

Lyme Disease and the Microbiome

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Abstract

Introduction. Lyme disease is a common vector-borne illness with broad public health concerns. We aimed to test the gut microbiome of subjects with Lyme disease compared to controls.

Material and Methods. We tested the gut microbiome of 35 Subjects with Lyme disease, and 19 healthy control subjects, using next-generation shotgun sequencing and analyzed the resulting data for relative abundance of the dozen most prevalent genera, mean relative abundance between groups, and beta diversity using principal coordinate analysis.

Results. There was a significant difference in the gut microbiome composition between subjects with Lyme disease (n=35), and their healthy counterparts (n=19). Both composition and principal coordinate analysis (PCoA) showed statistically significant, characteristic dysbiosis in referred Subjects carrying a diagnosis of Lyme Disease. Subject with a Lyme Disease diagnosis had significantly reduced abundance of bacterial genus Bifidobacteria (p<0.0001), and significantly elevated abundance of genus Bacteroides (p=0.01).

Conclusions. In our small study we identified Bifidobacteria as a key beneficial bacterial genus which is underrepresented in, and a potentially harmful genus Bacteroides, which is overrepresented in Subjects with Lyme disease. This dysbiosis of the gut microbiome we have found, has myriad effects on the overall health of the individual. Thus, illnesses and their associated treatments, which can have a detrimental impact on the gut microbiome or which fail to improve the gut microbiome, deserve further study.

Methods

Stool samples were collected from 35 Subjects with a history of Lyme disease, and 19 healthy control subjects, attending the GI clinic at Ventura Clinical Trials, in Ventura, CA. Demographic information for these individuals can be found in Table 1. Genomic DNA was extracted from each sample from which a library was prepared and sequenced using the NextSeq 550 by Illumina. Next, samples were analyzed using the OneCodex bioinformatics pipeline.

Results

Figure 2. Mean relative abundance plot of the top 12 most prevalent genera

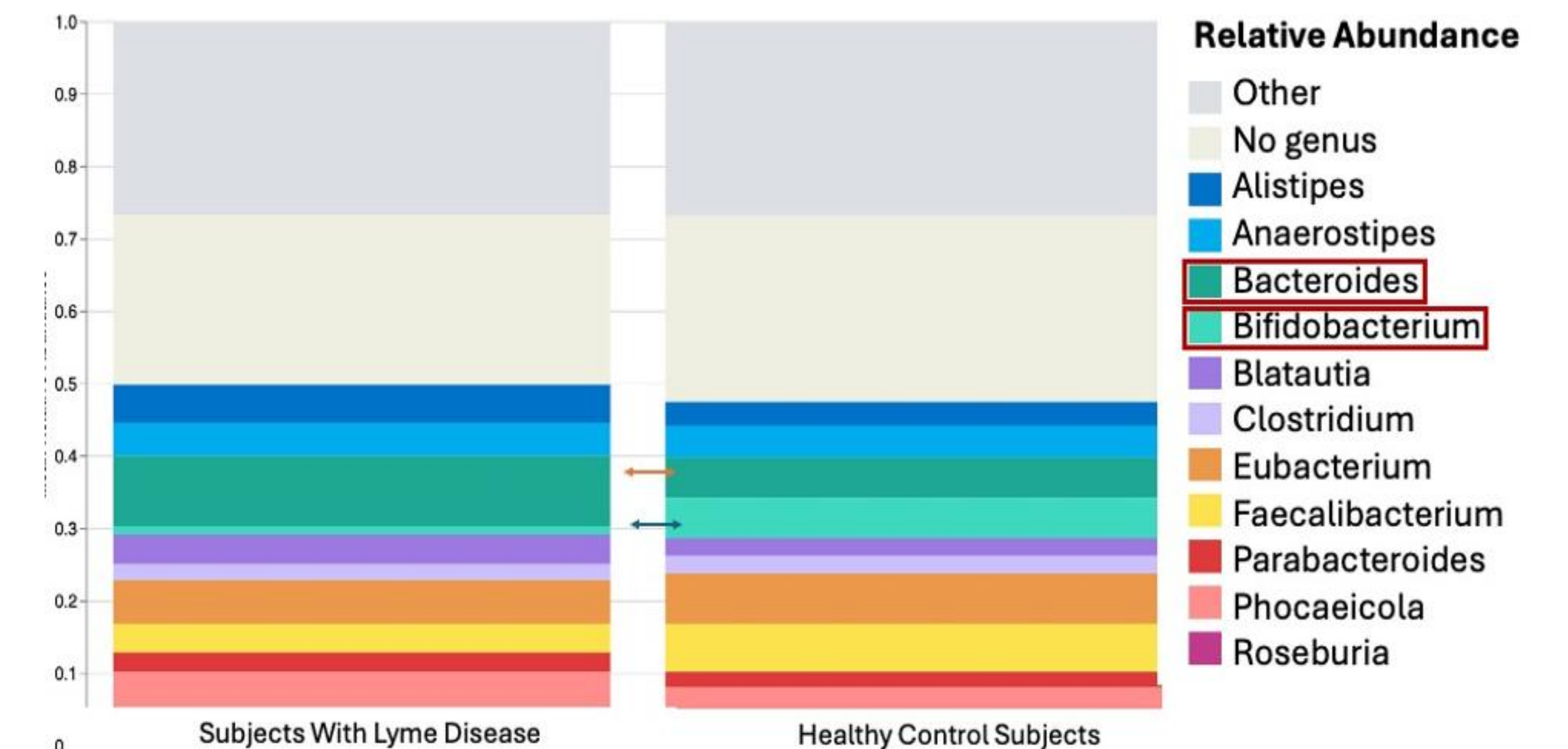
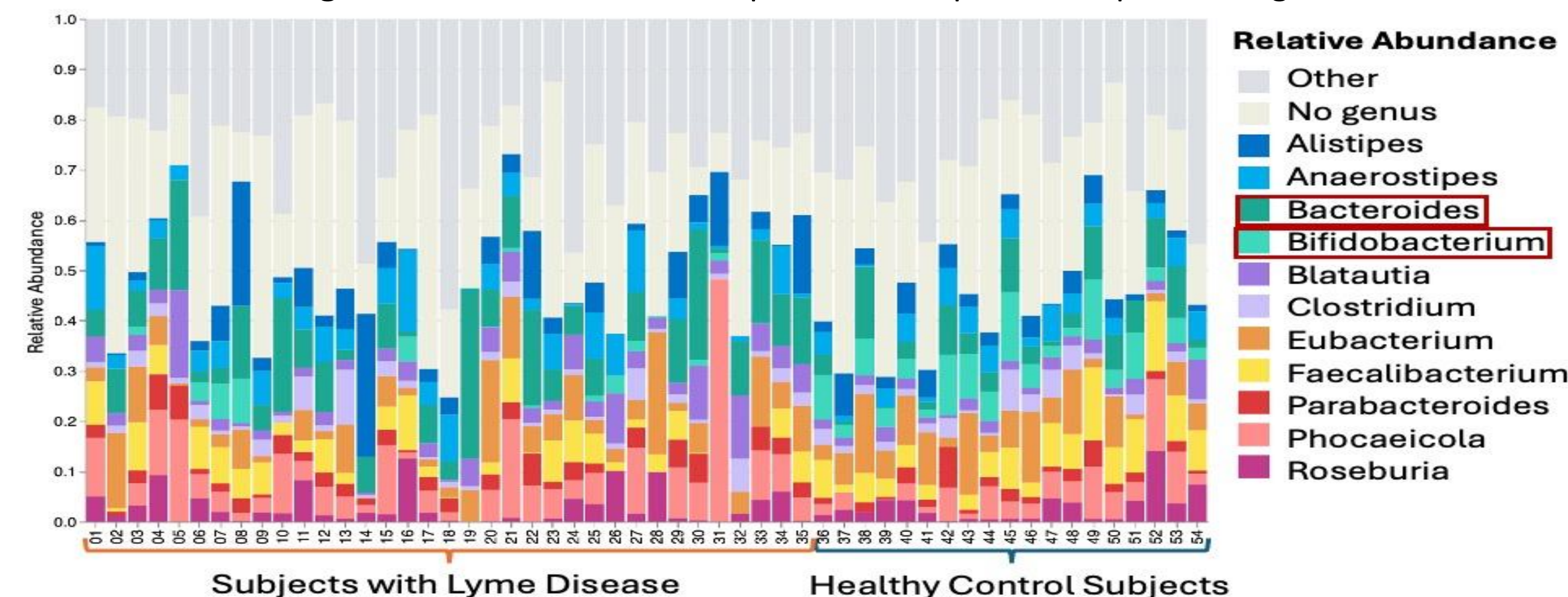


