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Regulation of Mesenchymal Stem Cell Fate Commitment

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Mesenchymal intricate stem cells (MSCs) represent a versatile population of multipotent progenitor cells with remarkable capacity for self-renewal and differentiation[1]. The fate commitment of MSCs is orchestrated by a complex interplay of intrinsic and extrinsic factors, encompassing signaling pathways, transcriptional regulators, epigenetic modifiers, and microenvironmental cues[2-5]. Key signaling pathways, such as Wnt, BMP, Notch, and TGF-β, intricately regulate MSC fate decisions by modulating the expression of lineage-specific transcription factors and downstream effectors[6-9]. Within this framework, Guo *et al*. (Prog Biochem Biophys, 2024, **51**(6): 1406-1417. DOI: 10.16476/j.pibb. 2024.0099) illuminates the pivotal role of PRMT7 in governing the adipogenesis of MSCs, furnishing novel scientific insights into the directed differentiation of MSCs and unveiling fresh targets for modulating their fate commitment.

PRMT7, a member of the protein arginine methyltransferase family, governs the post-translational modification of arginine residues in diverse protein substrates. Through its enzymatic activity, PRMT7 catalyzes the addition of methyl groups to arginine residues, thereby modulating protein function and cellular processes. Unlike other PRMT family members, PRMT7 predominantly catalyzes mono-methylation of arginine residues, exhibiting distinct substrate specificity and regulatory roles[10]. Central to its multifaceted functions, PRMT7 intricately modulates chromatin architecture and gene expression through histone methylation. By catalyzing the mono-methylation of histones, PRMT7 exerts fine-tuned control over transcriptional activation and repression, thereby shaping the epigenetic landscape crucial for cellular differentiation, proliferation, and development[11]. Guo *et al*. revealed a new target for PRMT7: IGF-1. The authors confirmed, through qRT-PCR and Western blot, that PRMT7 indeed exerts significant control over IGF-1 expression levels. It's a captivating discovery, yet the mechanism behind PRMT7's regulation of IGF-1 remains unclear. Whether it acts as a histone arginine methyltransferase, focusing on IGF-1's promoter region to regulate its expression, or directly affects IGF-1 by adjusting its post-translational modifications, is still uncertain. However, this finding opens up an intriguing avenue for further exploration.

Understanding the mechanisms underlying MSC fate commitment holds profound implications for clinical medicine and tissue engineering. This work presents groundbreaking scientific evidence supporting the targeting of PRMT7 as a potential approach for addressing obesity and obesity-related metabolic disorders stemming from adipocyte and adipose tissue dysfunction.

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