

The role of livestock in our ecosystems and economy



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The faecal microbiota during the pre-weaning period and its relationship with diarrhoea, health and performance in dairy heifer calves

Sabine Scully

Teagasc

UCD School of Veterinary Medicine





Calf health and diarrhoea

- Diarrhoeal disease
 - Most common cause of neonatal calf death
 - Morbidity and mortality:
 - 32% mortality in neonates in Ireland
 - morbidity reaches 50% globally
 - Short- and long-term economic and animal welfare implications

Predominant causes of death in calves in Ireland from birth to 1 yr. of age¹

	Neonatal (birth to 1mo)	Calfhood (1mo-5mo)	Weanling (6mo-1yr)
<i>GIT infection</i>	32%	15%	17%
<i>Systemic infection</i>	15%	8%	3%
<i>Respiratory infection</i>	8%	34%	41%

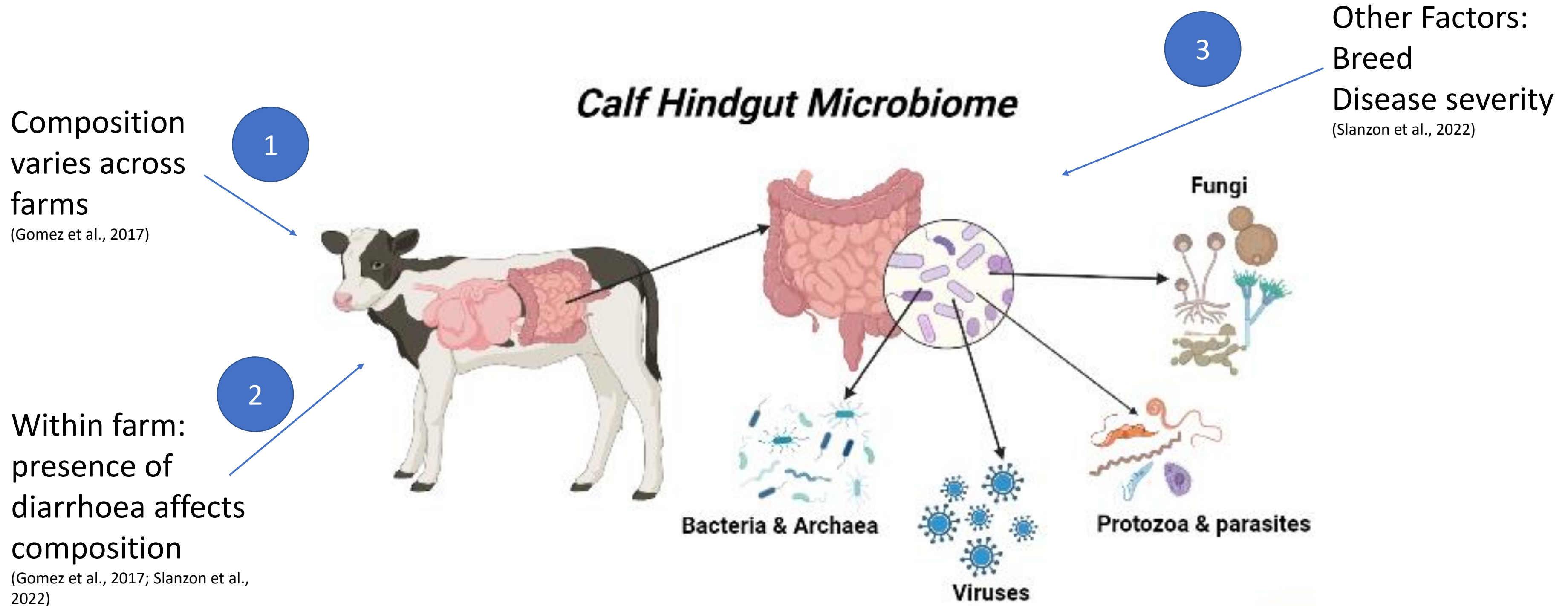
¹ Irish Department of Agriculture, Food and the Marine. 2023. All-Island Animal Disease Surveillance Report, 2022



Gut Microbiomes



Dysbiosis: loss of commensal microbes accompanied by proliferation of harmful pathogens
(Chase & Kaushik, 2019)





