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Global mRNA analysis to determine a transcriptome profile of cancer stemness in a mouse model.

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BACKGROUND: Striking similarities between stem cells and cancer cells have led to the concept of the existence of a cancer stem cell, a concept that has since been documented in many tumours including breast, brain and prostate tumours. Teratocarcinomas are malignant tumours occurring predominantly in the testes composed of undifferentiated stem cells and mature tissues. Cancer stemness was studied using the teratocarcinoma model of tumourigenesis. **MATERIALS AND METHODS:** The gene expression profile of murine embryonic stem cell lines was compared to its malignant counterpart, murine teratocarcinoma cell lines. Validation was performed using real-time quantitative PCR. **RESULTS:** A list of 1170 differentially expressed genes was obtained. Significant pathways involved in cancer stemness included oxidative stress and angiogenesis. Transcription factors and extracellular matrix molecules appeared prominently. **CONCLUSION:** Novel molecules have been highlighted including decorin, an extracellular matrix protein, which may provide opportunities for the investigation of innovative strategies in the future treatment of cancer.

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