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Presentation Title:	Knowledge-based metastatic prostate cancer targets discovery
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New targets and novel therapeutic strategies are urgently needed for the prevention and treatment of metastatic prostate cancer (MPC). Enhanced understanding of mechanism responsible for the prostate cancer metastasis progression will speed up the discovery of biologic targets that could be explored as novel therapeutics. In this study, bioinformatics analysis power and high throughput biological assay were integrated to explore a new approach in targets discovery of MPC. Firstly, based on multiple gene expression microarray datasets and Ingenuity software, fourteen MPC profiling molecules were identified. Functional analysis was performed to improve the molecules accuracy by co-localization and WebGestalt (Web-based Gene Set Analysis Toolkit) analysis. Next, a MPC network was developed from profiling molecules by assembling the essential signal pathways related tumor metastasis from KEGG (Kyoto Encyclopedia of Genes and Genomes) and protein-protein interaction. The key modulator molecules were scored by network topological analysis and further validated by high throughput siRNA (small interfere RNA) screening for cell migration/invasion using time-lapse imaging of human high metastatic potential prostate cancer cell (PC3). The invasive ability of tumor cells was significantly inhibited following siRNA treatment on a few genes, e.g., ARNT (Aryl hydrocarbon receptor nuclear translocator), RAP1A (Ras-related protein Rap-1A), CDN2C (Cyclin-dependent kinase 4 inhibitor C) and MAPK1 (Mitogen-activated protein kinase 1). It strongly indicated those genes as new promising targets for MPC management. The results demonstrated a new and effective systems biological approach for targets discovery in MPC.
Kemi Cui and Guangxu Jin contributed equally to this work

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