

Are there germline genetic variants that correlate with mutational events in adult brain tumours?

Xiajie Summer Zhang, Andrea Johns, Alexandre Xavier, Kelly Kiejda and Rodney J. Scott
School of Biomedical Sciences and Pharmacy, Faculty of Medicine, Health and Wellbeing,
University of Newcastle

The search for inherited predispositions to any form of brain tumour has been hampered by difficulties in accessing tumour and blood samples from patients diagnosed with these types of brain malignancy. The absence of material to study has resulted in little if any improvement in outcomes for the past 40 or so years. More recently, the collection of brain tumour material and constitutional DNA samples has been increasing and more information about the genetic basis of this disease is now forthcoming.

In the current study we undertook exome sequencing of 128 matched tumour and 140 constitutional DNA samples to determine if there was a genetic predisposition to brain tumours. In a first pass analysis we identified several somatic events, many of which had been previously reported, and compared these results to germline variants in an attempt to reveal any correlation between the two data sets.

The results revealed there was little if any cross over between the somatic events we identified and what was observed in the germline of these patients. We were able to correlate combinations of genes that were associated with outcome, some of which were linked to a particular poor prognosis.

In conclusion, we did not reveal any germline changes in genes that have previously been linked to brain tumour susceptibility, underscoring the rarity of these variants even in a selected population of patients. This suggests that epigenetic events are more likely to be associated with adult-onset brain tumour development.