



# Microbiability of feed efficiency related traits in pigs

2 December 2020 | L.M.G. Verschuren,  
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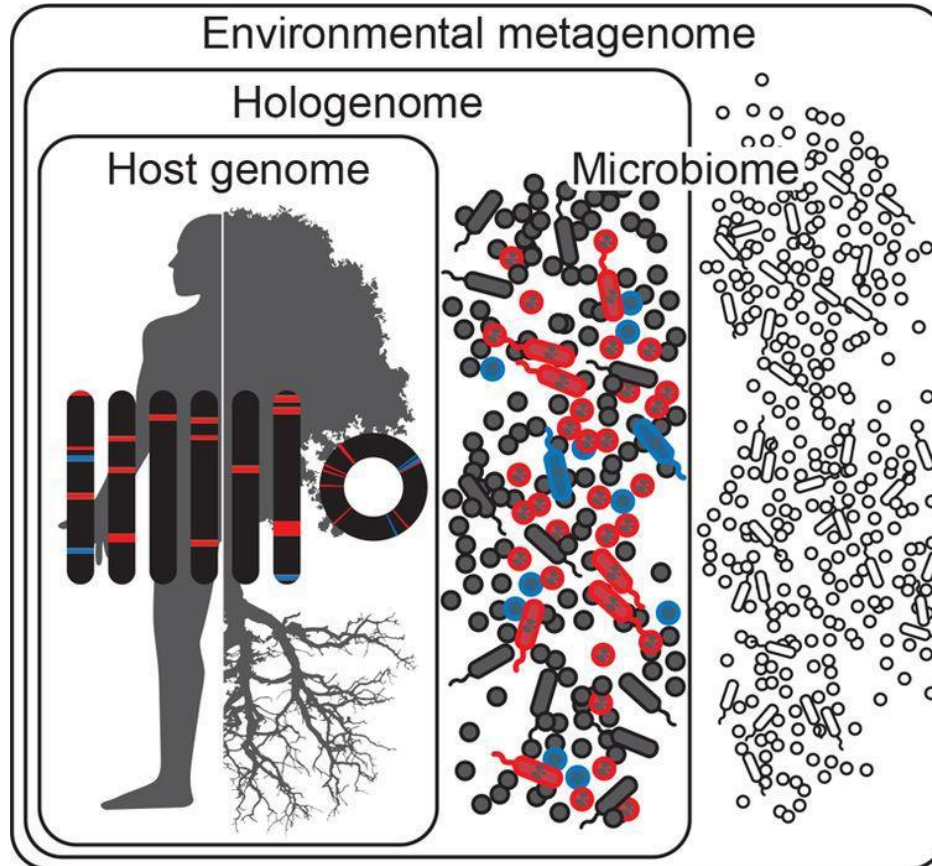
# Acknowledgement





