Changes in Gut Microbiota Control Metabolic Endotoxemia-Induced Inflammation in High-Fat Diet–Induced Obesity and Diabetes in Mice

Patrice D. Cani,1,2 Rodrigo Bibiloni,3 Claude Knauf,2 Aurélie Waget,2 Audrey M. Neyrinck,1 Nathalie M. Delzenne1, and Rémy Burcelin2

OBJECTIVE—Diabetes and obesity are characterized by a low-grade inflammation whose molecular origin is unknown. We previously determined, first, that metabolic endotoxemia controls the inflammatory tone, body weight gain, and diabetes, and second, that high-fat feeding modulates gut microbiota and the plasma concentration of lipopolysaccharide (LPS), i.e., metabolic endotoxemia. Therefore, it remained to demonstrate whether changes in gut microbiota control the occurrence of metabolic diseases.

RESEARCH DESIGN AND METHODS—We changed gut microbiota by means of antibiotic treatment to demonstrate, first, that changes in gut microbiota could be responsible for the control of metabolic endotoxemia, the low-grade inflammation, obesity, and type 2 diabetes and, second, to provide some mechanisms responsible for such effect.

RESULTS—We found that changes of gut microbiota induced by an antibiotic treatment reduced metabolic endotoxemia and the cecal content of LPS in both high-fat–fed and ob/ob mice. This effect was correlated with reduced glucose intolerance, body weight gain, fat mass development, lower inflammation, oxidative stress, and macrophage infiltration marker mRNA expression in visceral adipose tissue. Importantly, high-fat feeding strongly increased intestinal permeability and reduced the expression of genes coding for proteins of the tight junctions. Furthermore, the absence of CD14 in ob/ob CD14−/− mutant mice mimicked the metabolic and inflammatory effects of antibiotics.

CONCLUSIONS—This new finding demonstrates that changes in gut microbiota controls metabolic endotoxemia, inflammation, and associated disorders by a mechanism that could increase intestinal permeability. It would thus be useful to develop strategies for changing gut microbiota to control, intestinal permeability, metabolic endotoxemia, and associated disorders.

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Environmental factors, such as a fat-enriched diet and a sedentary lifestyle, are the causes of the great prevalence of obesity and type 2 diabetes in the population (1). Diabetes and obesity are characterized by a low-grade inflammation whose molecular origin is unknown (2,3). However, we have recently reported that moderate increase of plasma concentration of the inflammatory reagent, the bacterial lipopolysaccharide (LPS), increased during a fat-enriched diet, and defined metabolic endotoxemia (4). We demonstrated that LPS was responsible for the onset of metabolic diseases (4), because a continuous subcutaneous low-rate infusion of LPS induced most, if not all, of the features of metabolic diseases. Most importantly, the corresponding LPS receptor CD14 knockout mouse resisted the occurrence of the diseases. LPS is a major component of the outer membrane in Gram-negative bacteria. Although the reasons for its increase in plasma during high-fat feeding were undetermined, its levels were closely correlated but not causatively demonstrated, with changes in intestinal microbiota where the Gram negative–to–Gram positive ratio increased during high-fat feeding (4). Furthermore, dietary fibers, which reduce the impact of high-fat diet on the occurrence of the metabolic diseases (5), normalized the Gram negative–to–Gram positive ratio and plasma endotoxemia (6). These data strongly suggested that intestinal microbiota could be responsible for changes of metabolic endotoxemia and for the onset of the corresponding diseases, although the causative link between intestinal bacteria, endotoxemia, and metabolic disease was not shown. Gut microbiota has recently been proposed as an environmental factor involved in the control of body weight and energy homeostasis (7–12). Germ-free mice of the same age and genetic background as conventional mice fed with a normal low-fat diet had a 40% lower body weight (11), whereas germ-free mice colonized with the gut microbiota derived from the conventional mice increased their fat mass and developed insulin resistance within 2 weeks. In addition, germ-free mice restricted high-fat diet–induced body weight gain and fat mass development and had lower glycemia and insulinemia (9). Strikingly, these data did not provide any result with regard to the impact of the microbiota on endotoxemia and inflammation. Altogether, this evidence suggests that changes in intestinal microbial composition could be responsible for increased endotoxemia in response to a high-fat diet, which in turn would trigger the development of obesity and diabetes. Therefore, we aimed at changing the intestinal microbiota by means of an antibiotic treatment to reduce the elevated concentration of plasma LPS.
in high-fat diet–fed mice and in ob/ob mice. We further studied some mechanisms through which intestinal microbiota changes metabolic endotoxemia and the corresponding metabolic consequences.

