Faecal microbiome profiles can predict complex traits in pigs

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BREED4FOOD

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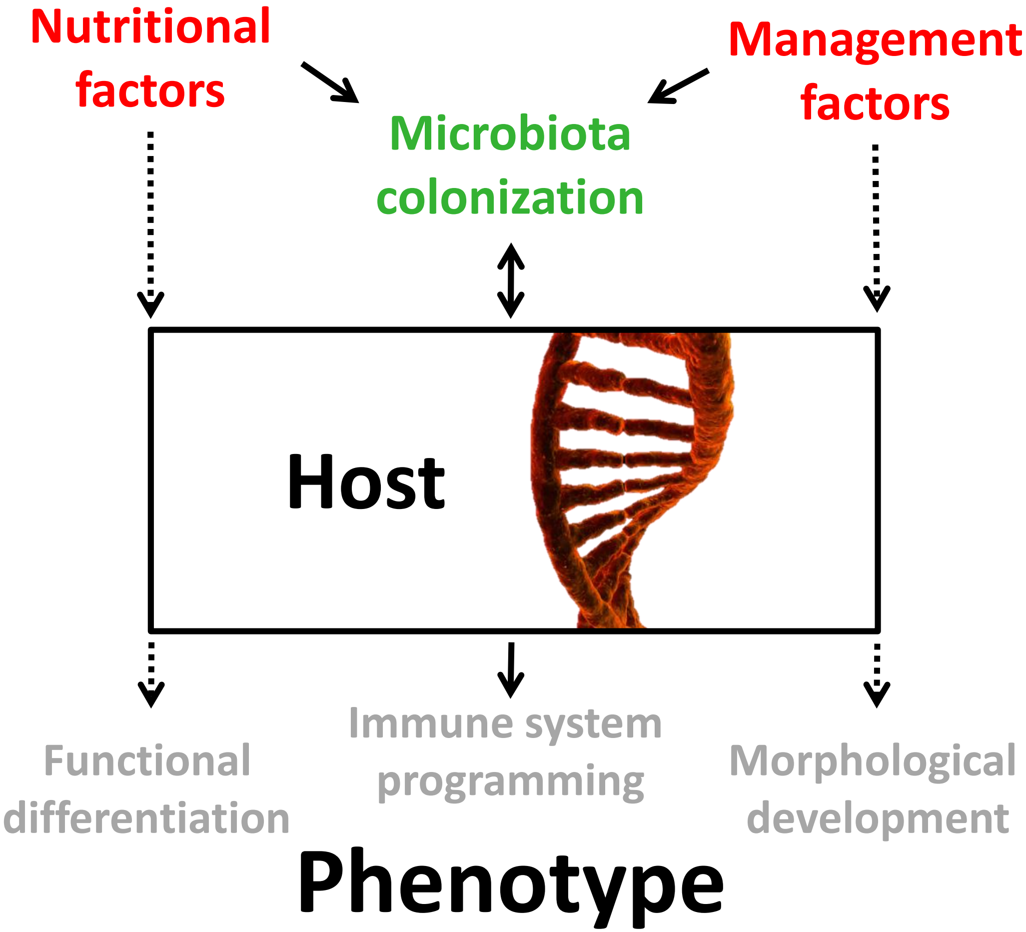
Early life microbiota drive health and metabolic phenotypes



