

Translational and functional oncogenomics. From cancer-oriented genomic screenings to new diagnostic tools and improved cancer treatment

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ABSTRACT

We present here an experimental pipeline for the systematic identification and functional characterization of genes with high potential diagnostic and therapeutic value in human cancer. Complementary competences and resources have been brought together in the TRANSFOG Consortium to reach the following integrated research objectives: 1) execution of cancer-oriented genomic screenings on tumor tissues and experimental models and merging of the results to generate a prioritized panel of candidate genes involved in cancer progression and metastasis; 2) setup of systems for high-throughput delivery of full-length cDNAs, for gain-of-function analysis of the prioritized candidate genes; 3) collection of vectors and oligonucleotides for systematic, RNA interference-mediated down-regulation of the candidate genes; 4) adaptation of existing cell-based and model organism assays to a systematic analysis of gain and loss of function of the candidate genes, for identification and preliminary validation of novel potential therapeutic targets; 5) proteomic analysis of signal transduction and protein-protein interaction for better dissection of aberrant cancer signaling pathways; 6) validation of the diagnostic potential of the identified cancer genes towards the clinical use of diagnostic molecular signatures; 7) generation of a shared informatics platform for data handling and gene functional annotation. The results of the first three years of activity of the TRANSFOG Consortium are also briefly presented and discussed.

Key words: cancer, DNA microarrays, genomics, RNA interference.

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