Searching for moreinformation about these taxa beyond greengenes

It's looks like the OTU that clusters with IL-6 is the L. gasseri/L. johnsonii group, which is interesting. I'll be interested to see if this holds.

If you want to figure out what the other Lactobacillus OTUs are, here's how. You might also see why I prefer the database approach we use in-house.

1) Go to Greengenes and get the accessions IDs for the taxa.

gg\_13\_5\_accessions.txt.gz

http://greengenes.secondgenome.com/downloads/database/13\_5

2) Go to NCBI, check 'nucleotide sequence' and search for the accession ID.

https://www.ncbi.nlm.nih.gov/

3) Go the NCBI Nucleotide BLAST

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE\_TYPE=BlastSearch&LINK\_LOC=blasthome

I'd suggest that you exclude the 'uncultured' organisms.

Take a look at the best hits. You'll note for this example, it looks as though the Greengenes OTU doens't align well with these lactobacilli at the other end of the sequence. You could check to see if it the original read had bad sequencing quality or could have resulted from a chimera. We only sequenced V1-V3, so focus in that area. L. gasseri and L. johnsonii have high sequence identity in the V1-V3 region, and I'm not sure the QIIME can properly separate the two without digging in more deeply, which is why I suggest L. gasseri/L. johnsonii group. (Note: L. taiwanesis just isn't typically observed vaginally.)

Plots of variables weights: interpretation is similar to interpretation of PCA variables plots. Cytokines (blue) projected in the same direction as taxa (red) have more similarity.

Recent cytokines analysis results from the pre-term birth paper.

1. Eotaxin, IL-1b, IL-6, and MIP-1b were significantly increased in pre-term birth samples

2. Previous report: elevated IL-1, IL-6, MIP-1, IP10/CXCL10 and other pro-inflammatory cytokines associated with PTB in blood, amniotic fluid or cervical-vaginal lavage samples.

3. Integrative sparse canonical correlation analysis to assess the association of specific bacterial taxa with the abundance levels of nine key cytokines: IL-1b, IL-6, IL-8, Eotaxin, TNF-a, IL-17A, MIP-1b, IP-10/CXCL10, RANTES)

5. IP-10/CXCL10, which functions to induce chemotaxis of immune cells and promotes apoptosis, cell growth and angiostasis, and is generally considered to be pro-inflammatory, was positively correlated with L. iners.

In women who went on to experience PTB:

1. In women who went on to experience PTB, the proinflammatory cytokines and dysbiotic taxa (e.g. A. vaginae, G. vaginalis and Megasphaera type 1) formed a tighter cluster, indicating a stronger positive correlation, but IP-10/CXCL10 did not correlate with L. iners.

2. BVAB1 was negatively correlated with IP-10/CXCL10.

Observations:

1. OTU 324 that clusters with IL-6 is the L. gasseri/L. johnsonii group

Other earlier exploratory findings:

1. L. crispatus was strongly associated with lower levels of a number of cytokines, including interleukins 12 and 17 (IL-12, IL-17), macrophage inflammatory protein (MIP1a), and vascular endothelial growth factor (VEGF).

2. BV-associated taxa, such as Sneathia, G. vaginalis, and BVAB1 were associated with very different cytokine profiles. For example, granulocyte colony stimulating factor (G-CSF) levels were lower when these taxa were abundant, but IL-9, IL-10, and tumor necrosis factor (TNF-a) levels were higher

3. Among communities dominated by L. gasseri, a significant correlation existed between EPA and MIP1a

4. And among communities dominated by BVAB1, a significant correlation existed between C16 DH SM and VEGF

5. Pro-inflammatory cytokines VEGF and IL-12 appeared to be grouped near taxon Coriobacteriaceae

6. pro-inflammatory cytokines IL-6 and MIP-1b formed a second group with taxa Clostridiales OTU22, L. gasseri, Lachnospiraceae OTU33, Peptoniphilus lacrimalis, Campylobacter ureolyticus, Actinomycetales OTU158, Finegoldia magna, and Dialister propionifaciens.