**TITLE PAGE**

**Title**: The Use of Antimicrobials as Adjuvant Therapy for the Treatment of Obesity and Insulin Resistance: Effects and Associated Mechanisms.

**Short Title:** Antimicrobials as Therapy for Metabolic Diseases.

**Authors:** Sandra Aparecida dos Reis [a]; Maria do Carmo Gouveia Peluzio [b]; Josefina Bressan [c*].

**Affiliations:**

[a] Department of Nutrition and Health, Universidade Federal de Viçosa, Viçosa, Minas Gerais, zip code: 36570-900, Brazil. E-mail address: sandra.reis@ufv.br

[b] Department of Nutrition and Health, Universidade Federal de Viçosa, Viçosa, Minas Gerais, 36570-900, Brazil. E-mail address: mcpeluzio@ufv.br

[c] Department of Nutrition and Health, Universidade Federal de Viçosa, Viçosa, Minas Gerais, 36570-900, Brazil. E-mail address: jbrm@ufv.br

***Corresponding author:** Department of Nutrition and Health, Universidade Federal de Viçosa, Viçosa-MG, zip code: 36570-900, Brazil. Phone: (31) 3899-1275. Fax: + 55 3899-2899. E-mail address: jbrm@ufv.br



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**ABSTRACT**

The intestinal microbiota has come to be considered an additional risk factor for the development of metabolic diseases. Considering the potential role of antimicrobials as modulators of the intestinal microbiota, they have been investigated for use in the adjuvant treatment of obesity and insulin resistance. In this regard, the present manuscript aimed to review the effect of regular use of antimicrobials on the treatment of obesity and/or IR, as well as its associated mechanisms. The regular use of antimicrobials does not seem to influence the body weight and adiposity of its consumer. Regarding IR, clinical trials did not observe positive effects, on the other hand, most of the experimental studies observed an increase in insulin sensitivity. The mechanisms used by antimicrobials that could lead to the improvement of insulin sensitivity are dependent on the modulation of the intestinal microbiota. This modulation would lead to a reduction in the stimulation of the immune system, as a consequence of improved intestinal barrier and/or the reduction of gram-negative bacteria in the microbiota. In addition, the secretion of GLP-1 would be modulated by metabolites produced by the intestinal microbiota, such as secondary bile acids and short chain fatty acids. Based on the results obtained to date, more studies should be performed to elucidate the effect of these drugs on obesity and IR, as well as the mechanisms involved. In addition, the cost-benefit of the regular use of antimicrobials should be investigated, as this practice may lead to the development of antimicrobial-resistant microorganisms.

**Keywords:** antibiotics, metabolic disease, intestinal microbiota, immune system, GLP-1.

## 1. Introduction

Microbiota is a term that originally refers to all commensal, symbiotic and pathogenic microorganisms that inhabit on the body surfaces of organisms.[1] In this sense, the term intestinal microbiota refers to all bacteria, fungi, yeasts, archea, viruses and protozoa that inhabit the intestine.[2]

In healthy adults, the intestinal microbiota can comprise more than 100 trillion microorganisms, hosting 500 to 1000 different species, which are predominantly anaerobic bacteria.[2, 3] This enormous microbial diversity is essential to human health because they produce a variety of compounds and perform metabolic activities, all of which are indispensable for the maintenance of homeostasis. As a result, the intestinal microbiota can be considered an additional organ in our body.[2]

In this way, when there is an imbalance in the composition of the intestinal microbiota, dysbiosis occurs. Dysbiosis strongly influences host susceptibility to chronic diseases, particularly those related to chronic low-grade inflammation, such as obesity and insulin resistance (IR). [1]

In 2004, Bäckhed et al. [4] proved for the first time that the intestinal microbiota is capable of increasing the risk of developing obesity and IR. In their experiment, they observed that although the food intake of conventional mice was lower (29% lower) than germ-free C57BL/6J mice, the latter's body fat mass was 42% lower. Furthermore, the conventionalization of the germ-free mice with the intestinal microbiota harvested from the conventional mice, led to a 57% increase in body fat mass and IR in a span of 2 weeks, despite a 7% reduction in food intake. Ever since, attempts have been made to identify microorganisms related to the increased risk of developing obesity and IR, as well as the mechanisms used by them. [5-9]