## Feed-a-Gene





# Introduction



 Host and symbiont genes that alone and/or together affect a holobiont phenotype

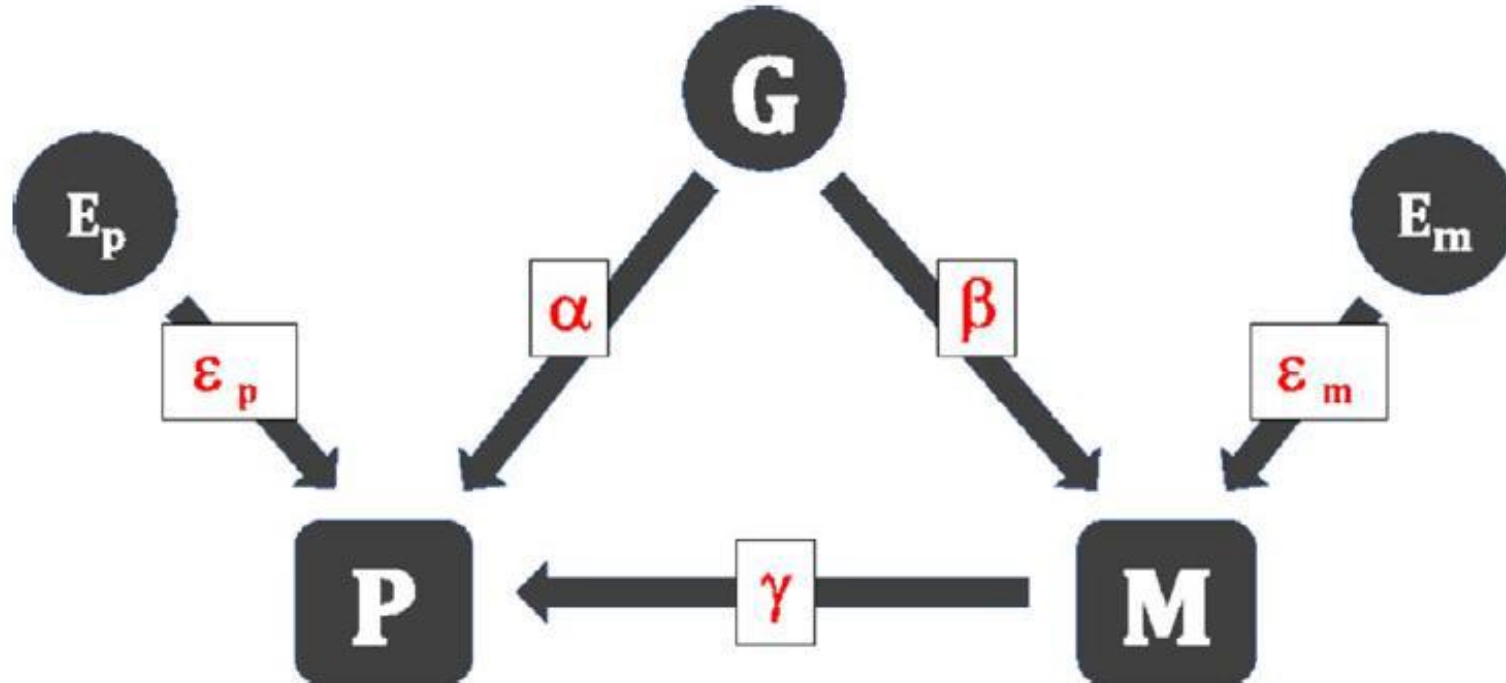
 Coevolved host and symbiont genes that affect a holobiont phenotype

 Host genes and symbionts that do not affect a holobiont phenotype

 Environmental microbes that are not part of the holobiont

Theis *et al.* (2016)

# Introduction



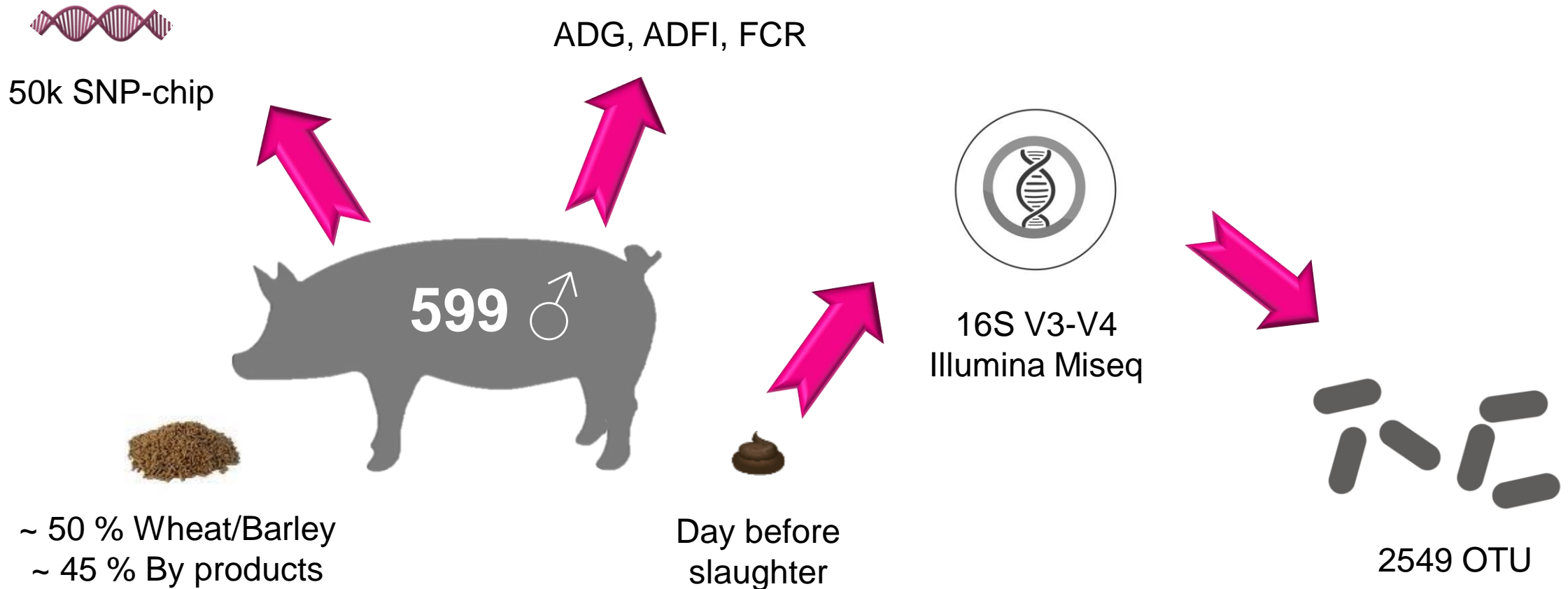
Maltecca *et al.* (2019)

