Expressional Analysis of Stem Cell Marker SALL4 in Mesencephalon during Chicken Embryogenesis

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Background
SALL gene family represent a group of evolutionary conserved zinc finger transcription factors which are involved in normal development. It includes four members (SALL1 to SALL4). SALL4 has significant roles in the maintenance of pluripotency and self-renewal, efficient proliferation /stabilization and cell fate decision of embryonic stem cells (ESCs). Our aim in this study was to analyze and quantify mRNA expression of SALL4 in mesencephalon, during different stages of chicken embryogenesis.

Materials and methods:
Ross fertilized eggs were incubated in 37°C -37.5°C in 60-65% humidified atmosphere. After beginning of embryogenesis, Mesencephalon mesencephalon part of the brain tissue was collected each day from the eggs embryos. Total RNA extraction and cDNA synthesis was performed from resected tissues. The synthesized cDNA was used as template for quantitative analysis of SALL4 mRNA expression using real time PCR assay.

Results:
The Real-time PCR analysis of SALL4 mRNA expression in mesencephalon tissues indicated that the level of gene expression is significantly variable during embryogenesis. While the basal SALL4 mRNA expression was detected during the rest of embryogenesis, the maximum copy number of SALL4 mRNA was quantified on 19 th day of chicken embryogenesis.

Conclusion:
Having analyzed the level of SALL4 mRNA expression in different stages of chicken embryogenesis, we can extrapolate that a probable relationship may be existed between expression of SALL4 in nerve centers of mesencephalon brain and development of optic organs.

Keywords: Expressionalanalysis, stem cell, mesencephalon.

Poster Presentation

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