Host genetics and hindgut microbiota jointly associate with milk yield and SCS in dairy cattle

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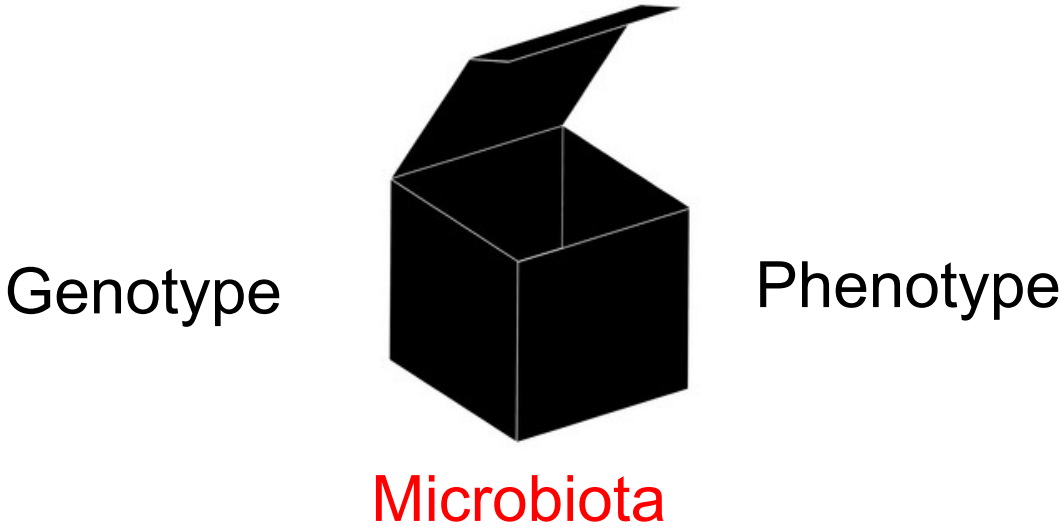
Introduction

- Gut microbiota are associated with host phenotypes (Berg et al., 2020).
- The effect of the microbiota on host phenotypes can be described by the microbiability (m^2).
- For rumen microbiota, the m^2 is 21.56% for milk protein yield (Xue et al., 2020). The m^2 was also reported for fatty acids (FA) (Buitenhuis et al., 2019) and CH_4 emission (Difford et al., 2018).
- There is emerging evidence that the hindgut microbiota is important for ruminant production efficiency and health, e.g., the m^2 for host oxidative stress (OS) is 43.1% based on 63 cows (Gu et al., 2023).

However, the effects of hindgut microbiota on milk yield and SCS in terms of m^2 is unknown.



Introduction

- The gut microbiota are known to be affected by host genetics in humans (Bonder et al., 2016), mice, pigs (Camarinha-Silva et al., 2017), and ruminants (Li et al., 2019).
- In dairy cattle, the heritability of rumen microbiota ranges from 0.13 to 0.61 (Martínez-Álvaro et al., 2022).
- The heritable and non-heritable rumen microbiota are reported to have different impacts on milk production traits (Zang et al., 2022).

However, to what extent the host genetics influence the hindgut microbiota is unknown.

Objectives:

- Estimate the m^2 of hindgut microbiota for milk yield and SCS;
- Estimate the h^2 of hindgut microbiota.

Materials and Methods- Animals and data

- **Animals:**

646 Holstein cows (433 primiparous and 213 multiparous) in the same dairy farm.

Lactation stage 1: DIM 40 -120; lactation stage 2: DIM 121 -190

- **Phenotype:**

Milk yield and SCS were recorded at the sampling date.

- **Microbiota and genotype data:**

Feces 16S rRNA sequence data and blood SNP genotype (150K)

Materials and Methods- statistical models

- **16S rRNA Sequence data processing**

  DADA2 plugin in QIIME2; SILVA database; 338F/806R primer

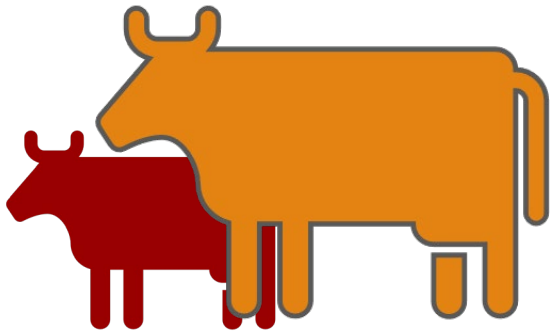
- **Estimate heritability and microbiability of milk yield and SCS**

$$y_{ijklmn} = \mu + TYM_i + parity_j + b_1 \times dim_k + b_2 \times e^{(-0.05 \times dim_k)} + AFC_l + G_m + M_n + e_{ijklmno}$$

$M = \frac{XX^T}{N}$ and $m^2 = \frac{\sigma_m^2}{\sigma_p^2}$ according to Difford et al., 2018.

