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Characterisation of Gut Microbiota in Ossabaw and Göttingen Minipigs as Models of Obesity and Metabolic Syndrome

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Abstract

**Background:** Recent evidence suggests that the gut microbiota is an important contributing factor to obesity and obesity related metabolic disorders, known as the metabolic syndrome. The aim of this study was to characterise the intestinal microbiota in two pig models of obesity namely Göttingen minipigs and the Ossabaw minipigs.

**Methods and Findings:** The cecal, ileal and colonic microbiota from lean and obese Ossabaw and Göttingen minipigs were investigated by Illumina-based sequencing and by high throughput qPCR, targeting the 16S rRNA gene in different phylogenetic groups of bacteria. The weight gain through the study was significant in obese Göttingen and Ossabaw minipigs. The lean Göttingen minipigs’ cecal microbiota contained significantly higher abundance of Firmicutes (P<0.006), Akkermansia (P<0.01) and Methanovibrioctactus (P<0.01) than obese Göttingen minipigs. The obese Göttingen cecum had higher abundances of the phyla Spirochaetes (P<0.03), Tenericutes (P<0.004), Verrucomicrobia (P<0.005) and the genus Bacteroides (P<0.001) compared to lean minipigs. The relative proportion of Clostridium cluster XIV was 7.6-fold higher in cecal microbiota of obese Göttingen minipigs as compared to lean. Obese Ossabaw minipigs had a higher abundance of Firmicutes in terminal ileum and lower abundance of Bacteroidetes in colon than lean Ossabaw minipigs (P<0.01). Obese Ossabaws had significantly lower abundances of the genera Prevotella and Lactobacillus and higher abundance of Clostridium in their colon than the lean Ossabaws. Overall, the Göttingen and Ossabaw minipigs displayed different microbial communities in response to diet-induced obesity in the different sections of their intestine.

**Conclusion:** Obesity-related changes in the composition of the gut microbiota were found in lean versus obese Göttingen and Ossabaw minipigs. In both pig models diet seems to be the defining factor that shapes the gut microbiota as observed by changes in different bacteria divisions between lean and obese minipigs.

Introduction

Obesity in humans has reached epidemic proportions worldwide, which is mainly due to a combination of inactive lifestyle and increased energy intake [1]. Obesity is a condition characterised by accumulation of fat in adipose tissue and a state of metabolic imbalance. The morbid conditions related to obesity such as abdominal obesity, insulin resistance and glucose intolerance, hypertension and dyslipidemia are together called the metabolic syndrome (MetS) [2]. Obesity and its co-associated morbidities namely cardiovascular disease, type-2 diabetes (T2D), fatty liver disease and hypertension pose a great economic burden in affected countries. Recently, the gut microbiota has been implicated as one of the influencing factors that further promotes obesity and metabolic disorders in obese subjects [3,4]. The gut microbiota is affected by dietary changes and is considered to be an environmental factor affecting the energy balance and whole body metabolism which may contribute to obesity and its metabolic disorders [3,5,6]. Recent studies have shown an altered gut microbiota characterised by reduced diversity in diet induced obese and diabetic mice as well as diabetic humans [6–10]. Other
studied in mice have demonstrated changes in the composition of the gut microbiota independently of the obese state and in response to high-fat/high-energy diet, suggesting other mechanisms that may contribute to obesity and metabolic syndrome [11,12]. In addition, Cani and colleagues [13–15] have provided evidence of a causal role of gut microbiota in the low grade inflammation in the gut of mice. The gut microbiota may lead to low grade inflammation induced by the lipopolysaccharides (LPS) present on the outer membrane of Gram-negative bacteria, causing activation of the innate immune response [16]. This low grade inflammation is connected to low, but constant levels of LPS in the circulation and to increased levels of adiposity and insulin resistance [13]. Together these findings suggest that high-fat diet (HFD) and obesity are associated with gut microbiota dysbiosis leading to alterations of gut barrier and resulting in an increased level of circulating LPS and a low grade inflammation (reviewed in [17]). However most of these studies are performed in mice that are genetically obese (ob/ob mice) and due to the many differences between humans and mice these findings may not be translated directly to humans [10]. Therefore, other animal models may provide better models for obesity-gut-microbiota related studies. Pigs are generally considered to be excellent biomedical models for nutritional studies because their gastrointestinal tract and physiology have similarities to humans, making the pig an excellent animal model in obesity related studies [19]. Pigs have already been used in a few obesity studies to investigate their gut microbiota [19,20]. Specifically, minipigs have a potential of becoming excellent animal models for gut microbiota related studies, due to their smaller size than domestic pigs and their tendency to become obese when fed ad libitum. In this study we investigate the composition of the gut microbiota in relation to diet, obesity and MetS in two pig models, Göttingen and Ossabaw minipigs. Female Ossabaw minipigs when fed high-fat/cholesterol, high-caloric diet develop symptoms of MetS with abdominal adiposity, glucose intolerance, insulin resistance and cardiovascular disease (CVD) [21–23] and therefore Ossabaw minipigs are considered one of the relevant animal models for obesity and MetS [24]. Göttingen minipigs are also used in diabetes research and are proposed to be good animal models for studying obesity and metabolic disorders caused by obesity [25–27]. To our knowledge the gut microbiota of Ossabaw and Göttingen minipigs have not been characterised previously, either in lean or obese states. Therefore, the objective of this study was to investigate the effect of obesity and diet on the composition of the gut microbiota in the two pig models of obesity. In Ossabaw minipigs the dietary regimen was very different between lean and obese animals and any differences found between these two groups will be a combined effect of obesity and different diet. In the Göttingen minipigs the diet composition did not differ much between lean and obese minipigs only the amount of food was different being, restrictive for the lean group and ad libitum for the obese group, and consequently group differences will most likely primarily be due to differences in obesity. We characterised the gut microbiota of Ossabaw and Göttingen minipigs by Illumina-based sequencing and further confirmed our findings using a high-throughput quantitative real time PCR (qPCR) platform.