RESEARCH DESIGN AND METHODS

Twelve-week-old male C57Bl/6J mice (Charles River, Lyon, France) and 6-week-old ob/ob (n = 13) mice (C57Bl6 background; The Jackson Laboratories, Bar Harbor, ME) were housed in a controlled environment (inverted 12-h daylight cycle, lights-off at 10:00 a.m.) with free access to food and water. The mice were fed a control (n = 13) (A01, Villemeizon sur Orge, France) or a high-fat, carbohydrate-free diet (high fat, n = 17) for 4 weeks. The role of the microflora was investigated by treating control (control antibiotic, n = 13), high-fat–fed (high-fat antibiotic, n = 17), or ob/ob (ob/ob antibiotic, n = 8) mice with antibiotics (1.0 g/l ampicillin [Sigma, St. Louis, MO] and 0.5 g/l neomycin [Sigma] in drinking water) during the experimental period. Ampicillin and neomycin are broad-spectrum antibiotics that are poorly absorbed (or unabsorbed as in the case of neomycin) and thus without any systemic effects (13). The high-fat diet contained 72% fat (corn oil and lard), 28% protein, and <1% carbohydrate, as energy content (5). To generate the ob/ob CD14−/− mice, CD14−/− mice (C57Bl6 background) were intercrossed with ob+/−, and F1 double heterozygotes were then used to generate the ob/ob CD14−/− and ob/ob genotypes. All of the following animal experimental procedures were validated by the local ethics committee, by the Rangueil Hospital animal ethics committee, and by the Université catholique de Louvain.

RNA extraction from cecal contents. Bacterial RNAs were extracted from cecal contents using BioRobot-EZ1 (Qiagen, Hilden, Germany), according to the manufacturer’s instructions. In a nutshell, cecal contents were homogenized in a bead beater for 2 min in a sterile microcentrifuge tube containing 0.3 g glass beads and 750 μl QIAzol lysis reagent. After the addition of 150 μl chloroform/isooamylalcohol (24:1), the samples were vortexed for 15 s and left to stand for 2–3 min at room temperature. Finally, the samples were centrifuged at 12,000 g for 15 min at 4°C, and 300 μl supernatant was loaded into the BioRobot equipment.

Denaturing gradient gel electrophoresis profiles of cecal bacteria. Bacterial RNA was amplified by RT-PCR targeting the V3 region of the 16S rRNA gene and using the universal bacterial primers HDA1-GC and HDA2 and a previously described program (14) (HDA1-GC, 5'-CGCGCCGGGCGGCCGTGCGGGGGGGGCTCATTACGGGAGGACAGCAT; HDA2, 5'-GTATACCGCGGCGGGCCTCATTACGGGAGGACAGCAT; and Qiagen, Hilden, Germany), according to the manufacturer’s instructions. Primers and probes used to detect Bifidobacterium spp. and Lactobacillus spp. were based on 16S rRNA gene sequences. The PCR amplification reactions were carried out as follows: 2 min at 94°C, 25 cycles of 30 s at 94°C, 30 s at 52°C, and 30 s at 72°C followed by 7 min at 72°C.

The mean relative proportion of each intestinal bacterial species was determined using an ABI Prism 7000 Sequence Detection System instrument and software (version 4.0.1, Applied Maths) at a sensitivity of 1–2%.

Fecal analyses. The content of the cecum was vacuum dried. The remainder of the nondigestible carbohydrates, proteins, and lipids were quantified as described previously (15,16). The total LPS content was extracted and measured as described previously (17,18).

Quantitative RT-PCR quantification of microbial cecal content. The cecal contents collected postmortem from mice were stored at −80°C. The QiAamp DNA Stool Minikit (Qiagen) was used to prepare DNA from stool samples according to the manufacturer’s instructions. The primers and probes used to detect Bifidobacterium spp. and Lactobacillus spp. were based on 16S rRNA gene sequences. PCR amplification reactions were carried out as follows: 2 min at 94°C, 15 cycles of 30 s at 94°C and 1 min at 60°C. Detection was carried out on an ABI Prism 7000 sequence detection system (Applied Biosystems, Foster City, CA). Each assay was performed in duplicate in the same run. The cycle threshold of each sample was then compared with a standard curve made by diluting genomic DNA (10-fold serial dilution) from cultures. Cell counts before DNA extraction were determined with the Neubauer hemocytometer. To determine the sensitivity and specificity of the assays, the PCR assays were confirmed using a set of intestinal bacterial species as controls. Group-specific primers based on 16 S rDNA sequences were used to amplify Bifidobacterium (CGCTCCCGGTGTCGGG; reverse Bifidobacterium, CCCCCACATCCAGCATCCA; BHQ-1-lacto, ATGGAGCAACGCCGC; forward F4/80, GCCAGTGAGGAAAGATAGTGT; forward RPL19, AATGGGCCGGCGGACTGGTG; forward occludin, ATGTCCGGCGAGATGCTCT; and reverse occludin, TTTGGCTGCTCTTGGGTGTAT) for intestinal bacteria.

