

# Effect of gut microbiota composition on carcass and meat quality traits in swine

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August 27, 2019

Ghent, Belgium

# Introduction

- The mammalian gastrointestinal tract is a home of a diverse micro-organisms which serve various biological functioning of the host.
- Commensal bacteria are often called the “forgotten organ” of the host.
- Gut microbiome constitutes a portion of the whole genome (Sommer & Bäckhed, 2013; Xiao et al., 2016) and has the potential to affect numerous biological activities that hosts lack.
- Previous researchers (Sandoval-motta, Aldana, & Martínez-romero, 2017) reported that microbial diversity of intestine accounted for significant amount of phenotypic variation for any trait.

# Objectives

- To estimate the microbiability and investigate its impact on heritability estimates of meat quality and carcass traits.
- To estimate the microbial correlation between the meat quality and carcass traits.

# Material and methods



Duroc ♂  
n = 28



Yorkshire x Landrace ♀  
Landrace x Yorkshire



Weaning  
15 – 24d

Mid-test  
115 – 124d

Off-test  
180 – 217d

Fecal sample  
n = 1205

Fecal sample  
n = 1295

Fecal sample  
n = 1283

Sample preparation → DNA extraction → Library construction

Sequencing → Data quality control

Operational taxonomic units (OTU)  
n = 1755

# Summary statistics of traits

N = 1,123

## Meat quality traits

Traits	Acronym	Mean	SD
Intra muscular fat, %	IMF	2.71	0.93
Minolta a*	MINA	3.79	1.10
Minolta b*	MINB	-0.15	0.91
Minolta L*	MINL	45.30	3.10
Ultimate pH	PH	5.64	0.18
Subjective color	SCOL	2.72	0.47
Subjective marbling	SMARB	3.10	0.83
Subjective firmness	SFIRM	3.04	0.99
Slice shear force, kg	SSF	15.9	3.65

## Growth and carcass traits

Traits	Acronym	Mean	SD
Carcass traits			
Loin depth, mm	LD	66.78	6.91
Back fat depth, mm	FD	22.62	4.88
Carcass average daily gain, g/day	CADG	560.00	70.00
Ham weight, kg	HAMWT	25.19	2.34
Loin Weight, kg	LOINWT	23.04	2.16
Belly weight, kg	BELLYWT	18.28	2.78

# Creation of M matrix

- **M** matrix was created as described by Camarinha-Silva et al. (2017).
- $\mathbf{M} = \frac{1}{N} \mathbf{X}\mathbf{X}'$ ;  $\mathbf{X}$  is matrix with dimension of  $n \times q$ , where  $n$  is number of animals and  $q$  is number of OTUs.
- $$\mathbf{X}_{ij} = \frac{\log \mathbf{P}_{ij} - \overline{\log \mathbf{P}_{oj}}}{sd(\log \mathbf{P}_{oj})}$$
- **P** is matrix of dimension  $n \times q$  where the elements  $\mathbf{P}_{ij}$  are the relative abundance of OTU  $j$  in animal  $i$ ,  $\mathbf{P}_{oj}$  is the vector of relative abundance of each OTU.
- **M** matrix was constructed for each stage.

**Objective 1 : To estimate the microbiability and investigate its impact on heritability estimates of meat quality and carcass traits.**

ASREML v4.

## Model

- Model 0 (only genomic information)  $y_{ijklm} = ELSE + a_l + p_{o(j)} + e_{ijklm}$
- Model 1 (microbiome at **Weaning**)  $y_{ijklmn} = ELSE + a_l + m_n + p_{o(j)} + e_{ijklmn}$
- Model 2 (microbiome at **Mid test**)  $y_{ijklmn} = ELSE + a_l + m_n + p_{o(j)} + e_{ijklmn}$
- Model 3 (microbiome at **Off test**)  $y_{ijklmn} = ELSE + a_l + m_n + p_{o(j)} + e_{ijklmn}$

$ELSE = \mu$  : mean

$D_i$ : fixed effect of dam line (2 levels)

$CG_j$  : fixed effect of replication (6 levels)

$G_k$  : fixed effect of gender (2 levels)

## Objective 2 : To estimate the microbial correlations between meat quality and carcass traits in swine.

- Data were analyzed using multi trait genomic model in ASREML v4.

