THE SUITABILITY OF FROZEN TISSUES FOR THE SINGLE-CELL TRANSCRIPTOMIC STUDIES OF ENDOMETRIOSIS

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1. WHY SINGLE-CELL STUDY?

Why analyse transcriptome at a single-cell level?

- Ectopic & eutopic endometrium are heterogeneous tissues
- Whole tissue analysis shows an average gene expression profile
- Single-cell analysis detects activated/suppressed processes in each cell type

2. CHALLENGE

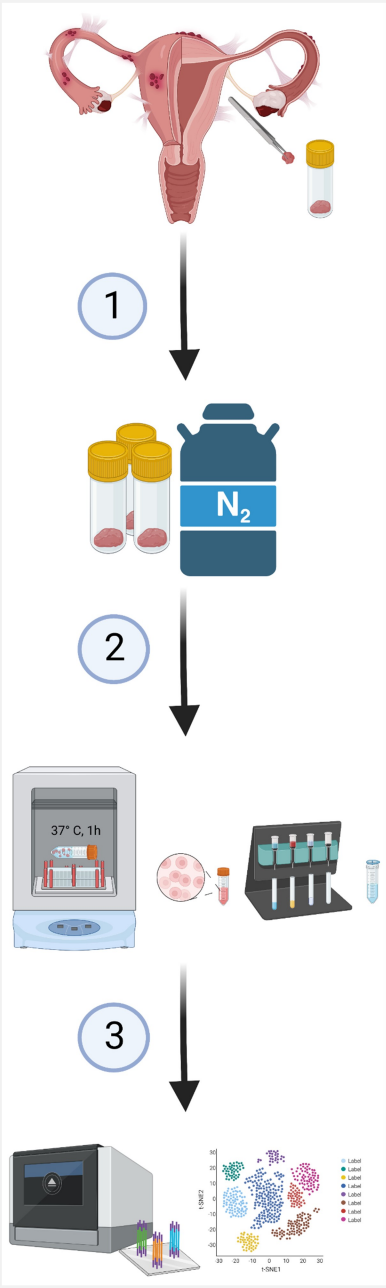
Current limitations for using fresh tissue biopsies:

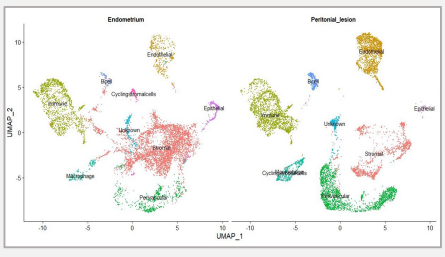
- Unpredictable laparoscopy results may jeopardize study design
- Proceeding with experiments immediately after sample collection
- The batch effect between multiple experiments in a study

Test: ① Sample collection & freezing ② Tissue processing ③ Seq & analysis

3. TEST RESULTS

1. Collection, cryopreservation of tissues and storage in LN2
2. 8 frozen paired samples: eutopic endometrium & peritoneal lesions (4 patients)
3. 10X GEMs generation, sequencing; BI Seurat integration & cluster analysis
4. 8 major cell types – in line with other scRNA studies
5. Smaller clusters of stromal & epithelial cells in lesions
6. Enriched pathways: cell adhesion & junction, actin binding, cell cycle, proliferation





4. CONCLUSIONS

1. Frozen tissue biopsies can be successfully used for single-cell transcriptomic studies as an alternative to fresh tissues
2. Comparable quality of results of cell populations from frozen and fresh tissue biopsies
3. Advantages: Processing of all the samples at a time avoids experimental batch variations, particularly with matched samples
4. General limitations: cell loss during the tissue processing steps

References: the graph is created with BioRender.com

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