Considering the high global prevalence of obesity associated with IR, its high morbidity and mortality rates and the economic impact of its treatment,[10] there are a growing number of studies that focus on new adjuvant therapeutic strategies for the treatment of obesity and IR through the modulation of the intestinal microbiota. In this regard, the role of antimicrobials has been investigated due to their potential to change the composition of the intestinal microbiota in a short or long term.[11]

Thus, the aim of this manuscript was to review the effect of regular use of antimicrobials on the adjuvant treatment of obesity and/or IR, as well as its associated mechanisms. For this purpose, a search was performed in the PubMed/Medline database

using the following descriptors: antibiotics OR antimicrobials, AND obesity OR overweight OR weight gain OR weight loss OR diabetes OR insulin resistance OR insulin sensitivity OR glucose intolerance, AND intestinal microbiota. A filter was used to select studies carried out during the last 10 years (February 2007 to February 2017). Clinical trials and experimental studies with obese individuals and/or IR individuals, of both sexes, and fully published in English were included. Studies with pregnant women, infants, children, and newborns were excluded. Similarly, studies with individuals who suffer from inflammatory bowel disease, diarrhea, or any type of infectious disease were excluded.

## 2. Antimicrobials

Antimicrobials are artificial substances synthesized in the laboratory, whose main function is to inhibit the growth of specific microorganisms. Antibiotics perform the same function as antimicrobials but they are produced from specific fungi or bacteria species. Due to the high demand for these drugs, antimicrobials are commonly used because they are easily produced on a large scale.[12]

Antimicrobials are being investigated for their possible use in the treatment of chronic non-infectious diseases, such as obesity and IR because of their potential modulatory effect on the composition of the intestinal microbiota. It is expected that the regular use of antimicrobials exert an "eubiotic effect". Consequently, bacteria related to the increased risk of developing obesity and IR would be eliminated and those related to the reduced risk of these diseases could proliferate and recolonize the intestinal environment.[13]

Over the last years, studies have attempted to identify a specific microorganism or group (core) of those that would be responsible for the development of obesity and/or IR.[14] Some studies have suggested that a greater abundance of bacteria of the phylum Firmicutes (gram-positive) and a lower of Bacteroidetes (gram-negatives) could be related to the increased risk of developing these diseases.[5-9] However, other studies have suggested otherwise.[15-17] Based on these findings, it is difficult to select an appropriate antimicrobial for the treatment of obesity and/or IR, since this drug acts more efficiently on bacteria of the gram-positive or gram-negative group. Thus, an antimicrobial should be selected according to a single bacteria group to be eliminated, and it is likely that within the gram-positive and gram-negative groups there are bacteria involved in the increase and decrease of the risk for the development of obesity and IR, which makes it difficult to obtain the “eubiotic effect”.

### *2.1. Treatment of Obesity and Insulin Resistance with Antimicrobials*

Regarding the effect of antimicrobial treatment on body weight and/or adiposity, most studies did not find changes in these parameters at the end of the treatment and/or in comparison to the placebo/control groups (Table 1 and 2). In order to reduce body weight and/or adiposity, an energy deficit must occur, however this does not seem to happen during the antimicrobial treatment, since some of the parameters that can influence energy metabolism were not modified, such as the quantity of energy harvested from the diet,[18, 19] substrate utilization,[20, 21] gastric emptying,[19, 20] appetite[20] and food consumption[18, 20, 22-26].

Concerning IR, studies suggest that antimicrobial treatment affects insulin sensitivity regardless of obesity (Tables 1 and 2). The intestinal microbiota has a modulatory potential on the immune system and incretins, while those play roles in insulin sensitivity. On this manner, studies that investigated the effect of antimicrobial treatment on IR have mainly evaluated whether the microbial modulation provided by this drug influences the activity of the immune system and the intestinal secretion of incretins.[27]

The activation of the immune system by the intestinal microbiota can occur through the interaction of lipopolysaccharide (LPS), present in the cell wall of gram-negative bacteria, with the CD14/TLR-4 complex, located on the surface of the immune cells. This interaction can trigger a chronic low-grade inflammatory process, which can impair host metabolism, contributing to the development of IR. For the host to absorb LPS, it is necessary that its intestinal barrier be altered, a process which may occur depending on the composition of the intestinal microbiota.[28] Thus, to prevent the absorption of LPS, the antimicrobial can reduce the population of gram-negative bacteria in the intestinal microbiota or maintain/improve the intestinal barrier of its host (Figure 1).

