

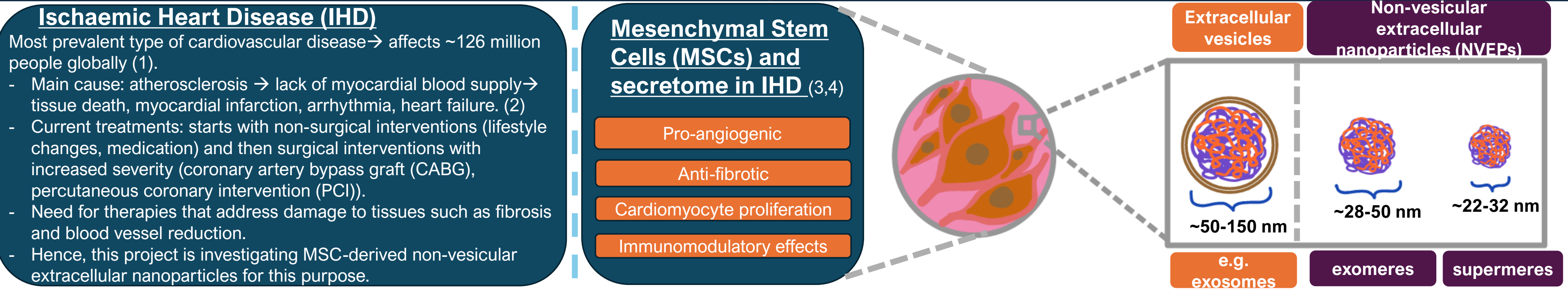
Investigating cardiovascular roles of non-vesicular extracellular nanoparticles



Annika Keshu¹, Lia DeBenedictis¹, Sinziana Popescu¹, Danya Agha-Jaffar¹, Gabrielle Johnston¹, Chris Cantwell², Rasheda Chowdhury¹, Costanza Emanuelli¹

[1] National Heart and Lung Institute, Imperial College London
[2] Department of Aeronautics, Imperial College London

Background



Hypothesis and Aims



Plan of Investigation and Progress

NVEPs

Isolation method

~70 million MSCs (~15 x T175s) are grown and kept in serum-depleted media for 48 hours prior to conditioned media collection. Subsequently subjected to filtration, concentration and a series of differential ultracentrifugation steps to isolate large EVs, small EVs, exomeres and supermeres (5,6). Schematic adapted from (5).

Cell-conditioned medium → 500g 10 min → Supernatant

2,000g 20 min → 0.22-µm filter → Concentrator → 3,500g 12-60 min → 10,000g 40 min → 167,000g 4 h → sEV → 167,000g 16 h → Exomere → 367,000g 16 h → Supermere

Protein yield

Isolated fractions are analysed by Pierce BCA (protein quantification assay) between each batch.

→ High variability in protein yield between different fractions and different batches.

→ Improved handling of protocol → improved yield.

Isolated fraction	Attempt 1	Attempt 2	Attempt 3	Attempt 4
sEVs	~100	~100	~100	~100
Exomeres	~180	~320	~180	~180
Supermeres	~180	~120	~250	~100

Characterisation

- Negative-stain (2% uranyl acetate) transmission electron microscopy was used with supermeres as a test case (shown below).
- Dynamic Light Scattering was also attempted → exomeres and supermeres not detected.

Challenges

- Heterogeneity in protein yield.
- Difficult/inconclusive characterisation as current automatic label-free methods (NTA) cannot resolve them.

Next Steps

Samples (n=3) will be sent for proteomics (Aim 1 to identify cargo) to identify MSC- exomeres/supermere markers. Currently, one batch is undergoing a pilot run to assess methodology.

This project focuses on the **Replacement** objective of the **3Rs** and as such I will be using **human-derived models** as outlined below.

Cells

- Treated and untreated cells will be assessed for viability, proliferation and angiogenesis (HUVECs)
- Experiments with AC16 are being conducted currently using a WST-1 assay. 40 ug/ml was used in initial experiment. Next step → dose response curve to find optimal dose.

Myocardial Slice

Untreated and treated (with NVEPs or relevant proteomic cargo) myocardial slices will be assessed in three ways:

Contractility

- Contractility will be measured via a tissue bath apparatus with a force transducer (trace shown above). This set-up is connected to a Micropace EP which stimulates the slice at 1Hz with a pacing current of 20-25mA with a 10ms duration.

MEA

Micro-electrode array (MEA) measurements (shown on the right) to extract time-domain (e.g. activation and end-point times) and frequency-domain features.

Immunostaining

Ki-67 (proliferation), collagen I and vimentin (fibrosis), isolectin-B4 (angiogenesis/microvascular rarefaction)

In silico electromechanical slice model

- Identification of existing ventricular electromechanical cell models/ electrophysiological model and contractility model that can be combined.
- Convert code from electrophysiological (EP) model and transfer into Nektar++
- Extend EP model implementation to include contractility-related equations to establish electromechanical coupling, confirm biological relevance and perform optimisation of parameters, if necessary.
- Translate from a single-cell scale to a 2D tissue level by creating a "fluid-like" mesh (homogenisation) with nodes connecting the single cells, allowing the simulation of electrical conduction and overall tension across a "tissue" of cardiomyocytes.
- Validate *in silico* response with data obtained from myocardial slices and their response with pharmacological agents with known effects e.g. lidocaine, carbonoxelone, dopamine.

Next Steps

Currently troubleshooting conversion in step 2 for repeated pacing.

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