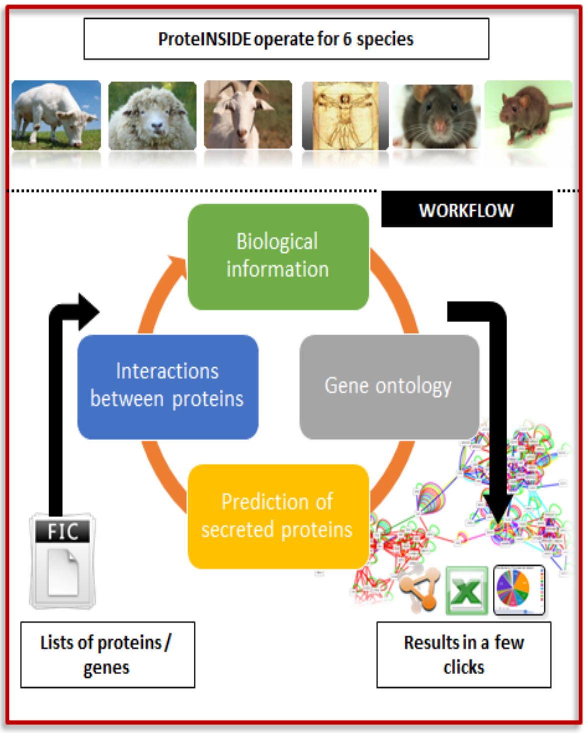
UMR1213 Herbivores

Animal Muscle Meat Team (Amuvi)

ProteINSIDE : a web service for the data mining of genomics datasets in ruminants

The challenge for scientists working in ruminants is to extract, from genomics experiments, relevant biological information in order to generate new hypotheses of research. We created ProteINSIDE, a web service for the data mining of genomics data in cattle, sheep and goat. The tool uses the knowledge available in ruminants and complement the missing information by using annotations available in monogastric (mouse, rat, man) species thank to orthology.

Transcriptomics and proteomics experiments produce large amounts of data to analyze. A robust and efficient way to mine such data is to use all in one tools, such as DAVID (Huang et al. 2009), BioMyn (Ramirez et al. 2012), ToppGene (Chen et al., 2009) Expander (Ulitsky 2010 et al.), PathwayStudio (Nikitin et al. 2003) or Ingenuity Pathway Analysis® (www.ingenuity.com; Redwood City, CA, USA). Unfortunately, such tools were not designed for the data mining of ruminant's data set and currently, the lack of dedicated automated tools hinders the efficiency and the robustness of the exploration in ruminants.



ProteINSIDE operate for 6 species

WORKFLOW

Biological information

Interactions between proteins

Gene ontology

Prediction of secreted proteins

FIC

Lists of proteins / genes

Results in a few clicks

We designed the online tool ProteINSIDE that provides an overview of the biological information stored in public databases (NCBI and UniProt) or provided by annotations according to the Gene Ontology. It also predicts proteins that are secreted (secretome) to search for proteins that mediate signalization between cells or tissues, and analyses protein-protein interactions to identify proteins contributing to a process or to visualize functional pathways or central proteins. Using lists of proteins or genes as a unique input, ProteINSIDE is an original all-in-one tool to mine genomic and proteomic data from cattle, sheep, goat, human, rat, and mouse. A user-friendly web interface provides access to create analyzes and view results that can be sorted online or directly downloaded as several file formats (image, pdf, tabular, spreadsheet, fasta…). ProteINSIDE's database collects and stores the biological information required to the efficient functioning of ProteINSIDE and is monthly updated to gather the last available knowledge. ProteINSIDE was successfully bench tested with 1000 protein identifiers from each species by comparison with DAVID, BioMyn, and AgBase designed for information retrieval and annotation, as well as with PrediSi, and Phobius that predict secreted proteins.

ProteINSIDE is freely available using a simple internet browser at www.proteinside.org and an example of results get using ProteINSIDE is provided on the home page of the website.

ProteINSIDE will be used to mine genomic data from many studies conducted worldwide to identify genes and proteins involved in a variability of the body composition of ruminants and thus the production efficiency of carcasses and meat. The integration of the published data will promote the discovery of genes or key proteins in the development of muscle and adipose tissue, because the variability of their expression or abundance will systematically be related to the variability of the mass of tissues. By this way, exploration of existing data will promote our understanding of the mechanisms controlling body composition while minimizing unnecessary duplication in research efforts.

Publication/patent:

Kaspric N., Picard B., Reichstadt M., Tournayre J., Bonnet M. ProteINSIDE to easily investigate proteomics data from ruminants: Application to mine proteome of adipose and muscle tissues in bovine foetuses. Plos One , 10 (5), e0128086

Kaspric N., Reichstadt M., Picard B., Tournayre J., Bonnet M. 2015. Protein Function Easily Investigated by Genomics Data Mining Using the ProteINSIDE Online Tool. Genomics and Computational Biology, (1)1, e16

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