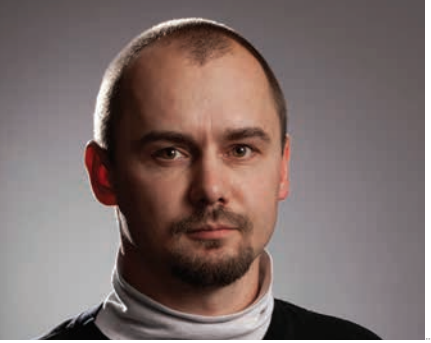

Laboratory of Epigenetic Regulations

RNA degradation, dsRNA, RNAi, miRNA, chromatin

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The zygotic genome activation is the first step in the execution of the genome-encoded programme that forms a new organism from a single fertilized cell and it is an essential event in the life of every sexually reproducing organism. The zygotic genome activation is closely associated with formation of pluripotency, i.e. the ability of cells to differentiate into any body cell type. Pluripotency is most studied in two artificial cell types, which maintain pluripotency during in vitro culture: embryonic stem cells (ESCs), which are derived from the inner cell mass of the blastocyst, and induced pluripotent stem cells (iPSCs), which form upon reprogramming gene expression in somatic cells with specific pluripotency factors that include transcription factors from the core transcription factor network controlling ESC renewal and pluripotency. A similar network forms in a stepwise manner during the mouse zygotic genome activation, which initiates at the early two-cell stage.

We study reprogramming of oocytes into pluripotent blastomeres of an early embryo (oocyte-to-embryo transition). This model is the natural parallel to the artificial reprogramming of somatic cells into iPSCs. The oocyte-to-embryo transition, however, is distinct. It is a unidirectional transient process executed by cytoplasmic factors, as demonstrated by animal cloning by nuclear transfer. Our primary research interest is in post-transcriptional mechanisms underlying oocyte-to-embryo transition. These mechanisms include control of maternal mRNA stability, small regulatory RNAs in miRNA and RNAi pathways, and production of maternal transcription factors, which will control gene expression in the embryo. Our goal is to understand how control of gene expression creates developmental competence in vivo.

Research of pluripotency is eminent for medicine and biotechnology, where pluripotency plays a role in an ever-growing number of applications. Understanding control of the oocyte-to-embryo transition will provide original insights into stem cell biology and will likely contribute to efficient and safe production of pluripotent stem cells, efficient cloning technologies, informative prenatal diagnostics, and understanding of pathology of sterility and developmental defects.

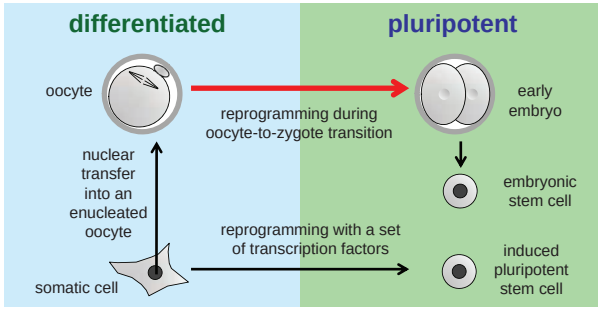

Fig. 1. Oocyte-to-zygote transition is a unique model for studying pluripotency. The mammalian oocyte is a highly specialized cell, whose cytoplasm is capable of reprogramming a genome to initiate development of a new organism. The blastomeres of the 2-cell embryo are totipotent as they can give rise to embryonic and extraembryonic tissues. The pluripotent embryonic stem cells, which have potential to give rise to any body cell type, are derived from the blastocyst, the final preimplantation embryo stage carrying the first defined cell lineages.

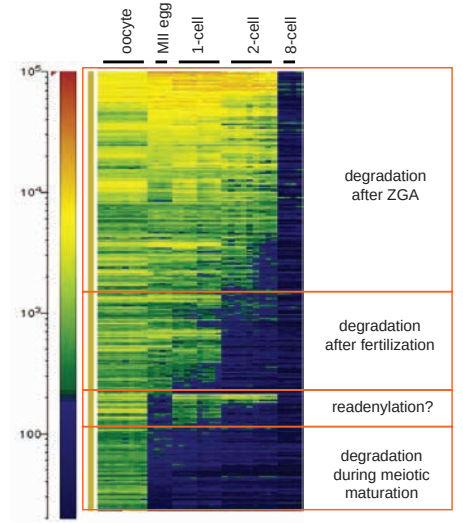

Fig. 2. Microarray analysis of maternal mRNA degradation. Shown are microarray data for 300 maternal transcripts. Colour scale indicates mRNA abundance at different stages.

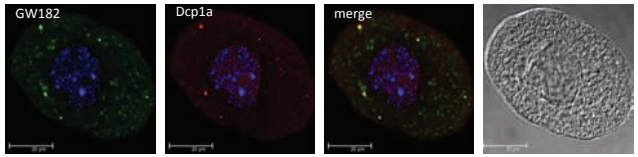

Fig. 3. Co-localization of p-body components GW192 and DCP1A in meiotically incompetent oocytes. P-bodies are centres of mRNA metabolism, including degradation and storage.

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From the left:
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Not in the picture:
Kateřina Chalupníková, PhD / Research Associate (maternity leave) · Matyáš Flemr, MSc / PhD Student · Martin Moravec / Diploma Student · Meyer Lansky / Administrative Assistant