

Reproduction in the Era of Genomics

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Fertility is the main key for enhancing milk and meat production and ultimately the farmer's livelihood. Therefore, efforts from researchers all over the world have been made in improving and controlling fertility of farm animals during the last decades. Earlier studies were mainly focused on characterization and understanding of general reproductive processes both in *in vivo* and *in vitro*. For instance, the cyclicity of estrus in females was one of the topics that have been intensively studied. This was led to more understanding of mechanisms regulating ovarian follicular turnover and how the hormones regulate it. All these researches have advanced in vivo embryo production and helped to set up in vitro embryo culture. Although our understanding of the controllers of reproductive events is increasing, the more clues and problems were raised. In parallel, reproductive biotechnology was revolutionized. With the recognition of efforts done in reproductive technology, the Nobel Prize in Physiology or Medicine 2010 was awarded to Robert G. Edwards "for the development of in vitro fertilization". The birth of Dolly on 1996 as the first ever organism to be cloned from adult cells has paved the way to a additional Noble prize in changing adult cells into stem cells, which can become any other type of cell in the body. At the same time, molecular biology techniques were more advanced to hold promise for more understanding of the gene function of cells involved in the reproductive process. Gene by gene analysis was first introduced as an attempt to investigate the fine-tuning of the different reproductive phenotypes. As more progress has been made in gene technology, a new concept has been presented which called reproductive genomics. This concept was developed as a collection of methods that profile specific cellular molecules at the genome level and Omics was given as name expressing all these tools. The Omics approaches are dealing with mRNAs (Transcriptomics), miRNA

(miRNAomics), proteins (proteomics), metabolites (metabolomics), lipids (lipidomics) and genomic modifications without changing DNA structure (Epigenomics). These approaches aim to define the gene pathways and networks governing reproductive processes. Furthermore, advancement of bioinformatics tools has enabled scientists to understand gene pathways and networks contributing to the complexity of reproduction in farm animals. The discovery of RNA interference (gene silencing by double-stranded RNA) was considered as a new powerful tool that could further expand our information on gene function. This is a pivotal time for scientists working in the area of reproductive biology and the related field of functional genomics. Different research areas in reproduction were deeply investigated using genomics tools. Identification of reliable molecular markers of oocyte and embryo quality one of the top issues that was focused during the last decade. Moreover, the impact of the environment and ART (Assisted Reproduction Technologies) on oocytes and early embryos of farm animals were explored in many publications. Maternal communications with gametes and embryos before and after fertilization are curial events of reproduction, which were recently highlighted. Other reproductive phenomena like cloning and stem cells research hold promise not only for improving farm animal but also for conservation of endangered species and regenerative medicine. Progress has been made also to discover the genes behind the reproductive diseases. With wide application of genomics based technologies in addition to next generation sequencing it will be possible to provide the breeding industry with essential tools for enhancing reproductive efficiency. Collectively, identification of genetic factors that compromise fertility of farm animals is the first step in eliminating this problem from the herd and thereby increasing reproductive outcomes.

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