In this way, it has been observed that the antimicrobial treatment can reduce the serum concentration of LPS,[11, 18, 23, 29-31] as well as pro-inflammatory cytokines.[11, 18, 23, 25, 29, 30, 32]. This result may be a consequence of the reduction in intestinal permeability caused by the treatment.[21, 30, 31] Regarding the gram-negative bacteria, it is observed that when an antimicrobial with spectrum of action against these bacteria is used its populations is reduced, however when an antimicrobial with spectrum of action against gram-positive bacteria is used the population of gram-negative increases, especially those belonging to the phylum Proteobacteria (Table 3). However, the treatment with an antimicrobial with spectrum of action against gram-positive bacteria is also capable of improving the intestinal permeability

of its consumers.[24] Thus, these antimicrobials can be used in the adjuvant treatment of IR as long as they do not increase intestinal permeability.

The incretin, glucagon-like peptide-1 (GLP-1), can regulate carbohydrate metabolism through the stimulation of insulin production by the pancreas in the postprandial state. GLP-1 is produced by the enteroendocrine L cells, mainly located in the ileum and colon.[33] It has been suggested that the intestinal microbiota is capable of regulating the production of this incretin, through the activity of some metabolites it produces[20], such as the secondary bile salts and short chain fatty acids (SCFA) (Figure 1). In this way, it is possible that changes in the composition of the microbiota caused by antimicrobial treatment could interfere in the production of GLP-1, and consequently IR.

Secondary bile salts are produced by some specific microorganisms found in the intestinal microbiota through the deconjugation, oxidation and dehydroxylation of primary bile salts. These secondary bile salts could bind to G-protein receptors, specifically TGR5, present in the L cell membrane, stimulating the production of GLP-1.[34, 35] In this regard, Reijnders et al.[21] and Vrieze et al.[22] observed that the treatment with vancomycin (1500 mg/day for 7 days) reduced fecal excretion of secondary bile salts and increased primary bile salts; while amoxicillin (1500 mg/day for 7 days) did not alter bile salt homeostasis in comparison to placebo. As a consequence of these effects, no differences were observed in fasting and postprandial serum GLP-1 concentrations, as well as IR-related parameters.

Considering that vancomycin acts mainly against gram-positive bacteria, which are the primarily responsible for initiating the production of secondary bile salts,[36] it is then probable that the changes in the intestinal microbiota composition associated with vancomycin treatment would have compromise the production of secondary bile salts (Table 3). Corroborating with this hypothesis, treatment with amoxicillin was unable to influence bile salt homeostasis, since the composition of the intestinal microbiota of the treated individuals remained similar to the placebo group (Table 3).

The modulation of the intestinal microbiota with the aim to increase the production of secondary bile acids should be carried with caution, since high concentrations of these bile acids may increase the risk of developing colorectal cancer because they increase local production of free radicals; stimulate the synthesis of prostaglandin E2; activate the β-catenin/Wnt signaling pathway and alter the intestinal barrier. Furthermore, secondary bile acids can prevent the repair of damaged DNA and favors the resistance of cancer cells to apoptosis. [37, 38]

Another metabolite capable of influencing the production of GLP-1 is butyric acid. This SCFA could interact with the G-protein receptors, stimulating the expression of the transcription factor cdx-2, which would act on the proglucagon gene promoter region increasing the expression of GLP-1.[39] The primary bacteria that produce butyric acid belong to the Firmicutes phylum, mainly the Clostridia IV and XIVa groups, being the main producing species *Faecalibacterium prausnitzii*, *Coprococcus eutactus* and *Eubacterium rectale*.[40]

Regarding the effect of antimicrobial treatment on the production of butyric acid, Reijnders et al.[21] observed that treatment with vancomycin (1500 mg/day for 7 days) reduced the fecal concentration of total SCFA and butyric acid. This result could be a consequence of the decrease in the bacteria population that produces butyric acid in the intestinal microbiota as a consequence of the vancomycin treatment (Table 3). Further, the authors observed that treatment with amoxicillin (1500 mg/day, for 7 days) did not alter the fecal concentration of this SCFA as well as the composition of the intestinal microbiota of the treated individuals compared with placebo.

The production of SCFA depends on the composition of the microbiota and the availability of substrate, mainly indigestible carbohydrates.[40] Obese and/or IR individuals tend to consume low amounts of fiber, thus, even if there is an increase in the population of SCFA-producing bacteria as a consequence of the antimicrobial treatment, it does not necessarily guarantee an increase in the production of SCFA.

