

Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems

Towards biomarkers of feed efficiency Using –omics approaches for biomarkers discovery

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Challenges and objectives

Feed conversion ratio (FCR): the classical measure of feed efficiency, calculated as ratio of feed intake to body weight gain.

Principles

What is a biomarker?

A biological molecule that can be used to follow normal or pathological processes in animals, and is objectively measured and evaluated to diagnose, monitor, predict, or evaluate susceptibility/risk in research, practice or personalized medicine.

- Residual feed intake (RFI): a measure of net feed efficiency, defined as observed feed intake - feed intake predicted from growth and maintenance requirements
- Feed intake, body weight and even body adiposity, must be recorded during a test period on each animal, which is time-consuming, expensive, and even difficult.
- Feed efficiency is integrative of many functional pathways related to diverse biological functions, and is highly variable

Providing proxies for feed efficiency

Molecular proxies for feed efficiency, that are involved in key biological pathways, may be useful to improve breeding schemes and avoid side-effects of selection.

Finding indicators of feed efficiency at different periods during growth

Biomarker can refer to one molecule or a combination of molecules.

Discovery process

Genes, transcripts, proteins, metabolites or non-coding regulatory RNAs from all over the body can be used as biomarkers.

They can be detected by spectroscopic, chemical, molecular or biochemical studies.



Feed efficiency is calculated after a long period of test, so that predictive indicators are in huge demand to incorporate feed efficiency in breeding programs or in decision nutritional support tools.

Search for biomarkers

- Hypothesis-based : a candidate in specific biological function is measured and related to feed efficiency traits
- **Discovery-based** : thousands to millions of molecules are assessed by high-throughput methodologies. The most discriminant molecules in the variability of feed efficiency traits are proposed.
- Relationships are modelled using regression, Partial Least Squares Discriminant Analysis (PLS) and Machine Learning Methods

Transcriptomics (gene expression)

(metabolite concentration)

Absorbance (target variation)

Experimental designs



Extremes for nitrogen efficiency or for whole feed efficiency



- Lines selected for digestive efficiency or for RFI
- Genotypes x diets to generate huge variability in nitrogen or feed efficiencies

Candidates need to be further evaluated on larger sets of animals reared in production conditions.

Expected outcomes

To learn more ...

Poster - Serum color and chicken digestive efficiency Sandrine Grasteau - Email: sandrine.grasteau@inrae.fr

Poster - Metabolomics on rabbit urine Mette Skou Hedemann - Email: mette.hedemann@anis.au.dk

Running slides - Biomarkers on urine, plasma & blood for pig efficiency traits Florence Gondret - Email: florence.gondret@inrae.fr

New traits to select animals for feed efficiency.

New indicators to evaluate and manage animals according to their own potential for feed efficiency (diets with high Lys content, tailored diets, etc.).



Feed-a-Gene Feed-a-Gene is a European H2020 project involving 23 partners which aims to adapt feeds, animals and feeding techniques to improve the

efficiency and sustainability of pig, poultry and rabbit production systems. It is coordinated by INRAE (France), started in March 2015 and will last 5 years. The project aims to reduce the environmental impact of monogastric livestock production by improving and diversifying animal diets and feed technologies and by integrating new selection criteria for these animals. The Feed-a-gene project further aims to develop new management systems for precision feeding and precision farming and to evaluate the overall sustainability of the different management solutions proposed in the project.







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