



Research We Fund



Project:

Design new treatments for patients with aggressive breast cancer using sequencing and drug response prediction

Research team:

Dr Delphine Merino

Institution: Olivia Newton-John Cancer Research Institute

Cancer type: Breast

Years funded: 2020-2022

What is the project?

Breast cancer is still one of the most common causes of death, for two reasons: firstly, some subtypes are difficult to treat and have an urgent need of new therapies, and secondly, when patients experience disease recurrence, treatment becomes limited. In collaboration with A/Prof Melissa Davis (bioinformatician at WEHI) and Dr Belinda Yeo (oncologist at the ONJCRI/Austin Health), we seek to identify the set of genes associated with favourable responses to drugs for different types of cancer. This will help predict whether patients are likely to respond to these therapies, which will assist clinicians in selecting the best drug for each patient.

What is the need?

While some drugs are known to be effective in patients with certain types of breast cancer, there are a range of responses, with some not responding at all. Many drugs also have distressing side effects. Understanding which genetic characteristics present in patient tumours can be associated with drug efficacy can help us to develop new tools to predict the sensitivity of the tumour to different therapies. This will both minimise the delivery of ineffective or potentially traumatic therapies and will help select which drugs in early development could be beneficial for improving patient outcomes and reducing deaths.

What are you trying to achieve?

In the short term this project will enable the development of diagnostic tools which identify sets of genes predictive of efficacy of drugs currently in the clinic or early development. Long term, this will guide therapeutic decisions, making them more personalised and effective.

Project timeline

Timeline	2020	2021	2022
Characterise genetic makeup of patient samples, analyse gene profiles and derive predictions of drug sensitivity			
Test the sensitivity of the samples to different drugs to validate and refine models			
Validate year 1 & 2 results in samples from ONJCRI Breast Cancer Biobank			

“ We seek to identify the set of genes associated with favourable responses to drugs for different types of cancer, to assist clinicians in selecting the best drug for each patient. ”

