Systems properties of insulin signaling revealed

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A team of Swedish researchers has characterized novel systems properties of insulin signaling in human fat cells. Their mathematical modeling, described in an article published June 20th in the open-access journal *PLoS Computational Biology*, provides further insight into energy level maintenance (via the hormone insulin) within our bodies.

Hampered insulin function is the cardinal cause of Type 2 diabetes, which currently affects nearly 250 million people worldwide. The disease causes a metabolic malfunction due to incorrect information transfer of insulin concentration in the blood to the internal fluid of cells (the cytosol). This information transfer occurs through a complicated network of protein-protein interactions. The skeleton of the network has been characterized, but systems details, including the relative importance and time-scales of the interactions, were previously unknown.

Due to the complexity of the network, it has proved difficult to achieve such a systems understanding through mere experimental techniques and reasoning. Therefore, the team experimentally collected time-series data from human fat cells in vitro and evaluated various mechanistic explanations by translating the explanations into corresponding mathematical models.

In this study, the modeling indicated that either receptor recycling between the membrane and the cytosol, or feedback from proteins activated further down in the network, are involved in the information transfer during the first minutes after insulin stimulation.

As more detailed data become available, the authors predict that mathematical modeling will become an increasingly important tool for data analysis, and for furthering understanding of insulin signaling and cellular control.

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