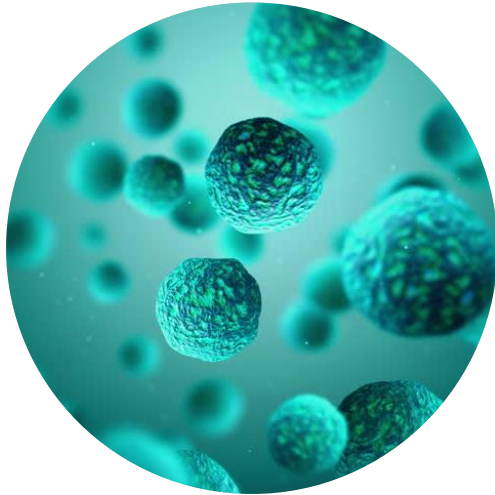
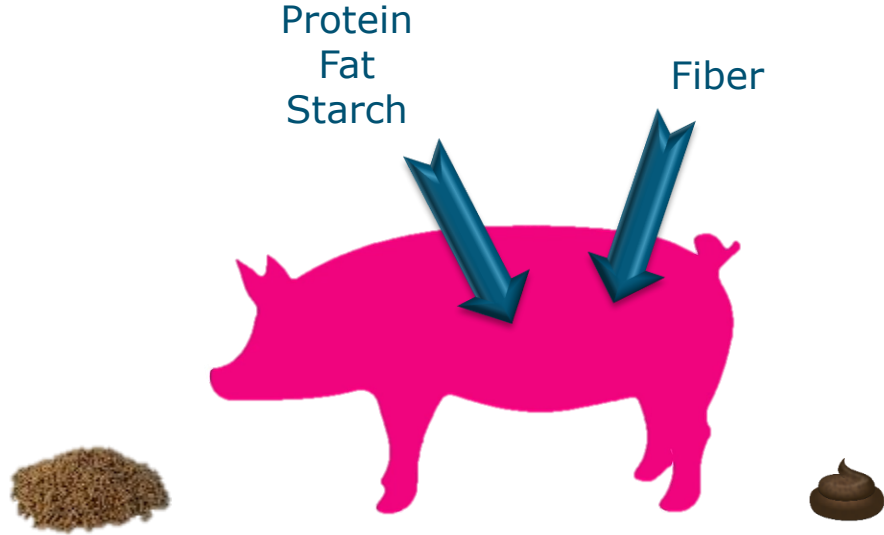


Microbiability of faecal nutrient digestibility in pigs

L.M.G. Verschuren, D. Schokker, A.J.M. Jansman, R. Bergsma, F. Molist and M.P.L. Calus



