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Agroscope

Protein efficiency in pigs: from phenotyping to estimating genetic parameters and beyond

Claudia Kasper
Animal GenoPhenomics Unit
Agroscope

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«The first generation»

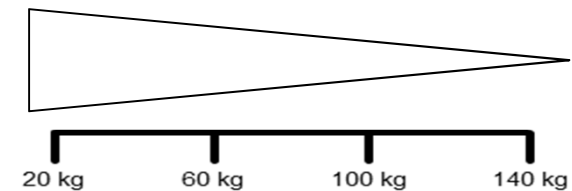


(Isabel Ruiz-Ascacibar Peter Stoll & Giuseppe Bee)

Protein requirement in finishing pigs is **lower** than assumed!

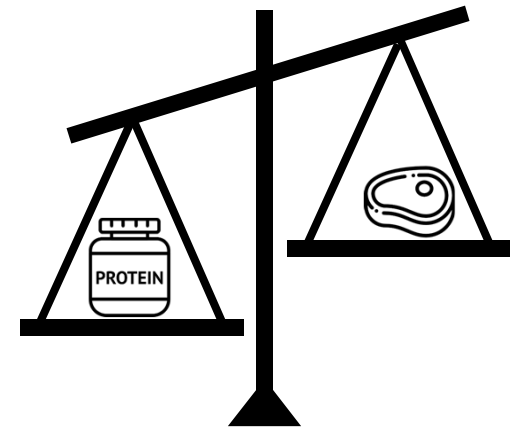
~ 30% of pigs in low-protein diets exhibited **similar growth rate** compared with pigs in control diets

Protein efficiency: ♂ > ♀ ≈ ♂



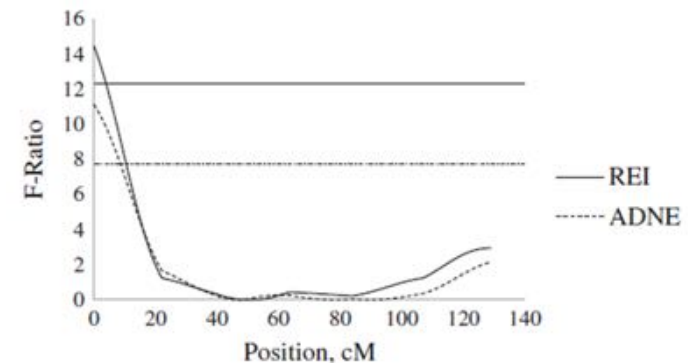
Protein efficiency

- New trait
- Economic and environmental importance
- Little information on differences and overlaps with classical feed efficiency traits
- Studies rare, not recent, use rough proxies



23 QTL for nitrogen excretion traits detected:

- some **unique** to nitrogen efficiency
- some **overlapping** with production traits





Can we breed pigs with increased **protein efficiency**?

Or is that already done via **FCR**?



Genetics of protein efficiency in pigs

- Project March 2018 – January 2023
- PhD Esther Ewaoluwabemiga



1. Pilot study

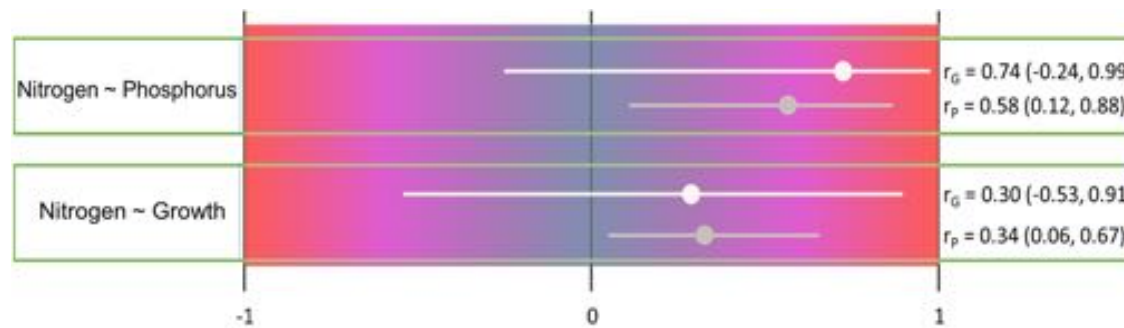
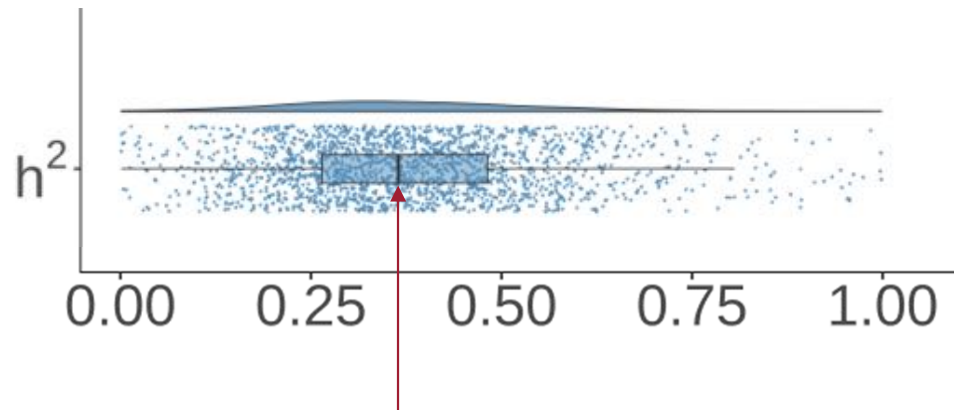
- N = 294
- 4 nutrition experiments
- ***I. Ruiz-Ascacibar, P. Stoll, G. Bee***
- 17 sires, 56 dams
- 2 diets (LP, C)
- several slaughter target weights
- PE via chemical analysis
- Animal model (Bayesian)