Materials and Methods

The studies in Göttingen minipigs were designed and performed at the University of Copenhagen in Denmark. The Ossabaw minipig studies were designed and performed at Indiana University School of Medicine. The diet and design of the two studies are different, therefore in this study we characterised the gut microbiota in the two pig models separately.

Göttingen Minipigs Study

Female Göttingen minipigs (n = 14) that were ovariectomized (Ellegaard Göttingen Minipigs A/S, Dalmoes, Denmark) were subsequently housed at two years of age in facilities provided by the University of Copenhagen (Taastrup, Denmark) until they were euthanized at approximately 41–47 months of age. Of the 14 minipigs, seven were allocated as the obese group. The obese minipigs had been given therapeutic peptides for pharmacological studies prior to the obesity experiments but were subjected to a suitable washout period before the start of the present experiments. The lean group (n = 7) were fed restrictively with 150 g of minipig chow (Altromin 9023, Christian Petersen A/S, Gentofte, Denmark), twice a day consisting of 19% protein, 8% fat and 73% carbohydrates. The obese group (n = 7) were fed ad libitum Altromin 9033 (minipig chow, Christian Petersen A/S, Gentofte, Denmark) consisting of 25% protein, 11% fat, 64% carbohydrates. At approximately 122 days before the end of the experiment the animals were weighed biweekly and the body-fat composition was measured by dual energy x-ray absorptiometry scanning (DXA-scanning) (Hologic Explorer, Santax Medico, Aarhus, Denmark) at the end of experiment and the absolute mass of fat tissue was obtained by using the scanner software package [28]. All the animals were euthanized by pentobarbitol. Colon and cecum samples with content were collected after the animals were euthanized. The samples were immediately frozen in liquid nitrogen and were subsequently stored at −80°C until further analyses.

Ossabaw Minipigs Study

The samples provided for this study were obtained from female Ossabaw minipigs that belong to Indiana University School of Medicine and Purdue University breeding colony (West Lafayette, IN, USA). The lean Ossabaw minipigs (n = 4) received a daily diet (standard chow) with a total caloric content of 2200 kcal and the calories provided by macronutrients were: protein 18.4%, fat 10.5% and carbohydrates 71.0%. The obese group of minipigs (n = 4) received a high-energy diet of 4500–6000 kcal daily provided: 16.3% protein, 42.9% fat and 40.8% carbohydrates (of which 20% came from fructose). Both groups were housed individually at an age of six months, were fed the respective diets for a period of 8–10 months, and were euthanized at the end of feeding experiments at an age of 14–16 months. All the minipigs were euthanized by cardiotomy while under anaesthesia by a combination of intramuscular injections of tiletamine-zolazepam (5 mg kg⁻¹), xylazine (2.2 mg kg⁻¹) and isoflurane (5%). Samples from colon and terminal ileum both including content were collected after the animals were euthanized and were immediately frozen in liquid nitrogen and subsequently stored at −80°C until further analyses.