Introduction

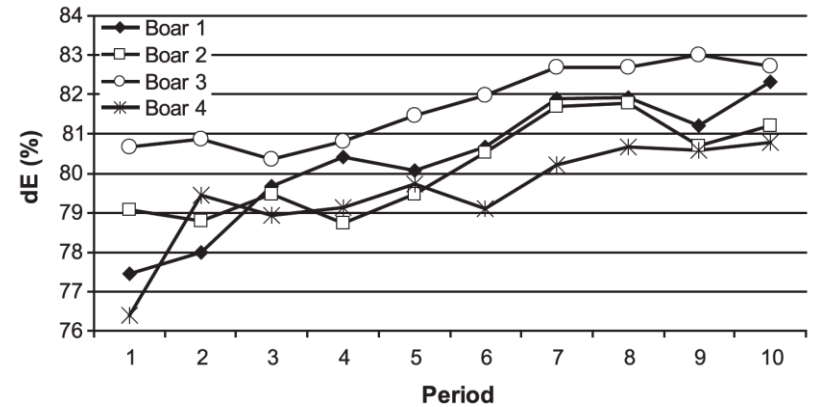


Faecal nutrient
digestibility
=
% of nutrients
disappeared in the GIT

Higher
=
More nutrients for
maintenance and
growth

Introduction

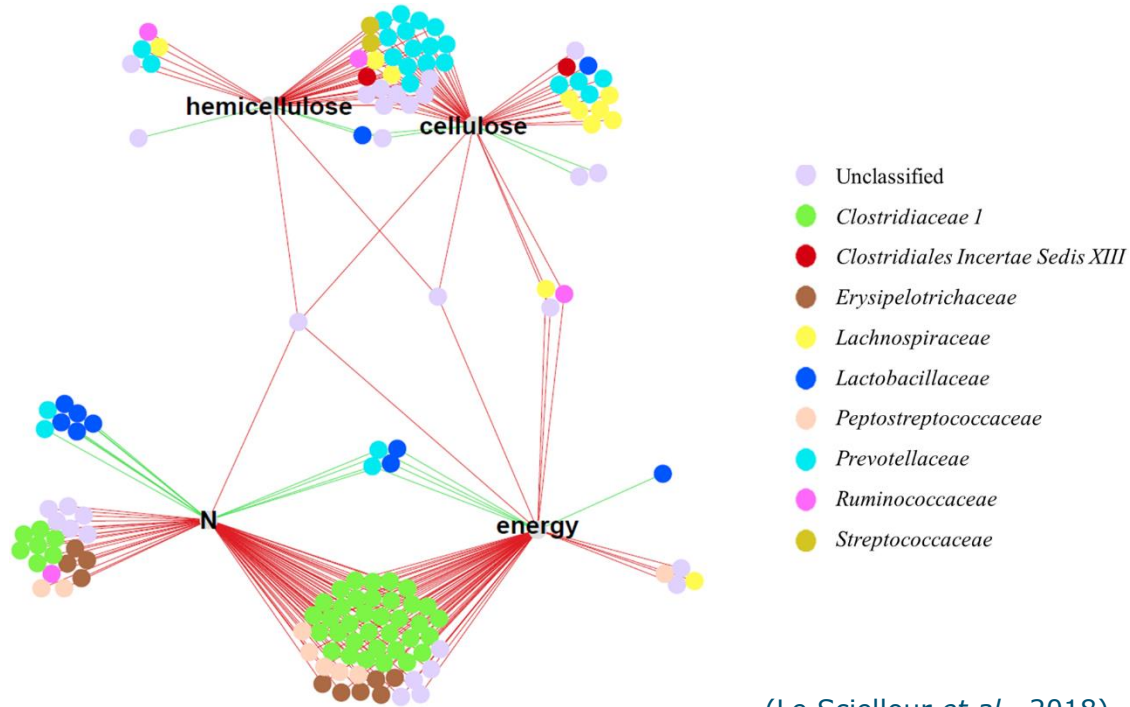
RFI ^a	High ^b	Low	SEM	Significance
CAID (%)				
Gross energy	81.67	83.05	0.37	0.029
Nitrogen	79.01	80.55	0.78	0.237
Ash	52.42	53.45	0.66	0.715
Dry matter	82.72	83.82	0.49	0.150
CATTD (%)				
Gross energy	82.89	84.25	0.39	0.031
Nitrogen	79.93	82.98	0.84	0.023
Ash	54.28	55.84	3.61	0.766
Dry matter	83.86	85.02	0.31	0.026



(Noblet *et al.*, 2013)

(Vigors *et al.*, 2016)

Introduction



Aim

- Use faecal microbial relationships to predict nutrient digestibility



Materials and Methods

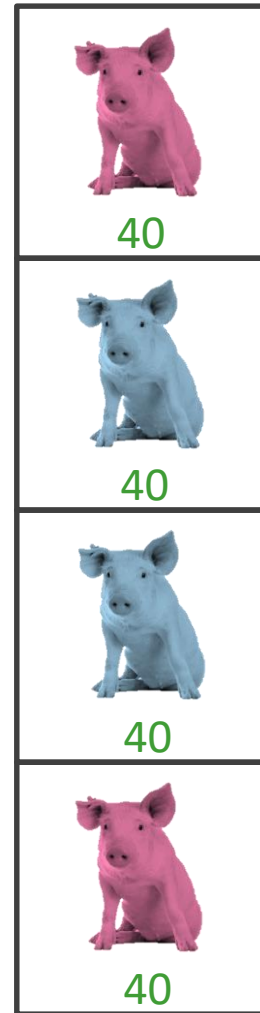
CS

~ 85 % Corn/Soybean meal
~ 10% By products



WB

~ 50 %
Wheat/Barley
~ 45 % By products



Day before slaughter



Materials and Methods (I)



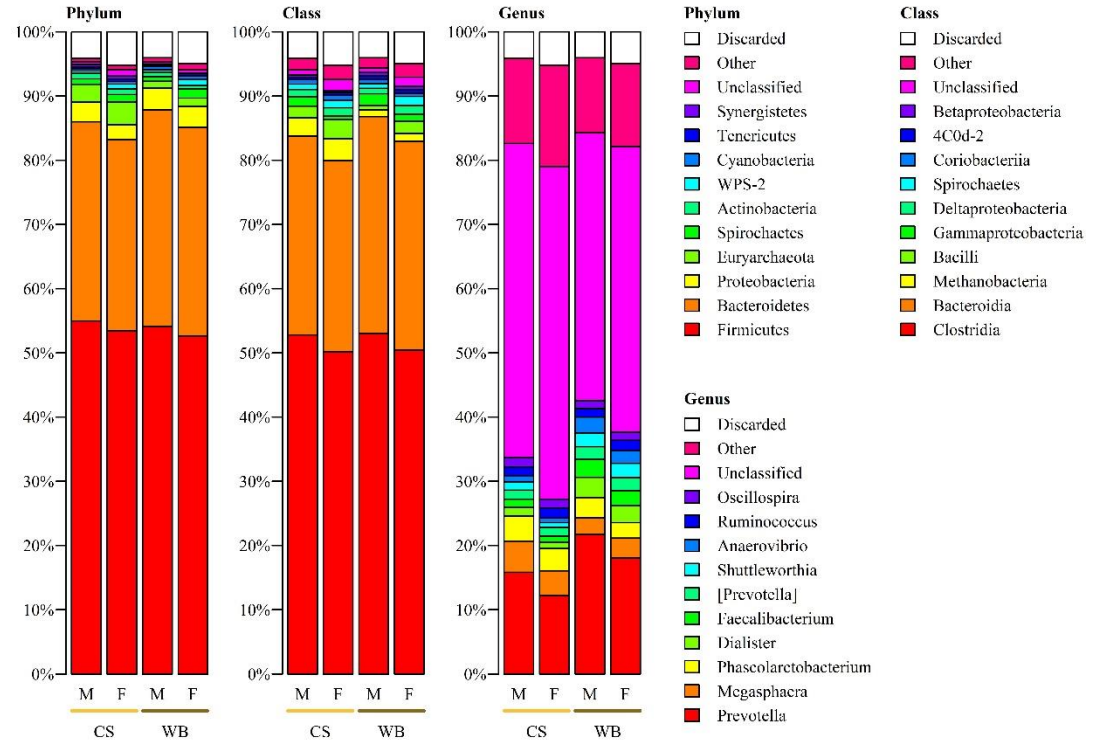
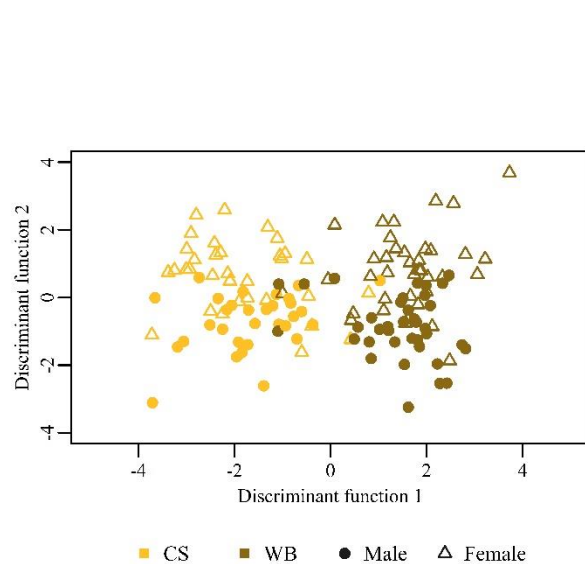
- Illumina MiSeq V3-V4 16S RNA sequencing
 - Cluster sequences into OTU
 - OTU filtering: mean relative abundance > 0.001 and present in $> 5\%$ of the animals
 - DAPC for diet, sex, and litter effects

