

## Global perspectives on trait ontology and phenotyping of livestock: examples from functional genomics and modeling in beef-producing animals

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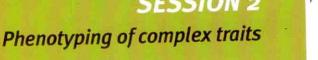
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We are entering a period where large-scale projects in life science are being developed, driven by the desire to explore biology as a whole rather than in pieces, to establish reliable relationship between genotype and phenotype, in a perspective of sustainable livestock breeding. This implies the use of the latest methods and technology for phenotyping and the development of large databases for modeling. In this context, accurate, precise, and comparable phenotypic information is critical for gaining an indepth understanding of the relationship between genes and phenotypes including the development of genomic selection. So far, it is indeed difficult or extremely difficult to combine genotype-phenotype data from multiple databases due to variability in phenotyping procedure and lack of breeding environmental data. As a consequence, it is necessary to define a common language developing an ontology which to univocally define traits and phenotypes, and later on, associated methods to capture relevant and comparable differences between animals. The ATOL (Animal Trait Ontology of Livestock) project is contributing to provide the organization and knowledge necessary for engaging livestock communities in the process of creating comprehensive phenotyping resources. This also implies a network of coordinated, advanced, and standardized phenotyping infrastructures, such as facilities for measuring well-known or new relevant traits by classic approaches, imaging techniques, and/or comprehensive description of molecular and metabolic patterns to develop strategies for multi-level data integration. Examples of such projects in functional genomics and in modeling will be given for meat-producing cattle.

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# "New technologies and new challenges for breeding and herd management"



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