To date, it has not been possible to determine a specific antimicrobial for the adjuvant treatment of obesity and/or IR that would provide positive results. It is likely that the findings so far were influenced by the different experimental designs (type, dose and duration of treatments), the population investigated and the animal models used. Furthermore, the pharmacokinetics, pharmacodynamics, path of administration and spectrum of action may influence the modulatory effect of an antimicrobial. Moreover, inherent consumer characteristics such as age, composition of the initial intestinal microbiota and lifestyle would also influence the modulatory effect of antimicrobials.[13]

Obesity is a complex disease, which requires a multiprofessional intervention for its treatment. Since antimicrobial treatment only acts on one casual factor, an investigation into the outcome of the treatment when associated with dietary re-education and the practice of regular physical activity is of great interest. In some cases the antimicrobial treatment was capable of restoring the metabolic flexibility of the liver, muscle and adipose tissue,[11, 23, 26, 29,

[41] which could contribute to weight loss if the treatment period is extended, however prolonged antimicrobial treatment is not recommended.

In general, studies suggest that, partially, of the effect of antimicrobial treatment on IR could be attributed to reduced interaction of LPS with the immune system. With regard to the production of GLP-1, the influence of antimicrobials appears to be limited. However, it is worth mentioning that the increase in GLP-1 production does not necessarily imply an improvement in IR, since some alterations in the insulin receptor could compromise the adequate binding of the insulin produced as a consequence of GLP-1 stimulation.

Thus, more studies are necessary for the mechanisms used by the antimicrobials that would lead to this improvement in obesity and IR can be better understood and afterwards amplified so that better results can be obtained.

**3. Main Limitations of the Studies**

Most of the experimental studies included in this review administered the antimicrobial by diluting a given amount of the drug in the drinking water of the animal model (Table 1). Although three of these studies[11, 18, 24] quantified the amount of water consumed by the animals, it is difficult to define the actual amount of antimicrobial consumed. Such information is essential for conducting further studies as well as justifying results. Thus, an alternative solution to this limitation would be the administration of the antimicrobial via gavage, ensuring that the pre-established dose is consumed.

The clinical trials, included in this review, did not evaluate the composition of the diets consumed by the participants. Diet exerts a great modulatory effect on the composition of the intestinal microbiota[3] and influences the modulatory potential of antimicrobials,[30] being therefore essential to verify if there were changes in diet during the treatment period, mainly in the consumption of macronutrients and fibers.

Another limitation concerns the use of absorbable antimicrobials such as norfloxacin, amoxicillin and ampicillin, which have limited effect on TGI levels, but could interfere with insulin sensitivity through its systemic activity.[11] Thus, it is suggested that studies aiming to investigate the effect of antimicrobials on obesity and IR through the modulation of the intestinal microbiota, should use only antimicrobials that act locally on TGI (non-absorbable).

## 4. Future Perspectives

The indiscriminate use of antimicrobials can lead to the development of antimicrobial- resistant microorganisms, which is a cause of great concern because of the risk of spreading infectious diseases.[42] Therefore, the choice of the type of antimicrobial as well as dose and duration of treatment should take into account the possibility of antimicrobial resistance, especially in clinical trials. Moreover, it should be investigated whether antimicrobial treatment provides better results than the regular consumption of probiotic, prebiotic or symbiotic foods. Since these foods can modulate the composition of the intestinal microbiota without contributing to the development of antimicrobial-resistant microorganisms.[43]

The modulatory effect of antimicrobials on the composition of the intestinal microbiota should be investigated in the long term, since their regular use may increase the proliferation of microorganisms that contribute to the development of other diseases.[13] Some studies observed that treatment with antimicrobials resulted in the increase of the Enterobacteriaceae family (Table 3), which comprises some species related to the increased risk of developing colorectal cancer.[44, 45]

As discussed earlier, the metabolites produced by the microbiota exert considerable influence on host metabolism.[27] In this sense, future studies on microbial treatment should make an effort not to only identify changes in the composition of microorganisms but also the metabolites produced by them.

