

Fabrication of Vascular Smooth Muscle-Like Tissues Based on Self-Organization of Circumferentially Aligned Cells in Microengineered Hydrogels

Tao Sun,^a Qing Shi,^{*ab} Qian Liang,^b Yibing Yao,^c Huaping Wang^b, Junzhong Sun^c, Qiang Huang^b and Toshio Fukuda^a

*Corresponding author. E-mail: shiqing@bit.edu.cn

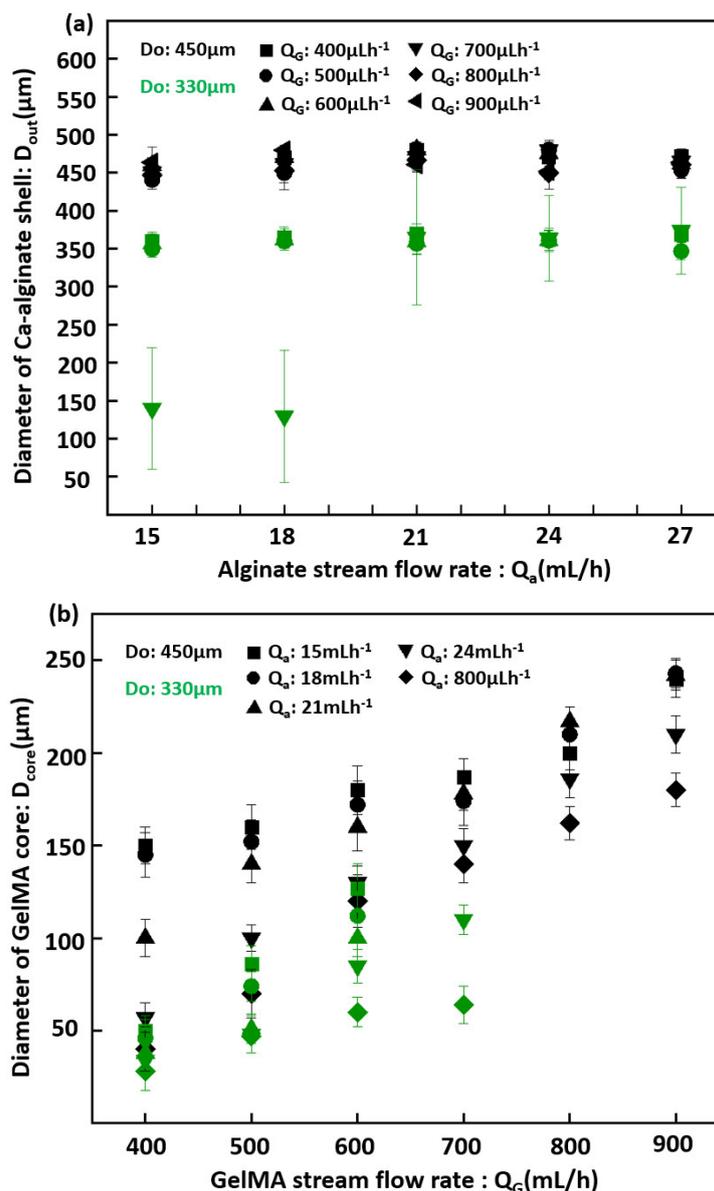


Fig. S1 Quantitative analysis of size of core-shell microfibers. (a) Diameter of Ca-alginate shell: D_{out} versus alginate solution flow rate: Q_a for different patterns of spinning orifice diameter: D_o and GelMA solution flow rate: Q_G ; (b) Diameter of GelMA core: D_{core} versus GelMA solution flow rate: Q_G for different patterns of spinning orifice diameter: D_o and alginate solution flow rate: Q_a .

Data are expressed as mean \pm standard deviation (SD) ($n \geq 50$).

