#12108: The role of personalized therapy in cancer associated depression among 10,673 patients

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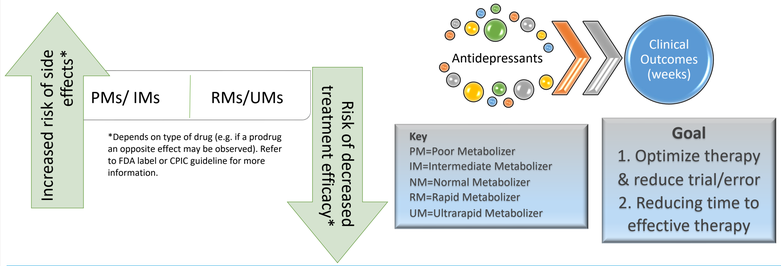
Background

- Pharmacogenomics (PGx) can help reduce the trial and error of antidepressant management in cancer patients.
- Depression is a major contributor to morbidity and mortality in cancer patients.

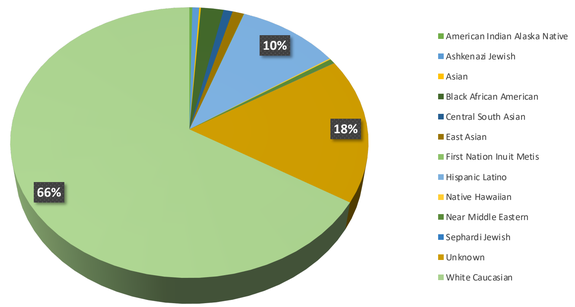


Methods

- Retrospective analysis of 10,673 patients genotyped for *CYP2D6* and *CYP2C19* was conducted (OneOme LLC, Minneapolis, MN).
- 1,616 tests were found to be ordered by oncologists and analyzed separately as a sample subset.
- Phenotype and allele frequencies were calculated and compared to self-reported ethnicity/race.

Results

Figure 1: Sample Population (n= 10,673) for General Analysis



- Utilizing PGx to guide drug selection and dosing for cancer patients with depression may reduce trial/error, time to effective therapy, limit burden, improve QOL.
- ~46-60% of patients may need a dose change or alternative antidepressant medication*

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*Based on CPIC guidelines[1]. Depends on a case-by-case scenario, medical condition, etc. This is only from a PGx perspective.

Figure 2: % PMs General Analysis

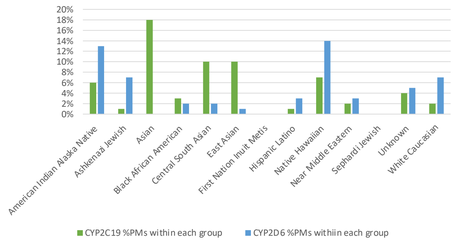


Figure 3: % UMs General Analysis

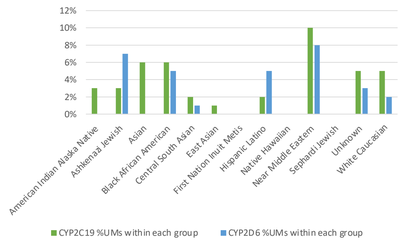


Figure 4: CYP2C19 General Analysis

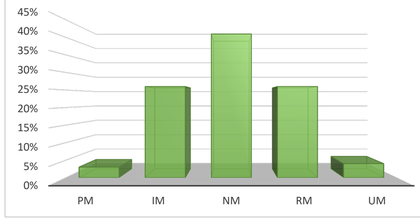
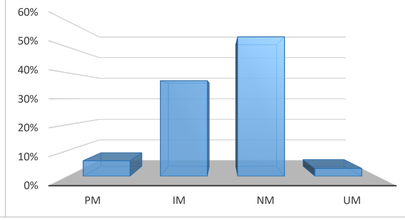


Figure 5: CYP2D6 General Analysis



Figures Key
Figure 1: % of sample population for general analysis
Figure 2: % PMs within each group oof the general analysis
Figure 2: % UMs within each group oof the general analysis
Figure 4: % phenotypes in total CYP2C19 general analysis

Figure Key
Figure 5: % phenotypes in total CYP2D6 general analysis (minus one sample)
Figure 6: % of sample population for sub-analysis
Figure 7: % phenotypes in CYP2C19 sub-analysis
Figure 8: % phenotypes in CYP2D6 sub-analysis

Figure 6: Sample Population (n=1,616) for Sub-Analysis

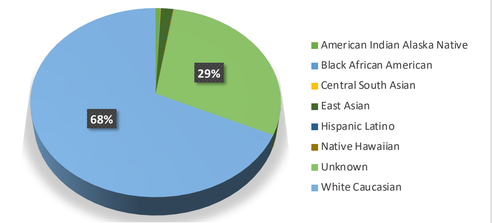


Figure 7: CYP2C19 Sub-Analysis

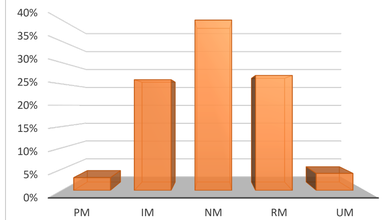
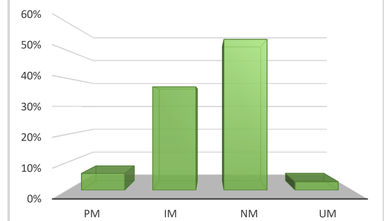


Figure 8: CYP2D6 Sub-Analysis



Gene	General Analysis (N=10,673)	Sub-analysis (N=1,616)
CYP2C19	3% PM 4% UM The highest percent of *CYP2C19* PMs at 11% was found within the collective Asian tested population.	3% PM 4% UM
CYP2D6	6% PM 3% UM Native Hawaiian and American Indian Alaska Native had more CYP2D6 PMs within the tested sets at 14% and 13%, respectively.	6% PM 3% UM

Future Directions for Research

- Further research is needed to determine the clinical outcomes as this was a retrospective analysis of limited data.
- A need for more specific demographic information.

References

1. Bousman, Chad A., et al. "Clinical Pharmacogenetics Implementation Consortium (CPIC) guideline for CYP2D6, CYP2C19, CYP2B6, SLC6A4, and HTR2A genotypes and serotonin reuptake inhibitor antidepressants." *Clinical Pharmacology & Therapeutics* 114.1 (2023): 51-68.