

Escherichia/Shigella at 1 month impact epithelial cells which expressed higher calprotectin and cathelicidin

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Escherichia/Shigella at 1 month impact epithelial cells which expressed higher calprotectin and cathelicidin

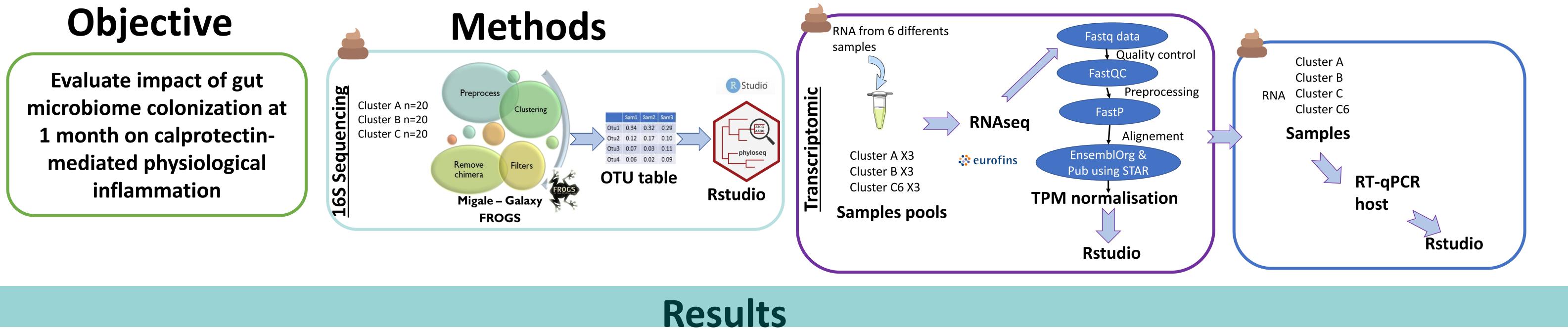


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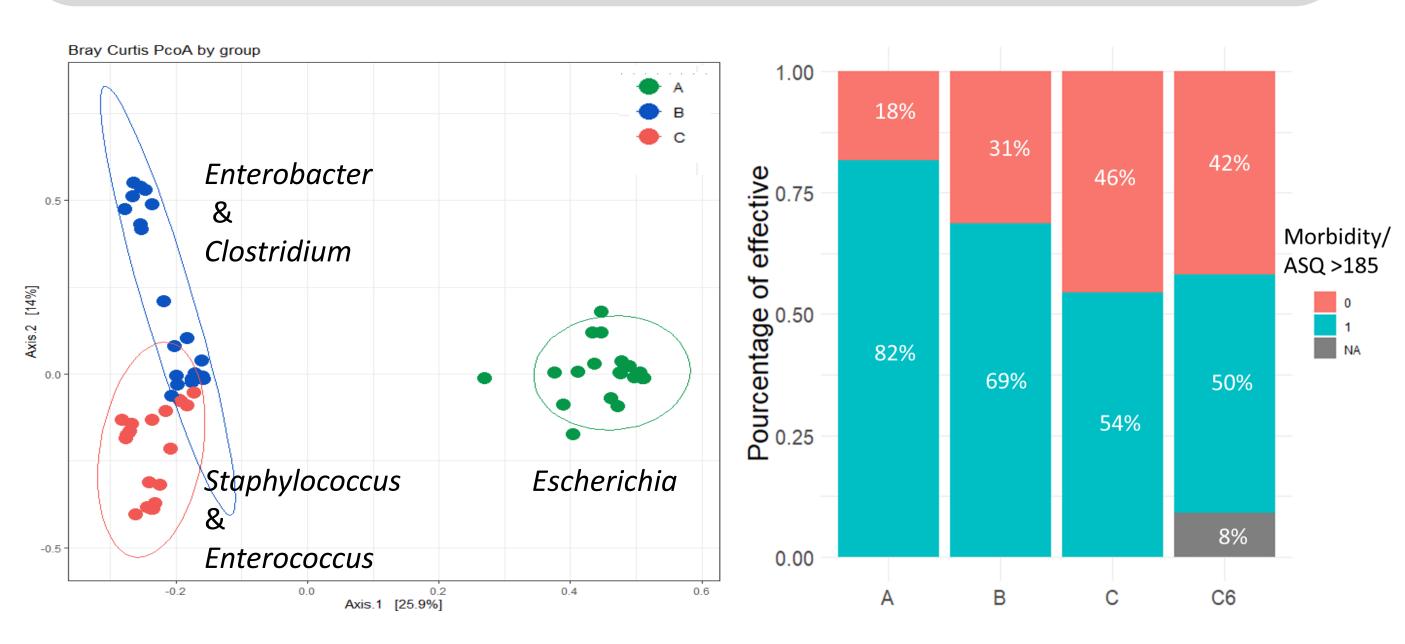
Background