Nutritional factors

Management factors

Microbiota colonization

Host

Functional differentiation

Immune system programming

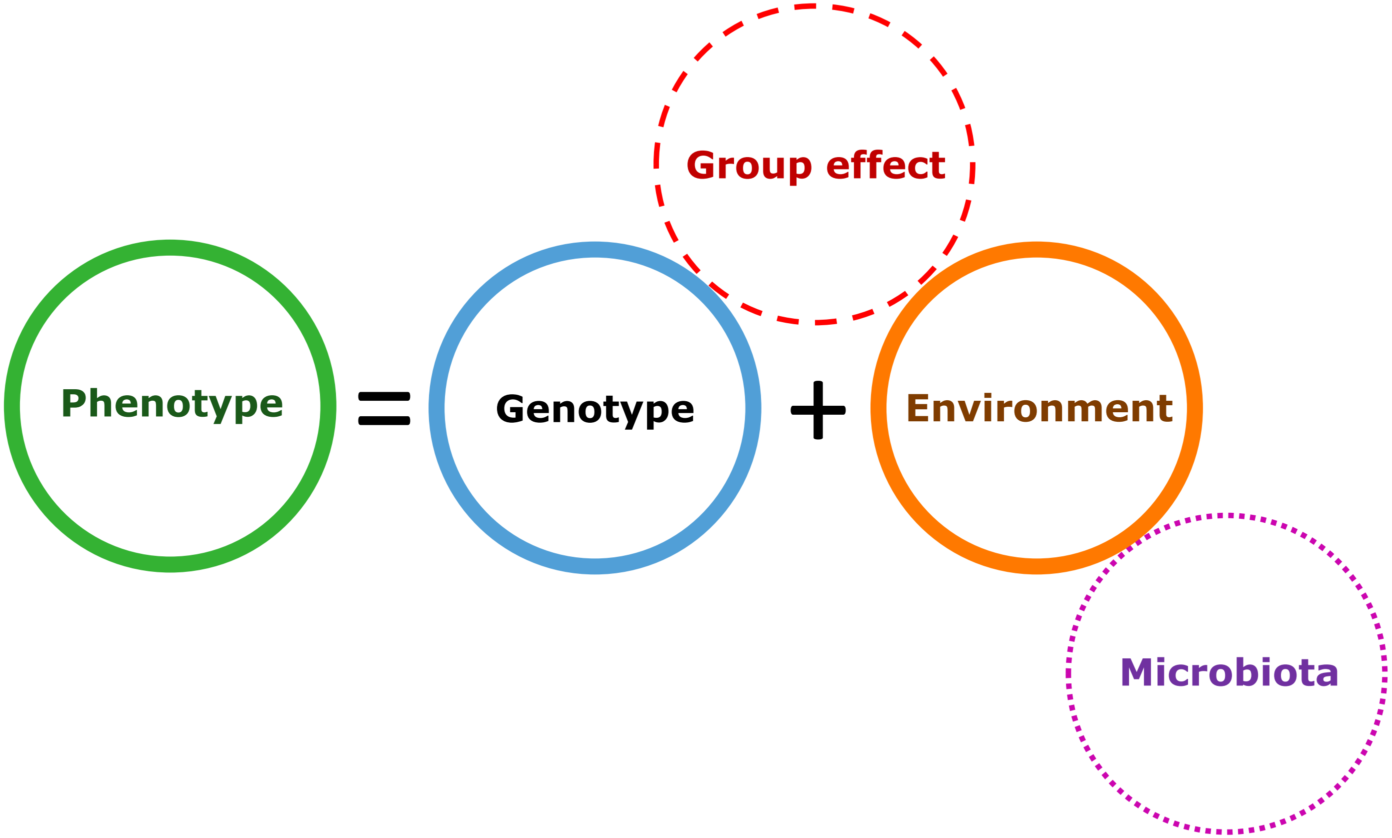
Morphological development

Phenotype

@DirkjanSchokker #wur_abg

Phenotypes <> complex traits

- Almost all phenotypes (traits) are quantitative or complex traits



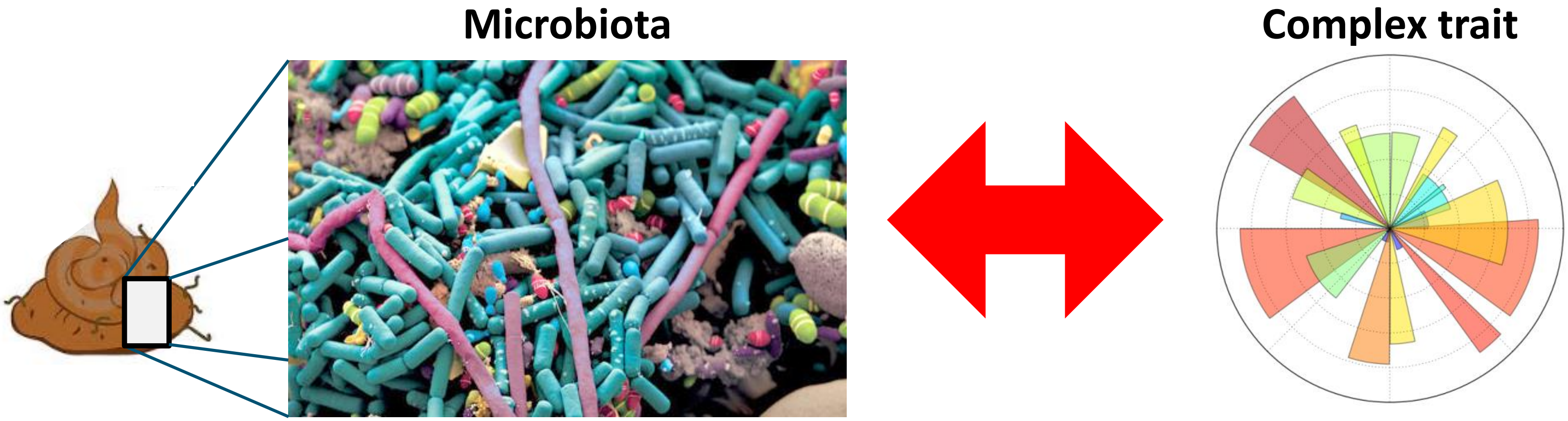
Group effect

Phenotype = **Genotype** + **Environment**

Microbiota

Objective

Identify **faecal microbiota profiles** associated to **important economical traits** in pigs



Details of the dataset

- Three-breed crossed pigs
  - S (LR x LW) or S (LW x LR)
- Phenotypic data were available for 160 animals
  - Start ±23 kg - Slaughter ±120 kg
  - 20 litters, ~ 50% ♀/♂
  - 2 batches
  - 16 pens
- 2 Diets
  - Corn/soybean meal (CS)
  - Wheat/barley/by-products (WB)

Analysis – model (I)

- Model: $\mathbf{y} = \mathbf{1}\mu + \mathbf{fe} + \mathbf{m} + \mathbf{e}$
  - $\mathbf{y}$ = vector of phenotypes
  - μ = general mean
  - $\mathbf{fe}$ = fixed effects (sex, diet & batch)
  - $\mathbf{m}$ = vector of microbiotic predictions $\sim N(0,\mathbf{M}\boldsymbol{\sigma}_m^2)$
  - $\mathbf{e}$ = vector of residuals

- Compute m^2 ("***<u>microbiability</u>***") as: $m^2 = \boldsymbol{\sigma}_m^2 / (\boldsymbol{\sigma}_m^2 + \boldsymbol{\sigma}_e^2)$
- Subsequently a leave-one out analysis was performed to test for significance

Results (I)

Trait	Sex	Diet	Microbiability	Accuracy
ADG	0.855	0.610	50% (±13%)	0.36
FI	**0.013**	0.822	60% (±13%)	0.28

- Only FI shows a significant effect of sex
- High microbiability values

