Inherent Differential Propensity of Dental Pulp Stem Cells Derived from Human Deciduous and Permanent Teeth

Abstract

Lately, several new stem cell sources and their effective isolation have been reported that claim to have potential for therapeutic applications. However, it is not yet clear which type of stem cell sources are most potent and best for targeted therapy. Lack of understanding of nature of these cells and their lineage-specific propensity might hinder their full potential. Therefore, understanding the gene expression profile that indicates their lineage-specific proclivity is fundamental to the development of successful cell-based therapies. Methods: We compared proliferation rate, gene expression profile, and lineage-specific propensity of stem cells derived from human deciduous (SCD) and permanent teeth (DPSCs) over 5 passages. Results: The proliferation rate of SCD was higher (cell number, 25 x 10(6) cells/mL; percent colony-forming units [CFUs], 151.67 +/- 10.5; percent cells in S/G2 phase, 12.4 +/- 1.48) than that of DPSCs (cell number, 21 x 10(6) cells/mL; percent CFUs, 133 +/- 17.62; percent cells in S/G2 phase, 10.4 +/- 1.18). It was observed that fold expression of several pluripotent markers such as OCT4, SOX2, NANOG, and REX1 were higher (>2) in SCD as compared with DPSCs. However, DPSCs showed higher expression of neuroectodermal markers PAX6, GBX2, and nestin (fold expression >100). Similarly, higher neurosphere formation and neuronal marker expression (NF, GFAP) were found in the differentiated DPSCs into neuron-like cells as compared with SCD. Conclusions: This study thus demonstrates that both SCD and DPSCs exhibit specific gene expression profile, with clear-cut inclination of DPSCs toward neuronal lineage. (J Endod 2010;36:1504-1515)

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