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**Detection and characterization of the feed intake response of growing pigs to perturbations***H. Nguyen Ba<sup>1</sup>, M. Taghipoor<sup>2</sup> and J. Van Milgen<sup>1</sup>**<sup>1</sup>INRA, UMR Pegase, Le Clos, 35590 Saint-Gilles, France, <sup>2</sup>INRA, UMR MoSAR, 16 rue Claude Bernard, 75231 Paris, France; hieu.nguyen-ba@inra.fr*

Improving robustness for farm animals is seen as a new breeding target. However, robustness is a complex trait and not measurable directly. Robustness can be characterized by examining the animal's response to environmental perturbations. Although the origin of environmental perturbations may not be known, the effect of a perturbation on the animal can be observed, for example through changes in voluntary feed intake. We developed a generic model and data analysis procedure to detect these perturbations, and subsequently characterize the feed intake response of growing pigs in terms of resistance and resilience as elements of robustness when faced with perturbations. We hypothesize that there is an ideal trajectory curve of cumulative feed intake, which is the amount of feed that a pig desires to eat when it is not facing any perturbation. Deviations from this ideal trajectory curve are considered as a period of perturbation, which can be characterized by its duration and magnitude. It is also hypothesized that, following a perturbation, animals strive to regain the ideal trajectory curve. A model based on differential equations was developed to characterize the animal's response to perturbations. In the model, a single perturbation can be characterized by two parameters which describe the resistance and resilience potential of the animal to the perturbing factor. One parameter describes the immediate reduction in daily feed intake at the start of the perturbation (i.e. a 'resistance' trait) while another describes the capacity of the animal to adapt to the perturbation through compensatory feed intake to rejoin the ideal trajectory curve (i.e. a 'resilience' trait). The model has been employed successfully to identify the ideal trajectory curve of cumulative feed intake in growing pigs and to quantify the animal's response to a perturbation by using feed intake as the response criterion. Further developments include the analysis of individual feed intake curves of group-housed pigs that can be exposed to the same environmental perturbing factors to quantify and to compare different pigs. This study is part of the Feed-a-Gene project and was funded by the European Union under grant agreement no. 633531.

**Layers response to a suboptimal diet through phenotype and transcriptome changes in four tissues***F. Jehl<sup>1</sup>, M. Brenet<sup>1,2</sup>, A. Rau<sup>1</sup>, C. Désert<sup>1,2</sup>, M. Boutin<sup>1,2</sup>, S. Leroux<sup>1</sup>, D. Esquerré<sup>1</sup>, C. Klopp<sup>1</sup>, D. Gourichon<sup>1</sup>, A. Collin<sup>1</sup>, F. Pitel<sup>1</sup>, T. Zerjal<sup>1</sup> and S. Lagarrigue<sup>1,2</sup>**<sup>1</sup>INRA, 147 Rue de l'Université, 75007 Paris, France, <sup>2</sup>Agrocampus Ouest, 65 Rue de Saint-Brieuc, 35000 Rennes, France; frederic.jehl@inra.fr*

Poultry meat and eggs are major sources of nutrients in the human diet. The long production career of laying hens expose them to biotic or abiotic stressors, lowering their production. Understanding the mechanisms of adaptation to stress is crucial for selecting robust animals and meeting the needs of a growing human population. In this study, financed by the French ChickStress and the European Feed-a-Gene (grant agreement no. 633531) programs, we compared the effects of a 15%-energy-reduced diet (feed stress, FS) vs a commercial diet (control, CT) on phenotypic traits and adipose, blood, hypothalamus and liver transcriptomes in two feed-efficiency-diverging lines. Phenotypic traits showed differences between lines or diets, but no line × diet interaction. In the FS group, feed intake (FI) increased and hens had lower body- and abdominal adipose weight, compared to CT group. We found no differences in egg production or quality. At the transcriptomic level, 16,461 genes were expressed in one or more tissues, 41% of which were shared among tissues. We found differentially expressed genes between lines or diet in all tissues, and almost no line × diet interactions. Focusing on diet, adipose and liver transcriptomes were unaffected. In blood, pathways linked to amino acids, monosaccharides, and steroid metabolism were affected, while in the hypothalamus, changes were observed in fatty acid metabolism and endocannabinoid signalling. Given the similarities in egg production, the FS animals seem to have adapted to the stress by increasing FI and by mobilizing adipose reserves. Increase in FI did not appear to affect liver metabolism, and the mobilization of adipose reserves was apparently not driven at the transcriptomic level. In blood, the pathways linked to metabolic processes suggest a metabolic role for this tissue in chicken, whose erythrocytes are nucleated and contain mitochondria. FI increase might be linked to the hypothalamic pathway of endocannabinoid signalling, which are lipid-based neurotransmitters, notably involved in the regulation of appetite.