

DMBT1 Longitudinal Differential Abundance - Otu Results

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Analysis description

Goal

Investigate the temporal relationship between

- **genotype** (KO vs WT),
- **histopathology** (hyperplasia/CIS and SCC) and

in terms of predictive power of the **microbial composition** (clr-transformed OTUs).

Methodology

For microbial compositions, I used the CLR-transformed counts (after zero-replacement). I applied our methodology to

- **All OTUs which are present (count above 0) in at least 5% of samples (187 OTUs).**

Hyperplasia/CIS vs SCC model

The model is given by

$$y(t) \sim \beta_{hp/cis}(t) + \beta_{scc}(t)\mathbb{I}[scc] + \beta_{ko}(t)\mathbb{I}[ko] + \beta_{scc:ko}\mathbb{I}[scc, ko] + \alpha\mathbb{I}[Female]$$

Here are the relevant quantities to study:

In particular, we plot:

- the estimated mean curve in each group
- the estimated differences

Results

OTUs with genotype differences

Early differences:

- Otu 0028: family *Porphyromonadaceae* (only sig. in SCC, but similar trend in HP/CIS)
- Otu 0113: family *Porphyromonadaceae* (only sig. in SCC, but similar trend in HP/CIS)
- Otu 0116: order *Bacteroidales* (only sig. in SCC, but similar trend in HP/CIS)

Midrange differences:

- Otu 0004: genus *Streptococcus*
- Otu 0033: family *Porphyromonadaceae*
- Otu 0050: family *Lachnospiraceae*
- Otu 0059: genus *Sediminibacterium* (only sig. in SCC, but similar trend in HP/CIS)
- Otu 0078: family *Lactobacillaceae*

Late differences

- Otu 0013: family *Comamonadaceae*
- Otu 0018: genus *Bradyrhizobium*

Overall differences

- Otu 0007: genus *Cupriavidus*

OTUs with histopathology differences

Early differences:

- Otu 0049: genus *Bacteroides* (only sig. in KO, but similar trend in WT)

Midrange differences:

- Otu 0015: order *Lactobacillales*
- Otu 0045: genus *Alistipes* (only sig. in KO, but similar trend in WT)
- Otu 0101: family *Porphyromonadaceae* (only sig. in WT, but similar trend in KO)
- Otu 0143: genus *Alistipes*

OTUs with genotype-hitopathology interactions

Early differences between genotypes within SCC (one is reverse of the other three):

- Otu 0014: family *Staphylococcaceae*
- Otu 0040: family *Porphyromonadaceae*
- Otu 0096: family *Porphyromonadaceae*
- Otu 0526: phylum *Bacteroidetes*

Midrange differences between genotypes within SCC:

- Otu 0257: genus *Streptococcus*

Late differences between genotypes within HP/CIS:

- Otu 0252: family *Coriobacteriaceae*

Overall differences between genotypes within SCC (reverse of each other):

- Otu 0009: genus *Staphylococcus*
- Otu 0322: family *Porphyromonadaceae*

KO SCC lower in early window:

- Otu 0039: family *Lachnospiraceae*
- Otu 0053: family *Porphyromonadaceae*
- Otu 0062: family *Porphyromonadaceae*
- Otu 0120: family *Lachnospiraceae*

Differences in histopathology early; differences in genotype within SCC

- Otu 0048: family *Lachnospiraceae*
- Otu 0192: family *Lachnospiraceae*

Odd behavior at week 12

- Otu 0046: family *Lachnospiraceae*
- Otu 0318: family *Lachnospiraceae*

Hard to describe/group

- Otu 0016: genus *Caulobacter*
- Otu 0084: family *Lachnospiraceae*
- Otu 0105: order *Bacteroidales*
- Otu 0133: phylum *Bacteroidetes*