Phenotyping



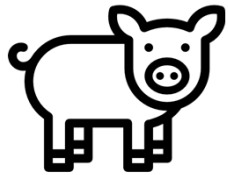
1. Pilot study



Protein efficiency is

- heritable
- genetic correlations with other traits unclear

2. Follow-up study



Larger **sample size**, improved **experimental design**,
additional phenotypes

PhD project of Esther Ewaoluwegbemiga

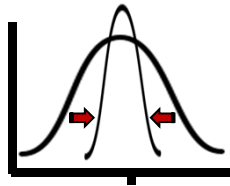


2. Follow-up study

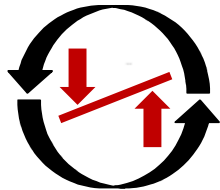
PhD project of Esther Ewaoluwegbemiga



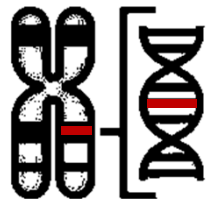
Goals:



Improved estimates of **genetic parameters** (Heritability, genetic correlations)

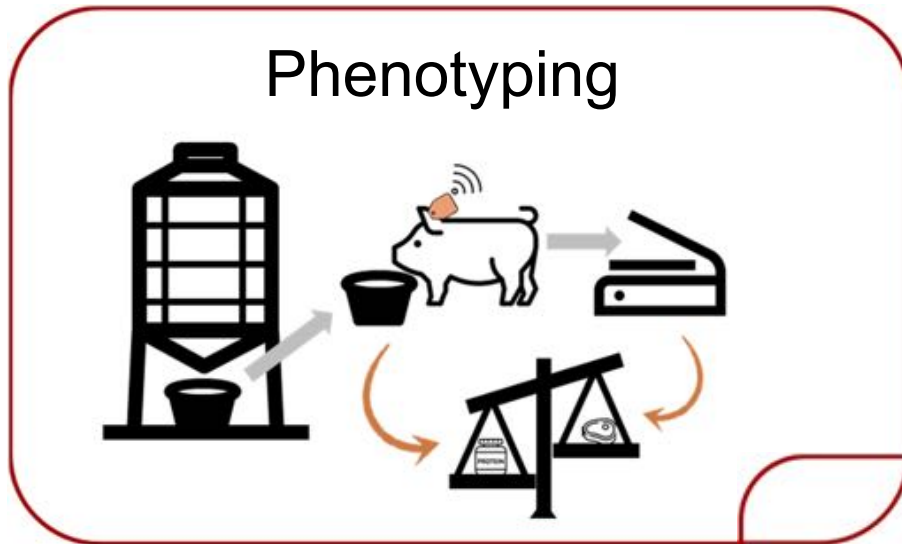





Estimation of **genetic and phenotypic correlations** with phosphorus efficiency, performance, meat quality, animal welfare




Identification of **genomic regions** associated with protein efficiency

Experimental design



-  682, ♀ & ♂
-  80% protein content soy-free
-  ca. 100 kg live weight

- ### Genotyping
-  ~1,000 pigs
 - HD- Genotyped and low-pass (1X – 4X) sequenced



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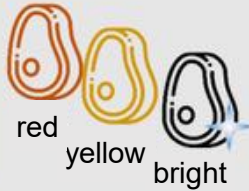
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**fondation
sur la croix**
Projekte Landwirtschaft



Additional traits

Meat colour



Intramuscular fat



Drip loss



Cooking loss



Sensory analysis



(N = 37)

