Systems genetics of stress responses in pigs

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BACKGROUND

Work hypothesis: antagonism between production traits and robustness

→ Study of genetic architecture of stress responses in pigs (hypothalamic–pituitary–adrenocortical axis) for the selection of more robust animals

DATA

Genotype

120 pigs

3 stress factors

Genotype

Restraint (ad stress, including behaviour)

ACTH (adrenal sensitivity to adrenocorticotropic hormone)

LPS (lipopolysaccharide inflammatory challenge)

Clinical measures (included: cortisol)

Metabolome (coming soon)

OBJECTIVES

➔ Data integration
➔ Biological model of stress responses (prediction of the most effective levers for genetic selection)
➔ Focus on G0 population (heterogeneous regarding stress responses)
➔ Validate the model on G3 population

EXPERIMENTAL DESIGN

➔ 120 Large White pigs
➔ 3 groups
➔ 4 (or 5) measurement points (0h, (10min), 1h, 4h, 24h)
➔ 52.5 % Female
➔ 28 Families

SELECTED EXPLORATORY ANALYSIS

Clinical biology normalization (quantile normalization)

Cortisol

Increase in response to all stress factors with varying kinetics

PERSPECTIVES

➔ Biological measures and metabolomic data integration
➔ Methodology development: studying relationships between two datasets (i.e.: metabolome and blood cell analysis) taking the longitudinal nature of the data into account
➔ Comparison of several approaches to find a common space of representation for all time steps (scaling effect depending on time, optimization among the time-dependant subspaces...)

High dimensionality handled by a regularized approach (sparsity under study)