In the future, it is necessary to investigate the minimum age at which antimicrobial treatment of chronic non-infectious diseases can be realized, since it has been suggested that the intake of antimicrobials during infancy may contribute to the development of obesity.[46] Another aspect to be investigated is the duration of the effectiveness of antimicrobial treatment after its discontinuation. It is possible that if there are no lifestyle changes, the composition of the intestinal microbiota could return to its initial state, accompanied with metabolic changes that lead to the development of obesity and IR.[20]

## 5. Conclusions

Regarding obesity, the effects of antimicrobial treatment appear to be limited. For IR, so far, positive results have been reported only in experimental studies, whereas in clinical trials no changes were observed. Regarding the mechanisms used, it was proposed

that antimicrobial treatment would interfere in the activation of the immune system by LPS and modulate the production of incretins, however the results are still inconclusive.

In this light, further studies are needed in order to better understand the effect of antimicrobial on obesity and IR. In addition, the risks associated with the regular use of this drug should be investigated, as well as comparing its effect with other potential modulators of the composition of the intestinal microbiota.

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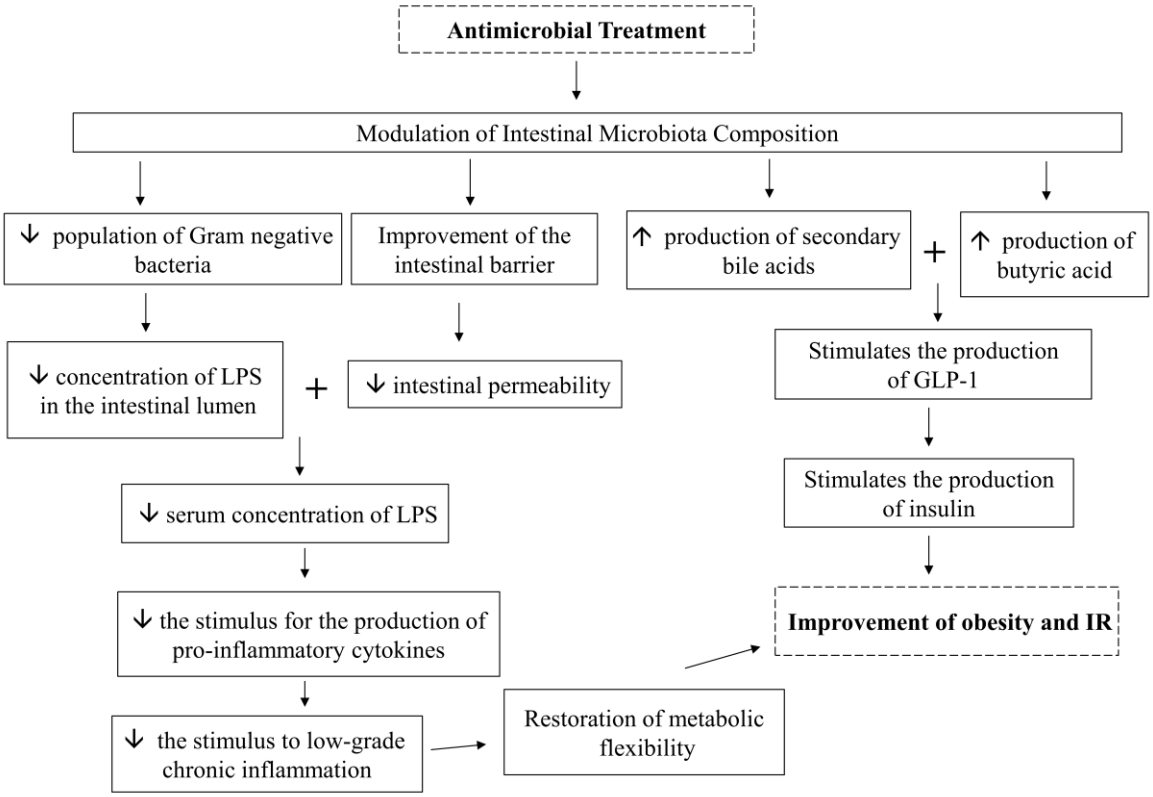


**Figure 1 -** The potential mechanisms used by antimicrobials to improve obesity and IR. The effects produced by antimicrobial treatment would be a consequence of the modulation of the composition of the intestinal microbiota. This modulation may lead to a reduction in the population of gram-negative bacteria, which contain LPS in their cell walls. Additionally, such modulation would improve the intestinal barrier, and consequently reduce intestinal permeability. All of these would culminate in reducing the stimulation of the immune system by LPS, decreasing the stimulus for low-grade chronic inflammation, that characterizes these diseases, and helping restore metabolic flexibility. Another mechanism is related to the increase in GLP-1 production, which would be a consequence of the activity of the metabolites produced by the microbiota, such as secondary bile acids and SCFA. The increase in the serum concentration of GLP-1 stimulates the pancreatic production of insulin.