Real-time quantitative PCR. Total RNAs from each individual adipose tissue were prepared using the TriPure reagent (Roche, Basel, Switzerland) as described previously (5). cDNA was synthesized using a reverse transcription kit (Promega, Madison, WI) from 1 μg total RNA. PCRs were performed using the ABI Prism 7000 Sequence Detection System instrument and software (Applied Biosystems) as described previously (5). Primer sequences for the targeted mouse genes are the following: forward tumor necrosis factor-α (TNF-α), TGGACAGTGATCCTGGAATCGT; reverse TNF-α, TTCGGAAGACCATTTAGGT; forward interleukin (IL)-1, TCCTGCAAGGTCAACAGAAG; reverse IL-1, CATCAGAGGGCAGAGGGAGAAC; forward plasminogen activator inhibitor 1 (PAI-1), AACGCTTGTTCTCATGCACGC; reverse PAI-1, CGGCCAGCAACGAGGAGAAAGA; forward ribosomal protein L10 (RPL10), CACGGCGAGGAGTCTGTTCA; reverse RPL10, GCTTGT; forward monocyte chemoattractant protein (MCP)-1, GCAGTTAACCCCCATCTCA; reverse MCP-1, CCCGCACTACTGGATGATCA; forward F4/80, TGAAAACGACGGCTGTG; reverse F4/80, GCCAGGGGAGAAGGATAGTGT; forward NADPH, GGGTGGGGGTGGACATTTC; reverse NADPH, TGACACAGGATGATGATGATG; forward trans-membrane protein of prostate 2 (STAMP2), GCATUTGCTTCTGCAGTCTG; reverse STAMP2, ATGGCACGATGGGAGGGTT; forward monocyte chemotactic protein (MCP)-1, AGTCCGGCCGATGCTCT; and reverse MCP-1, ATGGCACGATGGGAGGGTT.

Biochemical analyses. Plasma LPS concentration was determined using a kit (LAL kit endpoint-QCL1000; Cambrex, Teterboro, NJ) as described previously (11). Plasma IL-1β, TNF-α, IL-6, MCP-1, F4/80, and RPL19 rRNA levels as housekeeping gene, and the data were analyzed according to the 2−ΔΔCT method.

Adipose tissue morphometry and staining. The mean relative proportion and mean surface area of the adipocytes was estimated by a point-counting technique on paraffin-embedded tissue as described previously (4).

Intestinal permeability in vivo. This measure is based on the intestinal permeability to 4,000 Da fluorescent-dextran (Sigma-Aldrich, St. Louis, MO) as described previously (14). Briefly, 6-h–fasted mice were injected with fluorescent-dextran isothiocyanate (FITC)-dextran by gavage (600 mg/kg body wt, 125 mg/ml). After 1 h, 120 μl blood was collected from the tip of the tail vein. The blood was centrifuged at 4°C, 12,000 g for 3 min. Plasma was diluted in an equal volume of PBS (pH 7.4) and analyzed for FITC-dextran concentration with a fluorescence spectrophotometer (HTS-7000 Plus-plate-reader; Perkin Elmer, Wellesley, MA) at the excitation wavelength of 485 nm and the emission wavelength of 535 nm. Standard curves for calculating the FITC-dextran concentration in the samples were obtained by diluting FITC-dextran in nontreated plasma diluted with PBS (1:2 [vol/vol]).
RESULTS

Antibiotic treatment–associated changes in gut microbiota and endotoxemia during high-fat feeding.

We previously showed that high-fat feeding changed gut microbiota and increased plasma LPS levels, as defined by metabolic endotoxemia (4). This was confirmed as assessed by the DGGE analysis (Fig. 1A). Therefore, to establish a cause and effect relationship according to which changes in gut microbiota initiated metabolic endotoxemia, we used large-spectrum antibiotics to

