

How 'omics' are contributing to sustainable animal production

In association with



Torres Sweeney, full professor of animal genomics at the UCD School of Veterinary Medicine gives an overview of how 'omics' technologies are contributing to sustainable animal production

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Sustainable development can be defined as development that meets the needs of the present without compromising the ability of future generations to meet their own needs. Hence, sustainable agriculture relies on farming techniques that provide long-term protection to animal welfare, public health, rural communities and the environment, while enabling farmers to derive immediate adequate financial reward.

BREEDING ANIMALS FOR SUSTAINABLE ANIMAL PRODUCTION

Animal husbandry has a long history, evolving over time across many regions of the world. It began with domestication of food species including pigs (approximately 13,000BC), sheep (approximately 11-9,000BC) and cattle (approximately 8,500BC). The concept of selecting breeds that express desired traits became established during the Agricultural Revolution in the 18th century, whereby breeders promoted the selection of specific genetic lines that were adapted to survive and breed in the local climate/farming conditions while producing enough milk, meat, wool, eggs, etc. for local needs. However, the rapid increase in the global human population in the 20th century has promoted the need to select more productive animals and to farm more intensively. This has been particularly evident in cattle populations where selective breeding of dairy cows focused on increasing

milk production and selective breeding of beef animals focused on growth rate and carcase weight. While these breeding programmes have produced impressive gains in the selected traits, they have been to the detriment of other fundamental health, economic, and environmental traits. It is now clear that breeding programmes must incorporate a spectrum of traits that support the goals of sustainable animal production. Unfortunately, many of these traits are described as 'hard-to-measure' traits as measurements may require either prohibitive cost (feed efficiency); complex sampling (green house gas emissions); can only be measured late in life (longevity); in one sex (milk quality); when the animal is dead (meat quality); or require animals to be exposed to conditions that would hinder the ability to use the germplasm (eg. disease resistance). Many of these traits are quantitative/complex traits that are genetically influenced by a large number of genes/proteins as well as environmental factors such as nutrition. The overarching goal of our research programme is to support sustainable animal production using two complementary approaches. The first looks to identify and select the superior animals for the 'hard-to-measure traits', while the second strives to support their health and welfare by designing optimum diets. We use a spectrum of 'omic' technologies to understand the biology of these traits and how nutrition influences their expression.

WHAT ARE 'OMIC' TECHNOLOGIES AND HOW CAN THEY BE APPLIED TO RESEARCH QUESTIONS?

The suffix 'omics' is a relatively new term in biology that describes the collective characterisation and quantification of pools of biological molecules that underly the structure and function of an organism as follows:

- **Genomics:** is the study of the complete set of DNA of an individual. It involves the sequencing and analysis of genomes using high throughput/next generation DNA sequencing followed by bioinformatics, to assemble and annotate the structure and the function of entire genomes. It allows a high-resolution view of the genetic variants between individuals (eg. single nucleotide polymorphisms [SNPs] deletions, insertions, etc.) and the association between these variants and traits of interest. SNP chips can then be developed to rapidly screen a panel of SNPs in a large number of animals and predict the ability of the animals to express beneficial phenotypes.
- **Transcriptomics:** is the study of all of the RNA transcripts that are present in a cell at a particular time point. We routinely study mRNA, which are the messaging molecules sent from the DNA to inform the cell as to what protein to make at that time point. Measuring the expression of mRNA in different tissues or conditions, or at different times, gives information on how genes and traits are regulated. Next-generation sequencing can be used to identify all of the mRNA molecules that are expressed at a particular time point or in a variety of tissues as required. Quantitative polymerase chain reaction (PCR) allows the quantification of expression of specific genes of interest.
- **Epigenomics:** is the study of all of the reversible modifications attached to the DNA or to the histone molecules that house the DNA. These modifications can influence the rate of gene expression, without altering the DNA. A wide variety of environmental factors, such as stress and nutrition, can influence the epigenome.