Shear force



LMA



Backfat thickness



∅ Feed ingestion



ADG



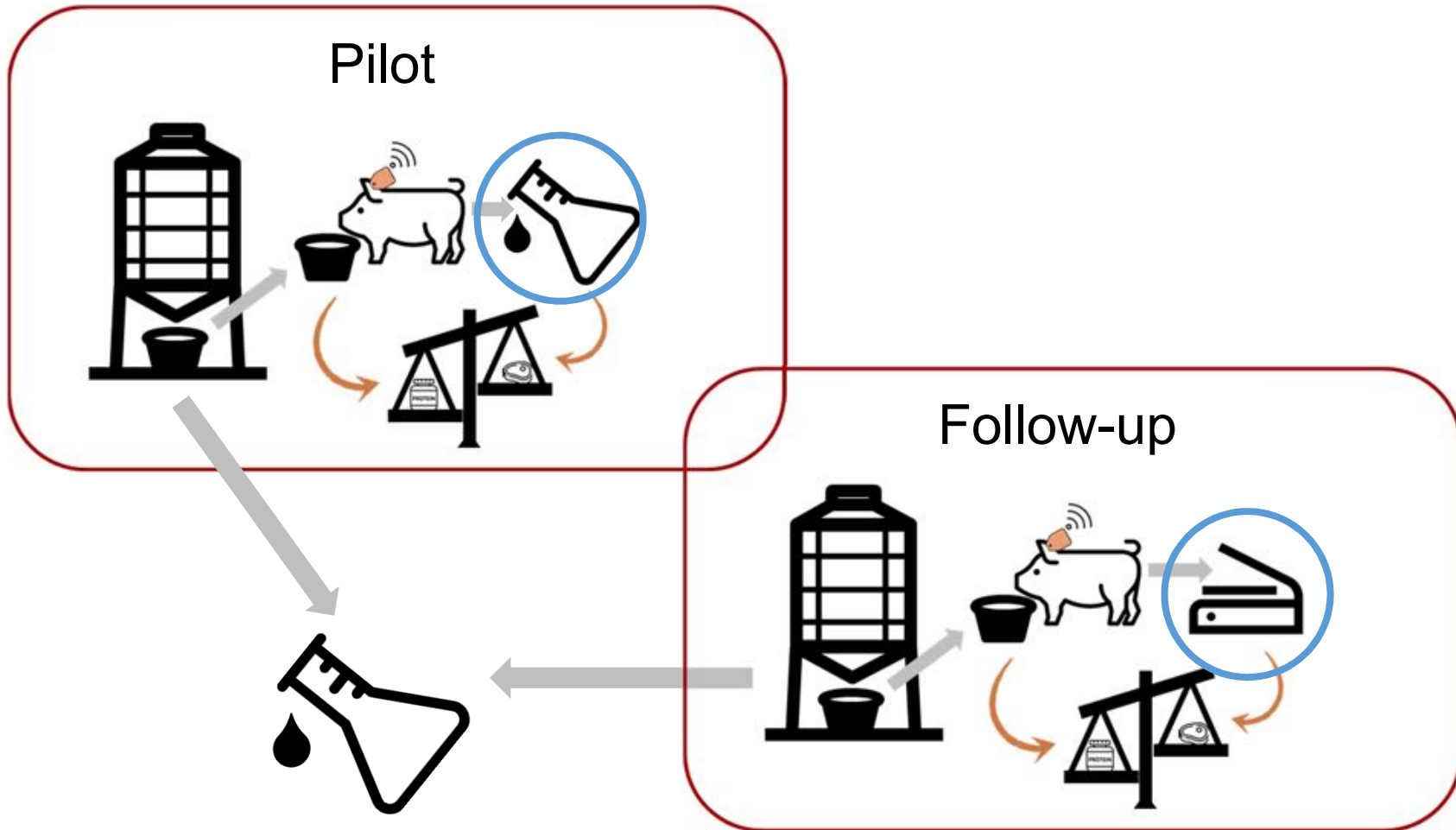
FCR



Phosphorus efficiency



Phenotyping



🇨🇭 Muscle mass in the carcass

Dual energy X-ray absorptiometry (DXA)



Protein efficiency of **62 pigs** of pilot study via
wet-chemistry + DXA

🇨🇭 Calibration study



62 pigs via wet-chemistry and DXA

$$\widehat{CP} = -482.745 + 0.23 \times \text{lean}_{\text{DXA}}$$

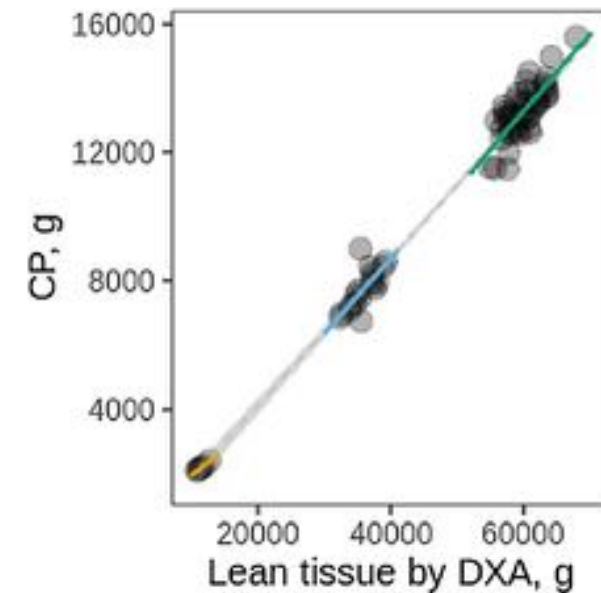
$$\widehat{P} = -6.388 + 1.09 \times \text{bone}_{\text{DXA}} + 1.09 \times \text{lean}_{\text{DXA}}$$

🇨🇭 Calibration study

📊 Calibration study **lean meat content DXA** vs. **protein/N content** by wet chemistry

📊 High **accuracy** ($R^2=0.98$) and **precision** (standardized error rCV=4.4%)

📊 Half **carcasses**, but also **live scans** (light anaesthesia)