**Table 1** – Main results of the experimental studies that evaluated the effect of antimicrobial treatment on obesity and IR.

| **Reference** | **Animal Model** | **Experimental Diet** | **Intervention (antimicrobial, dose and duration)** | **Main Results (intervention *vs* control group)** |
|---|---|---|---|---|
| Di Luccia et al. [18] | Male Sprague-Dawley rats with 14 weeks old | Diet rich in fructose (20.4%) | Ampicillin (1 g /L) and neomycin (0.5 g/L)<br>In the drinking water<br>8 weeks | Did not alter body weight<br>↑ insulin sensitivity and glucose tolerance |
| Hwang et al. [24] | C57BL/6J male mice with 8 weeks old | High-fat diet with 60% fat | Vancomycin (0.5 g/L) and bacitracin (1 g/L)<br>In the drinking water<br>4 weeks | Did not alter body weight and body fat mass<br>↓ insulinemia<br>↑ insulin sensitivity and glucose tolerance |
| Rajpal et al. [41] | C57BL/6 male mice with 14 weeks old | High-fat diet with 45% fat | Ceftazidime (50, 150 or 500 mg / kg) or vancomycin (50, 150 or 500 mg / kg) mixed in the diet<br>2 weeks | *Ceftadizime*: ↓ body weight and body fat mass (150 or 500 mg/kg); glycemia and insulinemia (500 mg/kg).<br>*Vancomycin*: ↓ body weight (150 mg/kg). |
| Rajpal et al. [41] | Mice Zucker (ZDF-Lepr$^{fa}$/Crl) males with 7 weeks old | Standard diet with 17% fat | Ceftazidime (500 mg / kg)<br>Via gavage<br>2 weeks | ↓ HbA1c, fasting glycemia and insulinemia<br>↑ body weight |

| Reference | Animal Model | Experimental Diet | Intervention (antimicrobial, dose and duration) | Main Results (intervention *vs* control group) |
|---|---|---|---|---|
| Del Fiol et al. [47] | Male Wistar rats | Standard diet | Amoxicillin<br>150 mg/kg<br>Via gavage<br>2 weeks | Did not alter body weight and body composition |
| Ghosh et al. [31] | Male LDLR-/- mice with 10 weeks old | Diet with 21% fat and 0.15% of cholesterol | Neomycin (100 mg/day)<br>polymyxin B (10 mg/day)<br>In the drinking water<br>16 weeks | Did not alter body weight and fasting glycemia<br>↑ glucose tolerance |
| Jena et al. [26] | Male Wistar rats with 8 to 10 weeks old | Diet with 65% of fructose | Cefdinir<br>Via gavage<br>4 weeks | ↓ body weight and fat mass, and glycemia<br>↑ glucose tolerance |
| Rune et al. [32] | Male C57BL/6NTac mice with 0 days old | High-fat diet with 60% fat | Ampicillin (1 g/L)<br>In the drinking water<br>5 weeks | Did not alter body weight and insulinemia<br>↓ HbA1c<br>↑ glucose tolerance |
| Bech-Nielsen et al. [48] | C57BL/6 female mice with 3 weeks old | Standard diet with 12.6% fat | Ampicillin (1 g/L) or erythromycin (1 g/L)<br>In the drinking water<br>5 weeks | Did not alter body weight<br>↓ fasting glycemia<br>↑ glucose tolerance |