FIG. 1. Antibiotic treatment–associated changes in gut microbiota, intestinal permeability, and endotoxemia during high-fat feeding. A: DGGE profiles generated from the cecal microbiota in mice fed normal diet (CT), normal diet and antibiotics (CT-Ab), high-fat diet (HF), or high-fat diet and antibiotics (HF-Ab) for 4 weeks. Each number and profile corresponds to a different animal. Bar = Dice’s similarity coefficient. B: Plasma endotoxin (LPS) concentration (EU/ml). Data are means ± SE. Data with different superscript letters are significantly different (P < 0.05), according to the post hoc ANOVA statistical analysis. C: Intestinal permeability assay: Plasma DX-4000-FITC (µg/ml). n.d., not detectable concentration. D and F: Epithelial tight junction proteins markers (ZO-1 and occludin mRNA concentrations). E and G: Correlations between intestinal permeability markers: plasma DX-4000-FITC and epithelial tight junction ZO-1 and occludin mRNA concentrations (P < 0.05). Inset corresponds to Pearson’s r correlation and corresponding P value. Data are means ± SE. Data with different superscript letters are significantly different (P < 0.05) according to the post hoc ANOVA statistical analysis.
modify the intestinal microbial community in mice and assessed the main features of high-fat diet–induced metabolic disorders. A 4-week antibiotic treatment strongly changed gut microbiota mRNA and bacterial content profile in both control and high-fat–treated mice (Fig. 1A; Table 1). DGGE profiles clearly showed that cecal bacterial composition and/or metabolic activity were strongly affected after a 4-week antibiotic treatment regardless of the diet (Fig. 1A). Similarity analysis of DGGE profiles of cecal bacterial communities showed that the profiles of chow-fed animals and those of chow-fed animals treated with antibiotics were only 44% similar. This difference was even more dramatic between the high-fat–fed and high-fat–fed, antibiotic-treated mice (high-fat antibiotic), where the profiles were only 22% similar. After antibiotic treatment, each individual animal showed identical bacterial profiles (Dice’s coefficient 100%). Moreover, we showed that of DGGE profiles of cecal bacterial communities showed that the profiles of chow-fed animals and those of chow-fed animals treated with antibiotics were only 44% similar. This difference was even more dramatic between the high-fat–fed and high-fat–fed, antibiotic-treated mice (high-fat antibiotic), where the profiles were only 22% similar. After antibiotic treatment, each individual animal showed identical bacterial profiles (Dice’s coefficient 100%). Moreover, we showed that

**TABLE 1**

<table>
<thead>
<tr>
<th>Bacterial quantification</th>
<th>Lactobacillus spp. (cells/g cecal content)</th>
<th>Bifidobacterium spp. (cells/g cecal content)</th>
<th>Bacteroides-Prevotella spp. (cells/g cecal content)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td>$6.6 \times 10^8 \pm 3.4 \times 10^8a$</td>
<td>$4.8 \times 10^6 \pm 1.1 \times 10^6a$</td>
<td>$4.7 \times 10^8 \pm 5.8 \times 10^8a$</td>
</tr>
<tr>
<td>High fat</td>
<td>$3.0 \times 10^7 \pm 5.7 \times 10^7b$</td>
<td>$5.9 \times 10^5 \pm 2.2 \times 10^5a$</td>
<td>$1.2 \times 10^9 \pm 6.4 \times 10^9b$</td>
</tr>
<tr>
<td>Control antibiotic</td>
<td>$2.1 \times 10^8 \pm 3.8 \times 10^8c$</td>
<td>$1.0 \times 10^4 \pm 4.9 \times 10^4b$</td>
<td>$5.1 \times 10^7 \pm 4.4 \times 10^7c$</td>
</tr>
<tr>
<td>High-fat antibiotic</td>
<td>$3.9 \times 10^8 \pm 5.3 \times 10^8c$</td>
<td>$4.5 \times 10^4 \pm 2.3 \times 10^4b$</td>
<td>$2.1 \times 10^6 \pm 1.9 \times 10^6a$</td>
</tr>
<tr>
<td>ob/ob control</td>
<td>$3.8 \times 10^9 \pm 1.2 \times 10^9a$</td>
<td>$8.5 \times 10^6 \pm 3.8 \times 10^6a$</td>
<td>$1.5 \times 10^8 \pm 7.6 \times 10^6b$</td>
</tr>
<tr>
<td>ob/ob antibiotic</td>
<td>$1.8 \times 10^8 \pm 5.7 \times 10^8b$</td>
<td>$1.4 \times 10^6 \pm 4.1 \times 10^6b$</td>
<td>Nondetectable</td>
</tr>
</tbody>
</table>

Data are means ± SE. Data with different letters are significantly different ($P < 0.05$) according to the post hoc ANOVA or Student’s $t$ test statistical analysis.

