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A study published in the open-access journal *PLoS Computational Biology* demonstrates how sophisticated mathematical modeling has encouraged the development of an optimally-timed vaccine for chronic myelogenous leukemia (CML).

Researchers Doron Levy (University of Maryland), Peter P. Lee (Stanford University), and Peter S. Kim (École Supérieure d'Électricité, Gif-sur-Yvette, France) collected data over four years from CML patients who were receiving therapy with the drug imatinib. They then developed a mathematical model that uses a patient's natural anti-leukemia response when treated with imatinib to improve leukemia treatment.

"By combining novel biological data and mathematical modeling, we found rules for designing adaptive treatments for each specific patient," remarked Professor Doron Levy. "Give me a thousand patients and, with this mathematical model, I can give you a thousand different customized treatment plans."

Levy indicates that it is both the drug and the body's natural immune response that are responsible for leukemia remission. "After starting imatinib, the anti-leukemia immune response gradually increases. However, it begins to weaken after it reaches a peak. This typically happens well into the treatment."

When this weakening occurs, cancer cells can begin to develop resistance to the drug, and the therapy can become ineffective. It is at this point that the immune system needs to be strengthened, and the authors suggest irradiated pre-therapy blood should be introduced into the patient. The researchers maintain that further studies are necessary and should lead to animal models and clinical trials.

Dynamics and Potential Impact of the Immune Response to Chronic Myelogenous Leukemia

Kim PS, Lee PP, Levy D
PLoS Computational Biology (2008). 4(6):e1000095.
 doi:10.1371/journal.pcbi.1000095
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