# Goal

**This study aimed to  
use microbial and genetic relationships  
to predict  
feed efficiency related traits  
in pigs**

# Materials and Methods

## Experimental set-up



# Materials and Methods

## Microbiability

The fraction of the phenotypic variance explained by the microbial variance (Difford et al., 2016).

In formula:

$$m^2 = \sigma^2_m / (\sigma^2_p)$$

Compare to heritability:

$$h^2 = \sigma^2_g / (\sigma^2_p)$$

# Materials and Methods

## Models

$$y = Xb + Zm + Uc + e \quad (1)$$

$$y = Xb + Wg + Uc + e \quad (2)$$

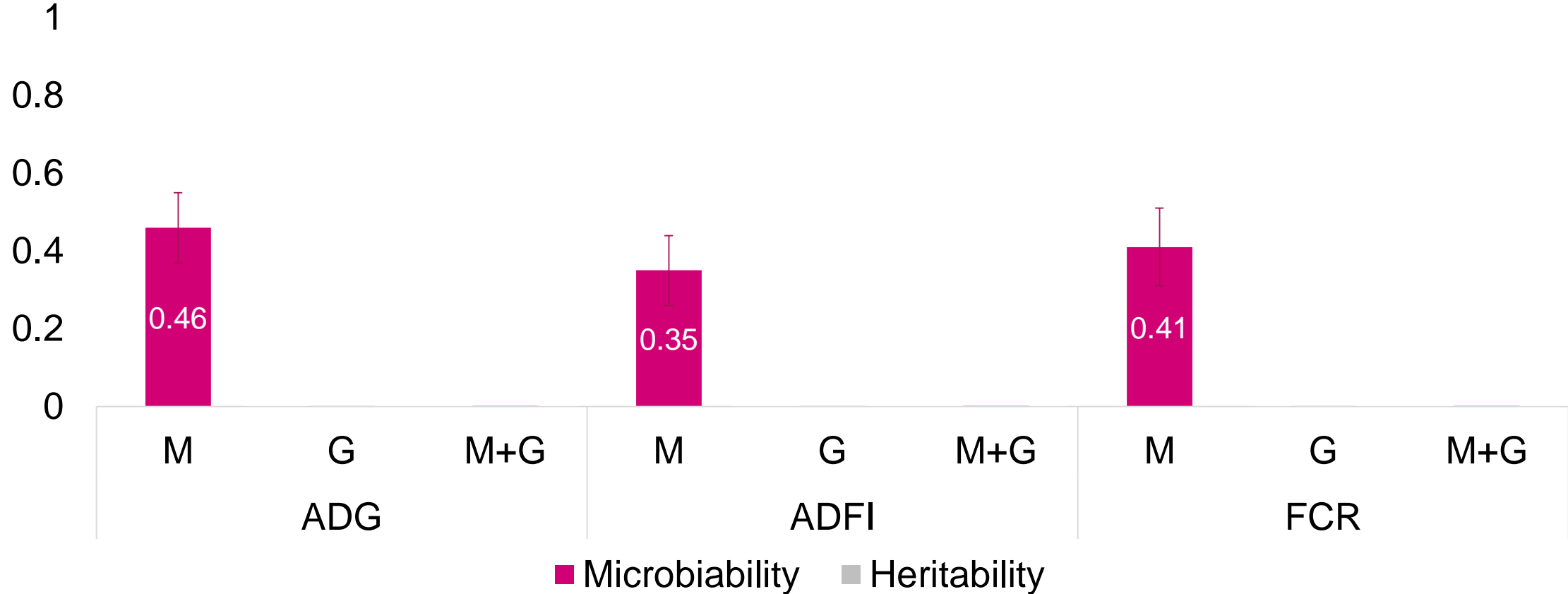
$$y = Xb + Wg + Zm + Uc + e \quad (3)$$

- $y$  = vector of phenotypes (one record per sample)
- $X$  = incidence matrix for the fixed effects for pen and co-variable weight at start experiment
- $b$  = fixed effects
- $Z$  = incidence matrix for OTU effects
- $m$  = random effect estimate of OTU
- $W$  = incidence matrix SNP effects
- $g$  = random effect estimates of SNP
- $U$  = incidence matrix for common litter effect (foster dam in case of cross-fostering)
- $c$  = random effect estimate of common litter
- $e$  = random residuals estimate