Table 1		
	Subjects with Lyme disease (n=35)	Healthy Control Subjects (n=19)
Age (mean, SEM, range)	48.57, 3.32, 12-88	44.42, 4.18, 20-87
Male (n, %)	14 (40%)	9 (47.37%)
Female (n, %)	21 (60%)	10 (52.63%)
Race	Number of Subjects (%)	Number of Subjects (%)
White	29 (82.86%)	17 (89.47%)
Asian	1 (2.86%)	2 (10.52%)
Other	1 (2.86%)	0 (0%)
Unknown	4 (11.43%)	0 (0%)
Number of Comorbidities	Number of Subjects (%)	Number of Subjects (%)
0	7 (7.53%)	14 (73.68%)
1	7 (7.53%)	2 (10.53%)
2	9 (9.68%)	0 (0.00%)
3	2 (2.15%)	1 (5.26%)
4	1 (1.08%)	1 (5.26%)
5	3 (3.23%)	0 (0.00%)
6 or more	6 (6.45%)	0 (0.00%)
Total (Mean per Subject)	93 (2.56)	9 (0.47)
Category of Comorbidity	Number of Comorbidities (%)	Number of Comorbidities (%)
Gastrointestinal	16 (17.20%)	4 (44.44%)
Autoimmune	14 (15.05%)	0 (0.00%)
Endocrine	4 (4.30%)	1 (11.11%)
Co-Infection	26 (27.96%)	1 (11.11%)
Other	33 (35.43%)	3 (33.33%)
State of Residence	Number of Subjects (%)	Number of Subjects (%)
In California	17 (48.57%)	10 (52.63%)
Outside California	18 (51.43%)	9 (47.37%)

Figure 1. Relative abundance plot of the top 12 most prevalent genera



Results

- Subjects with Lyme Disease were found to have markedly reduced relative abundance of *Bifidobacteria* (p<0.0001) when compared with Healthy Control Subjects as shown individually in Figure 1 and in the aggregate, in Figure 2.
- These data also show that the relative abundance of *Bacteroides* is much higher in subjects with Lyme disease than in their healthy counterparts (p=0.01).

Conclusions

Measures should be taken to ensure that populations have healthy levels of Bifidobacteria to aid in Lyme disease prevention. Further research is needed to confirm these findings.