DNA Extraction and Purification

The DNA was extracted from colon and cecum digesta of lean (n = 7) and obese (n = 7) Göttingen minipigs and from colon and terminal ileum digesta of Ossabaw lean (n = 4) and obese (n = 4) minipigs. Digesta from colon, terminal ileum and cecum (200 mg each) was used for DNA extraction by Maxwell® 16 Cell DNA Purification Kit (Promega Corporation, Madison, WI, USA) according to manufacturer’s instructions with an additional bead beating step in order to disrupt the cell wall of Gram-positive bacteria.
PCR Conditions
The DNA samples were used for amplification of the V5 region of the 16S rRNA gene. The PCR reactions were performed in duplicates of 49 μl per reaction consisting of 5 μl 5 X GoldTaq buffer (Applied Biosystems, Branchburg, NJ, USA), 20 μM of each forward and reverse primers, 2 μl dNTP (10 mM), 4 μl MgCl2 (25 mM), 0.5 μl AmpliTaq Gold® DNA Polymerase (5 U/μl) (Applied Biosystems), 31.5 μl H2O and 2 μl DNA of 100 ng μl–1. The PCR cycling conditions were an initial denaturing step of 94°C for 6 min, followed by 30 cycles of 94°C for 45 s, 57°C for 45 s, 72°C for 45 s and a final extension step at 74°C for 10 min. The amplification was performed using the V5 universal primer set in house design, forward primer 894F (5'-GGATTAG- TACCCNGGTAGTC-3') and reverse primer 926R (5'- CGGTCATTTCTTTAGTTT-3') using a T3 Thermocycler (Biometa GmbH, D-37079 Gottingen, Germany). The quantity and quality of the resulting PCR products were then assessed on an Agilent 2100 Bioanalyzer using the Agilent DNA 1000 kit (Agilent Technologies, Waldbronn, Germany). The amplified DNA was purified for primers and detergents using a Qiagen MinElute PCR purification kit (Qiagen GmbH, Hilden, Germany) according to the manufacturer’s instructions and then pooled together and finally 3.6 ng of DNA were submitted to the National High-Throughput DNA Sequencing Centre at Copenhagen University, Denmark, for sequencing on an Illumina HiSeq™ 2000 platform.

Sequence Analysis
The obtained sequences were sorted and normalized by BION-meta software [29] with the taxonomic classification according to the Greengene Database [30]. The software package can be obtained from: https://www.dropbox.com/sh/fumscuqanqquv/_.4H-XBsHQ. In brief, the sequences were initially de-multiplexed according to the primer and barcode sequences. Subsequently they were cleaned at both ends by removal of bases of a quality less than 96%. Identical sequences were further clustered and aligned into consensus sequences with a setting of 99.8% base quality. Consensus sequences of at least 40 nucleotides in length were further mapped into a table according to the individual barcodes. Finally, the consensus sequences were taxonomically classified against the Greengene SSU database using a word length of 8 and a match minimum of 30%. The top one percent of the obtained hits from the Greengene database was then used for taxonomical classification of the consensus sequences. The number of reads for each barcode was further normalized making it possible to do statistical analysis directly between individuals in the experiment. The Shannon-Weaver index of diversity (H') [31] was further calculated manually to estimate the diversity of the bacteria at genus level from the obtained normalized sequences. Prior to analysis, data were log transformed for normalizations and analysed using one-way ANOVA or two-way ANOVA when appropriate using GraphPad prism version 5.00 for Windows (GraphPad software, San Diego, CA USA). The Kruskal Wallis [32] or Bonferroni’s post hoc test [33] was further used to test for differences among groups. P-values <0.05 were considered significant. The abundances of bacteria in figures are represented as mean and error bars representing standard deviations.

