

Carcinogenesis Model Encompassing the Range of Prostate Cancer Progression and Metastasis

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Technology description

Currently there is a lack of information and models for understanding human prostate cancer progression. Most models currently available only allow for comparison of tumorigenic versus non-tumorigenic states. UCSF investigators have developed a series of human prostatic epithelial cell lines that encompass the range of prostate cancer progression. These cells are derived from the parental BPH-1 non-tumorigenic immortalized human prostatic epithelial cell line (see References below) using tissue recombination methods. Upon hormonal treatment, the cells exhibited either non-tumorigenicity, tumorigenicity, epithelial to mesenchymal transition (EMT), and metastasis. Progression uniquely occurs in initiated but non-tumorigenic epithelial cells and has been characterized by histopathological criteria, tumor mass size, and associated changes in expression of gene products.

Additional Information

Wang, et al. Cancer Research (2001) 61:6064-6072 Hayward, et al. Cancer Research (2001) 61:8135-8142

Application area

Testing novel therapeutic regimens specific to cancer state and progression.
Development of biomarkers for cancer.

Advantages

Advantages:- First prostate cancer progression model that metastasizes.- Display full range of clinical stages of prostate cancer relevant to human disease.- Allows comparison between each cell line/condition to evaluate genetic and epigenetic changes associated with tumor progression.- Genetically altered prostatic inducers can be incorporated into this model.

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