Genetics Systems of Stress Responses in Pigs

Valérie Sautron[1], Elena Terenina[1], Pierre Mormède[1] and Nathalie Villa-Vialaneix[2]

[1] GenPhySE, UMR 1388 INRA, 24 chemin de Borde Rouge, CS 52627 31326 Castanet-Tolosan cedex, France
(valerie.sautron@toulouse.inra.fr, elena.terenina@toulouse.inra.fr, pierre.mormede@toulouse.inra.fr)

[2] MIA-T, UR 0875 INRA, 24 chemin de Borde Rouge, CS 52627 31326 Castanet-Tolosan cedex, France
(nathalie.villa@toulouse.inra.fr)

1 Introduction

"Stress" is a generic term used to describe non-specific responses of the organisms to all kinds of challenges [1]. Stress is an important feature of robustness, as it has important consequences on resistance to diseases (via inflammation processes and immune function). Its main agents are the cortisol (numerous mammals, fish) or corticosteroids (rodents, birds), released by the surrenal cortex in response to the hypothalamic–pituitary–adrenocortical (HPA) axis activity.

Stress is frequently encountered in farm animals, and specifically in pigs. However, current breeding strategies have been favoring production traits to the disadvantage of robustness traits. According to the allocation of resources theory, there is an antagonism between production and robustness traits.

A major challenge for the production of food of animal origin is therefore to increase the robustness in farm animals while not significantly modifying production traits. Such an achievement would improve animal welfare by allowing better resistance to diseases and improving newborn survival, reproduction efficiency and adaptability to outdoor life. The strategy that we propose is to change the balance between production and robustness by selecting animals with higher HPA axis activity [2].

2 Objectives

The present paper aims at presenting the first results obtained in the project SusOStress funded by the ANR. This project aims at improving the knowledge about genetic bases of stress responses in pigs and delivering genetic strategies to animal breeders, in order to balance production objectives and robustness of the animals for a better trade-off between the production of food of animal origin and the respect of the environment and of animal welfare. It will include the investigation and modeling of the molecular mechanisms of genetic variability for stress responses in pigs, the study of the role of genetic variability in robustness and production traits and a genomic selection based on stress responses.

In this presentation, we will focus on the methodological challenge of integrating various data, collected at different levels of the living organisms, while taking into account the effect of a stress factor. These data were all collected on a G0 population (heterogeneous on stress response), before a divergent selection over 3 generations is being processed. The objective is to unravel the biological underlying stress responses in pigs and to propose a biological model of the stress response that will be validated on G3 generation.

3 Methods

3.1 Data

120 pigs (Large White), divided into 3 breeding groups, were submitted to 3 types of stress factors: adrenocorticotropin hormone (ACTH) injection, physical restraint and lipopolysaccharide (LPS)

injection. Blood was collected at 4 time steps (5 for restraint) on each pig before and after each experiment (e.g., t=0, t=+1h, t=+4h, t=+24h and additionally, t=+10min for restraint). The blood samples were collected for plasma total cortisol concentrations, clinical biologic measures and blood cell analyses alongside transcriptomic data (only for restraint stress) and metabolomic data. Each pig was also genotyped.

3.2 Analysis

Statistical analyses will include: extraction of differentially expressed genes linked to a biological phenomenon of interest (e.g., cortisol measures or time after stress factor) and integration of multiple high-dimensional data (genotyping, transcriptome, metabolome, biological measures...) using a methodology taking into account the longitudinal aspect of the data during integration. First exploratory analyses have been conducted on biological measures and transcriptomic data. Possible technical biases have been investigated using PCA. Correlations between variables of a certain type (transcriptome, clinical biology, blood cell analysis) at each measurement step have been studied.

4 Conclusions

The first analyses showed that:

• pigs responded at each type of stress factor with an increasing in the production of cortisol, ensuring the correct functioning of each experiment. However, some differences can be observed in the kinetic, depending on the type of stress factor;

• first exploratory analyses of clinical biologic data and blood cell analyses showed a group effect that could be reduced by quantile normalization (blood cell analyses) and global median normalization (clinical biologic data). Transcriptomic data showed a strong individual effect that needs to be reduced *(work in progress);*

• a current study aims at extracting the main correlations between two datasets while taking into account a time effect.

References

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