Cancer Genomics: Chapter 8. Preclinical Animal Models for Cancer Genomics

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Genome-wide association (GWA) studies and tumor-specific epigenome, transcriptome and genome sequencing projects are generating an ever-growing list of susceptibility alleles, as well as putative gain- and loss-of-function gene mutations associated with cancer. These genetic changes ultimately need to be validated to determine their contribution to the initiation, progression and likelihood of treatment response for various cancers. The bottle-neck is no longer obtaining sequence data or completion of the GWA studies, but rather the ability efficiently to validate candidate genes identified by these projects. In vivo studies in animal models are the "gold standard" for validation of these candidate drivers and modifiers of cancer. Furthermore, once a gene product or molecular pathway has been validated as playing an important role in the development or progression of cancer, animal models provide the necessary preclinical data for evaluation of the efficacy and toxicity of new therapeutics targeting that gene or pathway. As such, animal models play an essential role in cancer research by facilitating the translation of genomic discoveries into preclinical studies that precede new targeted therapies for cancer. In this chapter, we will discuss vertebrate and invertebrate animal models as they apply to cancer genomics, as well as key technologies employed. In particular, we will focus on the use of murine and zebrafish human tumor xenografts and transgenic models.

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