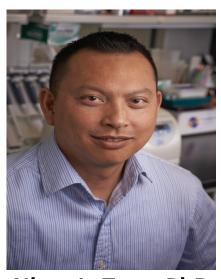
Keck School of Medicine of USC

Department of Translational Genomics - Virtual Distinguished Lecture Series



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"Genetics of Invasive Glioblastoma Cells"

Glioblastoma (GBM), the most common adult brain cancer, is among the most genetically heterogeneous, treatment resistant, and lethal of all human cancers. Despite the genetic heterogeneity, a unifying characteristic of GBM is aggressive cell invasion into the brain parenchyma, which prevents complete surgical removal, increases the risk profile of adjuvant therapies, and virtually assures tumor recurrence. Recurrent GBM tumors are generally less sensitive to therapy than the original tumor and in most cases are located in critical brain areas, preventing a second surgical resection. Most GBM molecular studies to date focus on primary, newly diagnosed tumors, and as a consequence our knowledge of recurrent GBM biology is limited. It is clear however, that primary and recurrent GBM are in some ways distinct diseases, with the latter tumors reflecting selective pressures exerted by the standard-of-care adjuvant treatment paradigm for primary GBM tumor treatment (radiation and temozolomide (TMZ). Paradoxically, even though the biology of recurrent GBM is not fully understood, most of the clinical trials testing new GBM therapeutic agents are in the setting of recurrence. Thus, additional studies focused on recurrent tumors are necessary in order to generate more molecular information on these tumors and to aid in the development of new therapies that target these aggressive cells. Accordingly, we have conducted comprehensive genomic and transcriptomic analyses of patient-matched primary and recurrent GBM patient tumor core specimens with the goal of identifying new therapeutic targets for recurrent disease. These initial studies have identified the important signaling node(s) in recurrent GBM and thus a potential vulnerability for targeted agents.