Objective

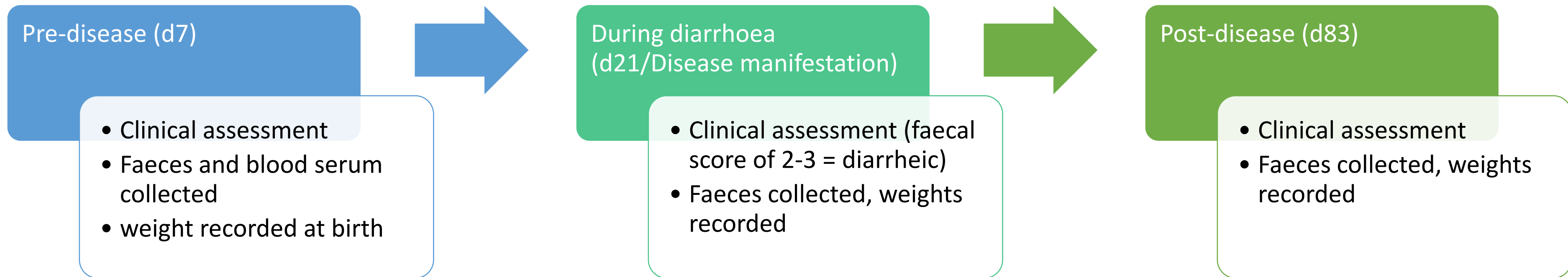
To explore the relationships of bacterial genera found to be significantly associated with health status in order to depict the dysbiosis of the hindgut microbiota





Animal model and data collection

51 spring-born, home-bred dairy heifer calves were observed and clinically assessed from birth to weaning and retroactively classified as **Diarrhoeic (n = 27)** or **Healthy calves (n = 24)**



150 faecal samples



Microbial DNA extraction
(Yu and Morrison, 2004)

Attachment of dual and Illumina
sequencing adapters



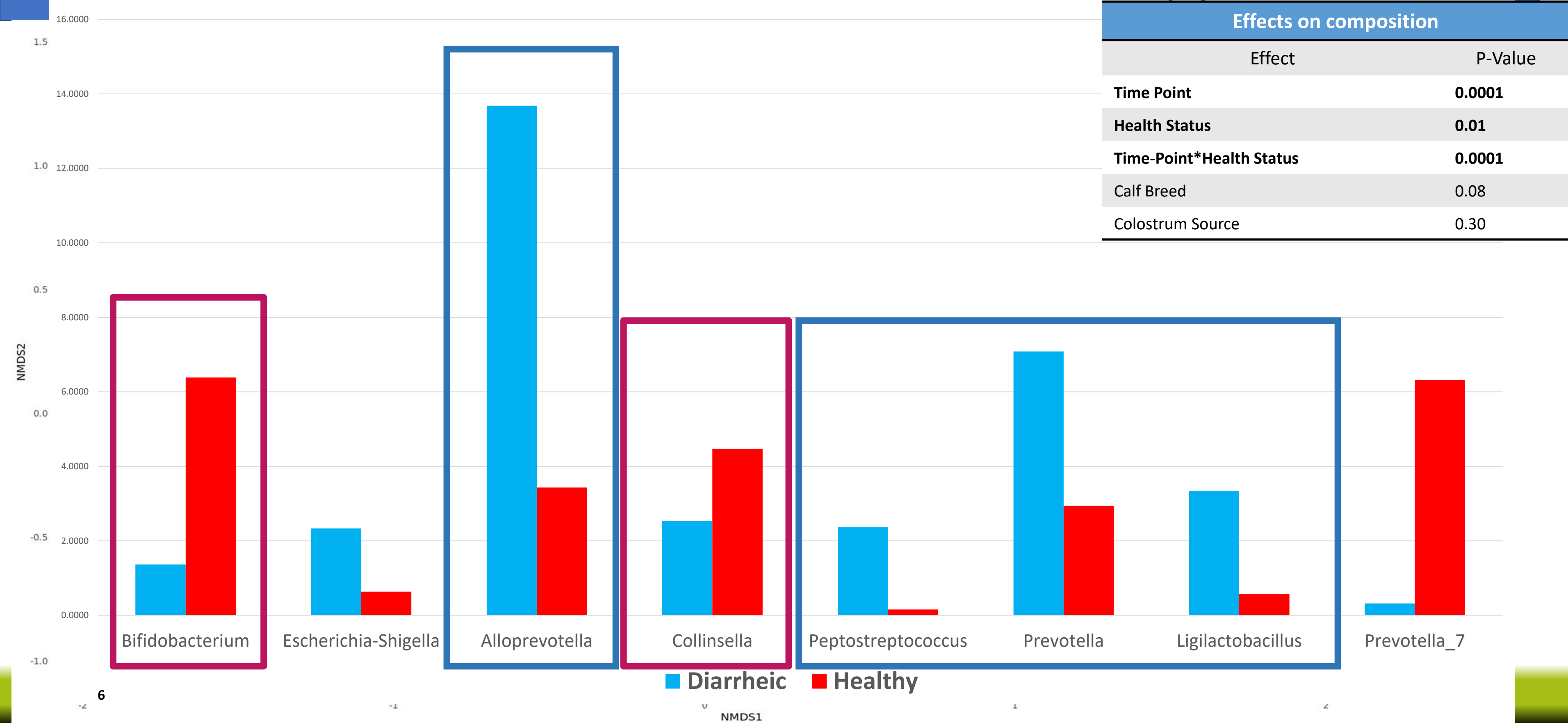
PCR amplification of
V4 region 16S rRNA
gene

