P-1096 - INTEGRATION OF CLINICAL, PSYCHOSOCIAL, COGNITIVE AND GENETIC MEASURES TO PREDICT ANTIDEPRESSANT TREATMENT OUTCOME IN MDD PATIENTS: A PRELIMINARY CLINICAL STUDY

K.Lin, G.Xu, Y.Guo, D.Rao, H.Ouyang, Y.Dang, M.Zhang, Y.Jia, C.Ma
[1]Guangzhou Psychiatric Hospital, [2]Psychiatriy, The First Affiliated Hospital of Jinan University, Guangzhou, China

Objectives: The main aim of this study is to investigate the capacity of a number of variables from four dimensions (clinical, psychosocial, cognitive and genetic domains) to predict the antidepressant treatment outcome, and combined the predictors in one integrate regression model with the aim to investigate which predictor contributed most.
Methods: In a semi-naturalistic prospective cohort study with a total of 241 fully assessed MDD patients, decrease in HAM-D scores from baseline to after 6 weeks of treatment was used to measure the antidepressant treatment outcome.
Results: The clinical and psychosocial model (R^2=0.451) showed that HAM-D scores at baseline and MMPI-2 scale paranoia was the best clinical and psychosocial predictor of treatment outcome respectively. The cognitive model (R^2=0.502) revealed that combination of better performance on TMT-B test and worse performance on TOH and WAIS-R Digit Backward testes could predict decline in HAM-D scores. The genetics analysis only found median of percent improvement in HAM-D scores in G-allele of GR gene BclI polymorphism carriers (72.2%) was significant lower than that in non-G allele carriers (80.1%). The integrate model showed that three predictors, combination of HAM-D scores at baseline, MMPI-2 scale paranoia and TMT-B test, explained 57.1% of the variance.
Conclusion: Three markers, HAM-D scores at baseline, MMPI-2 scale paranoia and TMT-B test, might serve as predictor of antidepressant outcome in daily psychiatric practice.

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