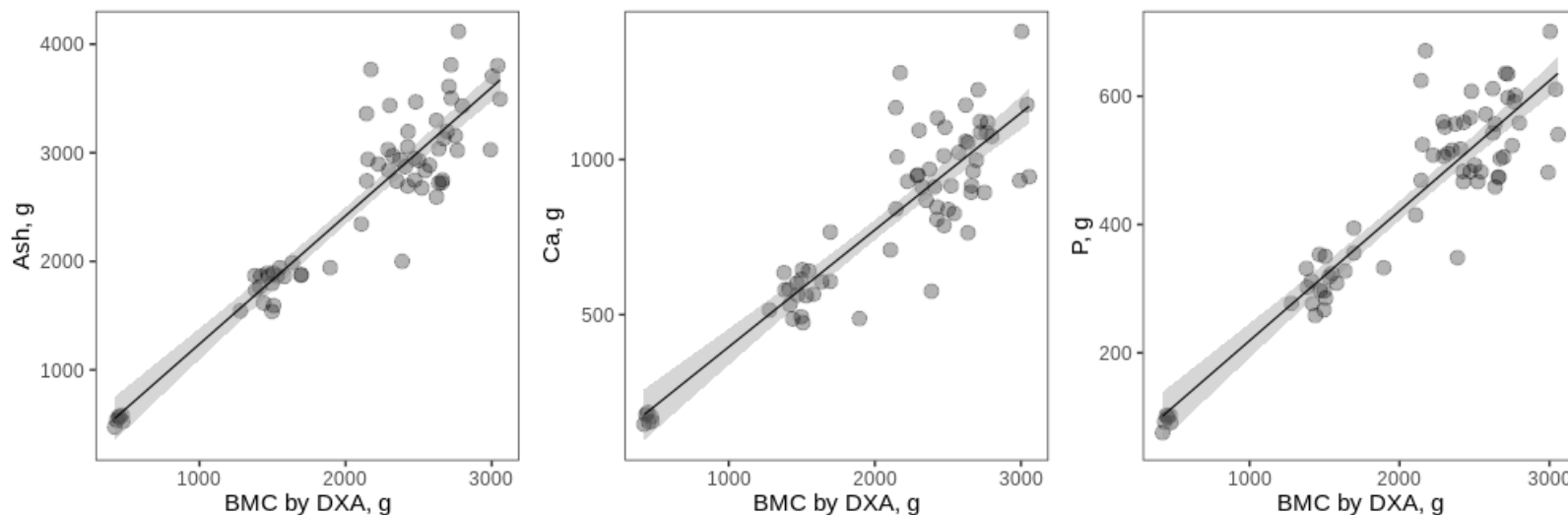
🇨🇭 Calibration study

📊 Bone mineralisation (ash, Ca & P) possible

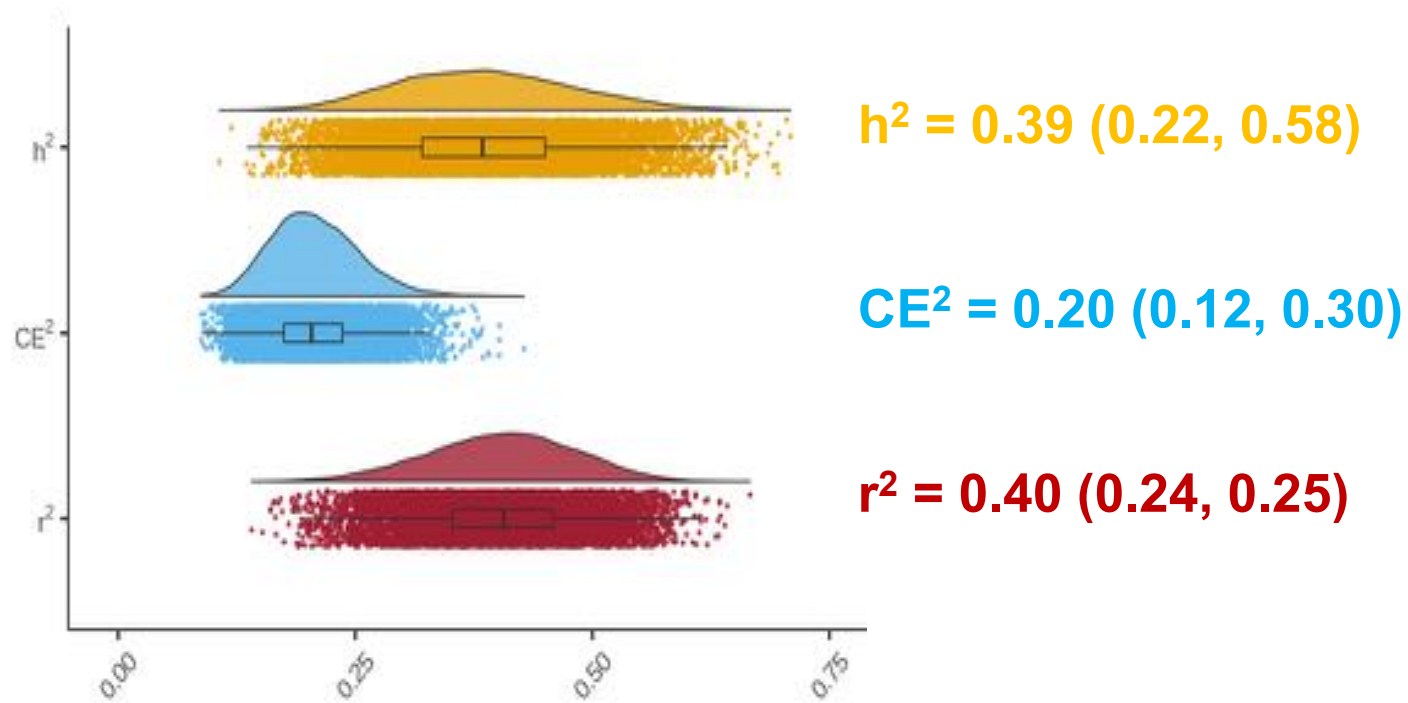
📊 Lower accuracy ($R^2=0.86$) and precision (standardized error rCV=13%)



continuous improvement of method! – N × 2



Heritability of protein efficiency



3. Full study

- Combination of different data sets from:
 - *Pilot study* (SMVG95, 96, 98 & 101)
 - *Follow-up study* (PigEff3)
 - *Further nutrition studies* (PigEff1 & 2)

■ N = 1,071

- Combination of different
 - Slaughter weights
 - Diets
 - Phenotyping strategies