Microbial Identification by 48.48 Dynamic Array
High throughput qPCR was performed by a 48.48 Dynamic Array Integrated Fluidic Circuits (Fluidigm, CA, USA). This platform combines 48 primers with 48 samples to run 2304 simultaneous qPCR reactions. In this chip, individual primer sets target the 16S rRNA gene DNA of different bacterial phylogenetic groups (Domain, Phylum, Class, Family, Genus and Species level) Hermann-Bank et al. (2013, in prep). Each sample consisted of 20 μmol L–1 forward and reverse primers, 1 × Assay loading reagent (Fluidigm, PN5000746), 1 × low EDTA TE buffer (AppliChem GmbH, Darmstadt Germany) and master mix consisting of: 20 X DNA binding dye sample loading reagent (Fluidigm, PN-100-0338), 20 X EvaGreen® DNA binding dye (Biortum, Heyward CA, USA) and 2 × Taqman master mix (Applied Biosystems). The 16S rRNA gene DNA concentrations were equilibrated to a concentration of 50 ng μl–1. In each run a non-template control (NTC) was included to detect any contamination or non-specific amplification. A melting curve analysis was performed for quality check of amplification and the non-specific reactions were excluded. The obtained C(T) values from the finally accepted values were subsequently exported to Microsoft Excel for further analysis. The relative proportion of bacteria representing each taxon was calculated based on the Livak method [34]. Hence, the relative quantifications of the PCR signal of the target 16S rRNA gene in the obese minipigs in each group was related to that of the lean minipigs which were considered to harbour the reference composition of the gut microbiota. Fold differences in the different bacterial groups were subsequently calculated by 2-ΔΔC(T) [34]. All the statistical analysis were performed on GraphPad Prism version 5.00 for Windows (GraphPad software, San Diego, CA, USA). The statistical analysis were performed by Mann-Whitney U test [35] and significant differences were considered when P<0.05.

Results
Phenotype of the Götttingen and Ossabaw Minipigs
The lean Götttingen minipigs (n=7) weighed 50.3±1.6 kg when the animals were euthanized, while the obese Götttingen minipigs (n=7) weighed 92.6±5.2 kg (Figure S1). Approximately four weeks prior to euthanasia and at the time of DXA scanning, the body weight of the lean minipigs was 49±1.6 kg with a body-fat percent of 26% (±4) and the obese minipigs had an average body weight of 87±5.3 kg with a body-fat percent of 42% (±4). The difference between body-fat and body weight in lean and obese minipigs was significant (P<0.001). There was no significant difference in blood triglycerides, total cholesterol and fasting blood glucose between lean and obese Götttingen minipigs. However there was a significant difference in fasting blood insulin levels between lean and obese Götttingen minipigs (P<0.01) (Table 1).

The obese Ossabaw minipigs (n=4) at six months of age weighed 43.3±6.6 kg and by the end of the experiment, at an age of 16 months they weighed 60.4±7.5 kg (Figure S2). At six months of age the obese Ossabaw minipigs (n=4) weighed 42.8±2.4 kg and at the end of experiments they weighed 98.3±2.9 kg (Figure S2). The obese Ossabaw minipigs displayed MetS with total blood cholesterol and triglycerides higher than the lean Ossabaw minipigs (Table 1). The fasting blood glucose levels showed a trend toward being higher in obese than in lean Ossabaw minipigs and a similar trend was observed in blood insulin levels in obese (34.7 pmol l–1) and in lean (15 pmol l–1) Ossabaw minipigs (Table 1).

Sequence Analysis
Obtained sequence files were analysed using the Bion-meta software [29]. A total of 603,926,924 reads were obtained from the Illumina sequencing. After de-multiplexing according to primer and barcode sequences a total of approximately 469 million remaining reads were 3’ and 5’ trimmed according to base
The abundance of Bacteroidetes was significantly higher in cecal (abundance of Bacteroidetes. The ratio of Firmicutes to Bacteroidetes (1.3) (P<0.0001). At family level, the 15 most abundant families of bacteria constituted 94.7% of all the phyla obtained from Illumina sequencing (Figure 4). The six most abundant phyla were: Bacteroidetes (39.2%), Firmicutes (27.3%), Proteobacteria (24.6%), Actinobacteria (20.8%), and Tenericutes (8.6%).