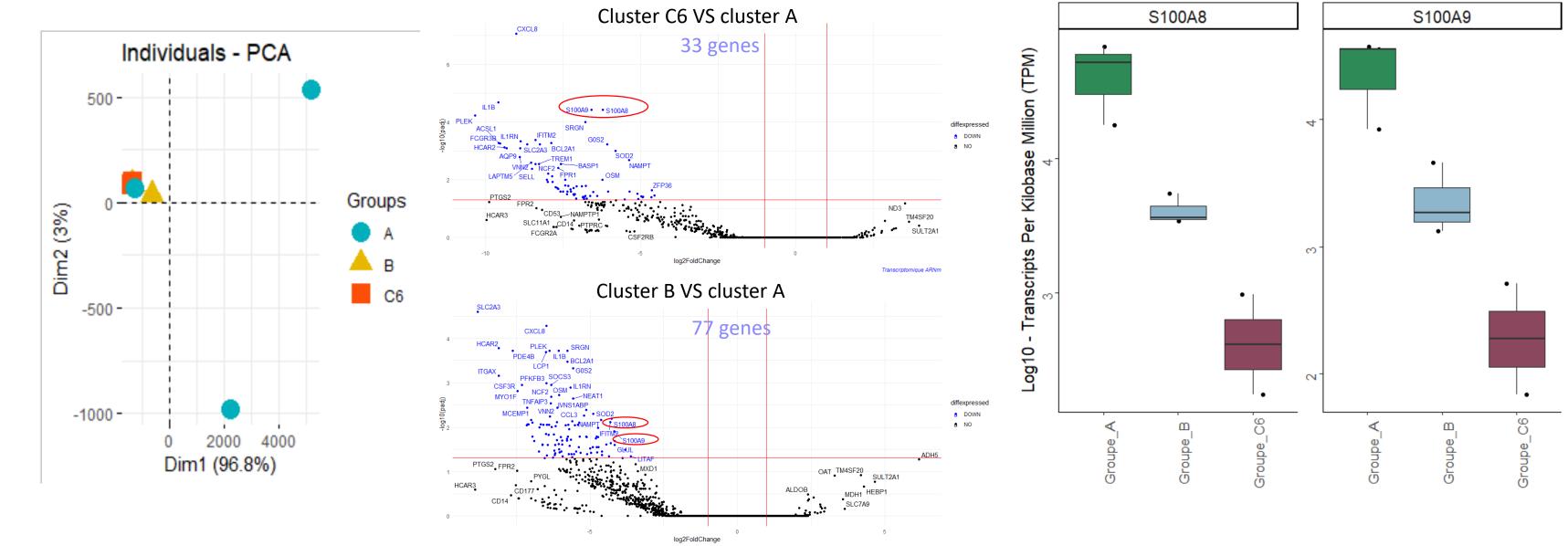
- Preterm birth are 1st cause of death in children under 5 years of age in the world
- Serious psychological and physiological consequences in the short and long term [1]
- High level of fecal calprotectin in healthy infants. Calprotectin is involved in inflammation and is a marker of leucocytes which produces antimicrobial peptides (alpha-defensines and cathelicidin) [2-3]
- Need to develop analyses on non invasive approach