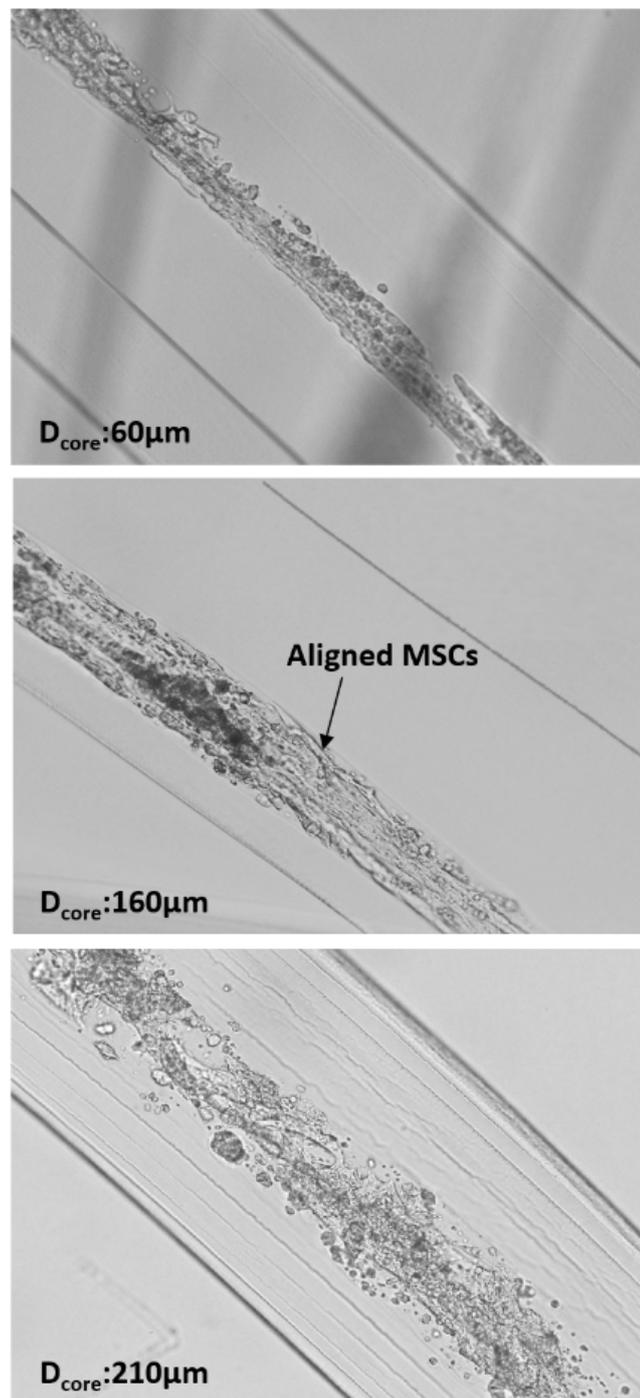


Fig. S2. The bright images corresponding to the immunofluorescence images in Figure. 2(c)



Fig. S3 the MSC elongation and orientation in the flow direction of the GelMA stream were evident immediately after fabrication

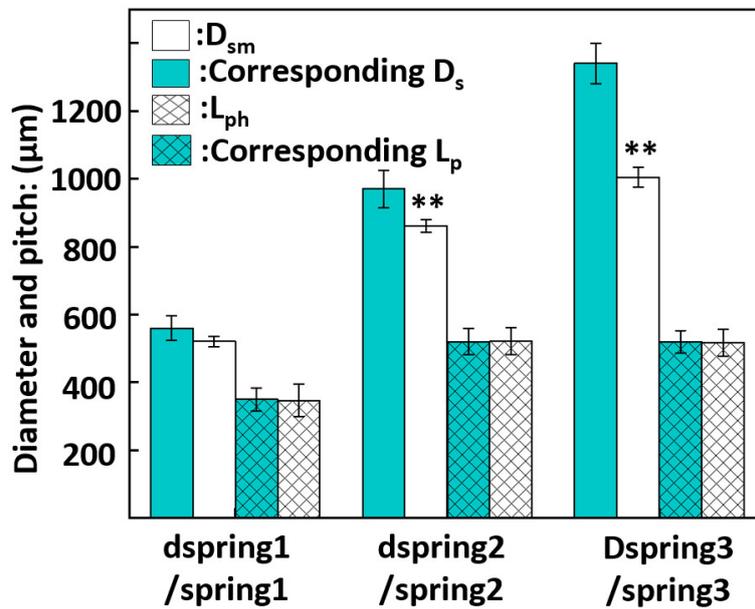


Fig. S4 The diameters : D_{sm} and L_{ph} pitches of the three dsprings vs. D_s and L_p of the corresponding three spring immediately after preparation. Data are expressed as mean \pm standard deviation (SD) ($n \geq 3$), ** $P < 0.05$ compared with D_{sm} and corresponding D_s for spring 2 and 3, respectively.