### Model:

$$y_{ijklmn} = \mu + D_i + CG_j + G_k + a_l + m_n + p_{m(j)} + e_{ijklmn}$$

$m_n$  = Random effect of microbiome at Mid test and Off test



# Predictive Ability

## ➤ Cross-validation

- 4-fold cross validation scheme
- Training set (~ 75% ) and testing set (~ 25%)
- Individuals were grouped based on sire relatedness

## ➤ 3 scenario

- Full: All markers and OTUs
- Informatively reduced: Informatively reduced markers and OTUs
- Randomly reduced: Randomly reduced markers and OTUs

# Model

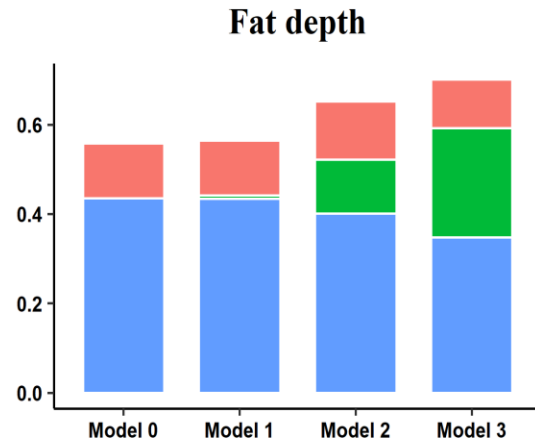
➤ 5 models for each scenario

- Null : 
$$y_{ijklm} = \mu + D_i + CG_j + G_k + p_{m(j)} + e_{ijklm}$$
- G (Genomic) 
$$y_{ijklm} = ELSE + a_l + p_{m(j)} + e_{ijklm}$$
- M (Microbiome) 
$$y_{ijklm} = ELSE + m_n + p_{m(j)} + e_{ijkmn}$$
- M+G (Both) 
$$y_{ijklm} = ELSE + a_l + m_n + p_{m(j)} + e_{ijklm}$$
- M+G+MG (Interaction): 
$$y_{ijklmn} = ELSE + a_l + m_n + am_{ln} + p_{m(j)} + e_{ijklmn}$$

