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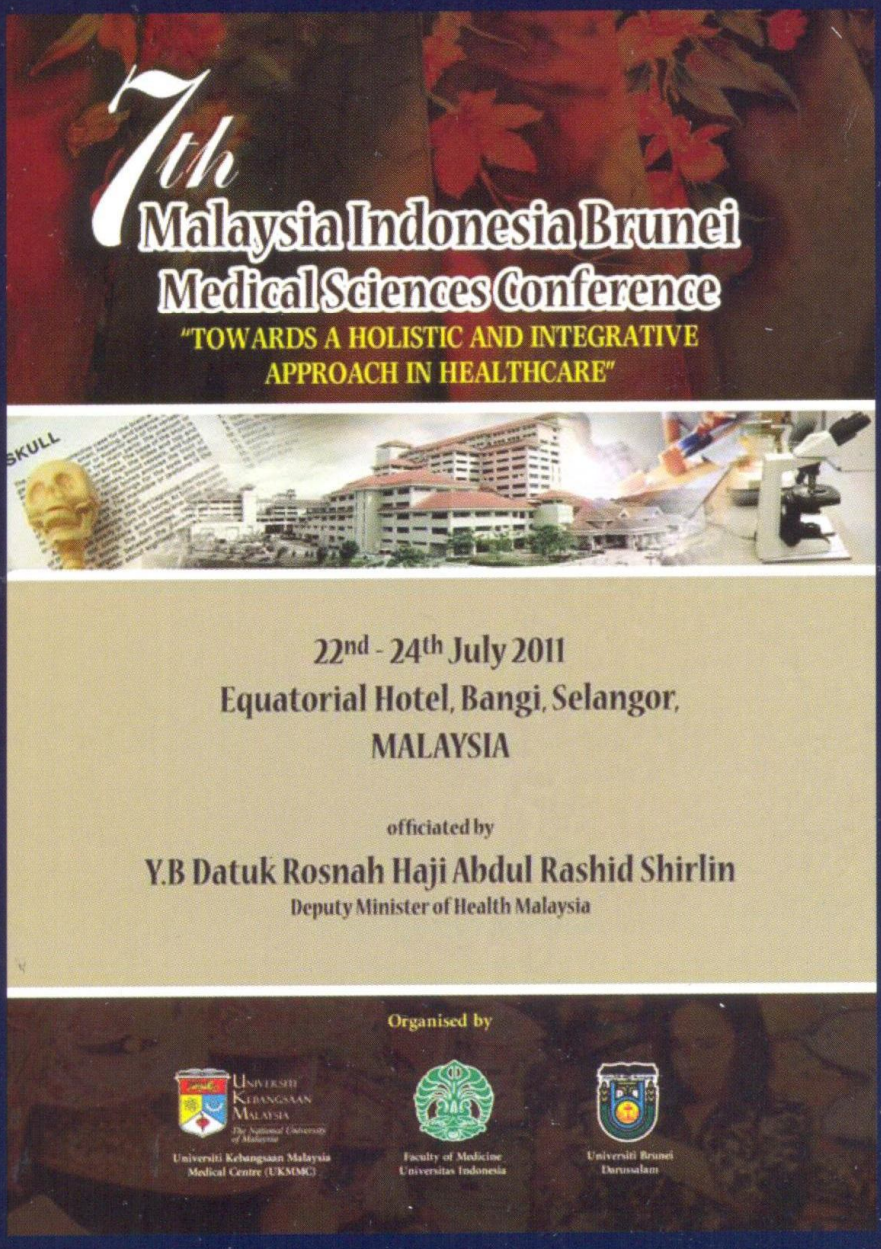

SENESCENCE-INDUCED GENES EXPRESSION OF EXPANDED HUMAN CORD BLOOD HAEMATOPOIETIC STEM CELLS

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Background:
The functions of haematopoietic stem cells (HSCs) include division, self-renewal and generation of specialized cells that make up the blood components. However, these functions could be impaired as demonstrated by many studies using human and animal models whereby HSCs eventually undergo replicative senescence. It is believed that accumulations of DNA damage, genetic modification and oxidative stress are responsible for the senescence but the specific mechanism remains unknown. This study aims to determine senescence-induced genes expression in expanded human cord blood (CB) HSCs by real time PCR.

Materials and Methods:
Human CB HSCs were isolated using immunomagnetic beads and characterized by immunophenotyping. These cells were expanded in culture medium. After 14 days, the cells were harvested, further characterized by immunophenotyping and its differentiation potential assessed by *in vitro* colony assay. Total RNA of the cells were extracted, transcribed to cDNA followed by real time PCR amplification with primers specific for *P16, P53* and *Rb* genes.

Results:
The expression of HSC cell surface markers and its differentiation potential were decreased. *P16*, *P53* and *Rb* genes were expressed more in the expanded cells compared to non expanded cells.

Conclusion:
The decrease in the expression of HSC cell surface markers and its differentiation potential were due to impairment of the expanded HSCs to divide and self-renew thus depletion and/or maturation of HSCs. This impairment could be explained by cell senescence since the expressions of *P16*, *P53* and *Rb* genes were observed.

Keywords:
haematopoietic stem cells, senescence-induced genes