2012 - 2021



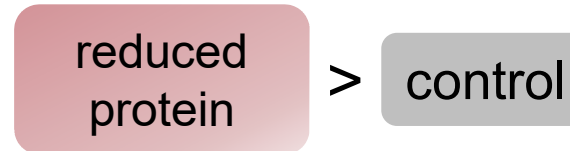


Effects on protein efficiency

- Slaughter weight



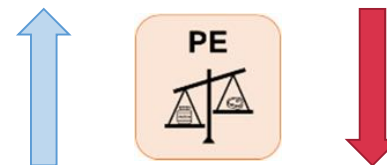
- Dietary treatments



- Sex



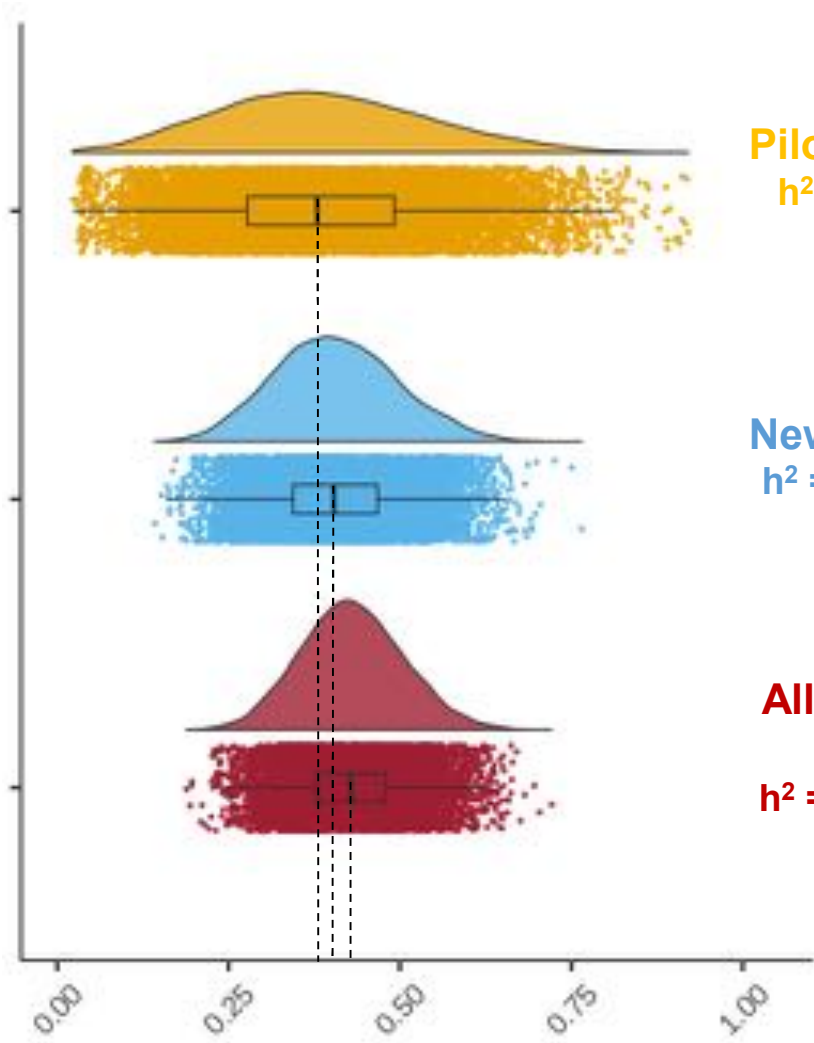
- Temperature





h^2 across studies

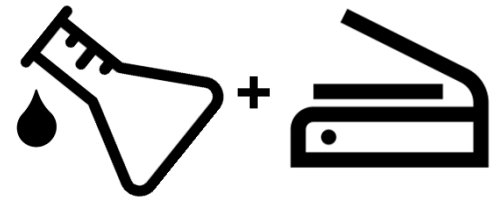
Phenotype



Pilot study (N = 294)
 $h^2 = 0.35 (0.10, 0.70)$

New data (N = 681)
 $h^2 = 0.40 (0.23, 0.58)$

All available data (N = 1,071)
 $h^2 = 0.44 (0.28, 0.58)$





h² of all traits



PE	0.43 (0.29 – 0.58)
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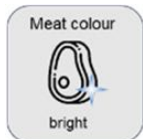
ADG	0.55 (0.36 – 0.72)
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FCR	0.47 (0.28 – 0.63)
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ADFI	0.61 (0.41 – 0.83)
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L*	0.21 (1.5 × 10⁻⁴ – 0.46)
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a*	0.77 (0.44 – 0.99)
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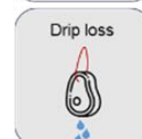
b*	0.39 (0.06 – 0.72)
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Protein Efficiency | SABRE-TP

