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What kinase gene expressed differently in primary and metastatic kidney cancer

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Background: Systemic treatment for metastatic clear cell (CC)-renal cell cancer (RCC) produces a median survival of only 1-2 years. Although understanding of biology leading to better treatments will likely require analysis of metastatic tumor tissue, most studies have analyzed the primary kidney tumor. We planned to study both primary and metastatic tumors to identify new kinase genes expressed in metastatic tumors compared to primary kidney tumors. These data may enable the design of new drugs, since it is relatively easier to design kinase inhibitors.

Methods: Samples of primary tumor, adjacent normal kidney, and metastatic tumor from 18 patients were available. RNA from samples was analyzed by Nanostring for levels of expression of 519 kinase genes. Over-expression was defined as >2-fold elevation compared to reference genes.

Results: Some of the top genes overexpressed in metastases compared to primary tumor and normal kidney were ROS1, EPHA3, PLK1 and CDK1. Some genes were under-expressed in tumors compared to normal kidney, suggesting that some kinase genes could protect against tumor growth.

Conclusions: We identified many genes overexpressed in metastatic CC-RCC tumor tissue, which may represent drivers of metastasis and targets for new drugs. Confirmation of findings is required before clinical trials of new drugs.

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