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To investigate patterns of survival and estimate conditional survival rates among brain cancer patients in Canada. METHODS: Canadian Cancer Registry data were obtained for all patients with primary brain cancer diagnosed between 1992 and 2008 (n=38,095). Follow-up ended with patient death or December 31, 2008, whichever occurred first. Crude Kaplan-Meier estimates were calculated at one, two, and five years post-diagnosis and also used to estimate conditional survival (restricted to 2000-2008). Age group, sex, residence and microscopic confirmation were considered in estimating rates for major histology types using multivariate models. RESULTS: The overall five-year survival rate was 27%. Oligodendrogliomas had the highest 5-year survival rate (65%, 95% CI: 62.5-67.4%) and glioblastomas the lowest (4.0%, 95% CI: 3.7-4.3%). Compared to Ontario, the age- and sex-adjusted 5-year glioblastoma survival estimates were lower in British Columbia, Alberta and Manitoba-Saskatchewan, lower in all other regions for diffuse astrocytoma, and lower in Manitoba-Saskatchewan for anaplastic astrocytoma. Estimates were significantly higher for oligodendrogliomas in Alberta, and for anaplastic oligodendrogliomas in Alberta and Quebec (P < 0.05). Longer term conditional survival rates (surviving an additional 2 years 1-4 years after diagnosis) varied by histologic group. CONCLUSION: There is a need to further explore the underlying reasons for the observed variation in survival rates by region in an effort to improve the prognosis of brain cancer in the Canadian patient population. Conditional survival information has value for clinicians as they plan the course of treatment and follow-up for individual patients.

Genetic Profiling of Radiation Induced Meningiomas

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One-third of all primary central nervous system tumors in adults are meningiomas, which arise from the meninges. Although the majority of meningioma cases are not associated with an environmental risk factor, it is well established that individuals receiving radiation treatment to the CNS are susceptible to radiation-induced meningiomas (RIMs). The genomic integrity of spontaneous meningiomas has been extensively profiled by whole genome sequencing and exome sequencing, providing a well-developed catalogue of meningioma associated mutations. In contrast, a comprehensive understanding of the molecular changes associated with RIMs is not available. Comparative genomic hybridization (CGH) has previously revealed that >90% of RIMs possess multiple regions of DNA copy number alterations, with the most common chromosomal loss being chromosome 1p and 22q. These CGH based studies of gross chromosomal alterations suggest that radiation induced meningiomas show no significant differences to spontaneous meningiomas. We have extensively characterized RIMs through the profiling of their global CpG methylation, gene expression and mutation signatures. The integration of these three platforms at base-pair resolution methylation has facilitated the identification of molecular changes that contribute to RIM. This is the largest cohort of profiled meningiomas to date, providing a robust characterization of unique RIM features that can be exploited for future therapies.