Claudia Kasper – Animal GenoPhenomics



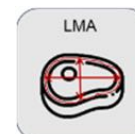
ShF	0.23 (3.5 × 10⁻⁶ – 0.48)
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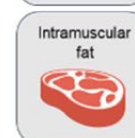
DL	0.13 (2.0 × 10⁻⁴ – 0.29)
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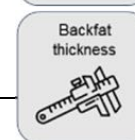
CL	0.31 (0.13 – 0.52)
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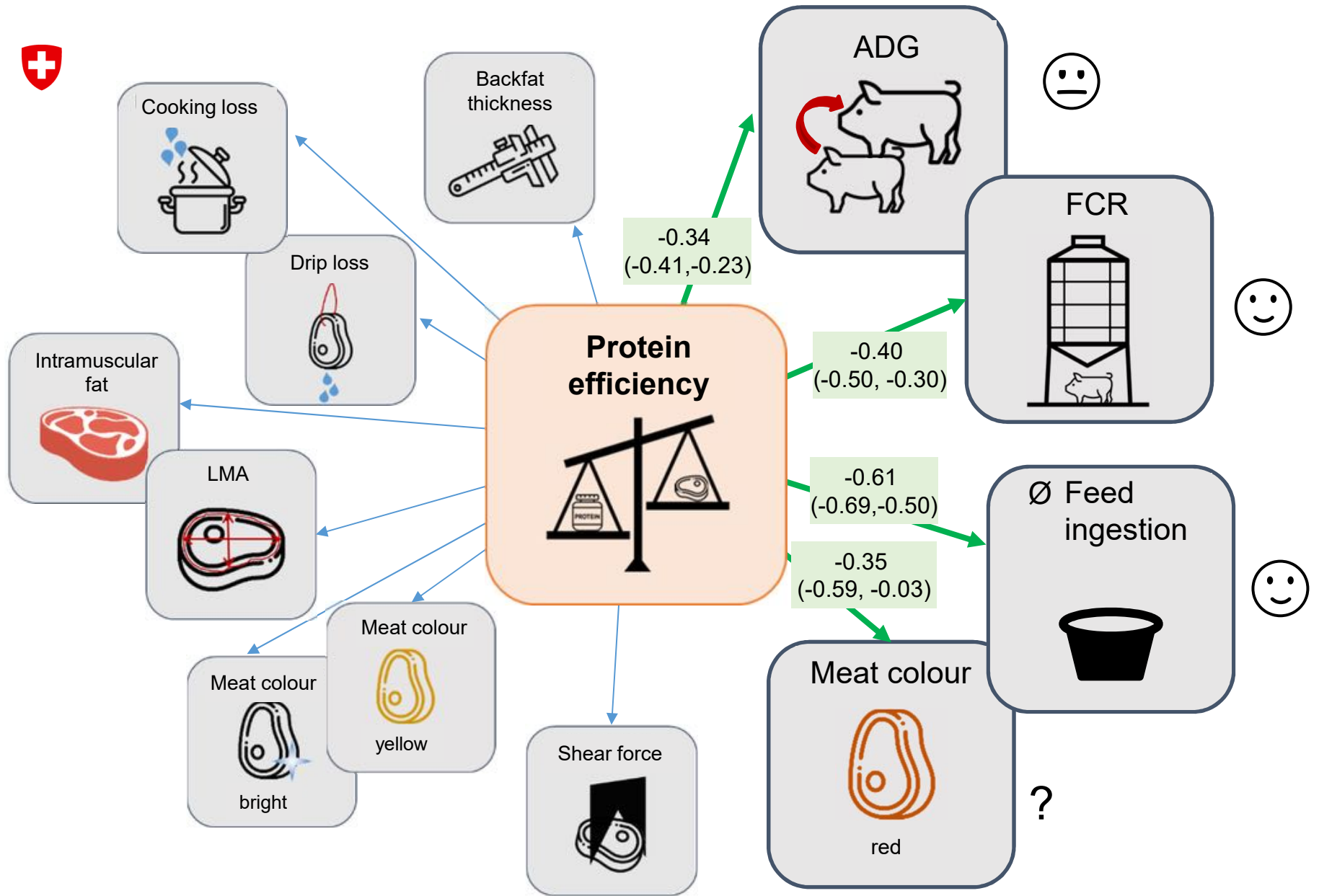
LMA	0.34 (0.09 – 0.59)
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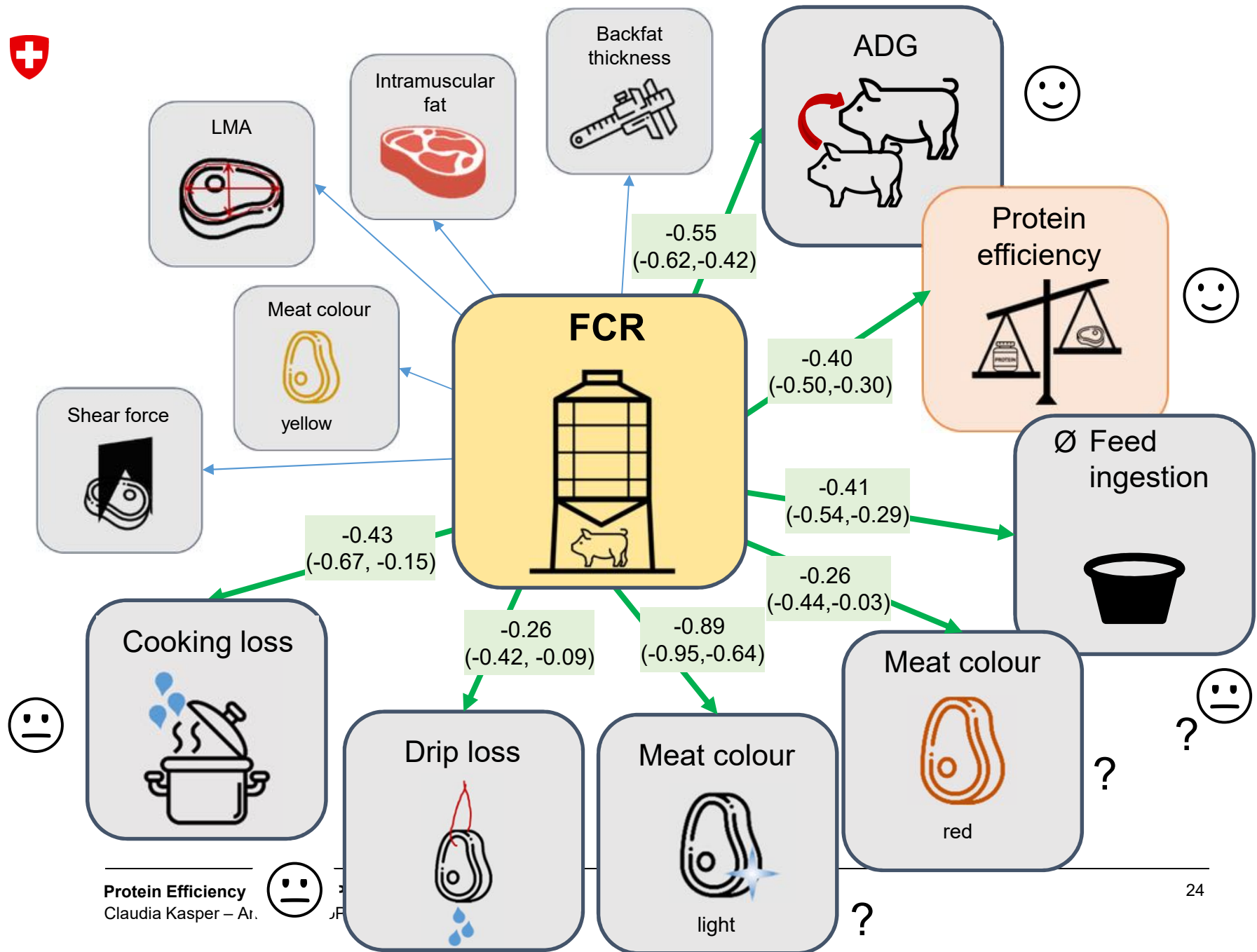