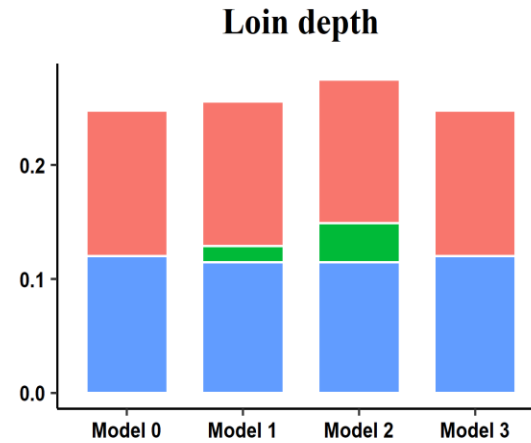
# Results

# Proportion of variance absorbed in carcass composition traits

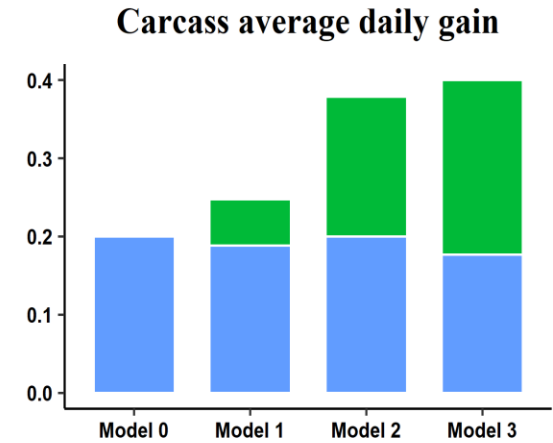
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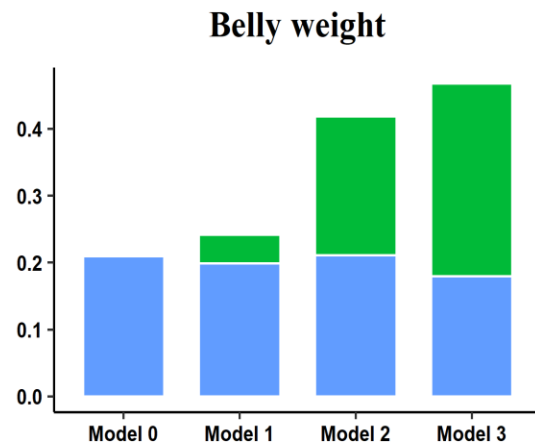
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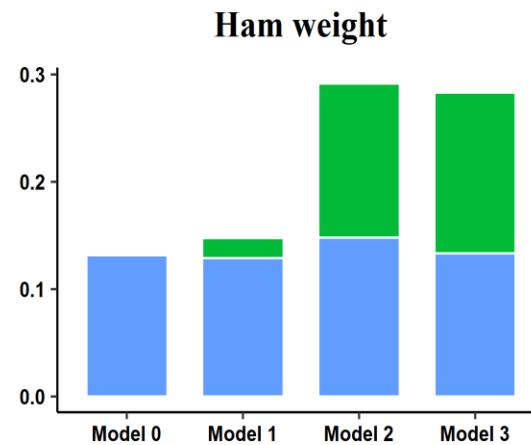
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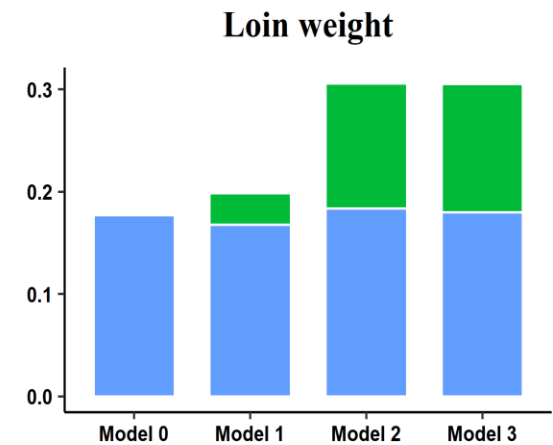
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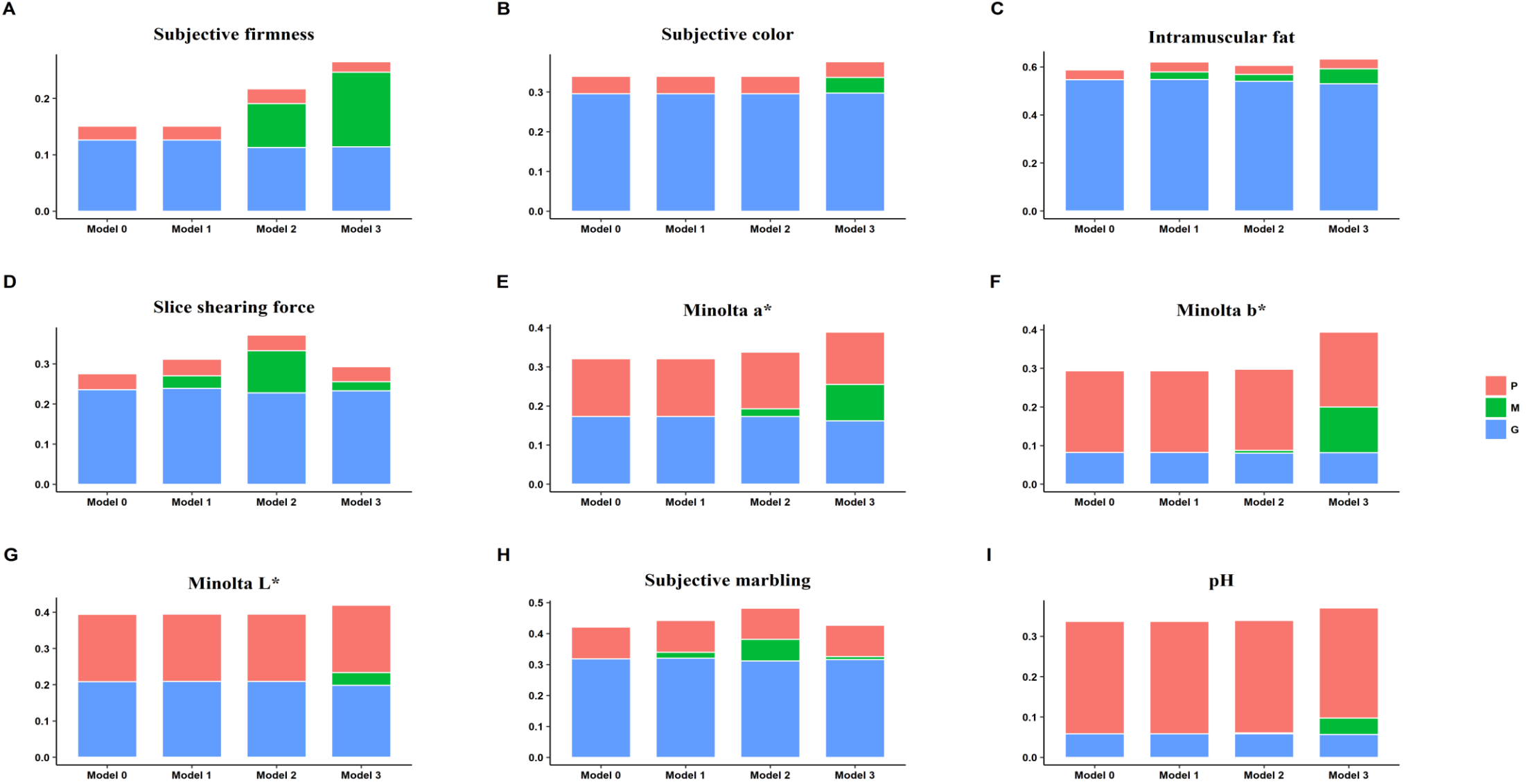
E