- **Estimate heritability of hindgut microbiota**

$$y_{ijkln} = \mu + TYM_i + parity_j + lact_k + G_l + e_{ijkln}$$



Results & Discussion– hindgut microbiota composition

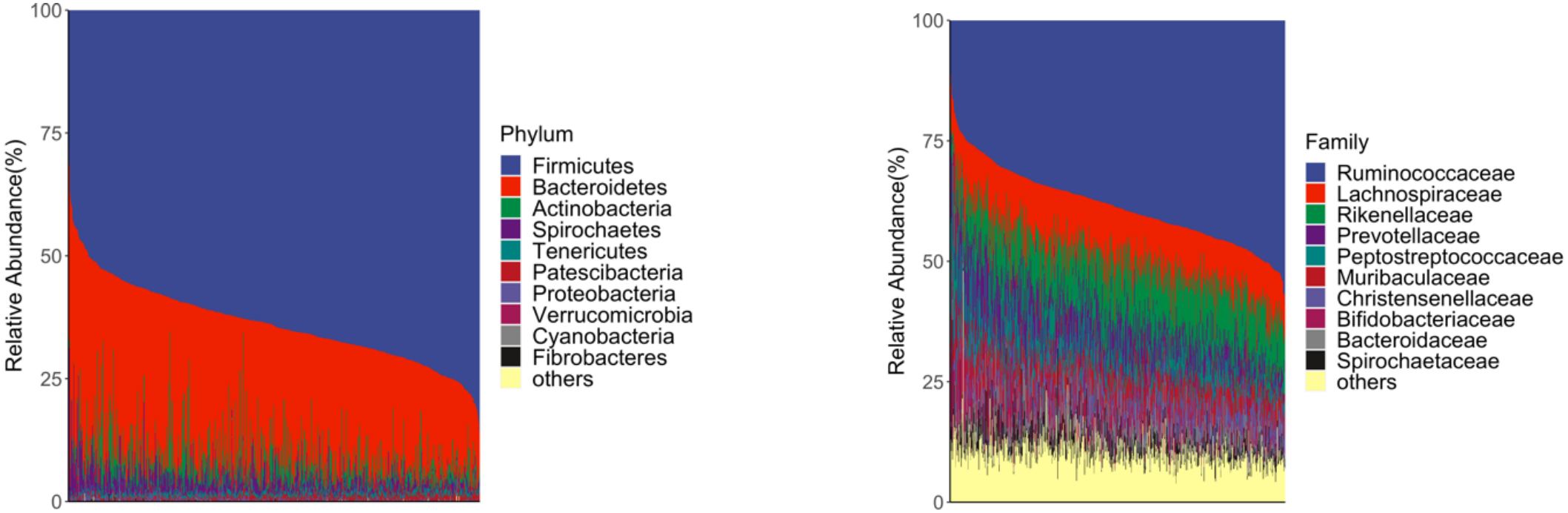


Figure 1. Relative abundance in Holstein hindgut microbiota at the phylum (A) and family (B) levels.

- 26,884 clean reads per sample; 14,238 unique ASVs; 1,616 ASVs in more than 10% of samples.
- 99.6% of ASVs had been assigned at the family level, 81% of ASVs had been assigned at the genus level.
- Phylum *Firmicutes* accounted for 64% and *Bacteroidetes* accounted for 28% of the total bacterial abundance.

Results & Discussion- m^2 of milk yield and SCS

Table 1. Heritability and microbiability of milk yield and SCS

Traits	individually h^2	individually m^2	simultaneously h^2	simultaneously m^2
Milk yield	0.31 (0.08[1])	0.29 (0.06)	0.23 (0.08)	0.26 (0.06)
SCS	0.11 (0.07)	0.07 (0.04)	0.13 (0.07)	0.07 (0.04)

[1] standard error.

- There are 11 bacterial taxa with effects on milk yield, including 1 class, 1 order, 1 family, 7 genera, and 1 species, as well as 47 ASVs (FDR < 0.01).
- There are 1 genus and 5 ASVs with effects on SCS (FDR < 0.05) .

Results & Discussion– Heritability of hindgut microbiota

Table 2. Heritability of hindgut microbiota

Microbiota	number	Significant	heritability
Phyla	10	4	0.16 ~ 0.21
Classes	16	2	0.15 ~ 0.18
Orders	22	7	0.13 ~ 0.21
Families	44	8	0.15 ~ 0.36
Genera	119	29	0.13 ~ 0.54
Species	11	1	0.32
Total	222	51 (23%)	0.13 ~ 0.54
ASV	1616	184 (11%)	0.11 ~ 0.53

- 51 in 222 microbiota taxa had significant heritabilities, of which 3 taxa had heritabilities higher than 0.30, and 48 taxa had heritabilities ranging from 0.13 to 0.29 (FDR < 0.01).
- 29 taxa belong to the phylum *Firmicutes,* and 8 belong to the phylum *Bacteroidetes* (FDR < 0.01).

