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

**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 Osabaw 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), Akkermensia (P<0.01) and Methanovibribacter (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.

**General information**
State: Published
Organisations: Section for Bacteriology, Pathology and Parasitology, National Veterinary Institute, Indiana University-Purdue, Novo Nordisk AS, Danish Genome Institute, University of Copenhagen
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Number of pages: 10
Pages: e56612
Publication date: 2013
Peer-reviewed: Yes

**Publication information**
Journal: P L o S One
Volume: 8
Issue number: 2
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
ISI indexed (2013): ISI indexed yes