

Mapping of prostate cancer genes opens the door to new treatments

Genetic changes during the initiation and progression of prostate cancer have eluded scientists to date. Now for the first time researchers have identified a specific gene expression profile of prostate cancer stem cells, with important implications for future treatments.

The findings, published in BioMed Central's open access journal Genome Biology, revealed 581 genes that are differentially expressed in certain prostate cancer cells, highlighting several pathways important in the cancer stem-cells biology, and offering targets for new chemopreventative and chemotherapeutic approaches.

The cells in the study represent less than 0.1% of prostate cancer tumors, and have properties that mark them out as cancer stem cells. The cells renew themselves, are highly invasive, and have a longer lifetime than normal stem cells. They also feature a primitive epithelial phenotype and can differentiate to recapitulate phenotypes seen in prostate tumors. The cells are found in all stages and types of prostate cancer.

Expression profiling of prostate cancers typically uses tumor cell mass samples to identify individual genes. In this study, researchers harnessed advances in microarray and target labelling technologies to produce a functionally annotated expression profile of these prostate cancer stem cells.

The team, from the YCR Cancer Research Unit at the University of York and Pro-cure Therapeutics Ltd, created a malignant stem cell signature by combining genes significantly overexpressed in stem cells with those significantly overexpressed in malignant stem cells. Quantitative RT-PCR, flow cytometry and immunocytochemistry were used to validate the gene expression changes.

Genes associated with inflammation were prominent in the cancer stem cell expression profile. Potential therapeutic target NF- κ B is known to promote cell survival. The researchers showed that an NF- κ B inhibitor triggered programmed cell death in cancer stem cells, but spared normal stem cells. This provides a potential therapeutic target for this rare group of cells, which are unlikely to be affected by current chemotherapy regimens.

“For the first time we are looking at the subpopulation of cancer cells which actually initiate new tumors” explains Anne Collins, who coordinated the study. “The genetic profiling we have carried out should stimulate new lines of research directed towards stem cell treatments for cancer”

Source: BioMed Central

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