Genetic parameters of nutrient efficiency in a Swiss Large White pig population: preliminary results

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Background

Pork production contributes to **environmental pollution**:

- emission of **nitrogen and phosphorus** compounds in manure
- import of **soy beans** for feed (domestic vegetable protein sources cannot meet protein requirement) and **mineral phosphorus** as feed additive

improve nutrient efficiency through selective breeding

Preliminary evaluation of the potential of breeding for higher nitrogen and phosphorus efficiency using data from previous experiments in Swiss Large White pigs.
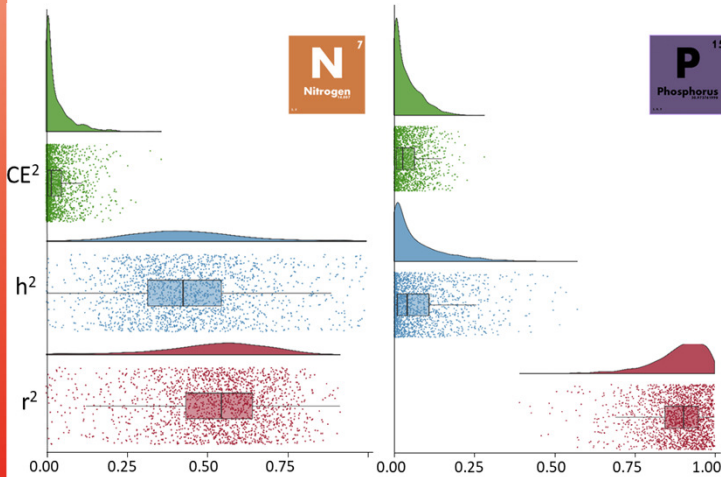

Fig. 1: Heritability (h^2, blue), common environment effect (CE^2, green) and residual variance (r^2, red) of nitrogen (left) and phosphorus efficiency (right). Posterior distributions of the respective variance components are presented as probability density functions (upper part). Points representing single estimates (mode of posterior distribution) are shown together with a box plot (with median, interquartile range and 5th to 95th percentile range).
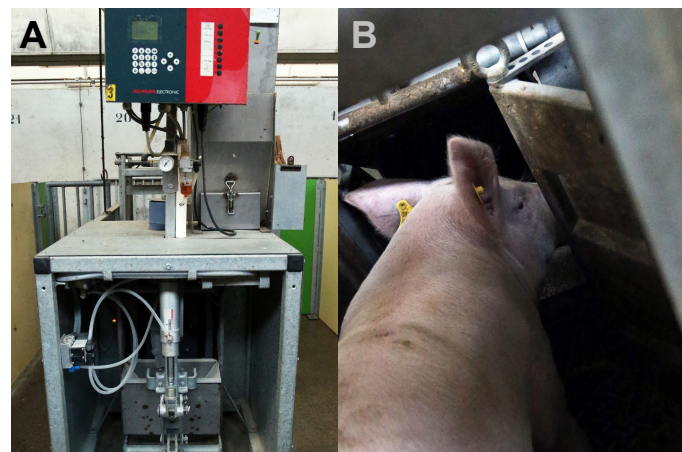
$$Nutrient\ efficiency = \frac{nutrient\ fixed\ in\ body}{nutrient\ intake}$$

Results

Heritability (Fig. 1)

- nitrogen efficiency: $h^2 = 0.400\ [0.07;\ 0.84]$
- phosphorus efficiency: $h^2 = 0.003\ [0.0002;\ 0.26]$

Genetic (r_A) and phenotypic (r_P) correlations of nitrogen efficiency (Fig. 2)

- phosphorus efficiency: $r_A = 0.74\ [-0.24, 0.99]$
  $r_P = 0.58\ [0.12, 0.88]$
- growth retardation: $r_A = 0.30\ [-0.53, 0.91]$
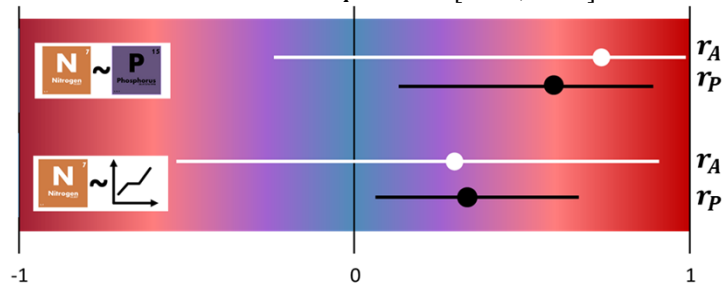 $r_P = 0.34\ [0.06, 0.67]$

Fig. 2: Genetic (white) and phenotypic (black) correlations of nitrogen and phosphorus efficiency (top) and nitrogen efficiency and growth retardation (bottom). Points represent the mode of the posterior distributions and bars the 95%-credibility interval.

Methods

294 pigs of the Swiss Large White dam line were raised on either a standard or a 20%-protein-reduced diet. Females, males and castrated individuals were tested. Nitrogen and phosphorus content of feed and whole body were determined by wet-chemistry analyses. Individual consumption was recorded by automatic feeders (Fig. 3). Growth retardation was calculated as the number of days an individual was behind the mean age at reaching the target weight for slaughter. Variance decomposition was carried out using univariate Gaussian Bayesian animal models. The models were corrected for fixed effects (age, weight, experimental run, diet, sex). Genetic correlations were estimated using bivariate Gaussian Bayesian animal models.

Outlook

In an ongoing experiment we collect a greater number of phenotypes in a paternal half-sibling breeding design. Instead of wet-chemistry analyses we will rely on body composition determined by dual-energy X-ray absorptiometry (DXA). All individuals will be genotyped on the 600K Axiom™ Porcine Genotyping Array.

Fig. 3: A) An automatic feeder with individual pig identification system as used in the experiments. **B)** A pig visits one of the autmatic feeders, which record the number of visits, the amount of feed and the length of the feeding bout of each individual **(Photo credits: Olivier Bloch, Agroscope).**

Agroscope   good food, healthy environment