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Mitra's CANScript validated for personalized cancer care

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Mitra Biotech, a cancer diagnostics company, announced that a study validating its flagship platform CANScript has been published in Nature Communications, an open access, multidisciplinary journal dedicated to publishing high-quality research in all areas of the biological, physical, chemical and earth sciences.

Papers published by the journal represent important advances of significance to specialists within each field.

The article 'Predicting clinical response to anti-cancer drugs using an ex vivo platform that captures tumor heterogeneity' was published in Nature Communications on February 27, 2015.

"The study is the first of its kind in delineating the importance of capturing tumor heterogeneity to elicit accurate prediction of clinical response," said Dr Leena Gandhi, one of leading oncologists and investigator at Dana Farber Cancer Institute at Boston, who is not associated with the study.

"This platform would not only be beneficial in enabling physicians to select the right mode of treatment, but also speed-up oncology drug development, thereby reducing go-to market time and costs," she added.

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Scientists from Mitra reported key findings that may open a new avenue in predicting clinical response to anti-cancer drugs.

The team showed that by maintaining the complex structure and behavior of tumors in tissue culture plates, CANScript can predict the response of individual patient tumors to anti-cancer drugs.

The findings is a result of collaborative efforts undertaken by a team from Mitra Biotech, Harvard Medical School, Dana Farber Cancer Institute, the Broad Institute at MIT along with other institutions in the United States and India.

"CANScript is a novel platform based on systems biology, and it has the ability to change the paradigm in cancer treatment," stated Dr Padhma Radhakrishnan, one of the senior team members.

Unlike other 3D technologies, CANScript facilitates a thorough understanding of the biology of a tumor in a truly personalized setting while maintaining the slices of tissues in a plate.

"We do not limit our analysis to a specific gene or a drug pathway; rather, we examine the complete tumor ecosystem in order to predict both positive and negative clinical responses using a common set up," said Dr Biswanath Majumder, the lead author of the paper.