| Reference | Animal Model | Experimental Diet | Intervention (antimicrobial, dose and duration) | Main Results (intervention *vs* control group) |
|---|---|---|---|---|
| Carvalho et al.[29] | Male Swiss rats with 6 weeks old | High-fat diet with 55% fat | Ampicillin (1 g/L), neomycin (1 g/L) and metronidazole (1 g/L) In the drinking water 8 weeks | Did not alter the size of adipocytes<br>↓ body weight<br>↑ glucose tolerance and insulin sensitivity |
| Murphy et al.[25] | C57BL/6J male mice with 7 weeks of age | High-fat diet with 45% fat | Vancomycin (2mg/day) Via gavage 8 weeks | Did not alter insulinemia<br>↓ body weight |
| Cani et al.[30] | Male C57BL/6J mice with 12 weeks old | High-fat diet with 72% fat | Ampicillin (1 g/L) and neomycin (0.5 g/L) In the drinking water 4 weeks | ↓ body weight, adipocyte size, insulinemia and fasting glycemia<br>↑ glucose tolerance |
| Cani et al.[30] | Male *ob/ob* mice with 6 weeks old | Standard diet | Ampicillin (1 g/L) and neomycin (0.5 g/L) In the drinking water 4 weeks | ↓body weight, adipocyte size, insulinemia and fasting glycemia |
| Chou et al.[23] | Male *ob/ob* mice | Standard diet | Norfloxacin (1 g/L) and ampicillin (1 g/L) In the drinking water 2 weeks | Did not alter body weight<br>↓ fasting glycemia and insulinemia<br>↑ glucose tolerance and insulin sensitivity |

| Reference | Animal Model | Experimental Diet | Intervention (antimicrobial, dose and duration) | Main Results (intervention *vs* control group) |
|---|---|---|---|---|
| Chou et al. [23] | Male C57BL/6J mice | Standard diet | Polymyxin B (0.5 g/L) and neomycin (1 g/L)<br>In the drinking water<br>2 weeks | Did not alter body weight and fasting glycemia |
| Membrez et al. [11] | Male *ob/ob* mice with 8 to 10 weeks old | Standard diet | Norfloxacin (1 g/L) and ampicillin (1 g/L)<br>In the drinking water<br>17 days | Did not alter body weight<br>↓ fasting glycemia and insulinemia<br>↑ glucose tolerance |
| Membrez et al. [11] | Male C57BL/6J mice 6 to 7 weeks old | High-fat diet with 60% fat | Norfloxacin (1 g/L) and ampicillin (1 g/L)<br>In the drinking water<br>17 days | Did not alter body weight<br>↓ fasting glycemia and glucose tolerance |

Abbreviations and symbols: HbA1c: glycated hemoglobin; ↑: increased,↓: decreased.

**Table 2 -** Main results of the clinical trials that evaluated the effect of antimicrobial treatment on obesity and IR.

| **Reference** | **Study Participants** | **Study Design** | **Intervention (antimicrobial, dose and duration)** | **Main Results (intervention *vs* placebo group)** |
|---|---|---|---|---|
| Mathur et al. [19] | 11 adult subjects, obese, pre-diabetic and with methane-positive breath | Transversal | Rifaximin (1650 mg/day) and neomycin (1000 mg/day)<br>10 days | Did not alter body weight<br>↓ fasting glucose and insulinemia |
| Reijnders et al. [21] | 57 adult Caucasian men, overweight or obese, glucose intolerant and insulin resistant | Randomized, double-blind, placebo-controlled | Amoxicillin or vancomycin 1500 mg/day<br>7 days | Did not alter body weight, size and number of adipocytes, fasting glycemia, insulinemia, HOMA index, and the sensitivity of adipose tissue and liver to insulin. |
| Mikkelsen et al. [20] | 12 adult male, Caucasian, healthy and eutrophic | Prospective with reassessment 180 days after the intervention | Vancomycin (500 mg/day), gentamicin (40 mg/day) and meropenem (500 mg/day)<br>4 days | Did not alter body weight, fasting glycemia, insulinemia, HOMA index, and serum concentrations of C peptide and HbA1c. |
| Vrieze et al. [22] | 20 Caucasian men with metabolic syndrome | Randomized, single blind, placebo controlled | Amoxicillin or vancomycin 1500 mg/day<br>7 days | Did not alter body weight, insulinemia and fasting glucose. |

Abbreviations and symbols: HbA1c: glycated hemoglobin; HOMA: homeostatic model assessment, ↓: decreced.

