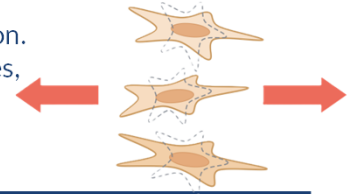


CellQ-Twin: A Soft Robotic Cell Stretcher for Multiaxial and Rhythmic Mechanobiology Studies

Background

- Mechanical forces regulate cell behaviour, function, and disease progression.
- Conventional static culture fails to reproduce physiological mechanical cues, limiting translational mechanobiology studies^[1].
- Existing cell stretching systems are often expensive and offer limited multiaxial control or imaging compatibility.



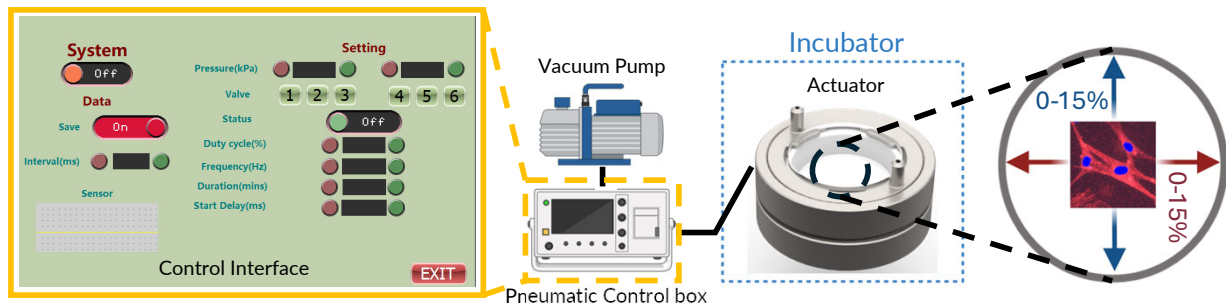
Concept - CellQ-Twin

Aim

To develop and validate a soft robotic platform for programmable multiaxial mechanical stimulation of cells.

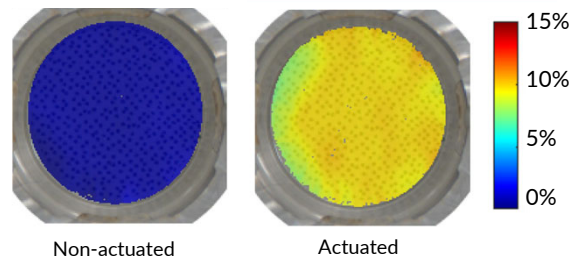
Key Features

- Soft robotic actuation for low-cost and scalable cell stretching.
- Programmable loading enables physiologically relevant strain waveforms (0–15% strain, up to 2 Hz).
- Independent control of strain along two axes across multiple culture chambers.



Mechanical Validation

- DIC confirmed a uniform and repeatable strain field across the culture membrane.
- Spatial strain variation was less than 1% within the cell culture region.
- Membrane strains of up to 15% were achieved and verified using ImageJ.



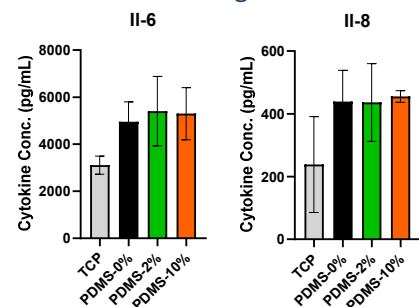
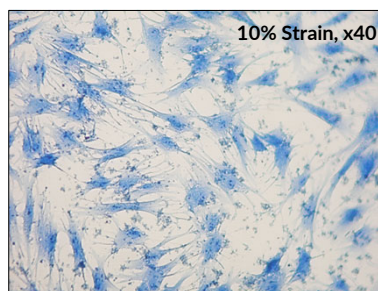
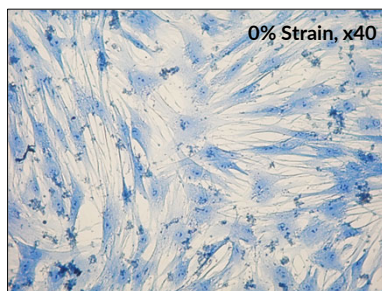
Preliminary Biological Evaluation

Methods

- BM-MSCs (N=3 donors) were seeded at 50,000 cells/well on collagen-coated PDMS membranes.
- Cells were exposed to cyclic stretch at 1 Hz and 2% or 10% strain for 8 h (N = 3).
- Cell viability, morphology, cytokine secretion (multiplex/ELISA), and gene expression were assessed (qPCR).

Key Findings

- BM-MSCs remained viable on collagen-coated PDMS under cyclic loading.
- 10% cyclic strain induced measurable morphological changes within 8 h.
- IL-6 and IL-8 secretion increased on CellQ-Twin, whereas MCP-1 remained unchanged.



Conclusion

- ✓ Soft robotic platform delivers programmable biaxial cyclic loading (0–15%, 2 Hz)
- ✓ Uniform membrane strain validated by DIC (<1% error)
- ✓ BM-MSCs remained viable under dynamic culture conditions
- ✓ Platform supports mechanotransduction and downstream molecular analyses.