



1. Identification of circulating markers of ovarian cancer

This project seeks to identify and characterize cancer-specific proteins circulating in plasma. Technologies being used include multiplexed protein labelling, protein fractionation and mass spectrometry. Ongoing work includes identification and validation studies for development of a screening test to detect early-stage cancers.

Ovarian cancer is currently one of the most common causes of cancer-related mortality for women. This is because most ovarian cancer patients have very few recognizable symptoms and are diagnosed at a late stage, when the cancer has already spread to other parts of the body. Survival of patients diagnosed with ovarian cancer diminishes rapidly as the cancer becomes more advanced. Early treatment, while the tumour is still confined to the ovary, provides the best prognosis for a full recovery. Unlike breast or cervical cancer, however, there is currently no suitable way to screen women regularly for ovarian tumours. The currently known molecular markers of ovarian cancer lack suitable sensitivity and specificity to be useful.

Our team is applying new proteomics technologies to identify proteins found in human plasma that may be useful in the development of an early stage screening test for ovarian cancer. Human plasma is a highly complex tissue that contains thousands of peptides and proteins, and is postulated to be a rich source of disease-specific information reflecting physiological, metabolic and disease-associated changes. The presence of certain molecules - proteolytic fragments of BRCA2 in the blood of ovarian cancer patients, for example - supports the hypothesized correlation of plasma protein levels with pathological conditions and suggests that plasma may provide a rich source of biomarkers with potential for development and application in a clinical context.

We have developed a comprehensive protein fractionation platform designed to identify proteomic changes in human plasma. A combination of several protein fractionation technologies including immunodepletion, FPLC, liquid phase isoelectric focussing and 2D PAGE with protein analysis techniques such as protein labelling and mass spectrometry is used to perform comparative analyses using plasma from ovarian cancer patients.



Using these strategies we can profile up to 4000 proteins in a single experiment, including low-abundance, biologically important proteins such as interleukins, cytokines and growth factors that are present at low nanomolar concentrations in circulation. Differences in expression levels between patients are used to infer the presence of tumours, and the proteins identified then proceed to validation studies.

The ultimate goal of our research is a routine diagnostic screening test that is able to detect cancers in their earliest stages. Early detection will significantly increase patient survival from this disease. Ongoing work includes identification and validation studies for development of a screening test to detect early-stage cancers.

Team – Circulating markers

- Dr Andrew N. Stephens
- Dr Adam Rainczuk
- Dr Katie Meehan
- Mrs Nicole Fairweather
- Ms Rebecca Crook

Collaborators - internal

- Associate Professor David M. Robertson, Group Leader, Reproductive Hormones, Prince Henrys Institute

Collaborators – external

- Professor Tom W. Jobling, Head, Department of Gynaecological Oncology, Monash Medical Centre



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