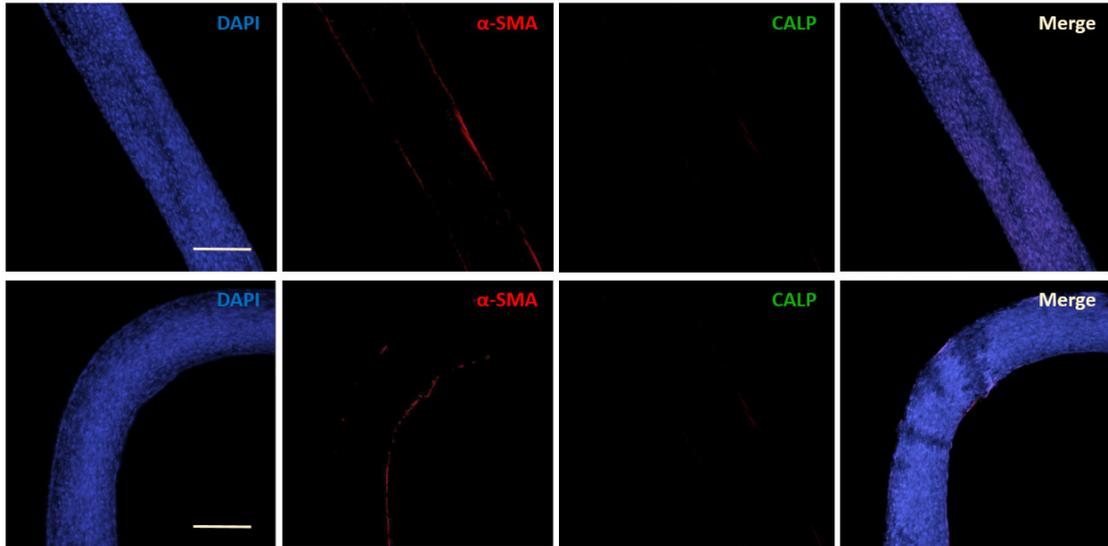


Fig. S5 Representative immunohistological images showing that only small amount of α -SMA⁺ MSCs were detected in the microfibers and the three springs in the absence of TGF- β 1, while the MSCs were negative for calponin

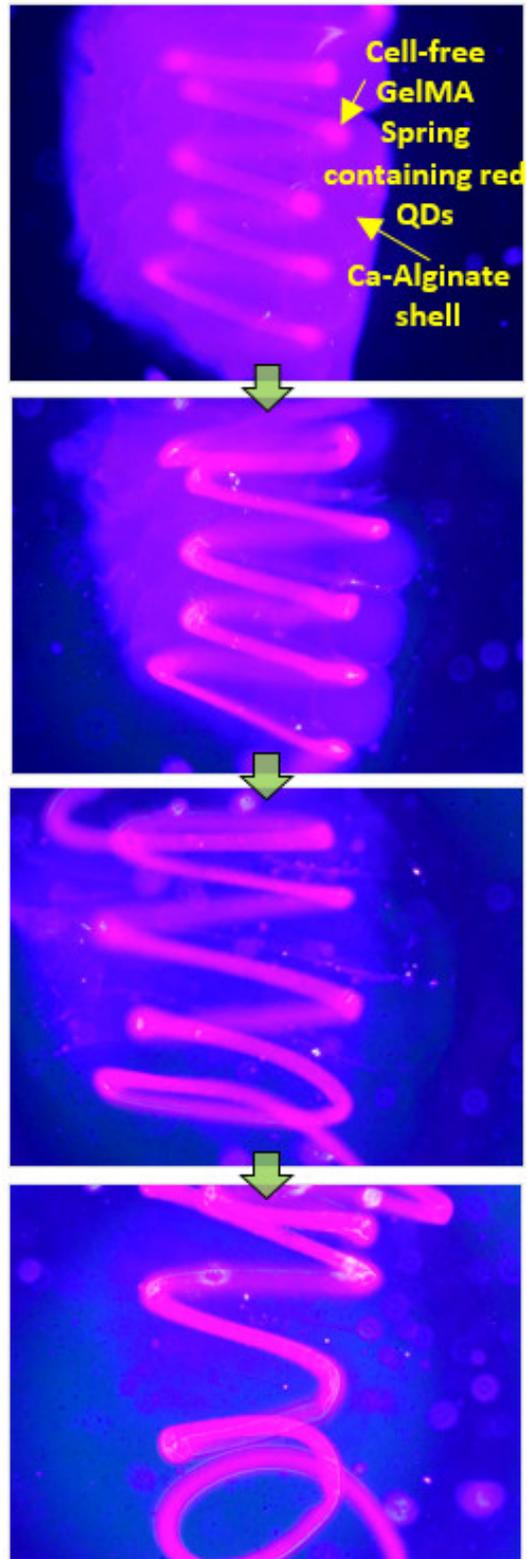


Fig. S6 Structural behavior upon degradation of the Ca-alginate shell for cell-free GelMA spring. Red fluorescent quantum dots (QDs) were encapsulated GelMA spring for easy observation.

