

UMR Herbivores

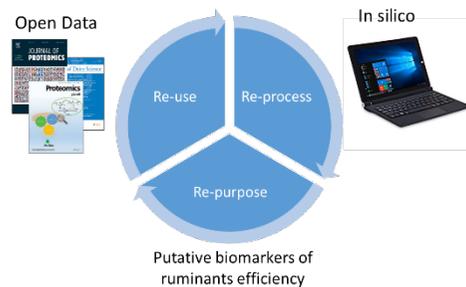
Team Biomarkers of performance, adaptation and qualities (Biomarkers))

Integration of public data for biomarker discovery

Open science makes scientific data accessible, the reuse of which promotes new discoveries. In order to characterise the efficiency and robustness of cattle, we aim to identify molecular markers to be included in phenotyping tools for the cattle production chain. To do this, one of our approaches consists of integrating the available data sets on proteins and mRNAs from bovine tissues and fluids. Three approaches are conducted: i) gene expression (mRNA and proteins) in muscle and adipose tissue is analysed to phenotype body and muscle adiposity; ii) plasma proteins are integrated to identify markers of tenderness and feed efficiency; iii) milk proteins are aggregated to propose markers of negative energy balance in dairy cows. Thus, by integrating public data with computer tools and without any new animal experimentation, we propose potential markers of the performance of beef and dairy cattle.

One way to improve the economic and environmental performance of ruminant production or to meet society's expectations is to develop tools for phenotyping the efficiency (optimal use of feed ingested for production) and robustness (maintenance of productive vs. non-productive functions, low levels of disease, etc.) of animals. This involves studying the physiological functions (growth, lactation, reproduction, immunity, etc.) that optimise production performance (efficiency) and the mechanisms that arbitrate priorities between these functions (robustness) when ruminants face constraints. Key tissues and organs (muscle, liver, mammary gland, adipose tissue ...) synthesise and secrete proteins, which participate in molecular dialogues between tissues or organs and in the prioritisation of functions (regulation of nutrient intake, metabolism and sharing ...) when faced with farm-related constraints. The aim is to use and integrate public 'omics' data, particularly transcriptomes and proteomes from different tissues and fluids, to identify molecular markers of cattle efficiency and robustness.

Data process #OpenScience3



Our approach to integrating public data aims to discover potential biomarkers of ruminant performance and to target the experiments to be carried out to confirm these biomarkers and include them in phenotyping tools for assessing animal efficiency or robustness. For example, meta-analysis of public transcriptomic data on muscle growth has identified genes linked to lipid metabolism and others that could induce or repress the differentiation of muscle progenitor cells towards the adipose lineage and thus contribute to the increase in muscle adiposity with the age of cattle (Bazile et al., 2018). Concerning meat quality, the integration of plasma proteome data has identified 63 potential biomarkers of bovine muscle tenderness (Boudon et al., 2018). Finally, the aggregation of proteins identified in healthy cow's milk produced an atlas of 4654 unique proteins present in milk. Data mining of this atlas targeted 6 milk proteins as potential biomarkers of negative energy balance in early-lactation dairy cows (Delosière et al., 2019). The integration of public data replaces animal experiments with computer and mathematical data processing, which constitutes an original approach to the discovery of biomarkers.

Data integration is one of the alternatives for the first stage of biomarker discovery [4]. We also carry out methodological developments to identify the greatest number of proteins in fluids and tissues when data is non-existent. The subsequent steps of verification and qualification of biomarkers consist in analysing the relationship between the abundance of the potential biomarker and the values of the phenotype targeted on animal cohorts different from those used for the discovery, and are in progress for the three examples cited above.

Publications

Delosière M., Pires J., Bernard L., Cassar-Malek I. & Bonnet M. 2019. Milk proteome from in silico data aggregation allows the identification of putative biomarkers of negative energy balance in dairy cows. *Scientific Reports*. DOI: 10.1038/s41598-019-46142-7

Delosière M., Pires J., Bernard L., Cassar-Malek I. & Bonnet M. Atlas of 4654 cow milk proteins distributed according to lactation stages and milk fractions. Data article soumis à *Data In Brief*.

Bazile J., Jaffrezic F., Laloë D. & Bonnet M. 2018. Meta-analysis of public transcriptomics data to understand and phenotype bovine body composition. Presented at 10. International Symposium on the Nutrition of Herbivores (ISNH10), Clermont-Ferrand, FRA (2018-09-02 - 2018-09-06). DOI: 10.1017/S2040470018000146

Boudon S., Henry-Berger J., Cassar-Malek I. 2018. Quest for plasma biomarkers for beef tenderness. Presented at 10. International Symposium on the Nutrition of Herbivores (ISNH10), Clermont-Ferrand, FRA (2018-09-02 - 2018-09-06). DOI: 10.1017/S2040470018000146

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