

Pathway to Ascertain the Role of Pharmacogenomics in Healthcare Utilization Outcomes [Response to Letter]

Paul Y Takahashi¹

Euijung Ryu²

James R Cerhan³

Suzette J Bielinski³

Janet E Olson³

¹Division of Community Internal Medicine, Department of Internal Medicine, Mayo Clinic, Rochester, MN, USA; ²Division of Biomedical Statistics and Informatics, Department of Health Sciences Research, Mayo Clinic, Rochester, MN, USA; ³Division of Epidemiology, Department of Health Sciences Research, Mayo Clinic, Rochester, MN, USA

Dear editor

We appreciate the thoughts of Dr. Roman and his comments. We understand that the number of identified pharmacogenomic genes continues to increase with time, and the clinical utility also increases with time and expert opinion. We chose these selected pharmacogenes because of their strong clinical practice recommendations and the data available at the time of the gene selection.¹ Due largely to the efforts associated with other initiatives within the RIGHT study, our clinical practice set up specific electronic medical record best practice alerts for these pharmacogenes, and it was believed that there was the potential for change in clinical care for patients with extreme phenotypes.² We did not design the study to specifically look at all pharmacogenomic genes.

We agree that the ideal goal would be to study specific drug/gene pairs. In our limitation section, we described the problems of not including specific drug/gene pairs and specific causes of hospitalizations or ED visits.³ In this real-world pharmacogenomic implementation study, we did not have a sufficient number of patients with the specific drug exposures, the high-risk genotypes, and clearly recorded electronic record documentation of side effects and lack of effectiveness. We also had to rely upon medication prescriptions rather than medications dispensed. Therefore, our alternate goal was to determine if PGx genes could be used as potential biomarkers for adverse health outcomes. In our previous pilot study, we found that patients with ultrarapid metabolizer of CYP 2D6 had higher risk of hospital utilization.⁴ Thus, we had hope that potentially expanding the number of pharmacogenomic genes would continue to show an effect. We agree and hope that as pharmacogenomics becomes more widespread, the ability to look at specific drug/gene pairing will be more feasible.

Lastly, we agree that there are practical limitations to the use of observational cohort studies to study pharmacogenomics. As described above, this includes the need for a very large sample size to compensate for the low likelihood of medication usage among those carrying the extreme phenotypes (those most likely to demonstrate a clinical effect), as well as inconsistent documentation of lack of efficacy and side effects. There is also the potential for bias and confounding in any observational design. However, there are also high costs involved with conducting clinical trials of pharmacogenomics which also limit the utility of this design for

Correspondence: Paul Y Takahashi
Division of Community Internal Medicine,
Department of Internal Medicine, Mayo
Clinic, 200 First Street SW, Rochester,
MN, 55905, USA
Tel +1-507-284-2511
Fax +1-507-266-2297
Email Takahashi.paul@mayo.edu

addressing many important questions. We look forward to seeing data from larger observational cohorts that may address some of the limitations inherent to our study.

Disclosure

We have nothing to disclose.

References

1. Bielinski SJ, St Sauver JL, Olson JE, et al. Cohort profile: the right drug, right dose, right time: using genomic data to individualize treatment protocol (RIGHT Protocol). *Int J Epidemiol.* 2020;49(1):23–24k. doi:10.1093/ije/dyz123
2. Caraballo PJ, Bielinski SJ, St Sauver JL, Weinshilboum RM. Electronic medical record-integrated pharmacogenomics and related clinical decision support concepts. *Clin Pharmacol Ther.* 2017;102(2):254–264. doi:10.1002/cpt.707
3. Takahashi PY, Ryu E, Bielinski SJ, et al. No association between pharmacogenomics variants and hospital and emergency department utilization: a Mayo Clinic Biobank retrospective study. *Pharmacogenomics Pers Med.* 2021;14:229–237. doi:10.2147/PGPM.S281645
4. Takahashi PY, Ryu E, Pathak J, et al. Increased risk of hospitalization for ultrarapid metabolizers of cytochrome P450 2D6. *Pharmacogenomics Pers Med.* 2017;10:39–47. doi:10.2147/PGPM.S114211

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