Abstract (English)

Oocyte-to-embryo transition (OET) is one of the most complex developmental events, during which a differentiated oocyte gives rise to a totipotent zygote. During OET a transcriptionally silent oocyte undergoes massive reprogramming of gene expression, which transforms it into a transcriptionally active zygote. Although numerous studies have contributed to understanding the mechanism of OET, many genes involved in OET are yet to be identified. A whole new level of possible regulation of OET came with the discovery of long non-coding RNAs (lncRNA). LncRNAs are pol II transcripts longer than 200 nucleotides, that are typically spliced and polyadenylated but do not encode proteins. While lncRNAs have been studied in many model systems including embryonic stem cells, their expression in oocytes and early embryos and contribution to OET were largely unexplored at the beginning of this project.

In my PhD project, I aimed to identify, annotate, and analyze lncRNAs expressed during OET. First, using RNA-Seq, 1600 highly reliable lncRNAs were identified and annotated in mouse oocytes and early embryos. Majority of lncRNAs were novel with expression exclusively at OET stages. A significant fraction of these lncRNAs was found associated with LTR retrotransposons, contributing to their novelty and evolution. Expression analysis of OET lncRNAs revealed, along with restricted maternal and zygotic expression profiles of OET lncRNAs, two unique classes of maternal lncRNAs. (I) A group of maternal lncRNAs were identified, which undergoes cytoplasmic polyadenylation, a mechanism which was previously associated with dormant maternal mRNAs, and (II) 100 lncRNAs with antisense pseudogene insertion were identified, which serve as substrates for endo-RNAi machinery in oocytes and give rise to endo-siRNAs. Finally, to study the role of lncRNAs during OET, loss of function mouse model of five selected lncRNAs were generated, of which three are reported here. Even though no phenotypic changes concerning fertility were observed, we validated cytoplasmic polyadenylation (i.e. lncRNA dormancy) and RNAi induction by maternal lncRNAs. Altogether, our study provides a comprehensive analysis of lncRNAs during OET, with the first look into contribution of LTR retrotransposons to lncRNA evolution in oocytes and zygotes, and the identification of two unique classes of maternal lncRNAs.