Human Ovarian Cancer Cell lines

A new set of 15 ovarian cancer cell lines are being accessioned into the ECACC General Collection. [1]

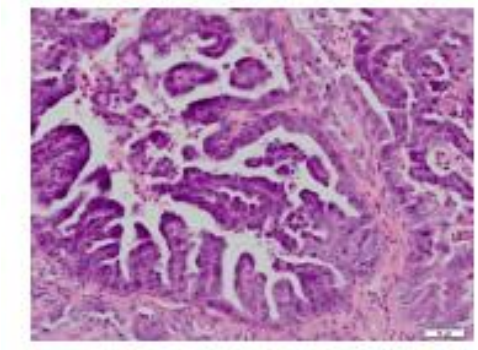

***Figure 1**: Histology of OCI-P7a tumour xenograft*

Ovarian cancer is the most lethal gynaecological malignancy with 80% of patients diagnosed in late stages and 80% suffering incurable relapse within 2 years. Drug resistance is a common problem faced in treatment and so *in vitro* models that more closely match the tumour conditions and behaviour in vivo is essential. [2][3]

These lines were generated to provide a new resource for ovarian cancer research that provides a larger number of cell lines than other collections that better mimic the phenotype of the source patient tumour.

These new lines have been characterised to ensure the genomic landscape, histopathology and molecular features of the original tumours is maintained and the molecular profiles and drug responses of these cell lines was compared to various groups of primary tumours with different outcomes.

In order to achieve this a new cell culture media was developed to increase the success rate of cell line development from diverse ovarian cancer subtypes to over 95% compared to standard culture media. This new media, called Ovarian Carcinoma Modified Ince Media (OCMI) allowed the continuous culture for approximately 60–300 population doublings with no decrease in growth rate, and upper limit of population doublings is yet to be found. Regular media resulted in growth arrest within 40 days of culture. (1)

The new collection is a valuable resource for the study of ovarian cancers and therapeutic development for their treatment, providing a greatly improved platform for *in vitro* and xenograft based investigations into high-grade, poorly differentiated ovarian cancers. Clear cell, Serous, Mullerian, Endometrioid, Carcinosarcoma and Mucinous tumour histologies are represented along with p53, PI3K and BRCA2 mutants identified.

These lines show high stability and consistency over time across their DNA, mRNA and protein profiles, and recapitulate clinically relevant patient populations. Unsupervised hierarchical clustering of the mRNA expression was used to identify two major clusters within the collection. There are 558 upregulated mRNAs in cluster 1 and 265 mRNAs in cluster 2. [1]

The mRNA expression signature was compared to that of two major studies (AOCS from Australia and TCGA from the USA). A close similarity was observed between the AOCS C1 and TCGA mesenchymal data sets and OCI cluster 1 poor outcome cell lines.

OCI cluster 1 lines showed an epithelial–mesenchymal transition-like signature associated with cancer stem cells, resistance to chemotherapeutic treatments and invasion of tumour cell clusters through the mesothelial lining of the peritoneal cavity. OCI lines in cluster 1 are also more resistant to Taxol and Cisplatin, both first-line treatments for ovarian cancer, compared with OCI cell lines in cluster 2 and pre-existing ovarian cancer cell lines. [1]

This suggests a potential for *in vitro* drug responses of these OCI lines to correlate with *in vivo* patient responses to drug treatments, a rarity in standard human tumour cell lines which often have reduced drug resistance compared to patient tumours. [1]

