The Clinical Impact Of An Antidepressant Pharmacogenomic Algorithm

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Abstract

BACKGROUND: Genes involved in the metabolism of antidepressants (CYP2D6, CYP2C19, and CYP1A2) and efficacy (GSK3β) of antidepressants have been associated with antidepressant treatment. Our study evaluated the impact of antidepressant treatment in patients with major depressive disorder (MDD) through a pilot study of an antidepressant pharmacogenomic (PGx) algorithm. This pilot study incorporated patients referred to a PGx laboratory for antidepressant or antipsychotic treatment.

OBJECTIVES: To determine the clinical impact of antidepressant treatment in patients with major depressive disorder (MDD). Two sided tests were used to compare PGx and TAU groups. Significance was set at 0.05.

Methods and Measures

Design: Prospective, randomized, double-blind, controlled study.

Subjects: Medically stable outpatients diagnosed by a board certified psychiatrist with either major depressive disorder (ICD codes 296.2, 296.3) or depressive disorder NOS (311.0). Signed informed consent and baseline HAMD-17 score < 25. PGx report had a low level of influence on treatment decisions in 8 (31%) PGx subjects. No difference in side effect frequency, intensity, or burden was found between treatment arms. Eight PGx and 1 TAU subject were remitters during the study (p = 0.01). Eight PGx and 1 TAU subject were responders during the study (p = 0.06, ns).

Results

Eight psychopharmacologists and 3 psychiatric nurse practitioners referred 66 patients to the study. Fifty-one patients were eligible for study enrollment and randomized to the PGx-treatment arm (PGx, n = 30) or treatment as usual arm (TAU, n = 25). One subject from each study arm did not complete the study. Mean age: PGx = 50.6 years; TAU = 47.8 years. PGx subjects were more likely to be female (66% vs 52%) and TAU subjects were more likely to be Hispanic (28% vs 9%). Study group sizes were small and the application of the PGx test was optional, yet clinical impact was found. PGx report had a low level of influence on treatment decisions in 8 (31%) PGx subjects. No difference in side effect frequency, intensity, or burden was found between treatment arms. Eight PGx and 1 TAU subject were remitters during the study (p = 0.01). Eight PGx and 1 TAU subject were responders during the study (p = 0.06, ns).

Conclusions

The PGx report provides patient genotypic and predicted phenotypic report influence at study end for each PGx subject. Patients in the PGx group were more likely to be female and Hispanic. The PGx report had a low level of influence on treatment decisions in 8 (31%) PGx subjects. No difference in side effect frequency, intensity, or burden was found between treatment arms. Eight PGx and 1 TAU subject were remitters during the study (p = 0.01). Eight PGx and 1 TAU subject were responders during the study (p = 0.06, ns).

References


Disclosures

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