- Here, we corrected for **batch** and not pen and litter (common environment)
- Our next step → implement this in the model

Analysis – model (II)

- Model: $\mathbf{y} = \mathbf{1}\mu + \mathbf{fe} + \mathbf{m} + \mathbf{c} + \mathbf{e}$

  $\mathbf{y}$ = vector of phenotypes

  μ = general mean

  $\mathbf{fe}$ = fixed effects (sex, diet & pen)

  $\mathbf{m}$ = vector of microbiotic predictions $\sim N(0, M\boldsymbol{\sigma}_m^2)$

  $\mathbf{c}$ = vector of litter (common env.) effects

  $\mathbf{e}$ = vector of residuals

- Compute m^2 ("***microbiability***") as: $m^2 = \boldsymbol{\sigma}_m^2 / (\boldsymbol{\sigma}_m^2 + \boldsymbol{\sigma}_e^2)$

Results (II)

Trait	Sex	Diet	Pen	Microbiability	Accuracy
ADG	0.241	0.949	**0.068**	38% (±13%)	0.08
FI	**0.010**	0.576	0.206	23% (±12%)	0.06

- ADG: Only trend for Pen
- FI: Sex difference is still observed
- Accuracies are not significantly different from 0

- Microbiability now in the range of 23-38%

Discussion

- **Phenotypes - complex traits**
  - Novel traits (*deep phenotyping)*
    - Performance parameters (ADG & FI)
  - Snapshot of microbiota data
    vs.
    longitudinal performance data
  - Possibility for health related traits or digestibility

Conclusions

- ***Microbiability* – possibility for breeding**
  - m^2 likely to be overestimated, because no animal genetic effect is included in the model
    - Need higher number of animals for better prediction
  - Costs for sequencing are still decreasing
  - Possibility to acquire faecal microbiota samples longitudinally

Thank you for your attention

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100years
1918 — 2018