

ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Stem Cells

ESPS manuscript NO: 18188

Title: Easily-handled method to isolate mesenchymal stem cells from coagulated human bone marrow samples

Reviewer's code: 02446023

Reviewer's country: United States

Science editor: Fang-Fang Ji

Date sent for review: 2015-04-12 00:06

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CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input checked="" type="checkbox"/> Grade A: Excellent	<input checked="" type="checkbox"/> Grade A: Priority publishing	Google Search:	<input checked="" type="checkbox"/> Accept
<input type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input checked="" type="checkbox"/> No	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		BPG Search:	<input type="checkbox"/> Major revision
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input checked="" type="checkbox"/> No	

COMMENTS TO AUTHORS

This is a well-designed study that clearly shows that urokinase-treated samples provides a superior method for obtaining useable mesenchymal stem cells. The methods of this study were sound and the conclusions followed logically from the data obtained. The study has significant relevance for stem cell therapies. Minor edit suggestions: Put spaces between values and units (e.g., 8 hr vs. 8hr or 8 mm vs. 8mm), this was not done consistently in the manuscript Also, a space between "Fig. and the number" (e.g., "Fig. 1" rather than "Fig.1" In statistical analysis section, use "A p-value" rather than "A P value"

ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Stem Cells

ESPS manuscript NO: 18188

Title: Easily-handled method to isolate mesenchymal stem cells from coagulated human bone marrow samples

Reviewer's code: 02398400

Reviewer's country: United States

Science editor: Fang-Fang Ji

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CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input checked="" type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input checked="" type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input type="checkbox"/> Plagiarism	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		[Y] No	<input checked="" type="checkbox"/> Major revision
		BPG Search:	
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		[Y] No	

COMMENTS TO AUTHORS

The manuscript by Wang et al. describes a simple procedure to isolate mesenchymal stem cells (MSCs) from coagulated human bone marrow samples. The data appear to be robust and the proposed methodologies effective. However, there are a few concerns that should be addressed prior to publication of the work, which are detailed below. 1. Each of the graphs in figure 2 lack a label on the Y-axis. Labels should be included for clarity. 2. Data in figure 2A is depicted as the number of CFU-F's. However, according to the methods colonies were counted in plates charged with 2 million bone marrow cells after 12 days of expansion. Normally, the CFU-F assay is performed on purified MSC populations plated at low density (100 cells in 10 cm dish). While it is possible to count colonies by the method described in the paper it is atypical of the standard CFU-F assay. Consequently, it would be beneficial if the authors included as part of Figure 3 lower power images of the Geimsa stained plates so that the overall number of colonies per plate is discernable. The high powered images in Figure 3 are valuable since they show the fibroblast-like morphology of the isolated cells. 3. Data in figure 2b-d would be more informative if each time point (0, 8, 16h)

were plotted individually as a function of passage. This would reveal whether populations isolated by different methods (urokinase, etc.) show similar growth kinetics, despite the fact that initial cell yields were significantly different. This information is more important than the effect of time left at 4 degrees.

3. Since the data in figure 2 includes multiple cell aliquots from multiple donors, it would be appropriate to analyze the data using ANOVA to see differences between treatment groups. For example, analyses can be performed to evaluate differences in yield based on isolation method (urokinase, etc.), and a similar analysis can be used to evaluate effect of time at four degrees. There is a lot of data represented here and the authors should take time to perform some multivariate analysis to extract as much information as possible. This approach will provide more valuable information than a simple Student's t test.

4. The authors state that prolonged storage at four degrees reduced the viability of the cells used in the study. Were any of the CFU-F data normalized to cell viability? If not how would this affect the data? The authors should at a minimum report the differences in viability between the stored samples.

5. Data in figure 5 are qualitative in nature. It would be useful if these data were quantifiable, which would allow the authors to compare the bi-lineage differentiation potential of MSCs prepared by the different treatments. Is it possible to quantify the data?