Does DNA Methylation Plays a Critical Role in Osteoblastic Differentiation of Mesenchymal Stem Cells (MSCs)?

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Received: February 27, 2012; Revised: January 16, 2013; Accepted: Jun 14, 2013

Keywords: Mesenchymal Stromal Cells; Cell Differentiation; Osteoblastic

Dear Editor,

Mesenchymal stem cells (MSCs) are characterized by ability to differentiate into several cell types and self-renewability. These stem cells have a limited capacity in cell lineage differentiation including osteogenic, adipogenic, chondrogenic, or myogenic lineages (1). Regarding their ease of isolation and specific characteristics, MSCs have been used widely in regenerative medicine and tissue engineering (2). In spite of identification of several signaling molecules in MSCs differentiation, controlling mechanisms in MSCs differentiation has not well been described. Recently, epigenetic mechanisms have been identified as the master regulatory mechanism in MSCs differentiation such as DNA methylation, histone modification and regulatory micro RNAs (2-4). In this report, we investigate DNA methylation status of ROR2 gene in osteoblastic differentiation of MSCs. We also show that ROR2 promoter was hypomethylated during osteoblastic differentiation for which the details can be found in Noruzinia et al. (5); While other important osteoblast specific genes did not evaluate. RUNX2 and OSX are two of the most known osteoblast specific transcription factors (6, 7). However, several other non-osteoblast specific transcription factors have been identified to control osteoblast differentiation, including TWIST1 (twist homolog 1), ZBTB16 (zinc finger and BTB domain containing 16), DLX5 and MSX2 (MSH homeobox homolog 2) (8, 9). Therefore, we suggest that those genes (such as RUNX2 and OSX) could be considered as a subject for future investigations.

Besides, it can be postulated that osteoblastic differentiation of MSCs may be influenced by mechanisms other than DNA methylation (10). Therefore, we suggest that other epigenetic mechanisms including histone modification and regulatory micro RNAs regarded in osteoblastic differentiation of MSCs should be considered for future studies.

Acknowledgements
None declared.

Authors’ contribution
None declared.

Financial Disclosure
There is no financial disclosure.

Funding Support
There is no funding or supports.

References


