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► To cite this version:

Isabelle Cassar-Malek, Brigitte B. Picard, Alain Boissy, Christine Leroux, Lenha Mobuchon, et al.. Exploiting the knowledge about model species and humans to revisit the biology of livestock animals. Workshop of translational biology in Agriculture and Medecine ‘From Bench to Bed in Medecine and from Pot to Plot in Agriculture’, Institut National de Recherche Agronomique (INRA). UMR Génétique Diversité et Ecophysiologie des Céréales (1095)., Oct 2014, Aubière, France. 1 p. hal-02799064

HAL Id: hal-02799064

<https://hal.inrae.fr/hal-02799064>

Submitted on 5 Jun 2020

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Exploiting the knowledge about model species and humans to revisit the biology of livestock animals.

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Based on a large panel of approaches from ‘-omics‘ technologies to integrative modelling, prediction and multicriteria evaluation tools, the research carried by UMR1213 Herbivores aims to improve the understanding of biological mechanisms that underlie phenotypes. Especially on-going studies try to make the link between expression of the genome and the phenotypic traits linked to production (e.g. development and quality of tissues and behaviours), efficiency, and adaptation to nutritional, management and climatic disturbances through functional genomics of animal tissues, fluids and behaviours. Due to the incompleteness of annotation of the genome of livestock animal and thus of relevant information, alternative strategies are to use model species (*in vivo* and *in vitro* approaches) or to mine genome-wide sets of data from international databases (*in silico* approach) thank to online and interactive workflows and databases that we are developing. The knowledge gained from the studies in non-ruminant and ruminant species will foster our understanding of biological mechanisms and minimize unnecessary redundancy in research efforts.

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