

# Combined transcriptomics and metabolomics in the whole blood to depict feed efficiency in pigs

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## The need to get deeper insights into feed efficiency variations in growing pigs

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- Pig production is facing several issues related to competition with feed resources, and competitiveness due to global trade
- The increase in size of pig farm led to environmental issues related to storage, treatment and use of effluents
- Feed represents between 60 and 70 % of the total cost of pork production

### Feed efficiency

- The ability of pigs to turn feed nutrients into lean growth rate
  - while maintaining physiological functions and health
  - by reducing effluent discharge

# The need to get deeper insights into feed efficiency variations in growing pigs

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## ➤ Feed efficiency

- A research priority to support sustainable meat production
- But a complex trait that integrates multiple biological pathways orchestrated in and by various tissues

## Primary avenues for exploration

- -omics technologies: produce large amount of data without a priori
- blood samples: minimally invasive way to summarize the activities of various tissues within the body

# Strategy: From single omics to multi omics analysis

The modalities are not independent

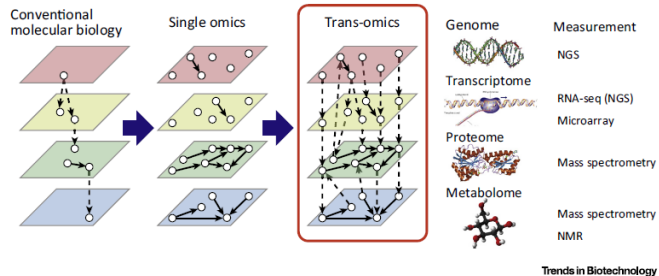


Fig. Linking the different levels of biological organization allows for a holistic view of biological entities (source: K. Yuri et al.)

Considering different levels of omics as a whole will help to understand biological systems, especially by considering the cascade of events and the interactions between entities

# Objectives

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## Starting hypothesis

Key drivers of the phenotypic divergence in feed efficiency can be better defined by

- considering the different levels of organization between biological entities
- integrating experimental data and knowledge bases

In this study, we have

- collected in 47 Large White pigs (132d of age) divergently selected for Residual Feed Intake:
  - transcriptomic data in the whole blood (60k porcine microarray)
  - metabolomic data in plasma (1H-NMR analysis and target gas chromatography)
  - phenotypic data (feed conversion ratio, body composition)
- access to pathways knowledgebase (Reactome)

## Identifying modules of co-expressed genes related to feed efficiency

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**Objective:** Build modules of co-expressed genes correlated with variations in feed efficiency and related traits

**Method:** Weighted Genes Co-expression Network Analysis (WGCNA)

### Results:

- 33 modules of co-expressed genes in the whole blood (13 to 2,491 unique genes)
- The eigengenes of 8 modules were significantly/tend to be correlated with :
  - Feed Conversion Ratio (FCR, on-farm measure of feed efficiency)
  - most of them were correlated with growth rate (ADG) and %loin muscle
- The eigengene of 1 module was significantly correlated with Daily Feed Intake
- Modules were enriched in ~ 3 different biological pathways (GO terms)