Illumina MiSeq
(500 cycle V2 kit)

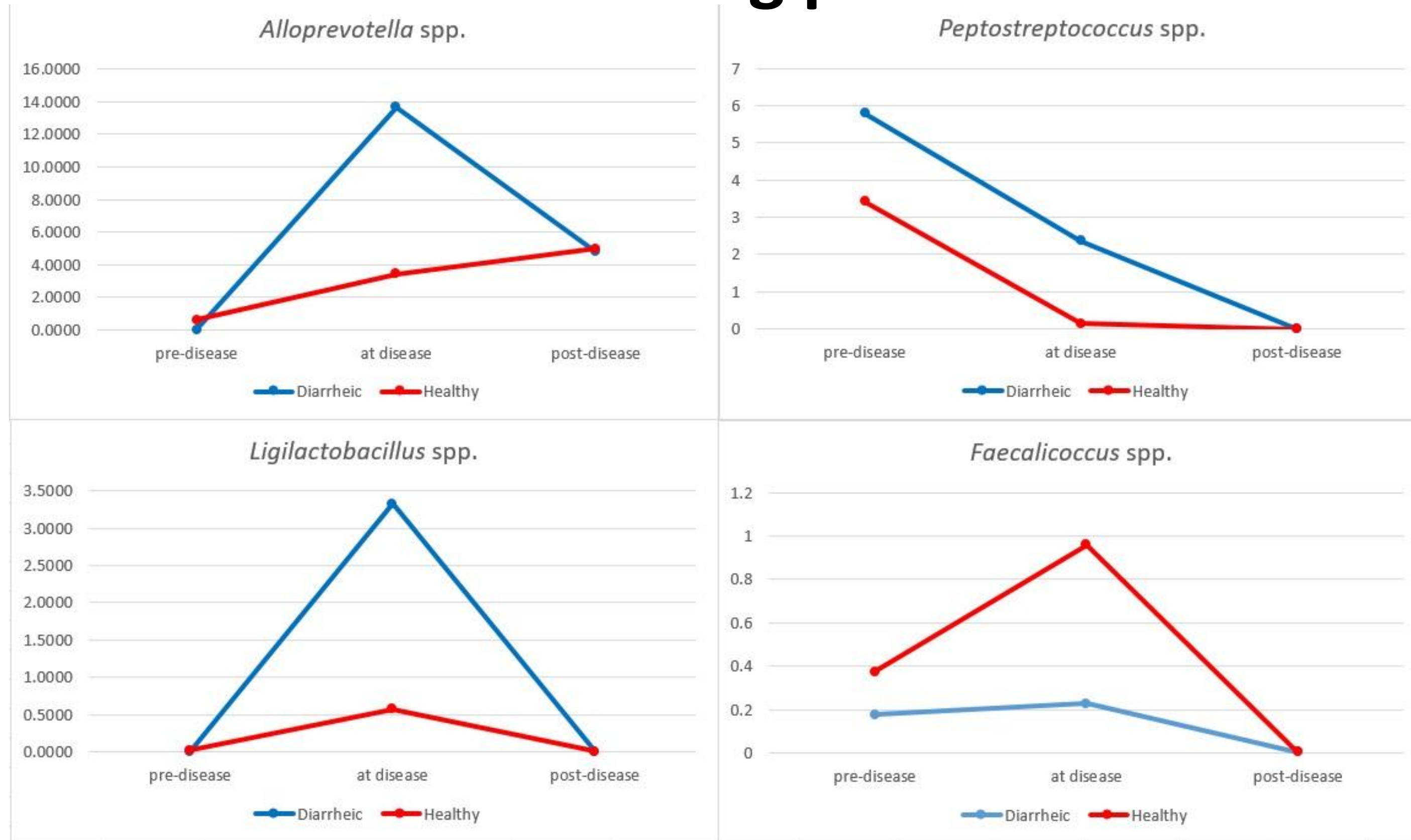


Microbial composition over the pre-weaning period

Relative Abundance at Disease Manifestation (B)



Changes in relative abundance over the pre-weaning period

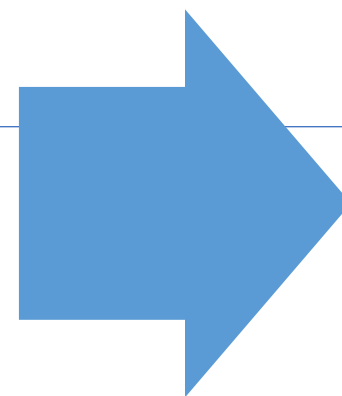


Associations: intra-ASVs

Intra-ASVs during disease manifestation

		<i>Alloprevotella</i>		<i>Bifidobacterium</i>	
	Negative	Positive	Negative	Positive	
Strong ($p \leq 0.01$) r_s : 0.60-0.79	<i>Faecalicoccus</i> <i>Akkermansia</i> <i>Intestinibacter</i>	<i>Prevotella_9</i>	None	<i>Prevotella_7</i>	
Moderate ($p \leq 0.01$) r_s : 0.40-0.59	<i>Bifidobacterium</i> <i>Prevotella_7</i> <i>Flavonifractor</i> <i>Dialister</i>	<i>Peptostreptococcus</i> <i>Prevotella</i> <i>Ligilactobacillus</i>	<i>Ligilactobacillus</i> <i>Prevotella</i> <i>Peptostreptococcus</i>	<i>Colinsella</i> <i>Faecalicoccus</i> <i>Flavonifractor</i> <i>Dialister</i> <i>Intestinibacter</i>	
Weak	<i>Butyricimonas</i>	<i>Alisonella</i>	<i>Escherichia-Shigella</i>	[f] <i>Ruminococcaceae</i>	

ASVs observed in diarrheic calves were negatively correlated to ASVs found to be associated with good gut health



ASVs observed in healthy calves have previously been associated with good gut health and are positively associated with one another



Associations: ASV's with calf performance

Faecal bacteria and calf performance

