

## Pharmacogenomics:

Faculty Presenter

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### Scholar Summary

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Dr. O'Donnell began his presentation by posing an important question: we know that no two patients are the same, so why aren't we better able to predict how a patient is going to react to therapies?

He went on to give some examples of how we may come to conclusions about drug effectiveness or side effects because we do not know enough about the genomics of a given population we are testing. For example, he discussed a NEJM article about SLCO1B1 variants and statin-induced myopathy; the takeaway is that we cannot consider genomics in a vacuum, as there are other factors that are important.

Dr. O'Donnell also spoke about the potential of genotype-directed dosing; he used the example of irinotecan and its active metabolite SN-38, which can lead to severe toxicity in patients with UGT1A1\*28 homozygous 7/7 genotype. He noted that we may be consistently underdosing some patients, because when testing max tolerated dose in clinical trials, we evaluate dosage on the patients who are the most sensitive to toxicity, which may not in fact be a majority of the population.

In the last portion of his talk, Dr. O'Donnell discussed some of his work at the University of Chicago creating a genomic prescribing system that is used by clinicians in their EMRs. The system contains information about 51 different medications in relation to the genomics of each particular patient. With the system, clinicians can more simply understand the risk of severe toxicities with different medications (based on published evidence) using a red, yellow, green light system. Additionally, the system can provide clinicians with pharmacogenomics alternatives when a patient is at risk for medication toxicity.

Overall this lecture was incredibly informative and really brought to light both the major challenges we face with pharmacogenomics and the potential of this field to enable us to better care for patients.