Melanoma Genome Project on track

By Susan Williamson | Posted in Genomics on 17 October, 2013

The Melanoma Genome Project (MGP), a large-scale national collaboration based at the Melanoma Institute Australia (MIA) and managed by the commonwealth infrastructure enabling body Bioplatforms Australia (BPA), is gearing up to deliver its data early in 2014.

The two-year project is analysing tissue from 500 patients with melanoma to identify common gene mutations that cause this deadly cancer and will ideally lead to more personalised treatments for patients.

“The samples come from an incredibly well-curated biobank at MIA,” said Anna Fitzgerald, project manager with BPA, explaining that the Melanoma Foundation established a tissue bank 12 years ago. “The Peter Mac and Ludwig Institutes have contributed samples as well. The samples have all gone through a single pathologist to ensure there is uniformity in the diagnosis.”

Although malignant melanoma represents only 15% of skin cancers, it accounts for almost all skin-cancer deaths - and Australia has the highest mortality rate from malignant melanoma worldwide.

Melanoma can rapidly metastasise, spreading via the blood from a primary tumour in the skin to form aggressive secondary tumours throughout the body. The median survival time is less than nine months and less than 10% of patients survive for five years.

Data from the MGP will be made publicly available in the International Cancer Genome Consortium (ICGC) repository, a readily accessible database for researchers.

To date, over 175 tumour-control pairs have been tissue and DNA quality control tested and most have been sequenced.

Whole genome sequencing (>60X coverage) and array comparative genomic hybridisation (aCGH) is being conducted at the Australian Genome Research Facilities, the Ramaciotti Centre at UNSW and John Curtin School of Medical Research at ANU (JCSMR), while aCGH, whole genome (>40X coverage) and exome sequencing (75X coverage) is taking place at Axeq Technologies (Macrogen) in Korea.

“We are using the BPA data - the first 150 sequences - like a pilot because transferring such huge amounts of data around is technically challenging,” said Fitzgerald.

The data is expected to be available in the ICGC database within the next couple of months.

Fitzgerald said it’s too early to tell whether any patterns are emerging. The aim is to finalise the data input by the end of this year and begin assessing patterns of activity and what the biology means at a meeting in early 2014.

“It is a large collaboration and analysing the data is an enormous task,” she added. “The project has been a massive education process. It has cost about $5.5 million to sequence tissue and controls for the 500 or so patients.”

The project is supported by the Australian and NSW Governments, Melanoma Institute Australia, Bioplatforms Australia on behalf of the Commonwealth Government and the Cancer Council NSW.