- Chemical analysis for nutrient digestibility
 - Dry matter, ash, organic matter, crude protein, crude fat, crude fibre and non-starch polysaccharides

Results & Discussion (I)

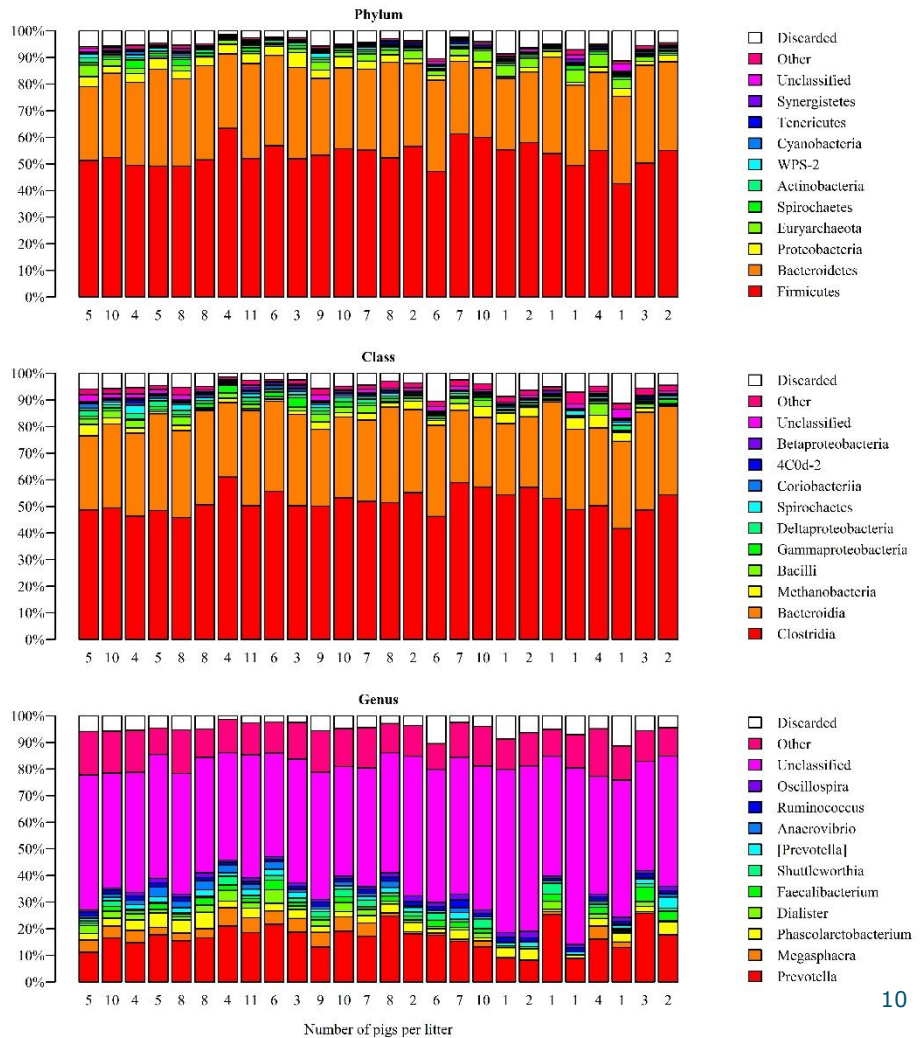
Index	Diet		Sex		P-value		
	CS	WB	M	F	Diet	Sex	Litter
Shannon	5.99	5.84	5.82	6.01	*	**	***
Chao	19925	19098	18587	20436	NS	NS	***