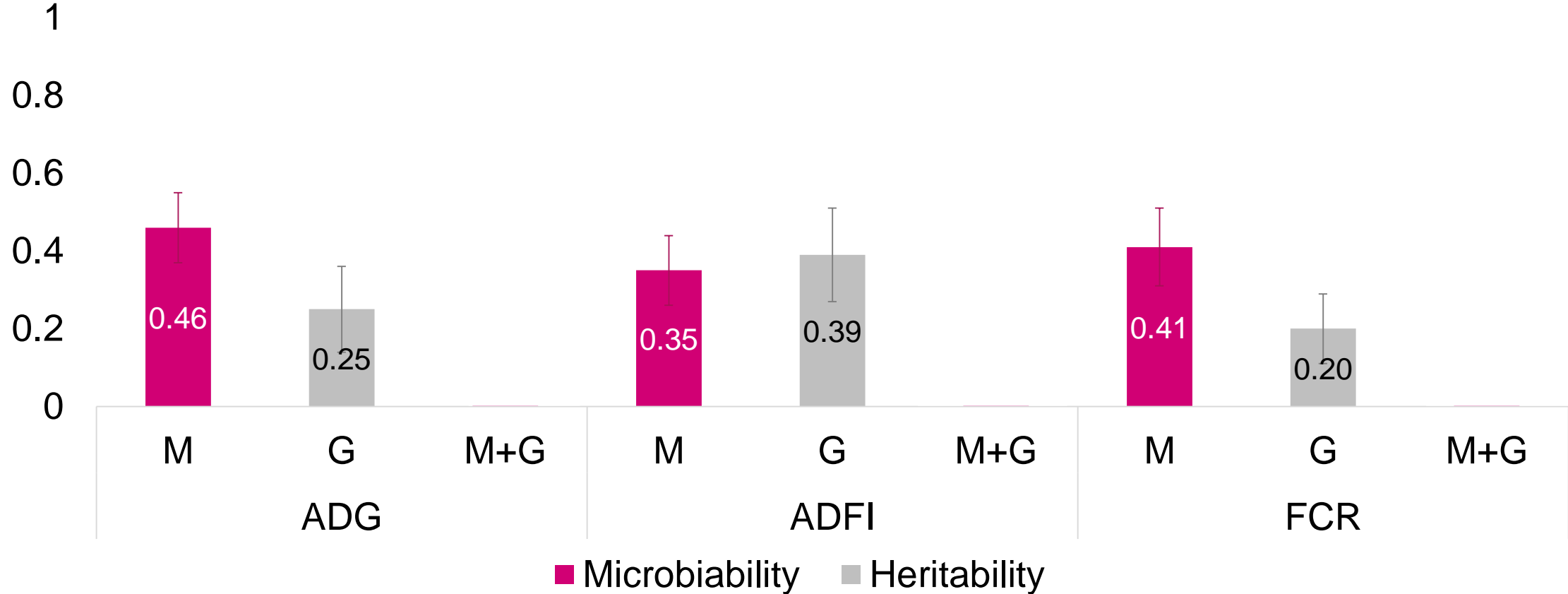
# Results

## Microbiability



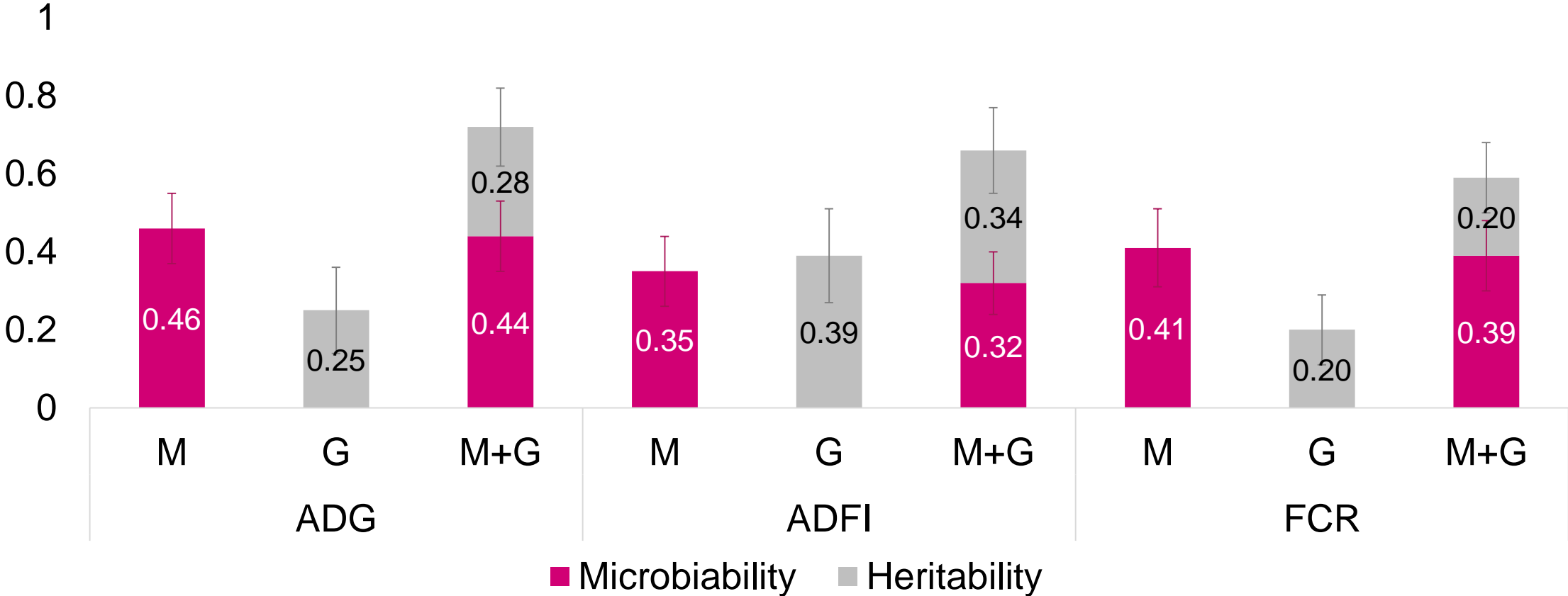
# Results

## Heritability



# Results

Microbiability and heritability combined



# Results

Accuracy

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## Microbial Prediction

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Trait	$r_m$	97.5% CI
ADG	0.45	0.38:0.51
ADFI	0.46	0.39:0.52
FCR	0.30	0.21:0.38

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# Results

## Accuracy

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Trait	Microbial Prediction		Genomic Prediction	
	$r_m$	97.5% CI	$r_g$	97.5% CI
ADG	0.45	0.38:0.51	0.20	0.13:0.27
ADFI	0.46	0.39:0.52	0.29	0.22:0.36
FCR	0.30	0.21:0.38	0.13	0.05:0.22

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# Results

## Accuracy

Trait	Microbial Prediction		Genomic Prediction		Microbial + Genomic Prediction	
	$r_m$	97.5% CI	$r_g$	97.5% CI	$r_{m+g}$	97.5% CI
ADG	0.45	0.38:0.51	0.20	0.13:0.27	0.49	0.42:0.54
ADFI	0.46	0.39:0.52	0.29	0.22:0.36	0.50	0.43:0.56
FCR	0.30	0.21:0.38	0.13	0.05:0.22	0.33	0.25:0.41

# Conclusions

- Variation in feed efficiency related traits is associated with variation in the fecal microbiome
- The fecal microbiome is a more accurate predictor of feed efficiency traits than the pig genotype
- Consequently, can we use the fecal microbiome to improve current selection?

**YES, to improve phenotypic predictions**

## Questions?