FIG. 2. Antibiotic treatment reduced the occurrence of visceral adipose tissue inflammation, oxidative stress, and macrophage infiltration markers in high-fat diet–fed mice. Inflammation: PAI-1, IL-1, and TNF-α mRNA concentrations (A, D, and G); oxidative stress: STAMP-2 and NADPHox mRNA concentrations (B and E); macrophage infiltration markers: MCP-1 and F4/80 mRNA concentrations (C and F), visceral adipose tissue oxidative stress levels (lipid peroxides concentrations) (H) in mice fed normal diet (CT), normal diet and antibiotics (CT-Ab), high-fat diet (HF), or high-fat diet and antibiotics (HF-Ab) for 4 weeks. Data are means ± SE. Data with different superscript letters are significantly different ($P < 0.05$) according to the post hoc ANOVA statistical analysis.
high-fat diet dramatically changed the gut microbiota content. This was characterized by a strong reduction of some Gram-positive and -negative bacteria (Lactobacillus spp., Bifidobacterium spp., and Bacteroides-Prevotella spp.) (Table 1). The reduced cecal microbiota content of high-fat antibiotic–treated mice only was associated with reduced metabolic endotoxemia to be similar to that of the control mice (Fig. 1B). Similarly, the cecal endotoxin content per gram of cecal content was significantly decreased after antibiotic treatment (cecal endotoxin content: control, 2.00 ± 0.04 log μg/g; control antibiotic, 1.30 ± 0.26 log μg/g; high fat, 0.93 ± 0.07 log μg/g; high-fat antibiotic, 0.02 ± 0.2 log μg/g). Moreover, we found that high-fat diet–induced metabolic endotoxemia depended on a mechanism involved in the control of gut permeability. We demonstrated that high-fat feeding dramatically increased intestinal permeability (Fig. 1C) by a mechanism associated with a reduced expression of epithelial tight junction proteins such as ZO-1 and Occludin (Fig. 1D–G), although only a tendency was observed for occludin. This effect was completely restored by the antibiotic treatment. These data suggest that gut bacteria are involved in the control intestinal permeability and furthermore in the occurrence of metabolic endotoxemia.

**Antibiotic treatment reduced the occurrence of adipose tissue inflammation, oxidative stress, and macrophage infiltration markers in high-fat diet–fed mice.** To causally link changes of gut microbiota to high-fat diet–induced markers of metabolic disorders, we quantified the mRNA concentrations of PAI-1, IL-1, and TNF-α in visceral (mesenteric) adipose tissue. All mRNA concentrations were increased in high-fat diet–fed mice when compared with control-fed mice. This increase was totally blunted in the high-fat diet–fed, antibiotic-treated mice (Fig. 2A, D, and G). Inflammation and metabolic disorders are frequently associated with oxidative stress in adipose depots (20–22). We found that high-fat feeding increased STAMP2 (21) and NADPHox mRNA concentrations and lipid peroxidation, which were totally normalized by the antibiotic treatment (Fig. 2B, E, and H). Similarly, the mRNA concentrations of chemokine MCP-1 and a marker specific of mature macrophages, F4/80, were increased in high-fat mice and totally normalized by the antibiotic treatment (Fig. 2C and F). The microflora therefore appears to be a key link between high-fat feeding, plasma LPS, and visceral adipose tissue inflammation. As reported for the visceral adipose depots, the mRNA concentrations of PAI-1, IL-1, TNF-α, and F4/80 were increased in the subcutaneous adipose depots of high-fat diet–fed mice as well (Fig. 3A, D, G, and F), whereas this increase was totally blunted in the high-fat diet–fed, antibiotic-treated mice. However, no significant change was observed for STAMP2, NADPHox, and MCP-1 mRNA (Fig. 3B, C, and E). Metabolic endotoxemia positively correlated with inflammation, oxidative stress, and macrophage infiltr-
treatment markers. To identify whether the changes of gut microbiota and metabolic endotoxemia controlled visceral adipose tissue inflammation, oxidative stress, and macrophage infiltration, we performed multiple correlation analyses between these parameters. Metabolic endotoxemia positively and significantly correlated with one another (Fig. 4A–D). Furthermore, these multiple correlations support a strong relationship between gut microbiota, endotoxemia, inflammation, and oxidative stress during high-fat diet feeding.

Antibiotic treatment prevented high-fat diet–induced adipocyte hypertrophy. We previously reported that a high-fat diet increased the adipocyte cell size (4), and here, we confirmed these data (Fig. 5A, B, and D). Furthermore, we also assumed that it could be due to a LPS-dependent mechanism (4). Therefore, we wondered whether reduced metabolic endotoxemia, induced by the antibiotic treatment, was associated with changes in adipocyte cell size. The mean adipocyte size was reduced in high-fat antibiotic–treated mice when compared with high-fat untreated mice (Fig. 5A, B, and D). These changes were accompanied with a lower cell density when compared with all of the groups (Fig. 5C).

