## **Neurological Disorders Essay**

## **Brain Tumour/Cancer**

## TILE: Advances in understanding and treating brain cancers

Dr Theo Mantamadiotis, PhD The University of Melbourne 28/06/2013

The most common and aggressive brain cancers are difficult to treat with existing drugs and radiotherapy and current best practice therapy shows that high grade brain cancer patients live for an average of 15 months after diagnosis. One of the reasons for the difficulty in treating this set of diseases is that brain tumour cells between patients vary in terms of the genetic mutations they carry. These genetic differences mean that tumour cell behaviours (growth, sensitivity to drugs/radiation) also differ. Therefore, standard treatments are a blunt instrument aimed at the 'average' patient, which in reality does not exist. 'Personalised medicine' provides a new perspective, where individuals should be treated according to their disease-specific genomic profile. Recent research shows that high grade brain tumours fall into a number of genetic categories which appear to correlate with disease aggressiveness, which implies that determining brain tumour genomic profiles will be useful in determining patient specific therapy. The best approach to advancing the personalized medicine approach is to decipher the different mechanisms underlying brain tumour biology and to then treat with drugs which will be most effective in targeting tumour specific biochemical pathways, which will be different for different patient subgroups.

Current approaches aimed at deciphering the underlying genetics of brain tumour biology have been greatly advanced by two separate medical research fields. The first has been used for the last 20 years and involves the ability to generate 'humanised' mouse models. This means that scientists can genetically manipulate mouse embryonic stem cells to introduce very specific mutations which be inherited by the mice. The enormous advance brought to biomedical research by this technology is highlighted by the awarding of the 2007 Nobel Prize in Physiology or Medicine to the pioneers of this technology. With the identification of human brain tumour mutations, scientists are now able to make mice which harbour human specific brain tumour mutations. These mice develop human-like brain tumours which allow scientists to understand the way tumour cells grow and more importantly perhaps these mice provide an opportunity to test new chemotherapeutic drugs quickly so that they can be fasttracked into human patient clinical trials. The second field which promises to accelerate the understanding of the nature of brain tumour biology involves the combined technological advances which enable complete patient genomic analysis and the use of new-generation super computers. The best way to understand this advance is to remind you that in the early 2000s the so-called Human Genome Research Project which enabled the complete genetic sequencing of one individual cost billions of dollars and engaged numerous laboratories over a number of years. The advent of new-generation sequencing technology and combined supercomputing power to analyse the sequencing data (literally billions of bits of data per genome) now allows a person's genome to be completely analysed in days in a single laboratory for about AUD\$1,500! This means that in the near future patient's genomes will be analysed to enable tailored therapy.

These advances are now providing an enormous amount of genomic data relevant to brain tumours which is currently being used and deciphered by many laboratories around the world. This research provides scientists and clinicians the tools to understand an individual patient's disease and to develop new drug which much more specifically target brain tumours. Ultimately clinicians will be able to treat an individual's brain cancer with specific tailored drug combinations to more effectively arrest tumour growth, thus providing a prolonged and better quality life to patients.