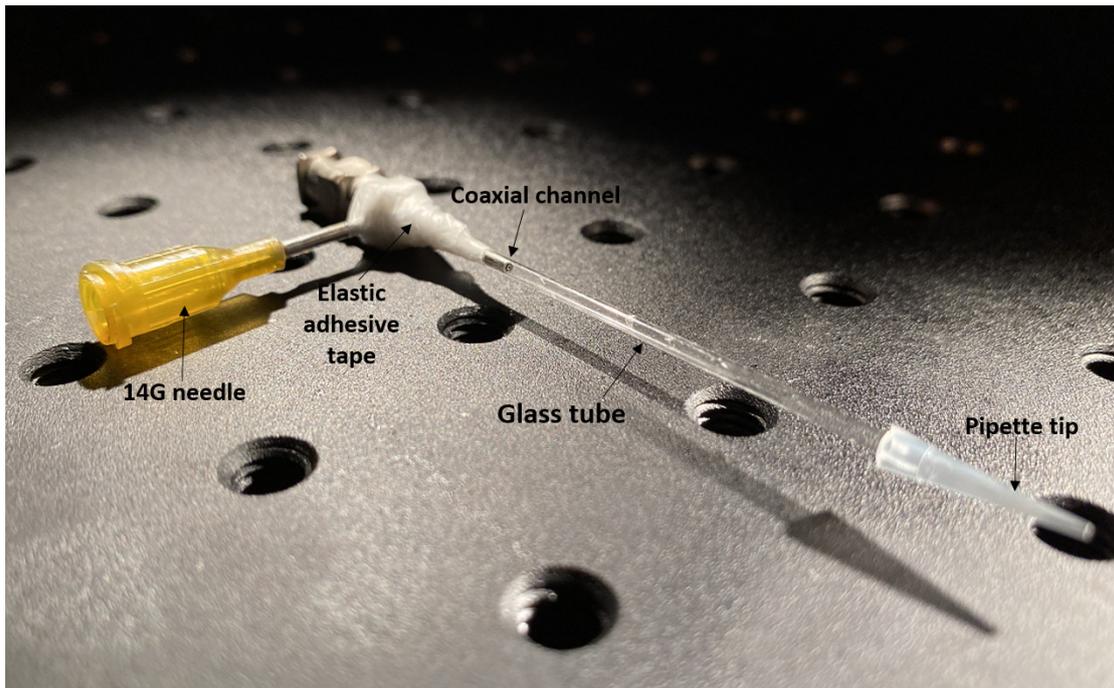


Figure. S7 Coaxial microfluidic device.