**Antibiotic treatment improved metabolic parameters of diabetes and obesity in high-fat diet–fed mice.** High-fat feeding induced glucose intolerance because the blood glucose concentrations were all higher than those of the control mice during the glucose challenge (Fig. 6A). High-fat mice treated with antibiotics exhibited improved glucose tolerance when compared with untreated mice (Fig. 6A). However, the blood glucose profiles and the calculated area under curve were still significantly different from the control-fed mice. Furthermore, glucose-induced insulin secretion, insulin resistance index, body weight gain, total energy intake, and visceral and subcutaneous adipose weight were significantly higher in high-fat diet–fed mice when compared with all of the other
groups (Fig. 6B–H). All of the parameters were corrected by the antibiotic treatment, except for the energy intake after high-fat diet feeding, which was worsened during antibiotic treatment (Fig. 6F). This increased energy intake could be related to an impaired energy harvesting. Fecal energy content per gram cecum content was similar between groups. It was \(3.16^{\text{a}} \pm 0.5\), \(3.28^{\text{b}} \pm 0.04\), \(3.11^{\text{a}} \pm 0.05\), and \(3.23^{\text{b}} \pm 0.08\) kcal/g, in control, control antibiotic, high fat, and high-fat antibiotic, respectively. However, the total cecal energy content was decreased after high-fat feeding (control \(0.45^{\text{a}} \pm 0.02\) vs. high fat \(0.19^{\text{c}} \pm 0.01\) g) and significantly increased after antibiotic treatment (control antibiotic \(1.36^{\text{a}} \pm 0.08\) and high-fat antibiotic \(0.82^{\text{a}} \pm 0.03\) g). Consequently, the total cecal energy content was increased fourfold in high-fat antibiotic \(2.85^{\text{d}} \pm 0.05\) kcal) when compared with high-fat mice \((0.68^{\text{d}} \pm 0.08\) kcal). A similar trend was observed in control \((1.42^{\text{d}} \pm 0.38\) kcal) versus control antibiotic \(4.63^{\text{b}} \pm 0.31\) kcal). The total cecal lipid content was sixfold increased in high-fat antibiotic \((34.38^{\text{d}} \pm 5.52\) mg) when compared with high-fat mice \((5.54^{\text{d}} \pm 0.44\) mg). This increase was more moderate in control \((8.81^{\text{a}} \pm 0.11\) mg) versus control antibiotic \((18.36^{\text{b}} \pm 1.84\) mg).

**Antibiotic treatment of ob/ob mice reduced endotoxemia.** To assess the contribution of gut microbiota to the development of metabolic endotoxemia and inflammation regardless of the high-fat feeding, we turned to ob/ob mice. These animals are characterized by higher inflammatory tone and plasma LPS concentration, whereas they are consuming a normal chow (23). Almost no bacterial RNAs were detected in any of the cecal contents of ob/ob mice. Antibiotic treatment, thus suggesting that similar to high-fat mice, the antibiotic treatment had a dramatic effect on the ob/ob intestinal microbial population. This could be due to the increased food intake and therefore antibiotic intake as well. Bacterial quantification confirms the DGGE profile and shows significant decrease in *Lactobacillus* spp., *Bifidobacterium* spp., and *Bacteroides-Prevotella* spp. (Table 1). Furthermore, our data showed that the treatment of ob/ob mice reduced metabolic endotoxemia (Fig. 7A and B). However, endotoxemia still remained higher than control values.

**Antibiotic treatment of ob/ob mice lowered the mRNA concentration of adipose tissue inflammatory markers and metabolic parameters of diabetes and obesity.** The mRNA concentrations of PAI-1 and F4/80 were significantly reduced in the visceral adipose depots and to a lower extent in the subcutaneous adipose depots of ob/ob antibiotic-treated mice (Fig. 7H, I, L, and M). Similarly, visceral adipose depot lipid peroxides, markers of oxidative stress, were twofold lower in antibiotic-treated mice (Fig. 7N). Moreover, glucose intolerance (Fig. 7C), insulin resistance index (Fig. 7F), glucose-induced insulin secretion (Fig. 7E), and visceral and subcutaneous adipose tissue weights (Fig. 7J and K) were reduced by the antibiotic treatment. However, no significant change of body weight was detected (Fig. 7G).

**The lack of the LPS receptor CD14 partially reverted inflammatory markers and metabolic parameters in ob/ob mice.** We and others previously demonstrated that the lack of LPS receptor protects against the high-fat diet–induced adipose tissue inflammation and metabolic disorders (4,24–28). To demonstrate that the LPS receptor might be involved in the inflammatory phenotype of ob/ob mice, we generated ob/ob CD14–/– mice. We showed here that in ob/ob CD14–/– mice, PAI-1 and F4/80 mRNA concentrations were reduced in the visceral adipose depots (Fig. 7H and L). This was accompanied by a reduction of oxidative stress markers (Fig. 7N). All of these parameters remained unchanged in the subcutaneous adipose depot when compared with ob/ob mice showing that CD14-mediated inflammation targeted visceral fat. Furthermore, blood glucose profiles, insulin resistance index, glucose-induced insulin secretion, visceral and subcutane-
ous adipose tissue weights, and lipid peroxidation were reduced in ob/ob CD14<sup>-/-</sup> mice compared with ob/ob mice (Fig. 7).