**Table 3** - Effect of the antimicrobial treatment on intestinal microbiota composition.

| **Reference** | **Sample** | **Method** | **Antimicrobial** | **Main results (antimicrobial *vs* placebo)** | |
|---|---|---|---|---|---|
| Mathur et al. [19] | Feces | q-PCR | Rifaximin and neomycin | - | ↓ *Methanobrevibacter smithii* species |
| Reijnders et al. [21] | Feces | Microarray (*Human Intestinal Tract Chip analysis*) | Vancomycin | ↑ Phylum Proteobacteria, members of the cluster of *Clostridium* IX, genus *Enterococcus* and species *Lactobacillus plantarum* | ↓ Phylum Firmitutes, members of the cluster of *Clostridium* IV and XIV as the species *Coprococcus eutactus, Faecalibacterium prausnitzii*, *Anaerostipes caccae* and *Clostridium leptum* |
| Di Luccia et al. [18] | Cecal content | Pyrosequencing | Ampicillin and neomycin | ↑ Phyla Proteobacteria and Bacteroidetes, and the class Bacteroidia | ↓ Class Bacilli, and genera *Coprococcus* and *Ruminococcus.* |
| Hwang et al. [24] | Cecal content | Pyrosequencing | Vancomycin and bacitracin | ↑ Phylum Proteobacteria and the specie *Escherichia coli* | ↓ Phylum Firmicutes, mainly the family Lachnospiraceae; and the phylum Bacteroidetes, mainly the family Porphyromonadaceae |
| Mikkelsen et al. [20] | Feces | Plating in specific media | Vancomycin, gentamicin and meropenem | - | ↓ Total anaerobes, coliforms, and the genera *Enterococci and Bifidobacterium* |
| Rajpal et al. [41] | Feces | Sequencing of metagenomic DNA | Vancomycin | ↑ Phylum Proteobacteria | - |
| Rajpal et al. [41] | Feces | Sequencing of metagenomic DNA | Ceftazidime | ↑ Phylum Firmicutes, mainly the genus *Lactobacillus* | ↓ Phylum Bacteroidetes and the class Clostridia |

| Reference | Sample | Method | Antimicrobial | Main results (antimicrobial *vs* placebo) | |
|---|---|---|---|---|---|
| Vrieze et al. [22] | Feces | Microarray (*Human Intestinal Tract Chip phylogenetic*). | Vancomycin | ↑ Phylum Proteobacteria, mainly the genera *Haemophilus* and *Serratia*, and the species *Escherichia coli* and *Lactobacillus plantarum* | ↓ Phylum Firmicutes, mainly the clusters of *Clostridium* IV and XIVa, and the species *Faecalibacterium prausznitzii* and *Eubacterium hallii* |
| Jena et al. [26] | Cecal content | Plating in specific media | Cefdinir | - | ↓ Family Enterobacteriaceae |
| Carvalho et al. [29] | Feces | Metagenomic analyzes (BLASTX) | Ampicillin, neomycin and metronidazole | ↑ Phylum Proteobacteria | ↓ Phyla Bacteroidetes, Verrucomicrobia and Firmicutes |
| Murphy et al. [25] | Feses | Pyrosequencing | Vancomycin | ↑ Phylum Proteobacteria; families Enterobacteriaceae, Streptococcaceae, Desulfovibrionaceae and Alcaligenaceae; genera *Lactococcus*, *Sutterella* and *Desulfovibrio* | ↓ Phylum Firmicutes and Bacteroidetes; families Clostridiacea, Bacteroidaceae, Porphyromonadaceae and Deferribacteres; and the genera *Bacteroides*, *Clostridium* and *Odoribacter* |
| Cani et al. [30] | Cecal content of the *ob*/*ob* mice | DGGE | Ampicillin and neomycin | - | ↓ Genera *Lactobacillus*, *Bifidobacterium*, *Bacteroides* and *Prevotella* |
| Cani et al. [30] | Cecal content of the mice feed with the high-fat diet | DGGE | Ampicillin and neomycin | ↑ Genera *Lactobacillus*, *Bacteroides* and *Prevotella* | ↓ Genera *Bifidobacterium* |

| Reference | Sample | Method | Antimicrobial | Main results (antimicrobial *vs* placebo) | |
|---|---|---|---|---|---|
| Chou et al. [23] | Feces | Plating in specific media | Norfloxacin | - | ↓ Family Enterobacteriaceae. |
| Chou et al. [23] | Feces | Plating in specific media | Ampicillin | - | ↓ Genus *Bacteroides*. |
| Membrez et al. [11] | Cecal content | Plating in specific media | Norfloxacin | - | ↓ Family Enterobacteriaceae. |
| Membrez et al. [11] | Cecal content | Plating in specific media | Ampicillin | - | ↓ Genus *Bacteroides*. |

Abbreviations and symbols: DGGE: gel electrophoresis with denaturing gradient, q-PCR: quantitative polymerase chain reaction, ↑: increased, ↓: decreased.