Microbiome of very preterm infants can be stratified in 4 clusters with different outcome

Cluster A genes library have a different gene expression pattern than the other tow groups





✓ Clusters are driven by 3 groups of dominant genus ✓ Cluster C6 has a lower abondance of bacteria to be detected

✓ Up-regulation of many genes for the cluster A against B and C6

✓ Calprotectin subunits (S100A8 and S100A9) are up regulated in cluster A.

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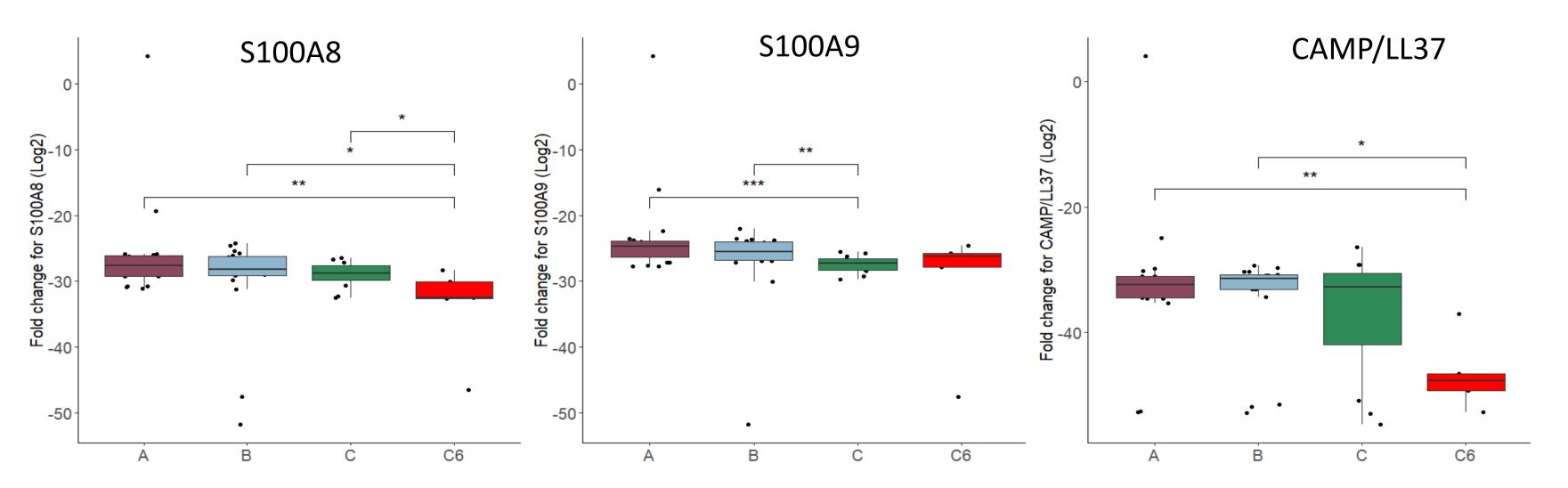
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✓ An increasing trend observed for is expression of calprotectin in group A.