II. Characterization of the Intestinal Microbiota in Ossabaw Minipigs

To characterise the intestinal microbiota of lean and Ossabaw minipigs, the colon and ileal microbiota were sequenced. Overall, the ten most abundant phyla constituted 99.7% of all the phyla obtained from Illumina sequencing (Figure 4). The six most abundant phyla were: Bacteroidetes (39.0%), Firmicutes (27.3%), Proteobacteria (24.6%), Actinobacteria (20.8%), and Tenericutes (8.6%).

`Table 1. Blood parameters in lean and Obese Ossabaw and Göttingen minipigs.`

<table>
<thead>
<tr>
<th></th>
<th>Lean (n=4)</th>
<th>Obese (n=4)</th>
<th>Lean (n=7)</th>
<th>Obese (n=7)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Body weight (kg)</td>
<td>60.4 ±6.6</td>
<td>98.3 ±2.9</td>
<td>50.3 ±1.6</td>
<td>92.6 ±5.2</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Triglycerides (mmol/l)</td>
<td>0.3 ±0.03</td>
<td>0.5 ±0.03</td>
<td>0.3 ±0.04</td>
<td>0.5 ±0.07</td>
<td>0.07</td>
</tr>
<tr>
<td>Total cholesterol (mmol/l)</td>
<td>2.0 ±0.1</td>
<td>12.9 ±2.0</td>
<td>1.8 ±0.1</td>
<td>2.0 ±0.1</td>
<td>0.2</td>
</tr>
<tr>
<td>Fasting blood glucose (mmol/l)</td>
<td>4.2 ±0.1</td>
<td>4.6 ±0.2</td>
<td>3.8 ±0.1</td>
<td>3.7 ±0.4</td>
<td>0.9</td>
</tr>
<tr>
<td>Fasting insulin (pmol/l)</td>
<td>15 ±3.5</td>
<td>34.7 ±7.5</td>
<td>141.2 ±32.4</td>
<td>39.2 ±9.9</td>
<td>0.01</td>
</tr>
</tbody>
</table>

`doi:10.1371/journal.pone.0056612.t001`
Ossabaw minipigs, with colon microbiota of lean Ossabaw minipigs consisting of 48.7% Bacteroidetes and 35.8% Firmicutes, while the obese Ossabaw minipigs had 45.7% Firmicutes and 35.9% Bacteroidetes in their colonic microbiota. Within the lean Ossabaw minipigs, a higher relative abundance of Bacteroidetes was observed in colon compared to terminal ileum. The obese Ossabaw minipigs had a higher ratio of Firmicutes to Bacteroidetes in terminal ileum and colon (3.9 and 1.3, respectively) as compared to lean Ossabaw minipigs (2.5 and 0.7, respectively).

There was a trend towards higher abundances of Proteobacteria and Spirochaetes in obese minipigs’ colon as compared to lean.

At class level the 10 most abundant classes constituted 98.2% of all the classes obtained from the normalized reads. Statistical analysis was performed on Clostridia, Bacteroidia, Bacilli, alpha-, beta-, delta-, gamma-, epsilon-Proteobacteria, Mollicutes and Actinobacteria. There was a higher abundance of Clostridia in colon of obese Ossabaw minipigs as compared to lean Ossabaw minipigs colonic microbiota and a higher abundance of Bacteroidia in lean colon with 48.5% (±9.8) of all bacteria as compared to colon samples from obese Ossabaw minipigs (35.5% (±14)). The class Bacilli (phylum Firmicutes), were highest in abundance in terminal ileum of obese minipigs. Overall the abundance of beta-Proteobacteria was...
higher in the microbiota from terminal ileum of both lean and obese minipigs compared to colon.

The families *Prevotellaceae*, *Clostridiaceae* and *Lachnospiraceae* together constituting 39.2% of all the normalized reads obtained at family level (Figure 5). *Prevotellaceae* was more abundant in lean Ossabaw minipigs than in obese Ossabaw minipigs with a mean relative abundance of 30.8% and 19.4%, respectively (Figure 5). There was a higher abundance of *Lactobacillaceae* in terminal ileum of lean minipigs compared to obese minipigs. The abundance of *Streptococcaceae* was highest in terminal ileum of lean minipigs and generally higher in terminal ileum than colon (Figure 5).

