KYVOR's CANLYTx™ Platform helps Doctors Treat Cancer with Precision.

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Abstract (300 word limit)

On a busy day, there was a call from an oncologist asking how our CANLYTx could help a CA endometrium first line therapy treatment negative female patient Mrs. Grace, aged 43 years.

A regular first line therapy with a combination of Platin, Doxorubicin and Paclitaxel was administered post diagnosis. Mrs. Grace was soon given the bad news that she had to undergo further chemotherapy with different chemo agents (chosen by trial and error) after a regular scan was done indicating progression of the tumor.

Two scenarios had risen due to the progression of Tumor for Mrs. Grace and it was at this stage we received the call from her doctor asking about our CANLYTx.

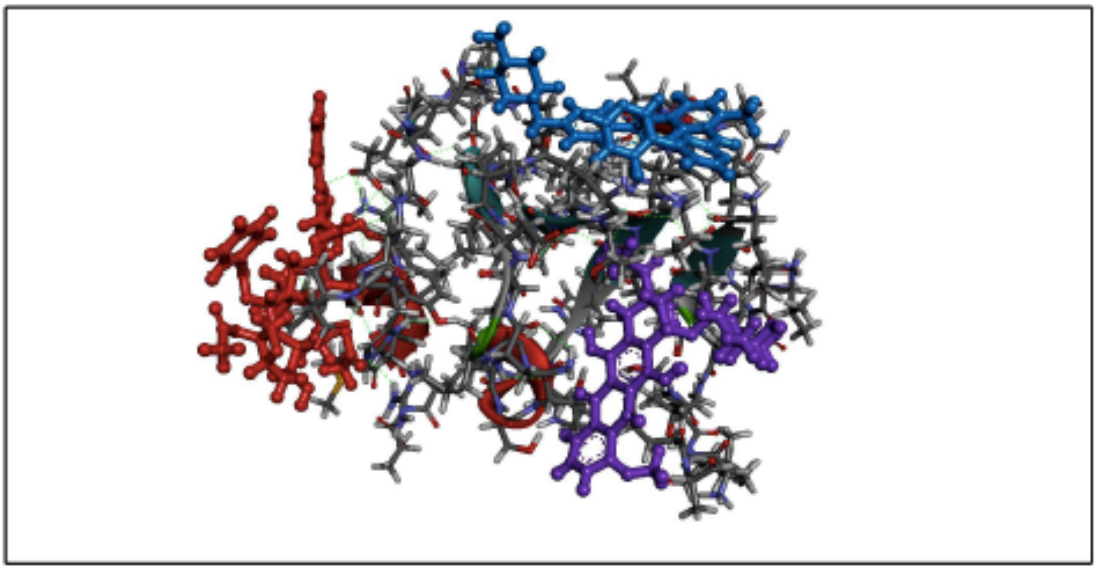
Now, we would like to demonstrate the extraordinary proficiency of whole exome sequencing with CANLYTx in such situations.

The process began with harvesting the DNA from the FFPE tumour block obtained from the diagnostic biopsy sample to perform whole exome assay. The resulting interpretation from this process revealed mutation in ABCB1 gene suggesting the use of Doxorubicin caused reduced drug clearance and hence addition of Imatinib along with the platins, doxorubicin and Paclitaxel would prove effective. Our CANLYTx platform recommends the use of Imatinib as it sensitizes endometrial cancer cells to Platins by targeting CD-117-positive-growth-competent cells and the platin resistance gene were not mutated. In addition, molecular simulation studies were carried out on the above combination to further validate the use of these agents. Our molecular simulation platform calculates a dock score using the concept of binding energy minimization between the agent and the target, the target being the mutant gene or its coding protein.
The database indicates that PARP inhibitors would be ineffective due to the absence of mutations in the associated genes. A routine targeted therapy targeting EGFR, BRAF gene would be ineffective due to the absence of protein coding mutations in the genes.

Next steps for the patient is the follow up for development of additional resistance mutations in the existing genes or newer genes by way of liquid biopsy from circulating tumour DNA or any other NGS technology beyond just testing for limited genes.

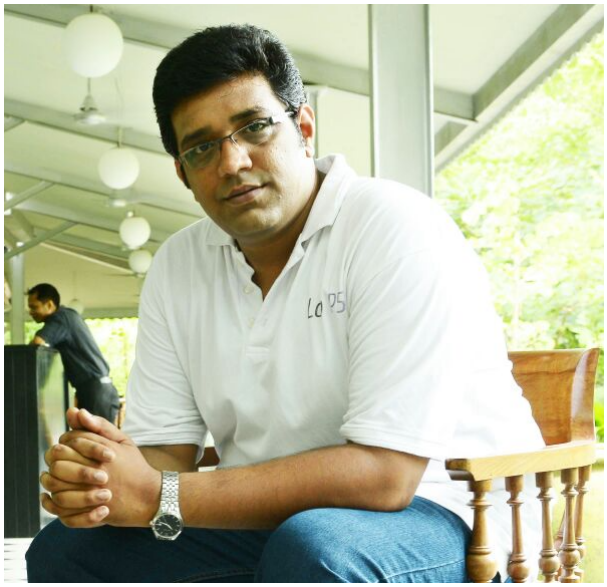
*Name changed to protect Identity.

Image



ABCB1 + PMS2 binding with (Cisplatin + Doxorubicin + Paclitaxel) + Imatinib

Biography (150 word limit)



An Inspiring life-sciences professional, Abilesh has a decade of experience in Medical informatics. Developed a keen interest in Personalized medicine, Cancer Genomics, drug discovery and earned his Masters degree in Medical informatics from the University of Manchester. He has been working on the technologies to personalize cancer treatments post his studies and went on to start this venture. He also worked on several bioinformatics methodologies and has identified a platform for effective cancer treatment. Abilesh is a go-getter and a creative soul wandering to explore new opportunities.

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Notes/Comments:

This is an abstract from a case study which I intend to present.