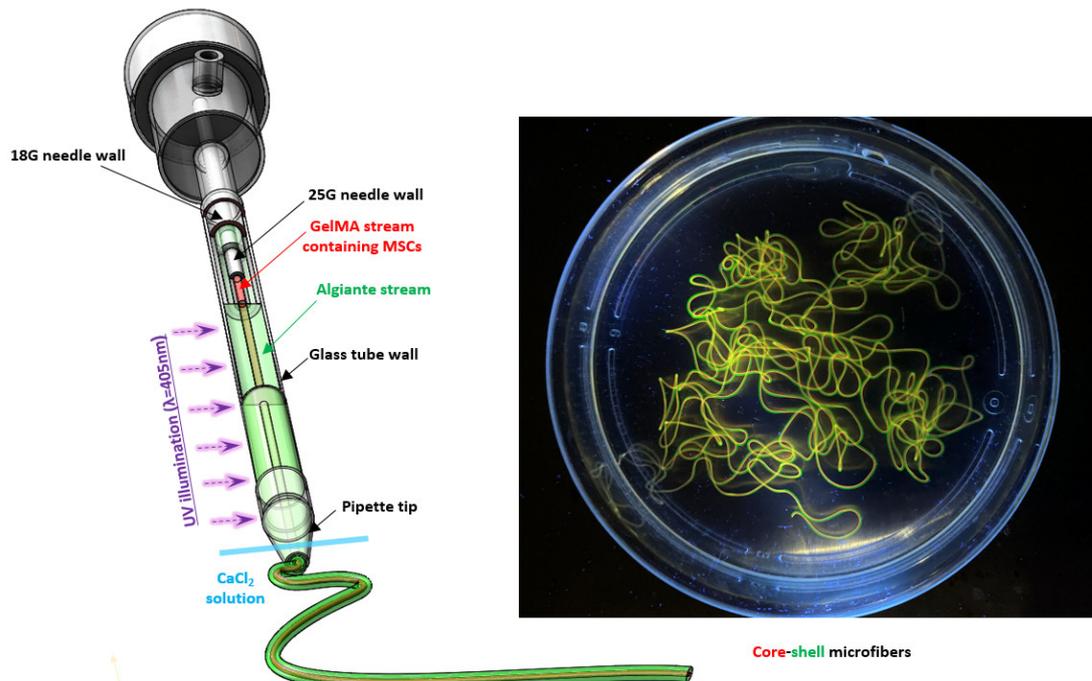


Figure. S8 Schematic of microfluidic spinning, and the spun core-shell microfibers.

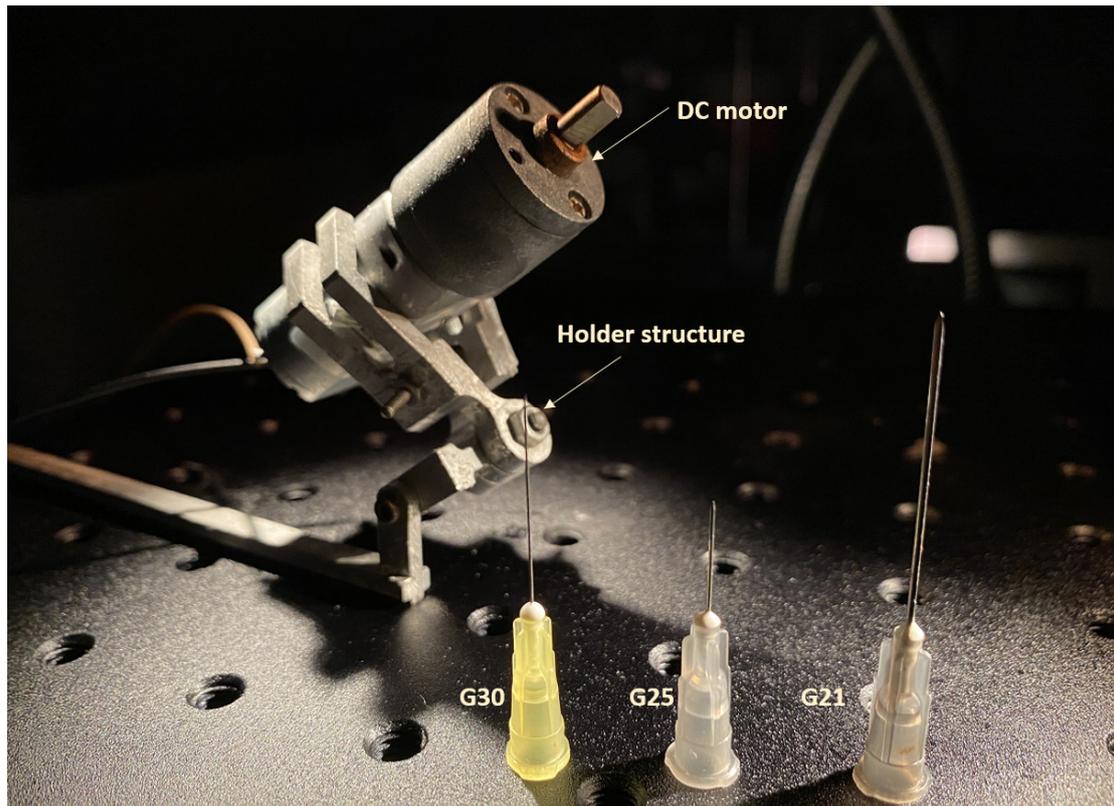


Figure. S9 Winding apparatus.

Gene	Forward Primer(5'-3')	Reverse Primer(5'-3')	Length(bp)
GAPDH	GACCTGACCTGCCGTCTA	GTTGCTGTAGCCAAATTCGTT	237
α -SMA	AGATCTCACTGACTACCTCA	CCAGAGCTACATAACACAGT	116
CALP	GAACGTGGGAGTGAAGTACGC	CAGCCCAATGATGTTCCGC	85
SM22	CCGTGGAGATCCCAACTGG	CCATCTGAAGGCCAATGACAT	104

Table S1 Primers used for RT-qPCR