✓ Cluster A and B at 1 month have better pronostic at 2 years

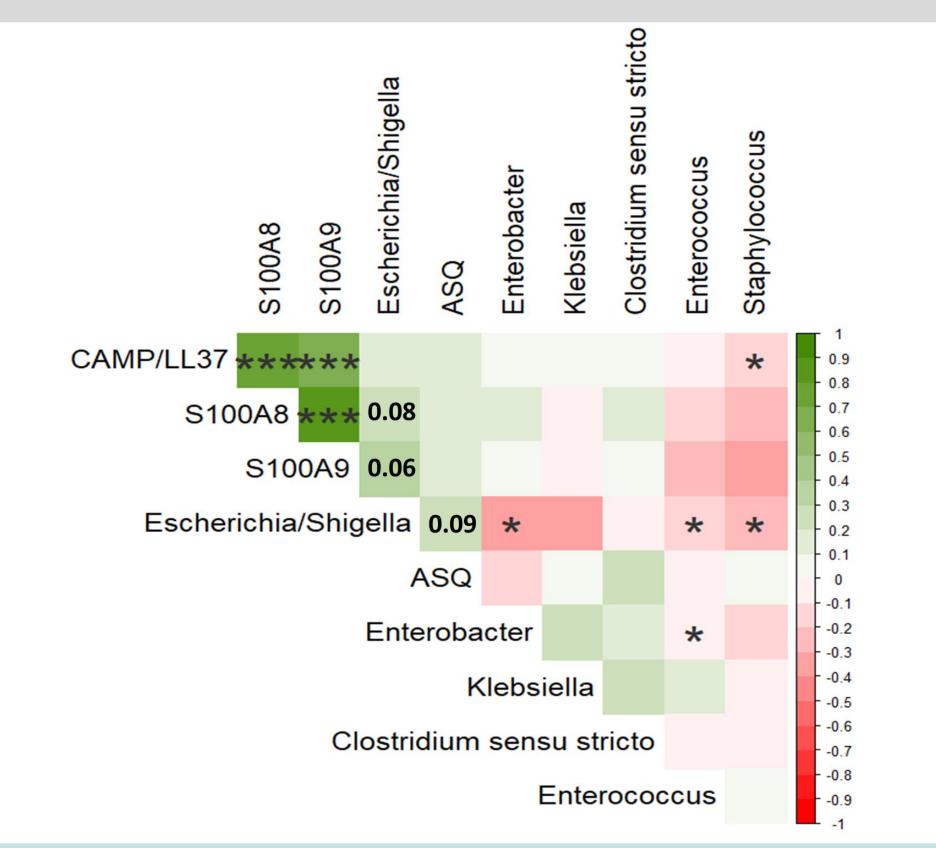
Expression of calprotectin and cathelicidin globally less expressed in children from cluster C and C6



✓ Globally, cluster A and B have a higher expression of calprotectin and cathelicidin. ✓ Cluster C6, with non detectable bacteria, has the lowest expression for calprotectin and cathelicidin.

No real impact of supernatant of bacteria on epithelial HT29 cells

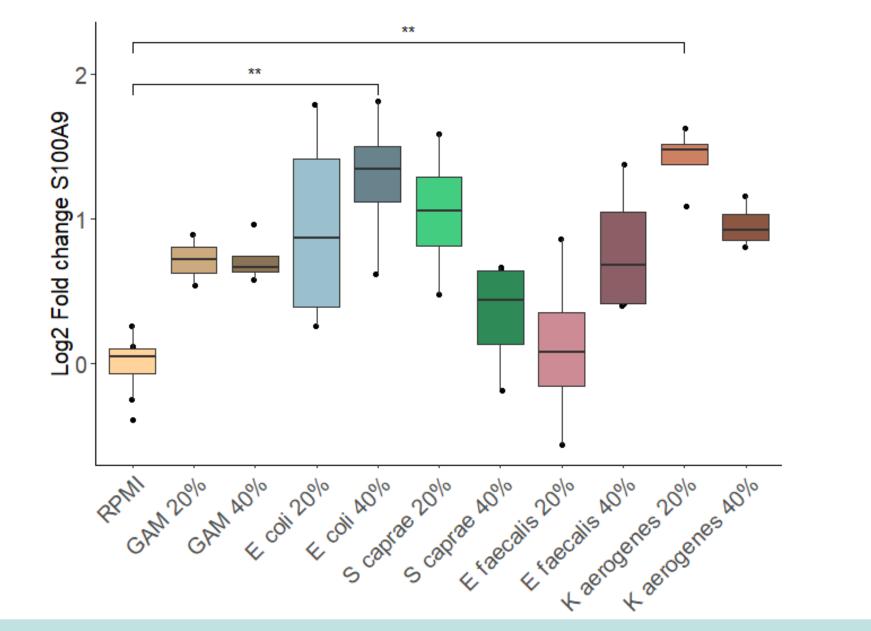
Calprotectin and cathelicidin correlated with gut microbiome



