

# **Umbilical Cord Blood Stem Cells - A Comparative Analysis of Differential Stromal Cell Lines Used to Support Natural Killer Cell Development**

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## **Abstract**

Based on murine models, the transfusion of natural killer (NK) cell that are derived from bone marrow stem cells can augment graft versus leukemia and prevent graft versus host disease; two major complications of allogeneic hematopoietic cell transplantation. Additionally, NK cell therapy has the benefit of potentially curing leukemia without the toxic side effects of chemotherapy. The NK development occurs in the bone marrow and then in the secondary lymphoid tissue (lymph nodes). NK cells may be used to target leukemic cells due to the ability to recognize and destroy them (Imai, 2005). One of the main obstacles to therapeutic use of NK cells is obtaining sufficient numbers to treat patients. We have devised a system to generate NK cells from hematopoietic stem cells (HSCs) that result in >2-3,000 fold expansion from a single stem cell. This developmental process is dependent on stromal cells and we have identified a number of different cell lines that support NK differentiation from HSCs. This research is a comparative analysis of differential stromal cell lines which support the NK cell generation from HSCs. The main purpose of the work is to compare the AFT, EL, HFWT, OP9, and UG cell lines in their ability to induce efficient NK differentiation HSCs. Our results show differences in five different cell lines in their ability to support NK development, NK cell counts and the ability to destroy leukemic cells. These findings will aid future clinical studies using these cells for leukemia treatment.

**Keywords:** *NK cell, Natural Killer Cell development, Stem Cell*

## **Biography**

“Yuri Na is a Ph.D. student at the University of Science and Technology as a researcher at Korea Research Institute of Bioscience and Biotechnology. She received a bachelor’s degree in Biology from the University of Minnesota Twin Cities. She is interested in the development of genomic prediction algorithm and software by artificial intelligence, open source platform for high-density genotyping technologies, and NGS-based genome platform.”