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High-resolution Characterization of Human Source-specific Mesenchymal Stem Cells for Therapeutic Use: "One Cell Source" does not fit all

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Substantial pre-clinical mechanistic understanding and therapeutic effectiveness have rapidly moved human mesenchymal stromal/stem cells (hMSCs) into clinical testing, with over 1000 trials registered. These versatile progenitor/stem cells possess multilineage differentiation capacity as well as profound immunomodulatory properties to even allow for unmatched use as off-the-shelf cellular products in many disease indications. But while the safety profile of this cellular product has been excellent, only a small proportion of trials have shown effective outcome. hMSCs possess donor-specific differences inherent in all live-cell products, and the availability of many tissues/organ sources for isolation adds to the complexity of this product. We have demonstrated that different tissue-specific hMSCs—including from the adult bone marrow (BM), fetal placenta, as well as pluripotent stem cell-derived including human embryonic stem cells (hESCs) and induced pluripotent stem cells (iPSCs)—may not be equivalent in terms of differentiation capacity or immunomodulatory properties. However, the current criteria used to classify this complex cellular product is functionally based, time-consuming, and decades old. To resolve the current therapeutic bottlenecks, it is necessary to utilize high-resolution technology which is rapid yet cost-effective. Whole transcriptome profiling technology has undergone tremendous advances, with many different types of platforms available to fit specific needs, ranging from the more established microarray to single-cell RNA sequencing. These comprehensive yet molecular technologies can help decipher tissue-specific hMSC differences at a high resolution, reveal if there are core subpopulations involved in therapeutic effects, and provide more up-to-date QA/QC criteria to improve clinical effectiveness of MSC therapy.