✓ Calprotectin and cathelicidin were positively correlated together

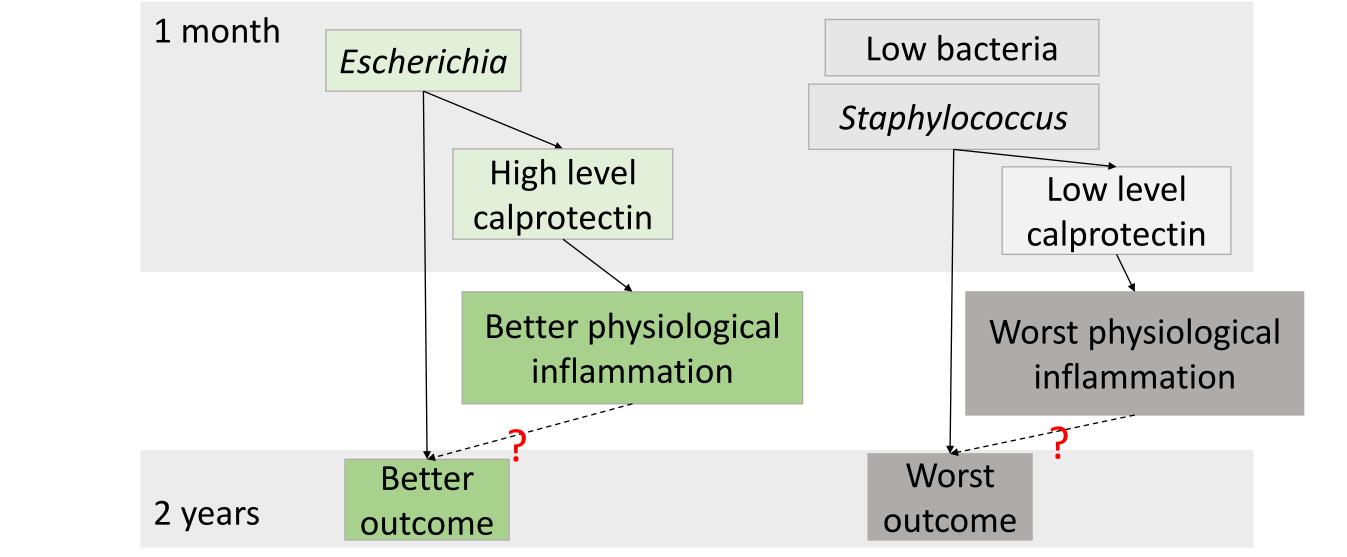
- Cathelicidin is negatively correlated with Staphylococcus (Driver of Cluster C)
- *Escherichia/Shigella* and calprotectin were positively correlated (NS)

Expression of S100A9 on HT29 cells with bacterial supernatant



✓ S100A8 was not detected in qPCR ✓ Escherichia coli and Klebsiella aerogenes increased significantly expression of S100A9

✓ ASQ at 2 years and *Escherichia/Shigella* were positively correlated (NS)



 \checkmark Gut microbiome at 1 month impact calprotectin and cathelicidin expression.

- ✓ Having *Escherichia* at 1 month increased the "physiological inflammation" with calprotectin and cathelicidin.
- ✓ Meconium ? Cells CCD 841 CoN ? Supernatant of isolates ?