Results & Discussion (I)



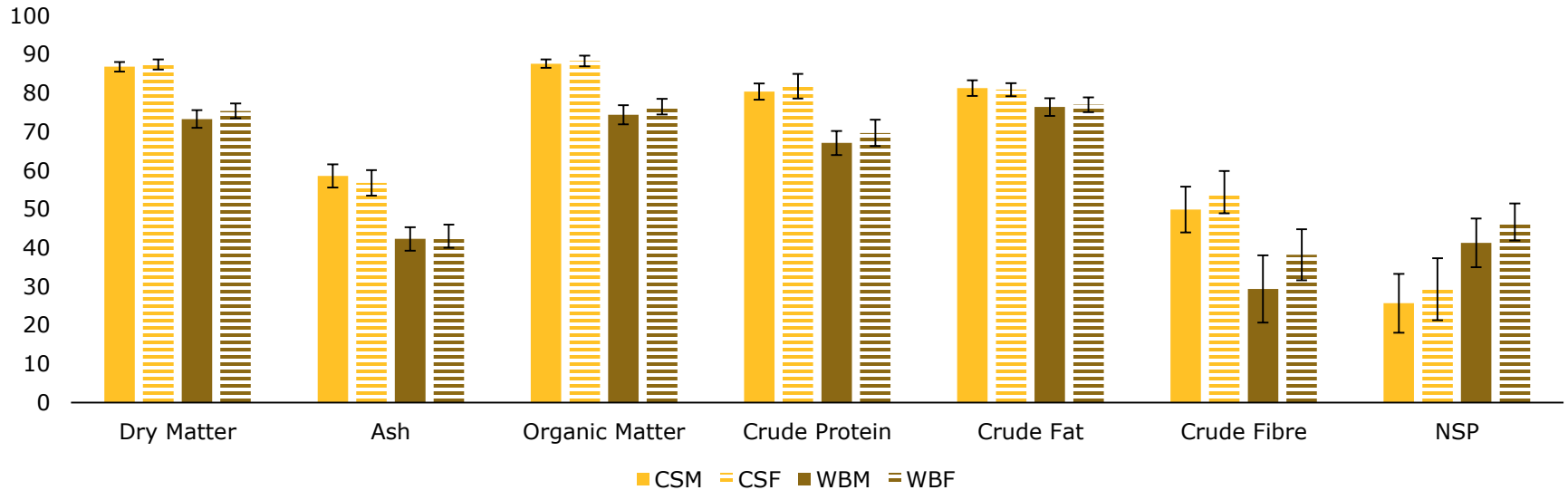
Results & Discussion (I)

The DAPC analysis could distinguish
 5 litters
 from the other
 21 litters
 based on the faecal microbial
 composition

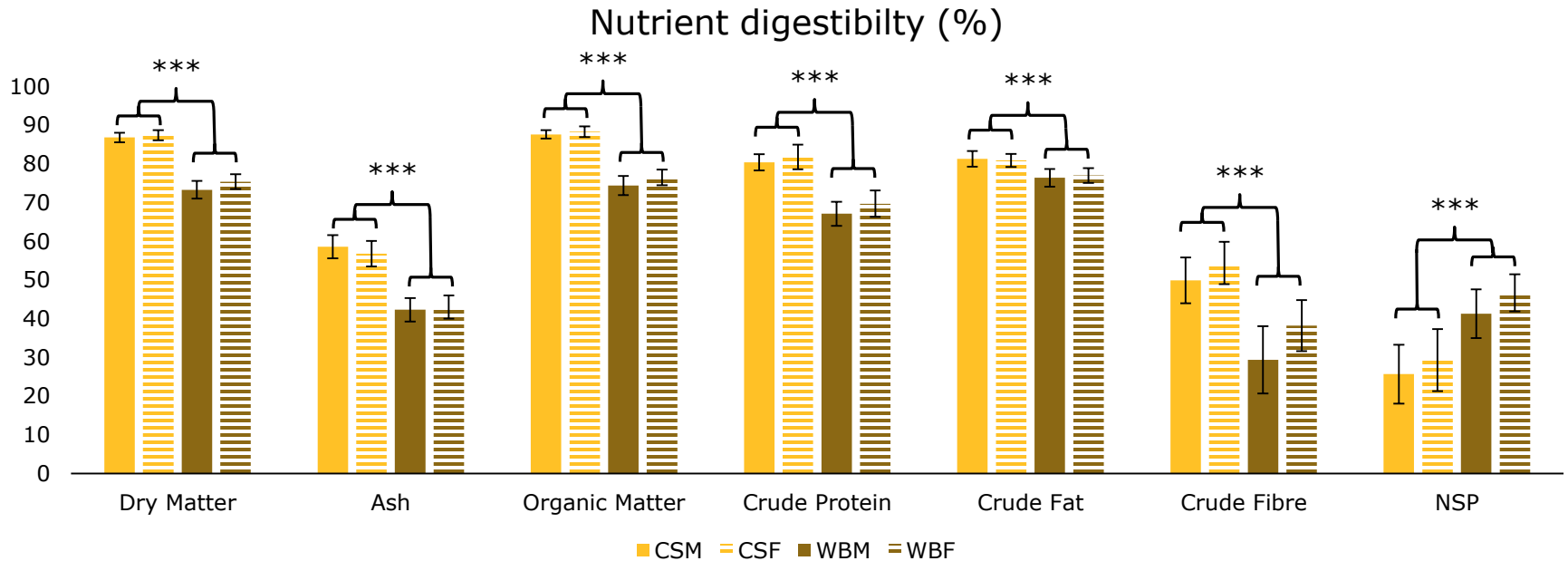


Results & Discussion (I)