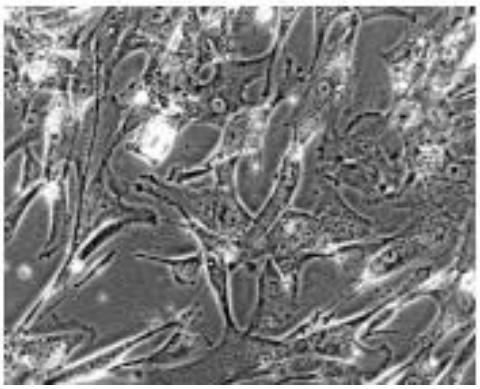

***Figure 2**: OCI-P7a culture, P33, 20x magnification*

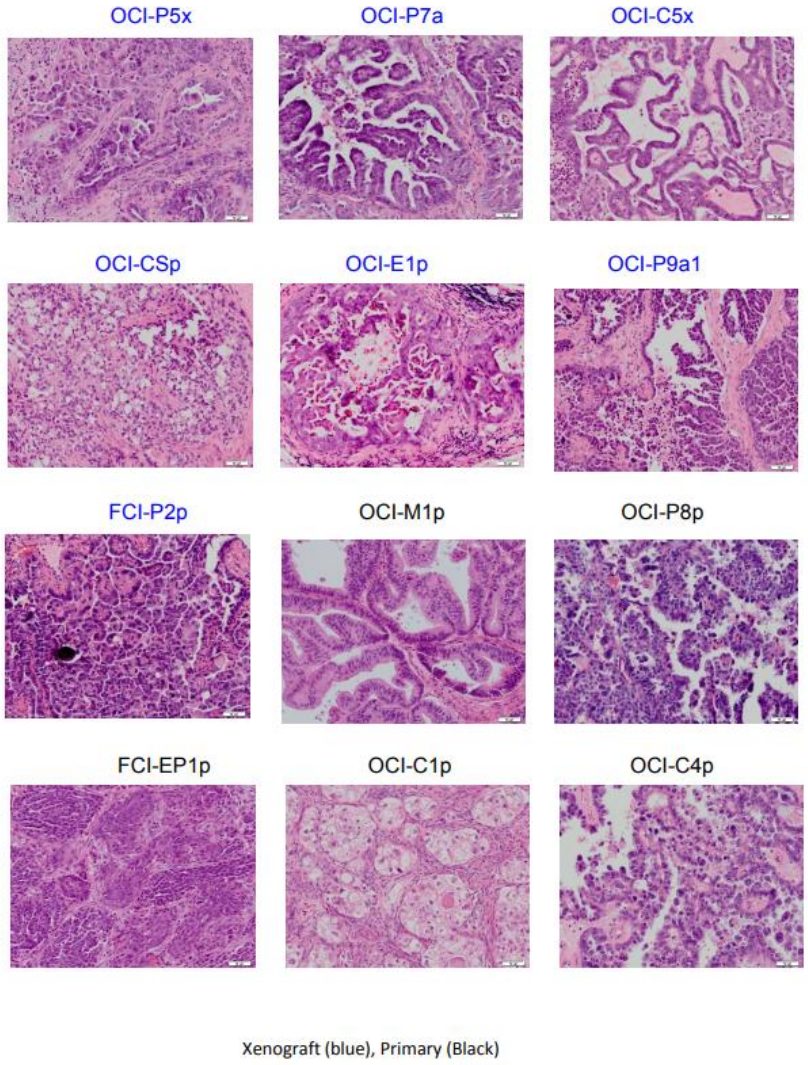

***Figure 3**: Histology of tumours formed by OCI cell lines*

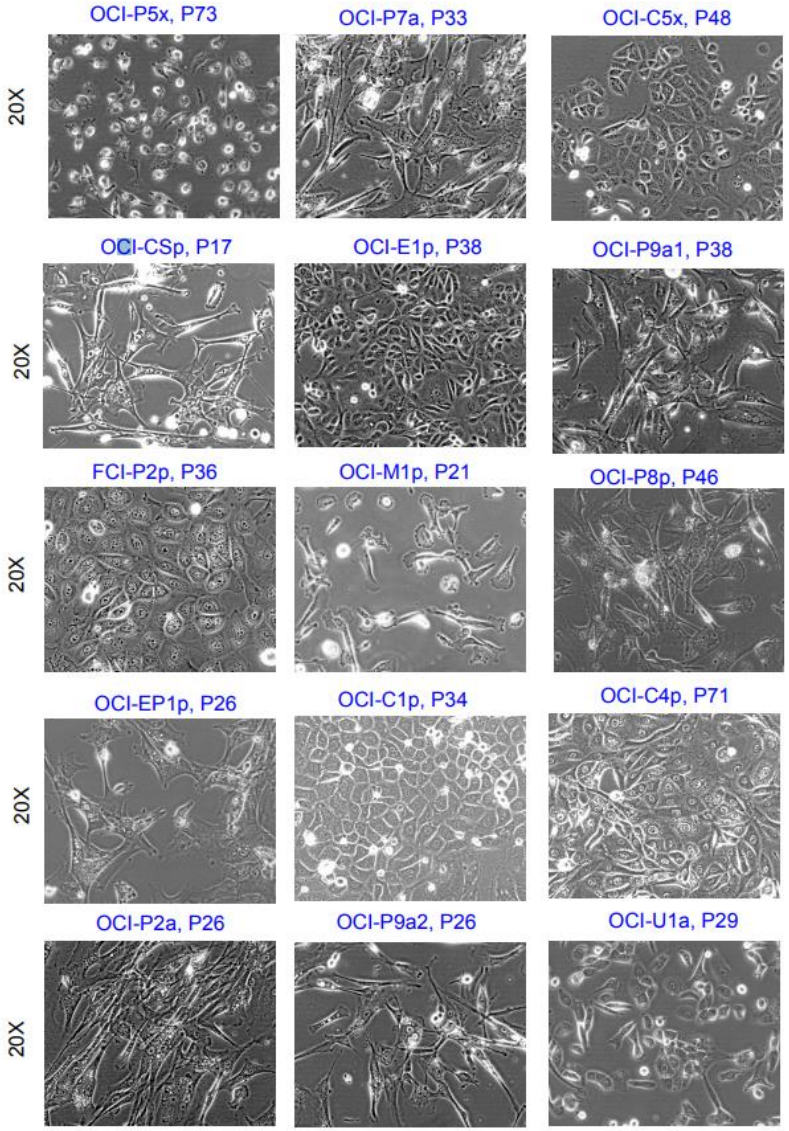

***Figure 4**: 20x images of OCI cell lines in culture.*

Related Cell lines:

ECACC Catalogue Number	Cell Line Name	Identified Cluster [1]
20012001	OCI-C1p	1
20012002	OCI-C4p	2
20012003	OCI-C5x	2
20012004	OCI-P2a	1
20012005	OCI-P5x	2
20012006	OCI-P7a	1
20012007	OCI-P8p	2
20012008	OCI-P9a1	1
20012009	FCI-P2p	2
20012010	OCI-CSp	1
20012011	OCI-U1a	2
20012012	OCI-E1p	2
20012013	OCI-EP1p	1
20012014	OCI-M1p	1
20012015	OCI-P9a2	2

These lines were originally collected at the Brigham and Women's Hospital and fall under the following IRB Approval (Protocol #: 2005-P-001862/1); in which the research activities in the proposal did not meet the definition of human subjects. All samples were taken from surgically discarded tissue that were anonymized without any patient information or identifiers.

References:

1. Ince, T., Sousa, A., Jones, M. et al. (2015) Characterization of twenty-five ovarian tumour cell lines that phenocopy primary tumours. Nature Communications 6: 7419. PMID: 26080861. https://doi.org/10.1038/ncomms8419

2. Tummala MK, McGuire WP. Recurrent ovarian cancer. (2005) *Clinical Advances in Hematology & Oncology*. 3(9):723-736. PMID: 16224447.

3. Tothill, R. W. et al. (2008) Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcome. Clin. Cancer Res. 14, 5198–5208. PMID: 18698038. DOI: 10.1158/1078-0432.CCR-08-0196.