- No significant correlations observed between ASVs and average daily gain
- Some correlations with Serum Ig G concentrations:

	Negative	Positive
Weak ($p \leq 0.05$) r_s: 0.20-0.39	<i>Alloprevotella</i> <i>Peptostreptococcus</i> <i>Prevotella</i> <i>Ligilactobacillus</i>	<i>Desulfovibrio</i> <i>Akkermansia</i> <i>Butyricimonas</i> [f] <i>Ruminococcaceae</i>
Moderate ($p \leq 0.05$) r_s: 0.40-0.59	None	<i>Prevotella_7</i> <i>Faecalicoccus</i>

Applications and future work



- Depicting dysbiosis of the hindgut microbiota:
 - development targeted treatments and preventative practices
- Exploring intra-ASV relationships:
 - Clearer image of bacterial interactions
 - Better products for good hindgut health and diarrhoea prevention
- Future work:
 - The function of these microbes in the gut
 - Changes in these functions and diarrhoeal disease

Conclusions

- Diversity and composition of the microbiota change based on time **AND** animal health status
- Changes in %RA **pre-disease to diarrhoeal incidence** confirms microbial dysbiosis
- *Alloprevotella* was negatively associated with genera associated with good gut health
- Correlations intra-ASVs describe changes in the hindgut microbiota and the dysbiosis associated with diarrhoea





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Thank you for your time

Sabine.Scully@Teagasc.ie

Office: +353 (0)46 906 1199

LinkedIn: Sabine Scully

Twitter: @SabsScully

