2014 Master Thesis Summary

Functional Analysis of Prdm14 in Breast Cancer

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Abstract

It has been known that several genes have been linked to human cancers especially that encode PR domain-containing transcriptional regulator. Particularly PRDM14, which is found to be critical for specification of germ cell fate, PRDM14 is expressed in proximal after embryonic day (E) 6.5. PRDM14 is expressed not only in PGCs but also in inner cell mass (ICM) and ESCs in normal condition. It has been shown that PRDM14 is overexpressed in breast cancer cell and tissues associated with gene amplification. Moreover, it has been shown that highly expressed PRDM14 promotes anchorage-independent growth and resistance for chemotherapy in breast cancer. However, it has been largely unknown the mechanism of tumor malignancy by overexpression of PRDM14. We previously have provided evidence that PRDM14 promotes active DNA demethylation through Ten-eleven translocation (TET)-mediated base excision repair pathway. To investigate molecular mechanisms of PRDM14 in breast cancer progression, I have tried to establish *PRDM14* knockdown (*KD*) and knockout (*KO*) breast cancer cell line using by lentivirus system and CRISPR/Cas9 system. Furthermore, I have tried to detect the interaction between PRDM14 and TET2 in MCF7 carrying doxycycline-inducible the expression of *PRDM14*.