IMF	0.85 (0.60 – 0.99)
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BT	0.46 (0.25 – 0.69)
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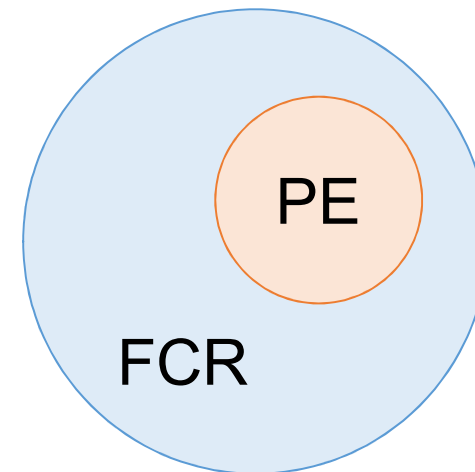
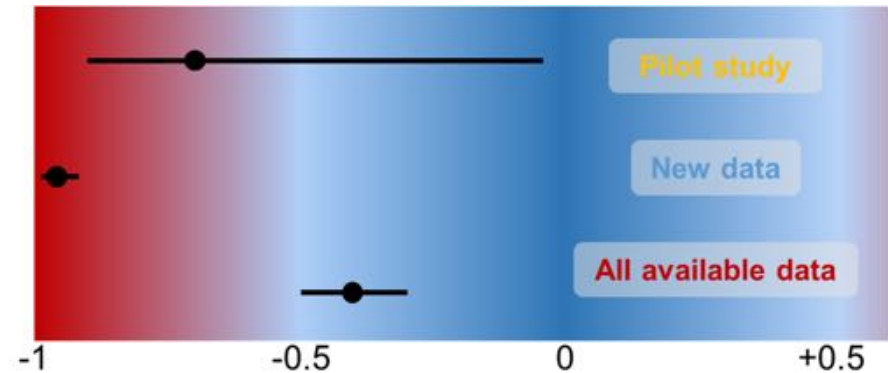




Protein efficiency = FCR?

- r_G (depends on subset!)
 - *Kasper et al. 2020 JABAG: (N=294)*
 $r_G = -0.70 [-0.90, -0.04]$
 - *PigEff3 data set: (N=510)*
 $r_G = -0.96 [-0.97, -0.95]$
 - *Total data set: (N=1071)*
 $r_G = -0.40 [-0.50, -0.30]$

- Physiology
- QTL
- Simulation study



Phenotyping

Wanted: prediction method!

Feeding patterns?

Protein
efficiency

- $R^2=0.33$
- $RMSE=0.02$

Energy
efficiency

- $R^2=0.54$
- $RMSE=0.02$

Lipid
gain

- $R^2=0.82$
- $RMSE=8.35$





Conclusions I

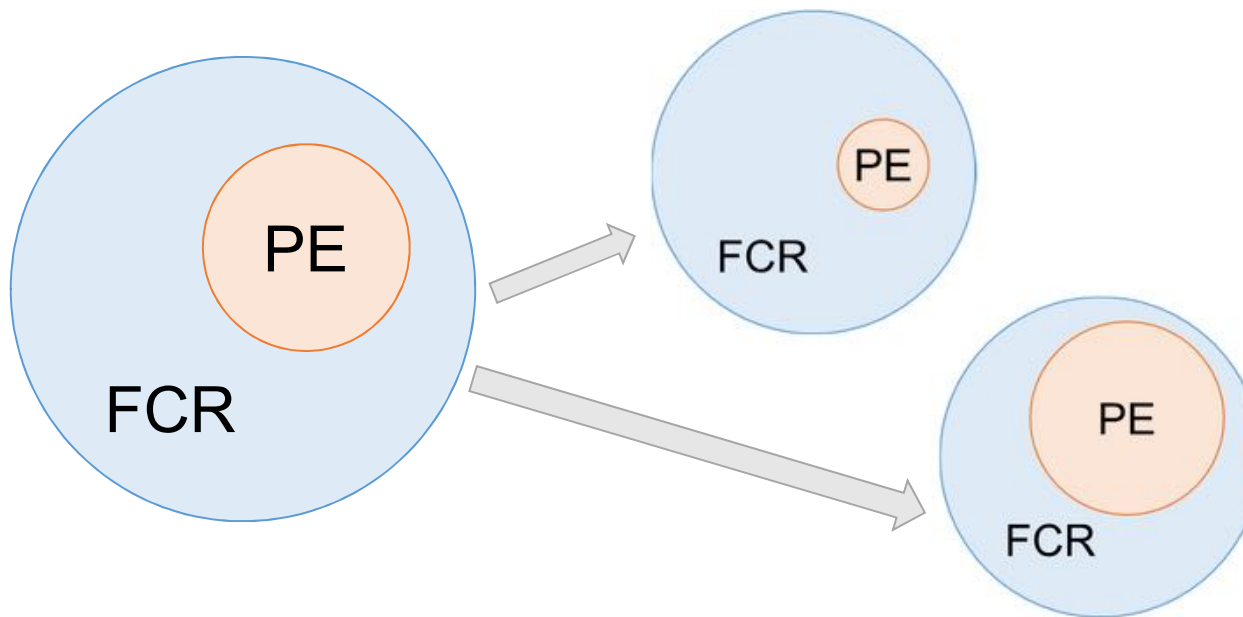
Phenotyping via DXA seems to work well

- *High-precision phenotyping* important -
 - new traits
 - small N
- Still *expensive* (1.1 M CHF ~ 1'500 CHF per pig)
- *Facilitate phenotyping*
- *Early phenotyping* for breeding but also nutrition studies



