CALIFORNIA STATE SCIENCE FAIR
2015 PROJECT SUMMARY

Name(s)
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Project Number
35766

Project Title
The 99¢ Clinical Trial: Accelerating Trials in Software for ErbB2 Pathways and Lapatinib on Metastatic Breast Cancer

Abstract

Objectives/Goals
6540 breast cancer clinical trials are being performed in the world and the drug life cycle takes an average of 14 years. The average pre-tax industry cost per new prescription drug approval (inclusive of failures and capital costs) is $2.55b. Accelerating fast failures can dramatically reduce drug approval costs and improve drug behavior predictability substantially. With this model software, pharmaceutical scientists can predict drug behavior in 21 min (instead of 21 days) by simulating virtual trials which are predictive pharmacogenomic models of ErbB2 activated signaling pathways in conjunction with Lapatinib (CAS 388082-78-8). Accelerating the experiment (1440 times faster) involves modeling the Mechanism of Action of Lapatinib ditosylate and Capecitabine in a cell region physiology exhibiting overexpression of ErbB2 (2-6 copies), a sub-cellular biomarker of advanced (Stage IV) metastatic breast cancer. The goal is to successfully complete a virtual trial in software to predict the drug response of Lapatinib for HER2-positive advanced metastatic breast cancer, in a digital micro-biopsy cell region matrix. The results will be validated with a corresponding clinical trial on women in China.

Methods/Materials
MacBook Air 4GB 1600 mHz Intel Core i5 was used for testing.

Results
It was observed that the natural DNA repair mechanisms remained unaffected by tumor growth, because the dysregulation of the Ras mediated MAPK signaling pathway only amplified cell proliferation signals. The Clinical Benefit Rate (CBR) was found to be in the range of [43.2%, 71.3%]. Also the adverse drug reaction (ADR) was in the proximity of 3.8% (at 5% level of significance) Lapatinib molecules were consistently engaged in a repair mechanism that increased their utilization and left a smaller quantity of substrate.

Conclusions/Discussion
I developed a clinical drug study tool, that follows a computationally and economically scalable (less than $1 per patient) model which simulates the ErbB2 signaling pathways and their response to Lapatinib.The software algorithms that I built would potentially allow pharmaceutical scientists to rapidly permutate over millions of patient biologies and candidate drug structures based on rule set specificity. All software is on GitHub and available upon request.

Summary Statement
The project involves pharmacological modeling of a advanced/metastatic breast cancer clinical trial in software based on measurement of drug response on pharmacogenomically generated patient biologies.

Help Received
Industry Drug Researcher Archana Gangakhedkar at Xenoport Clinically Validated Software Results