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EDITORIAL

# Focus on mammalian embryogenomics

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The term 'embryogenomics' was coined by Minoru Ko (2001) in his pioneering studies on the profiling of gene expression during mouse embryonic development. It refers to the area of research that combines embryological approaches and large-scale genomics analysis to provide an integrated examination of the morphogenetic processes that lead to the first patterning events at the onset of embryonic development. The term was rapidly adopted by those of us contributing to the development of embryo biotechnologies in domestic mammalian species and therefore interested in studying the extensive regulative properties of early mammalian embryos grown *in vitro* prior to their transfer to surrogate females. This was because the global analysis of the expressed genome (RNA, proteins) proposed by Minoru Ko appeared to be a valuable means of deriving key information from those expensive embryos. At that time dedicated molecular resources formed by cDNA or SAGE libraries and arrays, already accessible in both the mouse and human, were still under construction in domestic species (reviewed in Ko 2004). Since then, the tiny amount of biological material accessible from relatively few preimplantation embryos has become amenable to molecular analysis with the first techniques of RNA amplification (Brady *et al*. 1995, Kacharmina *et al*. 1999). However, the fidelity of the amplification procedures was still disputed when used in academic embryonic models (see for instance Baugh *et al*. 2001) or with samples of human tissues (Wang *et al*. 2000, Iscove *et al*. 2002).

It was to discuss these issues in the context of research conducted with embryos from domestic species that Marc-André Sirard (University of Laval) together with Andrew Watson (University Western Ontario) and Allan King (University of Guelph) launched the first 'Embryogenomics' meeting that took place in Quebec City in July 2002. This Canadian initiative was a marked success. It addressed recent progress and questions on cDNA library subtraction, SAGE analysis, use of heterospecific arrays, or RNA amplification procedures on oocytes or embryos from domestic species (see OECD proceedings, 2003). In the five intervening years, however, the landscape has dramatically changed. The power of the molecular resources and arrays in domestic species has been markedly improved with the availability of increasing Unigene entries and the near completion of genome assembly in *Bos taurus* and *Sus scrofa* (http://www.ncbi.nlm.nih.gov), as well as other marked achievements in the use of proteomic tools (2D-DIGE for example). This led us to follow up on the Canadian initiative and to organize a second Embryogenomics meeting, which was held in Paris during October 2007.

This Focus Issue of *Reproduction* summarizes the main data provided in the 20 talks that were presented and discussed during this meeting. These presentations were organized into six sessions. In this issue of the journal the contributing authors within each session of the meeting collectively provide an innovative review of their session. Altogether, these reviews cover the fields of oocyte and follicle development (Bonnet *et al*. 2008), embryonic cleavage and blastocyst formation (Duranthon *et al*. 2008), blastocyst elongation and differentiation (Blomberg *et al*. 2008), and epigenetic reprogramming (Niemann *et al*. 2008). The emerging fields of bioinformatics and RNA inhibition were also presented in two interactive sessions, one of which was on the interpretation of transcriptomic profiles and is presented here (Rodriguez-Zas *et al*. 2008*a*). These articles are complemented by three original papers provided by three of the participating groups (Mitko *et al*. 2008, Rodriguez-Zas *et al*. 2008*b*, Torner *et al*. 2008).

From discussions with colleagues who work with mice and who attended the meeting, it became evident that the embryos of domesticated artiodactyls, where implantation takes place several days after the onset of gastrulation, are invaluable models to study the respective contribution of embryonic and extra-embryonic tissues to embryo growth and differentiation. These embryos are increasingly being used to dissect the long-term developmental consequences of early perturbations to *in vivo*-derived or *in vitro*-produced embryos. Such studies do not prioritize the genetics of development but rather integrate developmental biology, physiology, and reproduction by considering the embryo together with its *in utero*


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(Spencer *et al*. 2008) or *in vitro* (Duranthon *et al*. 2008) environment. They provide further insights into the emerging related fields among which statistical network construction and functional genomics based on gain or loss of specific gene expression (using RNA inhibition or the sophisticated genetic constructs already largely used today in the mouse) will play an increasingly important role.

At the frontier of Embryogenomics, we foresaw the importance of large-scale epigenomics analysis, gene network modeling, and *in vivo* imaging for a comprehensive integration of molecular information to the study of basic biological processes at the cellular level of early embryo development. The conclusion of the meeting was that we should next meet probably within 2 years.

Finally, we would like to gratefully acknowledge the sponsors of the second Embryogenomics meeting held in Paris, as detailed in the acknowledgements and in the footnotes of the following review articles and research papers, as well as the Editorial Board of Reproduction who helped construct this Focus Issue.

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