Personalized medicine: Prediction of the efficacy of novel therapies in cancer

A study done at Technion shows that cell typing based on the expression of the metabolic genes enables **prediction of the patient's response to immunotherapy.** Based on this discovery, the researchers created a tool to predict which patients will respond to this therapy, emphasizing the importance of metabolism in the tumor microenvironment.

The introduction of immune checkpoint inhibitors (ICI) anti-cancer drugs is one of the most important revolutions in cancer medicine. These drugs are designed to deactivate a natural immune mechanism that can work against patients in the case of a cancerous tumor.

The immune mechanism in question is a network of "immune checkpoints." Its role, under normal conditions, is to prevent the immune system from reacting with excessive force that could damage healthy cells. In other words, it is a mechanism that regulates the immune system.

However, when faced with a cancerous tumor, that same mechanism may **prevent the immune system from attacking the cancer cells**. This is the background against which ICI drugs were developed: these drugs deactivate this mechanism, thereby "freeing" the immune system to attack the cancer cells. These drugs have caused a revolution in cancer medicine, leading to inhibition of tumor growth in many kinds of cancer.

Still, these drugs are effective in less than 40% of patients. The rest of the patients suffer from side effects of the drug without enjoying any benefit. While there have been efforts to determine in advance whether or not the drugs will be effective for specific patients, current tools for doing so – for example, based on a genetic signature or the amount of different cells, – are not accurate.

Prof. Keren Yizhak and Ofir Shorer from Technion's **Ruth and Bruce Rappaport Faculty of Medicine**, have developed a new tool for this type of assessment, based on the metabolism of immune cells in the tumor microenvironment. Since cancer cells and the immune system cells are found in the same environment, they are fighting for resources. Quantifying their metabolic demands enables successful prediction of the effect of ICI drugs on the individual patient. To accomplish that they analyzed single-cell RNA-sequencing of 1,700 metabolic genes, taken from more than one million immune cells of cancer patients treated with ICI.

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Tel: +972-77-8871992 :טל'
Fax: +972-4-8295940 :פקס

Technion City, Haifa 3200003, Israel
3200003 קרית הטכניון, חיפה
www.technion.ac.il

Prof. Keren Yizhak is a faculty member at the Ruth and Bruce Rappaport Faculty of Medicine and at the Henry and Marilyn Taub Faculty of Computer Science. **Ofir Shorer** is a graduate of the Technion's Excellence Program and is currently a doctoral student in the prestigious M.D./Ph.D. track, which combines a research doctorate with clinical studies, under the guidance of Prof. Yizhak.

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Captions:

1. Prof. Keren Yizhak
2. Ofir Shorer

Credit: Technion Spokesperson Office

For more information: Doron Shaham, Technion spokesperson - 050-3109088