At genus level, the 50 most predominant genera consisted of 93.1% of the entire genera present in all normalized reads. The two most abundant genera were *Prevotella* and *Clostridium* both consisting of 16.1% and 11.7% of all the normalized reads, respectively (Figure 6). In lean minipigs, the colonic microbiota had a higher abundance of *Prevotella* with a mean relative abundance of 28% (±5.5) while the obese minipigs had a mean relative abundance of 18.3% (±4.0) (Figure 6). However, *Clostridium* was more abundant in colonic microbiota of obese minipigs than lean minipigs (Figure 6). *Lactobacillus*, the fifth most abundant genus obtained from all the normalized reads, constituted 5% of the entire genera. There was a difference between the abundance of *Lactobacillus* within the microbiota of colon of lean Ossabaw minipigs having a higher abundance than the microbiota of obese Ossabaw minipigs (Figure 6). The abundance of *Streptococcus* in colon and terminal ileum was higher in obese Ossabaw minipigs than in lean Ossabaw minipigs (Figure 6). Overall, the abundance of *Streptococcus* was higher in terminal ileum than colon in both lean and obese group. There were several differences in bacteria belonging to different genera between the microbiota in colon and terminal ileum in both lean and obese minipigs. Generally *Parabacteroides* was more abundant in colon than terminal ileum (Figure 6).

## III. Fold-differences between Lean and Obese Minipigs in Selected Groups of Bacteria

The obtained results from high throughput qPCR showed several differences between lean and obese minipigs in both Gottingen and Ossabaw minipigs. There were many groups of bacteria that were not detectable by this qPCR system, such as *Verrucomicrobia*, *Bifidobacteriaceae*, *Cl. cluster IV, delta-, beta-, gamma-Proteobacteria*, *Enterococcus* and *Escherichia coli*.

In the obese Gottingen colon microbiota, there was a 7.8-fold higher abundance of *Bacteroidetes* than in the lean minipigs (Table 2). The only significant difference was found in relative abundance of bacteria belonging to the *Cl. cluster XIV* family, with a 7.6-fold higher abundance in colon of obese Gottingen minipigs as compared to the lean group (*P*<0.0001).

Actinobacteria had a 5-fold higher relative abundance in colon and terminal ileum of obese Ossabaw minipigs than lean minipigs. A 4-fold higher abundance of bacteria belonging to the genus **[Figure 3. Abundance of different genera in colonic and cecal microbiota of lean and obese Gottingen minipigs. Different genera in colon and cecum of lean and obese Gottingen minipigs. Parentheses indicates unknown genus belonging to an order or a family. doi:10.1371/journal.pone.0056612.g003](#)**
Bacteroides was observed in terminal ileum and colon of obese Ossabaw minipigs (Table 2).

**Discussion**

In this study we aimed to characterise the composition of the intestinal microbiota of two minipig models of obesity and the effect of diet and adiposity on gut microbial community in these minipigs. Gottingen minipigs have been used as obesity models and displayed minor abnormalities in glucose tolerance and insulin sensitivity [26], however the metabolic changes in lean and obese Gottingen minipigs on the diets used in the present study are not well described. Ossabaw minipigs have been used as animal models in studies of obesity related metabolic disorders such as cardiovascular disease and are predisposed to insulin resistance in response to obesity and high-fat feeding, which is unique in Ossabaw minipigs as opposed to other animal models [22]. Lee et al. [23] reported several differences in blood parameters such as cholesterol and triglycerides between lean and obese Ossabaw minipigs. The Ossabaw minipigs used in our study displayed metabolic syndrome with abdominal and visceral adiposity, high blood triglyceride levels and high total blood cholesterol [23]. To our knowledge the Ossabaw and Gottingen minipigs' intestinal microbiota has not been characterised before and this is the first study that investigated the relation between obesity and intestinal microbial community in Ossabaw and Gottingen minipigs by 16S rRNA gene sequencing using the Illumina technology.