DISCUSSION

We reported here that gut bacteria are involved in high-fat diet and ob/ob-induced metabolic endotoxemia, adipose tissue inflammation, and metabolic disorders. This effect could be mediated by a mechanism that could increase gut permeability and enhance LPS absorption. Antibiotic treatment significantly lowers plasma LPS levels, gut permeability, and the occurrence of visceral adipose tissue inflammation, oxidative stress, macrophage infiltration, and metabolic disorders. We therefore conclude that gut microbiota could control intestinal permeability, which determines the threshold at which metabolic endotoxemia-induced metabolic disorders occur.

We and others have recently demonstrated that the mechanisms of high-fat diet–induced inflammation and metabolic disorders were clearly linked to LPS (4,24–28). We here confirm these data and further demonstrate that this mechanism was linked to endotoxemia. We identified here that metabolic endotoxemia was due to changes in intestinal microbiota, because the antibiotic treatment, which dramatically reduced the local intestinal microbiota, restored normal plasma LPS values in high-fat diet–fed mice. High plasma LPS levels could result from an increased production of endotoxin by a change in gut
microbiota (4,6). Evidently, the intestinal epithelium acts as a continuous barrier to avoid LPS translocation, but some endogenous or exogenous factors may alter this function. Among the factors promoting a leaky gut and increasing plasma LPS levels, alcohol consumption (29–33), immobilization stress (33,34), and radiation (35) have been put forward. Most importantly, in most of these studies, antibiotic treatments were also administered and resulted in reduced plasma and cecal LPS levels. In addition to these factors, we further showed that reduced endotoxemia was due to a change in the microflora profile. High-fat feeding decreased the number of bifidobacteria (4,6). This group of bacteria has been shown to reduce intestinal LPS levels in mice and to improve the mucosal barrier function (36–38). Furthermore, we have shown that prebiotics increased the number of bifidobacteria and reduced the impact of high-fat diet–induced metabolic disorders (6). Interestingly, bifidobacteria do not degrade intestinal mucus glycoproteins like other pathogenic bacteria do. This effect promotes a healthier microvillus environment by preventing permeability and bacterial translocation (39,40). In the present study, we further provide evidence that the mechanisms involved in the development of metabolic endotoxemia and the corresponding metabolic disorders in response to high-fat feeding are associated with an increased intestinal permeability. The modulation of gut bacteria after high-fat diet strongly increased intestinal permeability by reducing the expression of genes coding for tight junction proteins ZO-1 and occludin. Moreover, our data demonstrate that gut bacteria are clearly

FIG. 7. Antibiotic treatment of ob/ob mice reduced endotoxemia. ob/ob mice treated with antibiotic and ob/ob CD14−/− mice exhibited lower mRNA concentration of adipose tissue inflammatory markers and improved metabolic parameters. A: DGGE profiles generated from the cecal microbiota in ob/ob mice (Ob) or ob/ob mice treated with antibiotic (Ob-Ab) for 4 weeks. Each number and profile correspond to a different animal. B: Plasma endotoxin (LPS) concentration (EU/ml). C: Plasma glucose (mmol/l) after an oral glucose load (1 g/kg) in ob/ob mice (Ob), ob/ob mice treated with antibiotics (Ob-Ab) for 4 weeks, or ob/ob CD14−/− mice. The inset represents the area under curve (AUC) of the same groups. D: Plasma insulin concentration (pmol/l) 30 min before (~30) and 15 min after (15) oral glucose administration of the same groups. E: Glucose-induced insulin secretion after oral glucose administration. F: Insulin resistance index. G: Body weight gain. J: Subcutaneous adipose tissue weight (percent body weight). K: Visceral adipose tissue weight (percent body weight). H and L: Visceral adipose tissue PAI-1 and F4/80 mRNA concentrations. I and M: Subcutaneous adipose tissue PAI-1 and F4/80 mRNA concentrations in ob/ob mice (Ob), ob/ob mice treated with antibiotics (Ob-Ab) for 4 weeks, or ob/ob CD14−/− mice. N: Visceral adipose tissue oxidative stress levels (lipid peroxides concentrations) in the same groups. Data are means ± SE. Data with different superscript letters are significantly different (P < 0.05) according to the post hoc ANOVA statistical analysis.
involved in the present mechanism because antibiotic-treated mice exhibited normal intestinal integrity, although the mice were still eating a high-fat diet. We therefore, suggest that high-fat feeding changes gut microflora, which then increase intestinal LPS permeability (Fig. 1C). It is noteworthy that the antibiotic treatment reduced the intestinal content in LPS, which could contribute as well to the reduced metabolic endotoxemia. We report here that changes in feeding habits or the antibiotic treatment profoundly affect the fecal content in energy. The lipid content was dramatically increased in mice treated with antibiotics, suggesting that intestinal flora contributes to energy harvesting or absorption. This observation is also supported by data from literature (7–12). Together, these data emphasize the role of gut microbiota in the development of high-fat diet-induced metabolic disorders.