Results & Discussion– Heritability of hindgut microbiota

Traits	V_p	V_e	V_g	h^2	se	Taxa	Abundance	Phyla	Classes	Orders	Families
p_Firmicutes	0.15	0.12	0.02	0.16	0.07	Phylum	63.87	Firmicutes			
f_Lachnospiraceae	0.16	0.11	0.04	0.27	0.08	Family	11.18	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae
f_Ruminococcaceae	0.07	0.06	0.01	0.20	0.08	Family	38.72	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae
f_Peptococcaceae	1.14	0.97	0.17	0.15	0.07	Family	0.17	Firmicutes	Clostridia	Clostridiales	Peptococcaceae

- 3 families, 24 genera and 1 species in *Firmicutes* have significant heritability (FDR < 0.01).
- Genera *Coprococcus* 3 and *Syntrophococcus* in *Firmicutes* have significant effects on milk yield (FDR < 0.01).

Results & Discussion- Heritability of hindgut microbiota

Traits	V_p	V_e	V_g	h^2	se	Taxa	Abundance	Phyla	Classes	Orders	Families	Genera
p_Bacteroidetes	0.18	0.14	0.04	0.21	0.08	Phylum	27.66	Bacteroidetes				
c_Bacteroidia	0.15	0.13	0.02	0.15	0.07	Class	27.66	Bacteroidetes	Bacteroidia			
o_Flavobacteriales	0.89	0.77	0.12	0.13	0.07	Order	0.02	Bacteroidetes	Bacteroidia	Flavobacteriales		
f_p_2534_18B5_gut_group	5.44	3.50	1.94	0.36	0.08	Family	0.45	Bacteroidetes	Bacteroidia	Bacteroidales	p-2534-18B5 gut group	
f_p_251_o5	2.13	1.62	0.51	0.24	0.08	Family	0.06	Bacteroidetes	Bacteroidia	Bacteroidales	p-251-o5	
f_Bacteroidales_UCG_001	1.16	0.89	0.27	0.23	0.08	Family	0.02	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales UCG-001	
g_dgA_11_gut_group	2.09	1.71	0.37	0.18	0.08	Genus	0.06	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	dgA-11 gut group
g_Odoribacter	0.91	0.76	0.14	0.16	0.07	Genus	0.01	Bacteroidetes	Bacteroidia	Bacteroidales	Marinifilaceae	Odoribacter

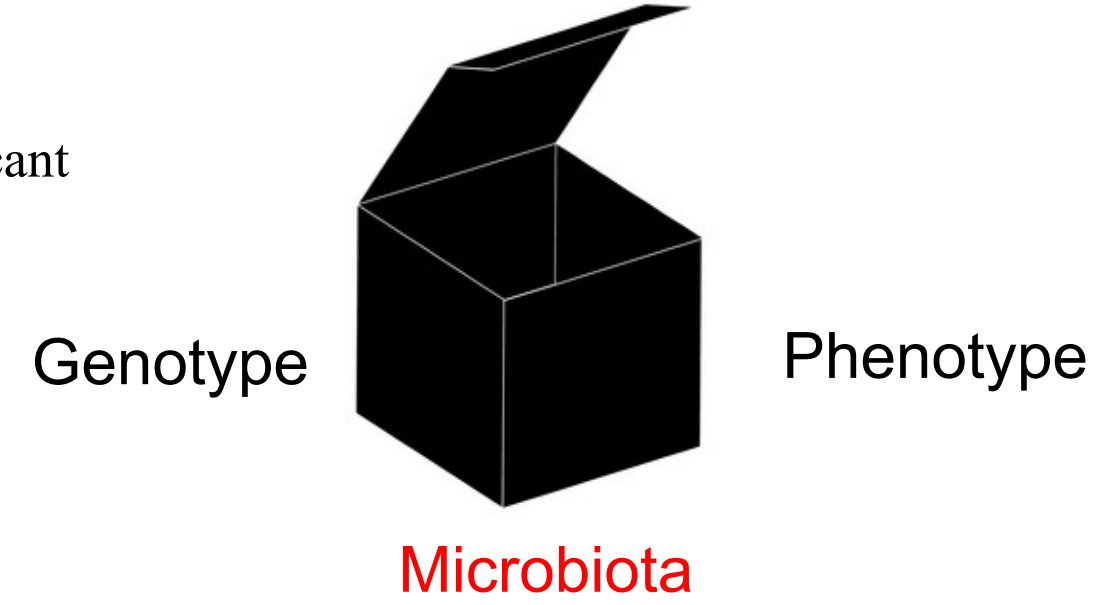
- 1 class, 1 order, 2 families, and 2 genera in *Bacteroidetes* have significant heritability (FDR < 0.01).

Next plan and take home messages

- **Next Plan:**

  The genetic correlation and GWAS for hindgut microbiota.

- **Conclusions:**
- Hindgut microbiota composition is different from rumen microbiota composition.
- The m^2 is 0.26 for milk yield and 0.07 for SCS.
- 23% of hindgut microbiota and 11% of ASVs have significant h^2 and are mainly in phyla *Firmicutes* and *Bacteroidetes*.



Suggestions and questions

Thanks for your attention