In this study we characterise the Gottingen minipigs' cecal and colonic microbiota in relation to obesity which was induced by overeating and not high-fat/high-energy diet. In the cecum microbiota of Gottingen minipigs there were several differences related to their metabolic state, while no differences were seen in the microbiota in colon. Interestingly the ratio of Firmicutes to Bacteroidetes was opposite to the findings in Ossabaw minipigs, as the lean Gottingen minipigs had a higher abundance of Firmicutes relative to Bacteroidetes. These results are however in agreement with the findings in diabetic mice and humans [7,36]. One of the interesting findings was the higher abundance of bacteria belonging to phylum Tenericutes (class Mollicutes) in obese Gottingen minipigs compared to their lean counterparts. The bacteria belonging to this phylum have previously been shown to be increased in diet-induced obese mice [9]. Noteworthy was the differences observed in Bacteroides between lean and obese Gottingen minipigs, with higher abundances in obese minipigs which has previously been reported to be connected to gut microbiota of T2D in humans [7]. In brief, the cecal microbiota of obese Gottingen minipigs was different from that of lean minipigs with higher abundance of bacteria belonging to phyla Bacter-
Table 2. Fold-differences in the relative abundance of bacteria between lean and obese minipigs.

<table>
<thead>
<tr>
<th>Phylum</th>
<th>Göttingen (cecum)</th>
<th>Göttingen (colon)</th>
<th>Ossabaw (TI)</th>
<th>Ossabaw (colon)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Firmicutes</td>
<td>1</td>
<td>N.D.</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
<tr>
<td>Bacteroidetes</td>
<td>&lt;2</td>
<td>7.6*</td>
<td>&lt;2</td>
<td>1</td>
</tr>
<tr>
<td>Actinobacteria</td>
<td>&lt;1</td>
<td>&lt;1</td>
<td>5.0</td>
<td>5.5</td>
</tr>
<tr>
<td>Fusobacteria</td>
<td>N.D.</td>
<td>1</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
<tr>
<td>Spirochaetes</td>
<td>3.3</td>
<td>N.D.</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
<tr>
<td>epsilon-Proteobacteria</td>
<td>N.D.</td>
<td>2</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
<tr>
<td>Lactobacillaceae</td>
<td>&lt;1</td>
<td>&lt;1</td>
<td>1</td>
<td>&lt;1</td>
</tr>
<tr>
<td>Streptococcaceae</td>
<td>&lt;1</td>
<td>&lt;1</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
<tr>
<td>Cl. Cluster IV</td>
<td>&lt;1</td>
<td>N.D.</td>
<td>&lt;2</td>
<td>&lt;1</td>
</tr>
<tr>
<td>Cl. Cluster XIV</td>
<td>&lt;1</td>
<td>7.6*</td>
<td>&lt;1</td>
<td>&lt;1</td>
</tr>
<tr>
<td>Bacteroides</td>
<td>N.D.</td>
<td>N.D.</td>
<td>4.6</td>
<td>4.3</td>
</tr>
<tr>
<td>Cl. Perfringes</td>
<td>N.D.</td>
<td>3.5</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
</tbody>
</table>