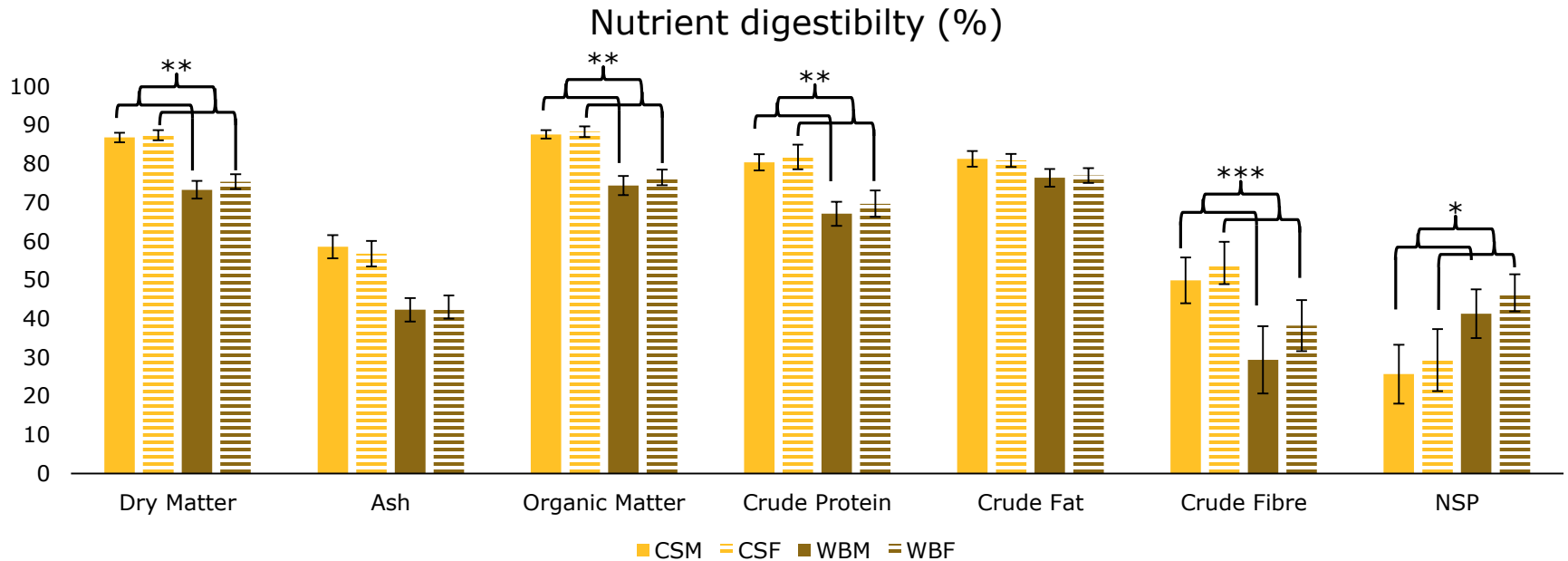
Nutrient digestibility (%)



Results & Discussion (I)



Results & Discussion (I)



Materials and Methods (II)

Microbiability

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

In formula:

$$m^2 = \sigma^2_m / (\sigma^2_m + \sigma^2_e)$$

Materials and Methods (II)

■ Model: $\mathbf{y} = \mathbf{Xb} + \mathbf{Zm} + \mathbf{Uc} + \mathbf{e}$

- \mathbf{y} = vector of phenotypes
- \mathbf{Xb} = fixed effects (sex, diet & pen)
- \mathbf{Zm} = random effects of OTU $\sim N(0, \mathbf{M}\sigma^2_m)$
- \mathbf{Uc} = random effects of common litter (foster dam) $\sim N(0, \mathbf{I}\sigma^2_c)$
- \mathbf{e} = vector of residuals $\sim N(0, \mathbf{I}\sigma^2_e)$