# Relationships between transcriptomic and metabolomic levels

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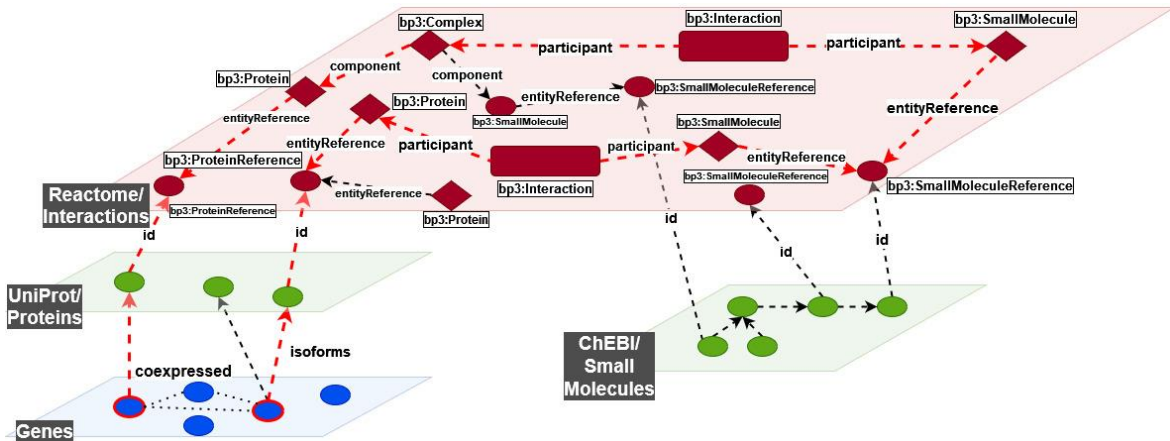
**Objective:** Determine lipids and metabolites profiles

**Method:** Construct lipids and metabolites profiles using PCA, calculate coefficient correlations between dimensions of the PCA and WGCNA eigengene modules

## Results:

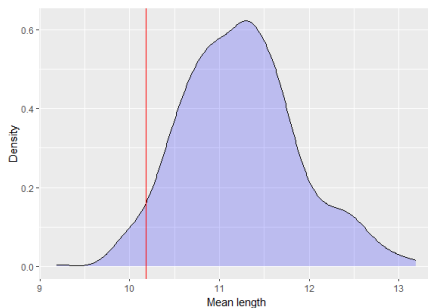
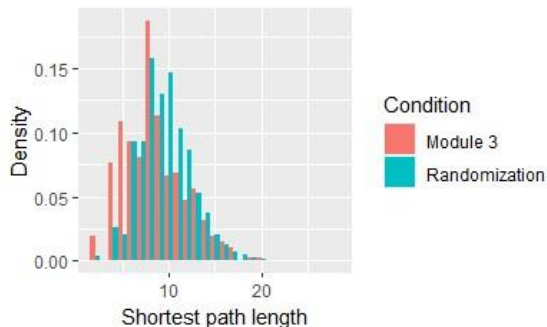
- There were few significant associations between the two -omics levels
- Example of significant association: the module Royalblue (81 genes)
- Co-expressed genes mainly involved in immunity (T and  $\beta$  cells signaling) and cell development — polyunsaturated fatty acids (omega-6 and omega-3) concentrations

# Integration of -omics levels on a same Reactome graph to explore connections using Web Semantic technologies on public databases and ontologies





# Graph traversal results on the Royalblue module



	Royalblue module	Random modules (*)
Average shortest path length	8,5	9,7
Proportion of paths with biochemical reaction encompassed	41,5%	38,3%
Proportion of paths with small molecule encompassed	41,2%	25,0%

(\*) same number of genes - average for 500 randomizations

## Conclusion: Insights on feed efficiency in pigs

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- Identifying co-expressed and co-regulated gene modules (patterns with different structures than random) related to feed efficiency: architecture of the trait
- These modules also regulate lean growth rate
- Among the biological processes over-represented within the modules, several are linked to immunity (+ cell development and protein localization)
- Interconnecting these modules with metabolic profiles suggests links between immunity and fatty acid % concentrations (relevant for future nutritional recommendations to obtain good synergy between production and health)
- Further methodological work is needed to better understand and identify key regulators of these networks thanks to knowledge graph

additional informations in : <https://doi.org/10.21203/rs.3.rs-2946807/v1>

# Acknowledgment



UMR **PEGASE**



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github: [cjuigne/multiomics\\_and\\_feed\\_efficiency](https://github.com/cjuigne/multiomics_and_feed_efficiency)



**INRAE**

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**METAPROGRAMME DIGIT-BIO**



(Digital biology to explore and predict living organisms in their environment)