

Predicting drug responsiveness in cancer patients

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Drugs such as everolimus that target the protein mTOR are used to treat several forms of cancer, but not all patients respond to the treatment. A team of researchers, led by Alberto Bardelli, at the University of Turin Medical School, Italy, has now identified a way to help predict which patients will respond to such drugs.

Specifically, the team found that human [cancer](#) cells with [mutations](#) in the PIK3CA gene responded to everolimus in vitro except when a KRAS gene mutation was also present. Importantly, in a cohort of metastatic cancer patients, the presence of KRAS gene mutations was associated with lack of response to treatment with everolimus therapy.

These data suggest that by looking for the presence or absence of PIK3CA and KRAS mutations in a person's tumor it will be possible to predict whether or not that person will benefit from treatment with a drug that targets mTOR. However, as noted in an accompanying commentary, by Morassa Mohseni and Ben Ho Park, at The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, Baltimore, while these data have enormous potential to change clinical practice, larger prospective studies are required to verify them.

More information: [www.jci.org/articles/view/3753 ...fd893349707da2f3dddf](http://www.jci.org/articles/view/3753...fd893349707da2f3dddf)

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