Preface

Proper embryogenesis requires well-orchestrated events. After fertilization, initially maternal factors stored in the egg lead the development and the zygotic genome is dormant. Then, zygotic genome controls the development by initiating its own transcription. Successful transition into this event, zygotic genome activation (ZGA), is critical for embryo survival. Previous studies have demonstrated that dramatic degradation of maternal mRNA occurs and activation of specific zygotic genes is involved during ZGA. However, specific pathways and factors involved in the process have not been fully elucidated. One of the main obstacles to investigating the process is limited tools available for molecular analyses of the event. Specifically, due to the limited amount of samples (DNA, RNA, and protein) available from early stage embryos, assessing the global profile of gene expression at the RNA and protein level has been a challenge. Similarly, following specific changes in epigenetic marks such as DNA methylation and histone codes during ZGA has been difficult. Recent technological advancements in molecular analyses now allow us to follow these changes at higher accuracy. Advanced next-generation sequencing technology allows the expression profile of transcripts during ZGA to be detected and analyzed. In addition, advancement in data processing allows us to effectively utilize mass data analysis approaches to investigate gene expression patterns during ZGA. Sensitivity of quantitative PCR is sufficient to assess the level of mRNA, small RNA, and long noncoding RNA. Immunocytochemistry, based on either antibody or fluorescence in situ hybridization (FISH), can now visualize the presence of specific epigenetic marks or RNA. The ability to alter genes during embryogenesis has not been widely available to study ZGA, at least in mammals. This is due to difficulty in generating and maintaining genetically modified animals for embryo collection. The application of siRNA technology now allows us to alter the level of transcripts during embryogenesis and the use of gene editing technology such as CRISPR/Cas9 system allows us to completely remove the function of target genes during embryogenesis. These technological advancements can overcome traditional barriers we have had that discourage us from investigating events of ZGA. This volume of the Methods in Molecular Biology series provides an overview of ZGA and use of the recent tools that can be used to elucidate the events during ZGA. We expect that new findings will emerge as now more practical approaches are available to monitor the changes we see during ZGA.

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