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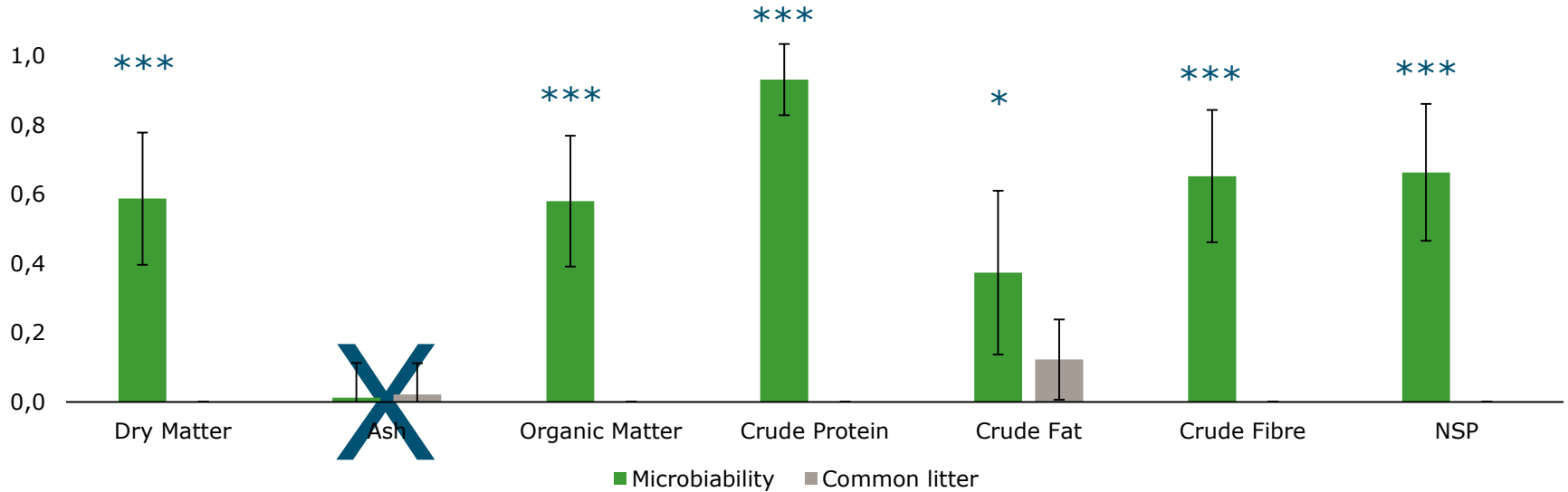
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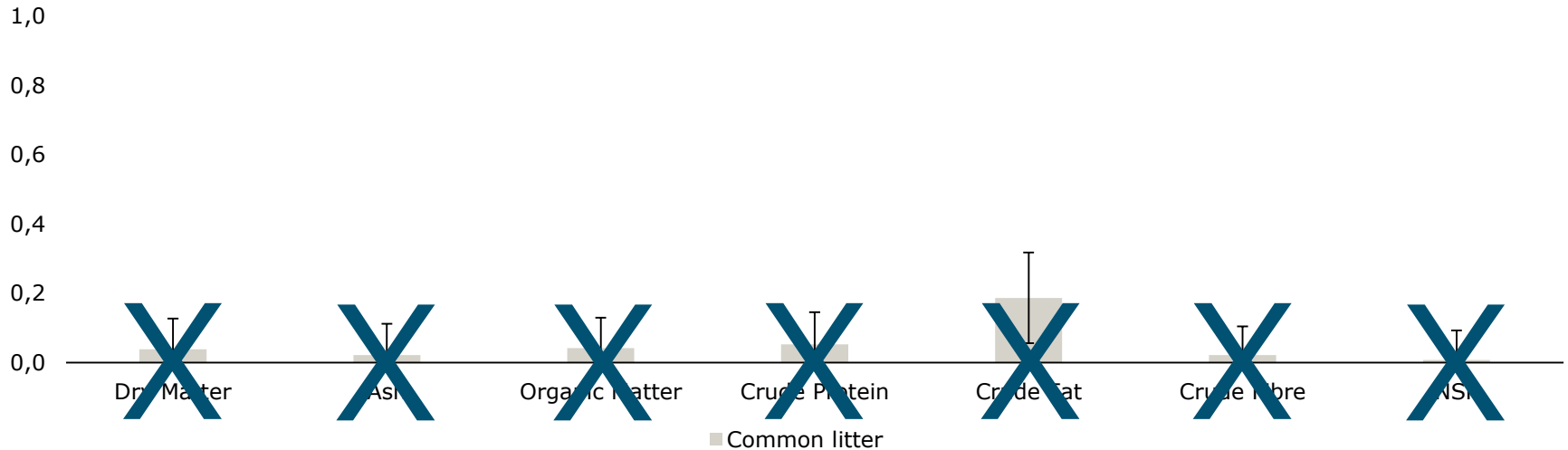
Results & Discussion (II)

