

An overview of in vitro, in vivo, and computational techniques for cancer-associated angiogenesis studies

ABSTRACT

Angiogenesis is a crucial area in scientific research because it involves many important physiological and pathological processes. Indeed, angiogenesis is critical for normal physiological processes, including wound healing and embryonic development, as well as being a component of many disorders, such as rheumatoid arthritis, obesity, and diabetic retinopathies. Investigations of angiogenic mechanisms require assays that can activate the critical steps of angiogenesis as well as provide a tool for assessing the efficacy of therapeutic agents. Thus, angiogenesis assays are key tools for studying the mechanisms of angiogenesis and identifying the potential therapeutic strategies to modulate neovascularization. However, the regulation of angiogenesis is highly complex and not fully understood. Difficulties in assessing the regulators of angiogenic response have necessitated the development of an alternative approach. In this paper, we review the standard models for the study of tumor angiogenesis on the macroscopic scale that include in vitro, in vivo, and computational models. We also highlight the differences in several modeling approaches and describe key advances in understanding the computational models that contributed to the knowledge base of the field.