F



# Proportion of variance absorbed in meat quality traits



# Microbial and genomic correlation meat quality traits

## Mid test

	SMARB	SFIRM	SSF	FD	CADG	HAMWT	LOINWT	BELLYWT
SMARB		0.39±0.33	<b>-0.72±0.28</b>	<b>0.46±0.24</b>	-0.21±0.28	-0.27±0.29	-0.34±0.32	-0.02±0.26
SFIRM	<b>0.42±0.18</b>		<b>-0.93±0.11</b>	NC	<b>0.86±0.17</b>	<b>0.62±0.24</b>	<b>0.58±0.26</b>	<b>0.87±0.16</b>
SSF	0.08±0.16	-0.23±0.21		<b>-0.70±0.21</b>	<b>-0.68±0.22</b>	-0.45±0.25	<b>-0.50±0.25</b>	<b>-0.55±0.24</b>
FD	<b>0.22±0.11</b>	NC	<b>-0.44±0.13</b>		<b>0.68±0.15</b>	<b>0.50±0.19</b>	<b>0.44±0.21</b>	<b>0.74±0.11</b>
CADG	0.02±0.17	0.03±0.23	0.19±0.18	0.21±0.15		<b>0.98±0.02</b>	<b>0.95±0.03</b>	<b>0.98±0.01</b>
HAMWT	-0.13±0.18	0.11±0.24	0.27±0.20	0.01±0.15	<b>0.67±0.11</b>		NC	<b>0.96±0.03</b>
LOINWT	-0.09±0.17	0.10±0.23	0.11±0.18	-0.14±0.15	<b>0.69±0.09</b>	<b>0.53±0.11</b>		<b>0.94±0.06</b>
BELLYWT	0.31±0.17	0.35±0.23	0.18±0.15	<b>0.57±0.11</b>	<b>0.79±0.06</b>	<b>0.42±0.17</b>	<b>0.42±0.15</b>	

Numbers highlighted in bold are significant ( $P < 0.05$ );  
Microbial correlation above diagonal and genomic correlations below diagonal.