m^2 and c^2 of faecal nutrient digestibility



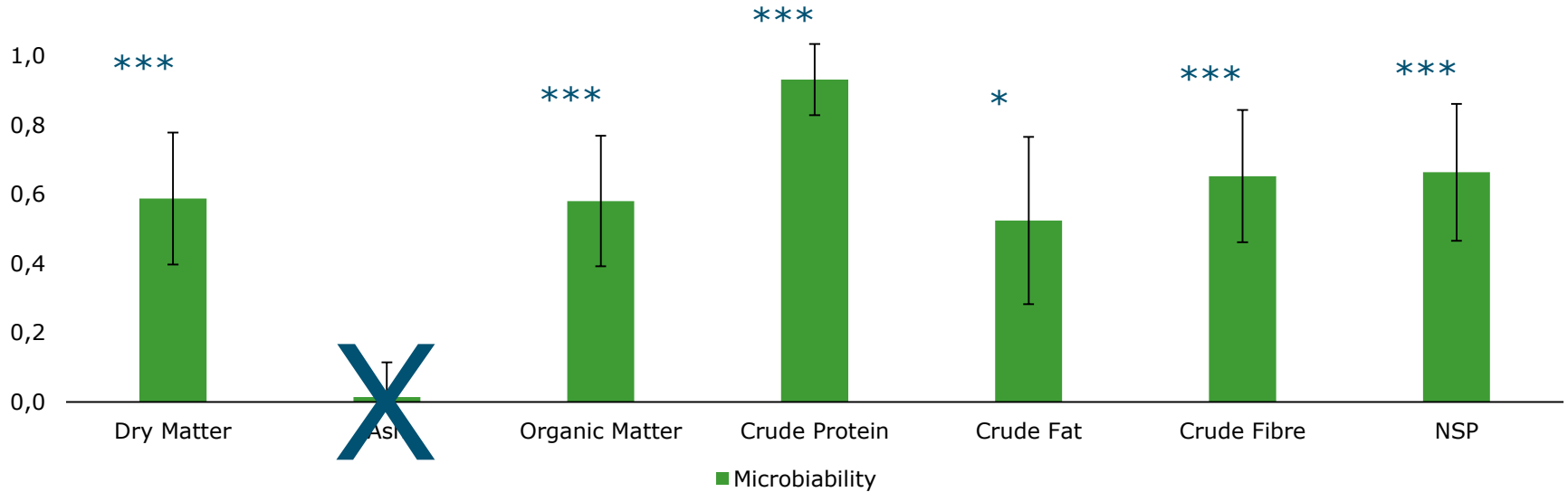
Results & Discussion (II)

Common litter effect of faecal nutrient digestibility



Results & Discussion (II)

Microbiability of faecal nutrient digestibility



Results & Discussion (III)

OTU	Phylum	Class	Family	Genera	Contribution to m ² of CP
OTU843086	Bacteroidetes	Bacteroidia	[Paraprevotellaceae]	[Prevotella]	1.08
OTU130147	Bacteroidetes	Bacteroidia	[Paraprevotellaceae]	[Prevotella]	0.94
OTU781124	Bacteroidetes	Bacteroidia	[Paraprevotellaceae]	[Prevotella]	0.85
OTU753291	Bacteroidetes	Bacteroidia	[Paraprevotellaceae]	[Prevotella]	0.52
OTU424454	Bacteroidetes	Bacteroidia	[Paraprevotellaceae]	[Prevotella]	0.49

Greengenes core set 13_8

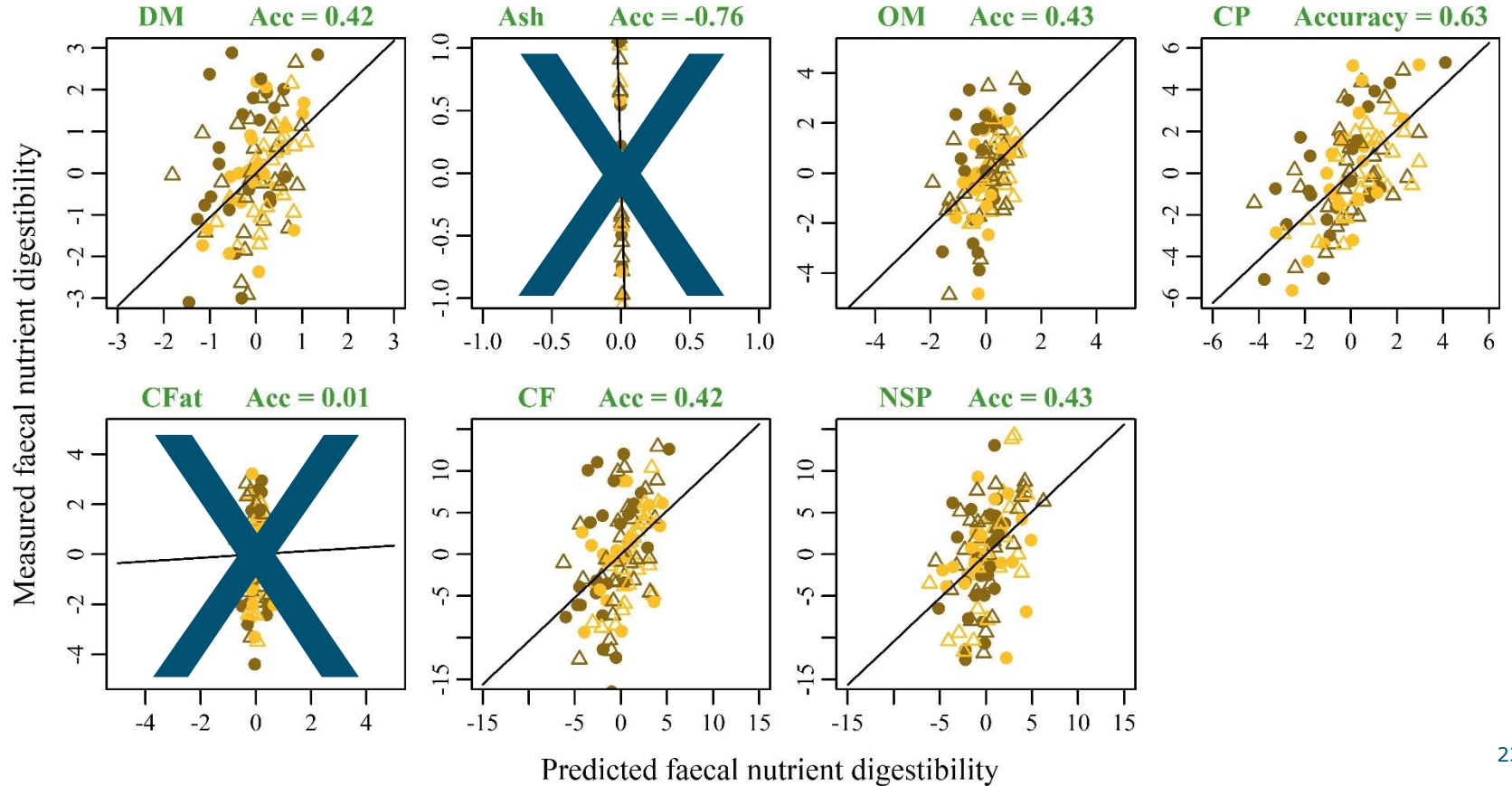
Materials and Methods (III)