Conclusions II

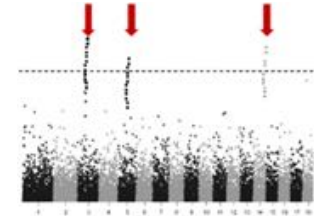
- Protein efficiency \neq feed efficiency
- Protein efficiency \subseteq feed efficiency
- Interpret r_G with caution!
- Simulation needed to disentangle selection for both traits





Outlook

Genomewide association study – *in progress*



Improved phenotyping method – *to do*

**Breeding and selection simulation to disentangle
FCR and protein efficiency** – *to do*

Functional genetics / eQTL – *to do*

Collaboration!



Thank you!



Esther Ewaoluwagbemiga (PhD student)

Swine Research Unit:

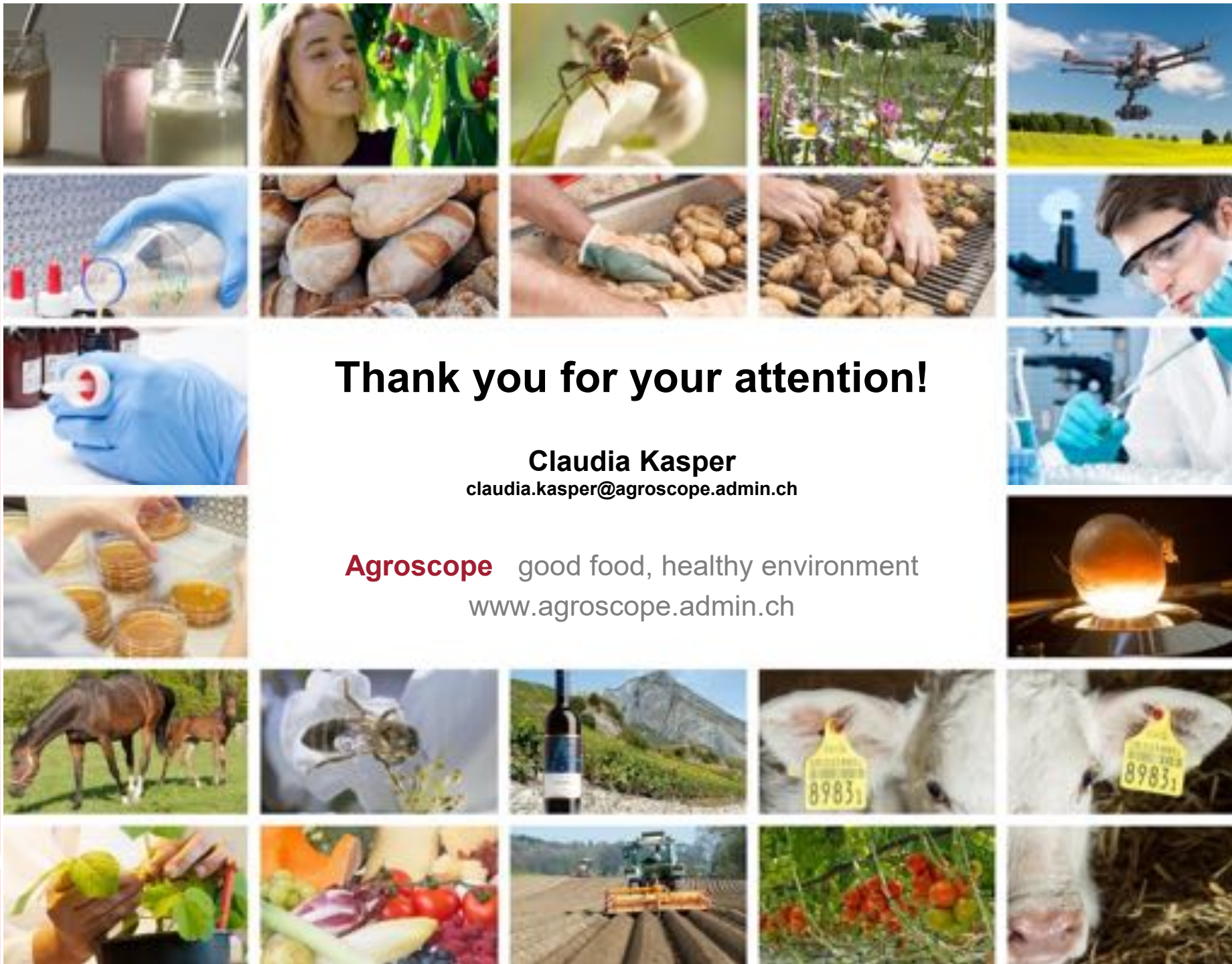
- Guiseppe Bee (pig nutrition)
- Marion Girard (pig nutrition)
- Patrick Schlegel (Suissebilanz, nutrient cycles, DXA)
- Catherine Ollagnier (veterinarian)

Experimental Farm and Abattoir:

- Guy Maïkoff
- Bertrand Egger
- Fabrice Sansonnens

Chemistry and Biology labs:

- Sébastien Dubois
- Paolo Silacci



Thank you for your attention!

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