# Microbial and genomic correlation meat quality traits

## Off test

	SCOLOR	IMF	SFIRM	MINA	MINB	PH
SCOLOR		-0.28±0.57	0.07±0.31	0.29±0.44	-0.26±0.39	<b>0.90±0.25</b>
IMF	-0.22±0.13		<b>0.91±0.17</b>	<b>0.55±0.28</b>	<b>0.75±0.27</b>	0.10±0.47
SFIRM	0.18±0.19	0.29±0.17		0.26±0.27	0.12±0.26	<b>0.73±0.35</b>
MINA	<b>0.45±0.16</b>	<b>0.29±0.14</b>	-0.53±0.28		<b>0.78±0.16</b>	0.33±0.36
MINB	-0.94±0.22	<b>0.78±0.16</b>	-0.03±0.32	-0.10±0.27		0.38±0.38
PH	0.13±0.50	-0.18±0.25	0.44±0.36	-0.04±0.33	-0.47±0.42	

Numbers highlighted in bold are significant ( $P < 0.05$ );  
Microbial correlation above diagonal and genomic correlations below diagonal

# Microbial and genomic correlation of carcass composition

## Off test

	FD	CADG	HAMWT	LOINWT	BELLYWT
FD		<b>0.71±0.11</b>	<b>0.59±0.16</b>	<b>0.55±0.17</b>	<b>0.94±0.05</b>
CADG	0.14±0.15		<b>0.97±0.02</b>	<b>0.91±0.05</b>	<b>0.94±0.03</b>
HAMWT	-0.10±0.17	<b>0.63±0.13</b>		NE	<b>0.87±0.06</b>
LOINWT	-0.13±0.15	<b>0.67±0.10</b>	NE		<b>0.82±0.08</b>
BELLYWT	<b>0.49±0.13</b>	<b>0.78±0.07</b>	0.34±0.19	<b>0.40±0.16</b>	

Numbers highlighted in bold are significant ( $P < 0.05$ );