▪ Model: $\mathbf{y} = \mathbf{Xb} + \mathbf{Zm} + \mathbf{Uc} + \mathbf{e}$

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Subsequently a leave-one out analysis was performed to test for predictive capacity

Results & Discussion (III)

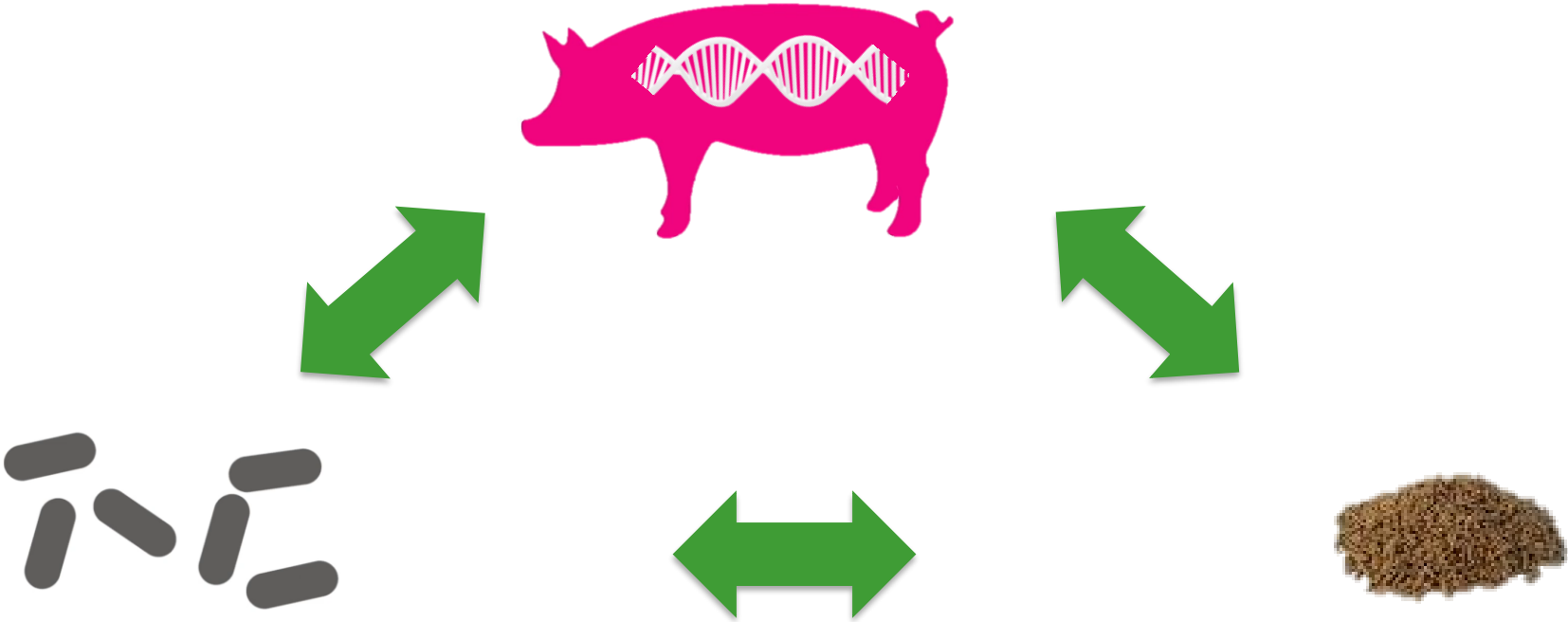


Conclusion

- Prediction of faecal digestibility using metagenomic profiles:
 - Possible for DM, OM, CP, CF, and NSP
 - Accuracies too low for nutrition studies; BUT promising to rank animals

- No effect of common litter on faecal digestibility of nutrients

Future



Acknowledgement



Animal Breeding
& Genomics



Animal nutrition



Take home message

Faecal digestibility of DM, OM, CP, CF, and NSP can be predicted based on metagenomics

The predictions can subsequently be used as phenotypes in genetic or genomic selection