These results demonstrate that the gut bacteria determines the threshold at which metabolic endotoxemia occurs during high-fat diet feeding. However, the role of gut microbiota on the development of metabolic endotoxemia-induced inflammation and metabolic disorders is poorly defined. Therefore, we characterized several inflammatory markers and found that the increase in PAI-1, IL-1, and TNF-α mRNA concentrations after high-fat feeding was completely abolished by the antibiotic treatment. This mechanism does not depend on the amount of fat ingested because it was even increased by the antibiotic treatment. Oxidative stress is frequently associated with inflammation and metabolic dysfunction in adipose depots (20–22). We similarly found that the antibiotic treatment totally normalized lipid peroxidation in the visceral adipose depots and normalized the inflammatory/oxidative stress factor STAMP2 (21) and NADPHox mRNA concentration in the visceral and subcutaneous adipose depots. Furthermore, we found that antibiotic-treated mice exhibited normal F4/80 and MCP-1 mRNA concentrations in the visceral adipose depot. Our result are in agreement with data from the literature, because we and others have previously shown that high-fat feeding is associated with adipose tissue macrophage infiltration (F4/80-positive cells) and chemokine MCP-1 (4,41,42). Moreover, our multiple correlation analyses strongly suggest that inflammation, macrophage infiltration, and oxidative stress markers are induced by LPS-dependent mechanisms and controlled by the antibiotic treatment. We here also further demonstrated that the modulation of gut microbiota improved high-fat diet–induced glucose intolerance, body weight gain, and fat mass development. These results are in line with our and other previous data showing that in the absence of metabolic endotoxemia or LPS receptor, dietary lipids are not sufficient to induce metabolic disorders (4,6,25,28).

To assess the contribution of gut microbiota to the development of metabolic endotoxemia and inflammation regardless of the high-fat feeding, we focused on ob/ob mice. These animals are characterized by different gut microbiota (8,12), higher inflammatory tone, and endotoxemia when compared with wild-type mice (23). Antibiotic treatment dramatically changed the ob/ob mice gut microbiota; reduced Lactobacillus spp., Bifidobacterium spp., and Bacteroides-Prevotella spp.; and lowered metabolic endotoxemia. Furthermore, these parameters were associated with a significantly lower inflammatory tone in ob/ob antibiotic-treated mice. To demonstrate that the LPS receptor is involved in the regulation of inflammation and metabolic disorders in response to changes of gut microbiota, we therefore generated ob/ob mice lacking the LPS receptor CD14 (ob/ob CD14<sup>−/−</sup>). Inflammation and macrophage infiltration markers were reduced in the visceral adipose depots and to a lower extent in the subcutaneous adipose depots of ob/ob CD14<sup>−/−</sup> mice. The latter set of data demonstrates that metabolic endotoxemia measured in ob/ob mice is, at least in part, involved in the inflammatory phenotype. In ob/ob mice, the lowering of metabolic endotoxemia, by means of the antibiotic treatment, and of LPS action in the ob/ob CD14<sup>−/−</sup> mice are associated with a significantly increased glucose tolerance and reduced visceral and subcutaneous adipose depot weights. Interestingly, we also found that ob/ob mice treated for 4 weeks with an endotoxin inhibitor (43) administered via osmotic mini-pumps improved glucose tolerance and lowered adipose tissue fat mass (Supplemental Fig. 2). This pattern is similar to that observed in antibiotic-treated mice. This confirms that the gut microflora and the consequent increased bacteria-derived factor LPS exert a key role in the development of adipose depots and inflammation in ob/ob mice. Altogether, these data demonstrate that changes in gut microbiota and metabolic endotoxemia play a role in the ob/ob phenotype.

In the quest for non–gut-dependent sources of endotoxemia, periodontitis could also be linked to the development of metabolic disorders (44). Several studies reported that the treatment of periodontitis with antibiotics was associated with improved metabolic parameters (45). Nevertheless, the impact of such antibiotic treatment on gut microbiota has not been investigated but could play a part in the improved metabolic phenotype.

In summary, first, we have demonstrated that in high-fat diet–fed mice, the modulation of gut microbiota is associated with an increased intestinal permeability that precedes the development of metabolic endotoxemia, inflammation, and associated disorders (Fig. 8). Second, we found that in ob/ob mice, gut microbiota determines the concentration of plasma LPS and is a mechanism involved in metabolic disorders. Altogether, we demonstrate that gut microbiota sets the threshold for metabolic endotoxemia.
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