Microbial correlation above diagonal and genomic correlations below diagonal

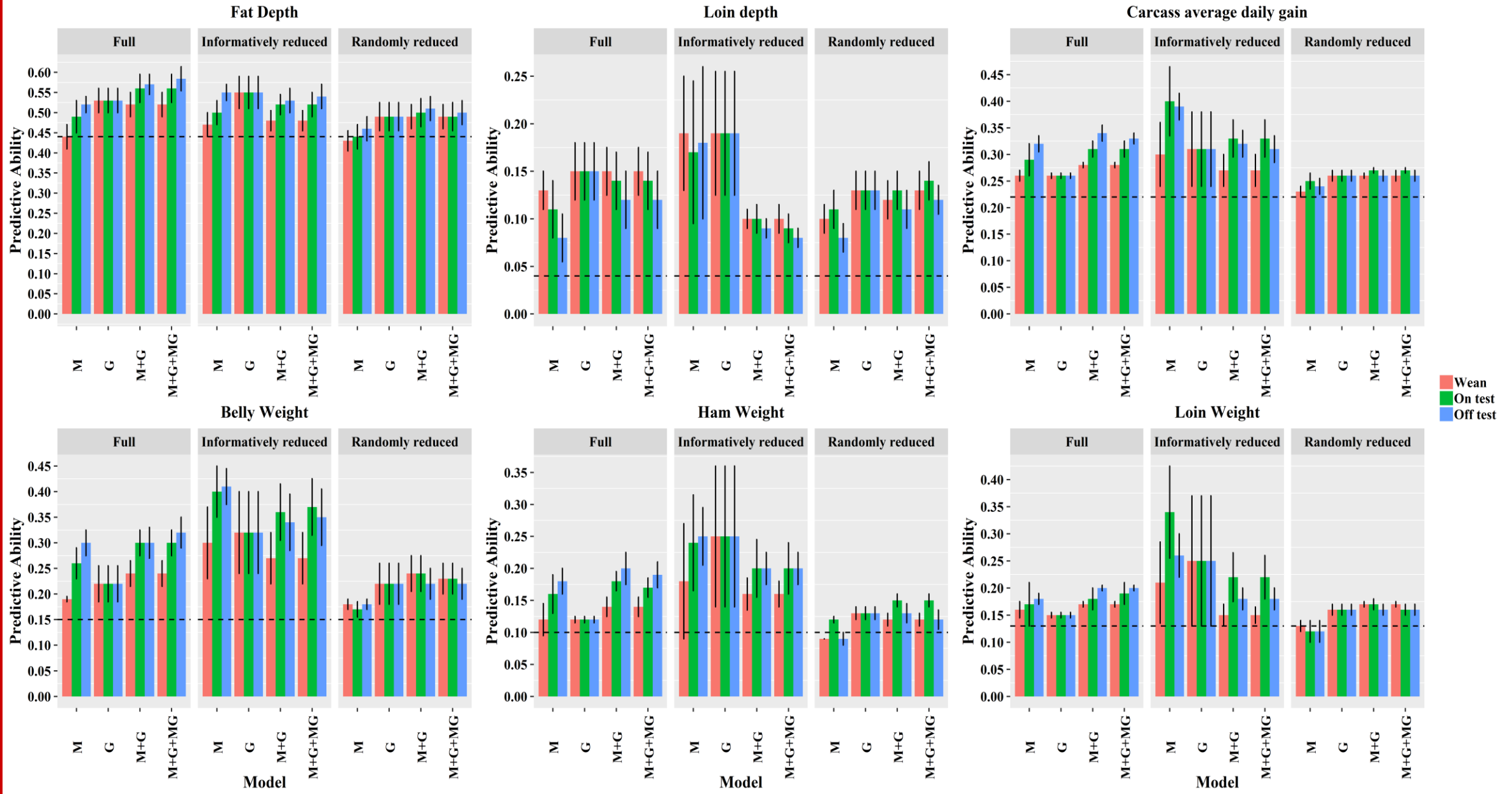


# Microbial correlation of meat quality and carcass composition traits at Off test

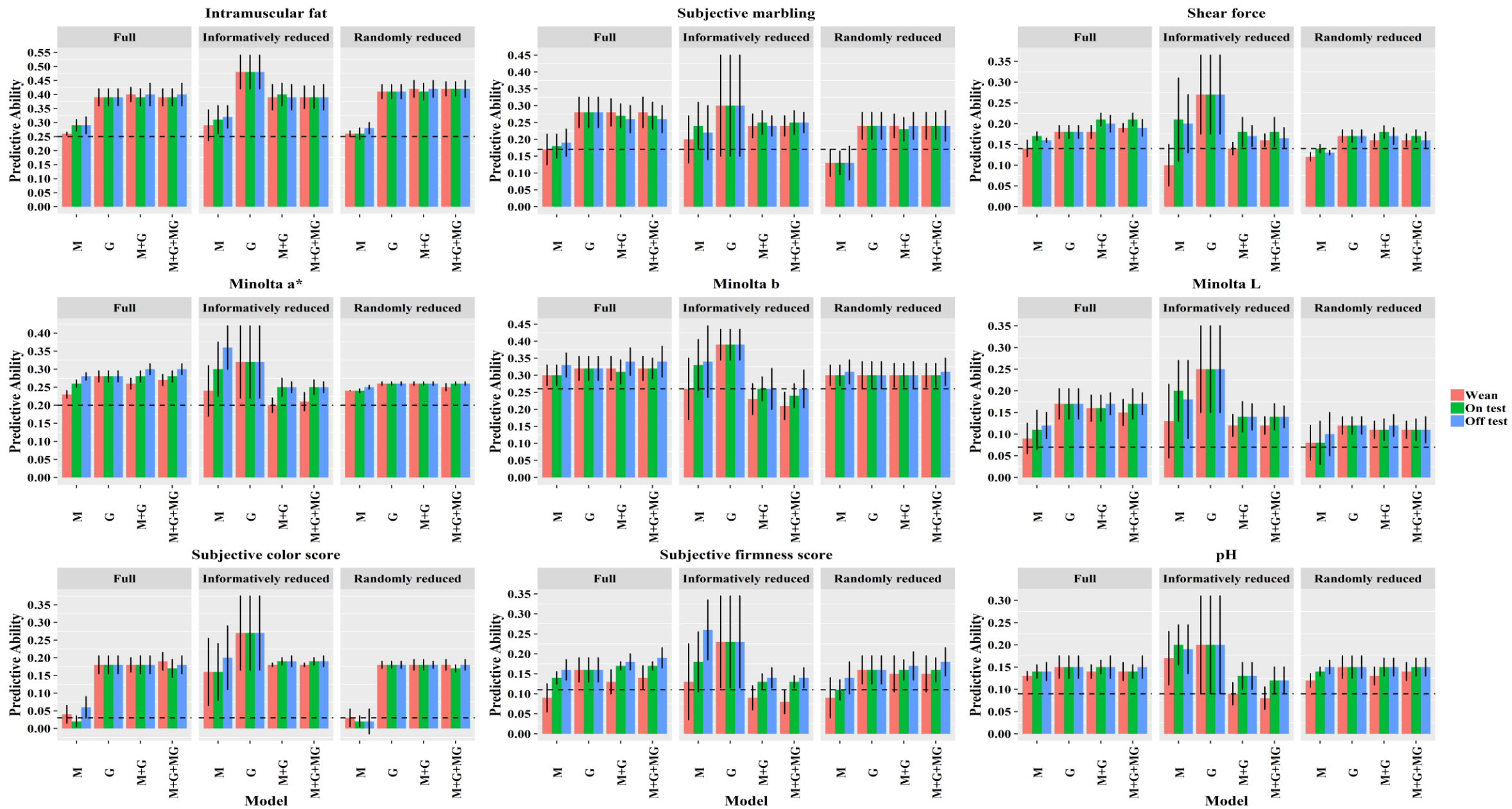
	FD	CADG	HAMWT	LOINWT	BELLYWT
SCOLOR	-0.29±0.37	-0.09±0.35	0.16±0.38	-0.25±0.35	-0.32±0.37
IMF	<b>0.90±0.14</b>	0.43±0.33	0.29±0.27	0.21±0.30	<b>0.73±0.18</b>
SFIRM	NE	0.31±0.19	0.18±0.24	-0.01±0.20	<b>0.50±0.18</b>
MINA	<b>0.53±0.18</b>	<b>0.66±0.17</b>	0.11±0.27	0.08±0.30	<b>0.41±0.21</b>
MINB	<b>0.43±0.19</b>	<b>0.58±0.18</b>	0.12±0.25	-0.13±0.28	0.35±0.20
PH	0.17±0.31	0.27±0.35	NC	NC	0.11±0.32

Numbers highlighted in bold are significant ( $P < 0.05$ )

# Predictive ability of carcass traits



# Predictive ability of meat quality traits



# Conclusions

- Adding microbiome information did not affect the estimates of genomic heritability of meat quality traits but changed the estimate of carcass composition traits
- Microbial correlation was highest for carcass composition traits than meat quality traits.
- Microbial correlation was greater at off test than on test and weaning.
- High microbial correlations among different traits suggests that genetic correlations among traits are partially contributed by the correlations among the gut microbiota composition.

# Acknowledgements