Relative abundance of bacteria in different phylogenetic groups in cecal and colonic microbiota of obese Göttingen minipigs and in ileal and colonic microbiota of obese Ossabaw minipigs, estimated by qPCR dynamic array. N.D. stands for Non Detectable. *indicates values with significant difference of \( P < 0.05 \).
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In Ossabaw minipigs, we report that the gut microbiota in relation to obesity was different between lean and obese Ossabaw minipigs. Our data suggest that obesity and/or HFD affected the gut microbiota of obese Ossabaw minipigs, since they had an overall different gut microbial community as compared to their lean counterparts. HFD has previously been shown to affect the gut microbiota both in obesity and independently of the obese state [11] and ingestion of HFD has been implicated in causing metabolic disorders observed in obese pigs and mice [26,40]. In our study the obese Ossabaw minipigs received HFD which also could have caused the differences observed between lean and obese Ossabaw minipigs. At phylum level the only differences between the lean and obese Ossabaw minipigs were observed in abundance of Firmicutes and Bacteroidetes, with higher abundance of Firmicutes in obese minipigs and higher abundance of Bacteroidetes in lean minipigs. Our results are in agreement with studies in obese humans [8], mice [6] and pigs [19] that displayed only obesity, while the results contrasts several human studies in subjects with T2D [7,41]. However, at lower taxonomic levels, more differences were observed between lean and obese Ossabaw minipigs. A marked difference was observed in the abundance of the families Prevotellaceae and Lactobacillaceae, especially genera Prevotella and Lactobacillus, which had higher abundances in lean Ossabaw minipigs while these results are opposite to the findings reported previously with higher abundance of Prevotella in diabetic humans and mice [7,36]. Our results are, however, in agreement with those reported by Turnbaugh et al. indicating that the state of obesity shapes the gut microbiota [10]. Nonetheless, diet is also a factor that may have caused the changes we observed here. Furthermore, the abundance of Lactobacillus was significantly lower in colon of obese Ossabaw minipigs as compared to lean Ossabaw and this result has been shown before in mice fed a HFD [42], implicating diet as a factor that shapes the intestinal microbiota. HFD has been implicated in changing the gut permeability by modulating the gut microbiota. A positive correlation has been observed between higher abundances of Lactobacillus and colonic transepithelial resistance [42]. The lean Ossabaw minipigs had a higher abundance of Lactobacillus in their colonic microbiota compared to obese and did not display metabolic dysfunction as compared to obese Ossabaw minipigs. The low abundance of Lactobacillus observed in obese Ossabaw minipigs could have caused changes in their intestinal permeability; however the intestinal permeability was not measured in our study. Increased gut permeability has been postulated to be related to metabolic endotoxemia, causing metabolic dysfunctions such as T2D. In case of Lactobacillus, the gut microbiota may have contributed in shaping the metabolic profile observed in obese Ossabaw minipigs by changing the gut permeability. Together our results suggest that the obese Ossabaw minipig’s gut microbiota display a profile that resembles the intestinal microbiota observed in obese mice and humans in response to HFD.

According to our data, the gut microbiota of obese Ossabaw minipigs displays the characteristic of obese gut microbiota and not MetS. One explanation for these results could be that these minipigs had to receive the HFD for a longer time in order to induce insulin resistance in them. However, it must be mentioned that the data from Ossabaw minipigs are based on a small number of animals and therefore, a larger population would provide a better understanding of the Ossabaw minipig’s gut microbial community.

Obese Göttingen minipigs display a specific gut microbiota that has previously been connected to metabolic disorders such as T2D. Even though obese Göttingen minipigs do not display metabolic disorders to the extent of that of obese Ossabaw minipigs, their gut microbial profile have similarities to those found previously in T2D mice. Therefore, Göttingen minipigs have great potential for being used in obesity related gut microbial...
studies. Here it is reported that certain group of bacteria flourish best under HFD conditions such as Firmicutes as observed in Ossabaw minipigs, while others such as the genus Bacteroides flourished due to obesity under other diet conditions such as overeating as observed in obese Goettingen minipigs. Together, these findings can be used to approach the obesity-related gut microbiota by exploring how the microbial community co-occur in periods of high energy feed and how this diet affects the community and its stability over a period of time. Such information can be used to develop probiotic strains to change the gut microbial community into a composition that protects against increased gut permeability, low grade inflammation, obesity and the obesity-related metabolic disorders.

In conclusion, obesity is connected to radical changes in several bacterial groups as observed in obese Goettingen minipigs. Our data suggest diet as an important factor that shapes the gut microbial community as shown in Ossabaw minipigs. However, it must be kept mind that our data is based on low number of animals and the Ossabaw study needs further investigation in a larger population. Here we show that both Ossabaw and Goettingen minipigs may be useful animal models in studying gut microbiota and provide a better understanding of obesity and metabolic syndrome and the relationship to the gut microbiota. Together, these findings can be used to approach the obesity-related gut microbiota to develop probiotic strains.

References


Supporting Information

Figure S1 Weight progression in obese Goettingen minipigs over a period of 122 days. (TIF)

Figure S2 Weight progression in obese Ossabaw minipigs in duration of 32 weeks. (TIF)

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Author Contributions

Performed the animal experiments regarding Goettingen minipigs: SGM SC BOC. Performed the animal experiments regarding the Ossabaw minipigs MS MA. Edited the manuscript: RP H-CI MB SG MB SGM MB. Provided the BION-meta software sequence analysis tool: NL. Conceived and designed the experiments: MS MA SC BOC SG RP MB. Performed the experiments: RP. Analyzed the data: RP H-CI. Wrote the paper: RP.