microreviews and Technoreviews will be directed to Elizabeth Hartland.

In the event of a potential conflict of interest with a particular editor, authors may request another editor to handle their manuscript.

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Every effort will be made to ensure rapid publication. Authors will normally receive reviewers' comments within four weeks of submission. To ensure the best service to authors and reviewers, manuscripts may be immediately returned to authors without scientific review following editorial assessment if it is deemed not suitable for *Cellular Microbiology* or if extensive revisions are required.

To maintain current scientific reviews, revisions of manuscripts should be resubmitted within 3 months of the editor's decision. Additional time for resubmission required to conduct specific experimental protocols may be requested in advance.

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