P-708 - GENETIC RISK FACTORS FOR INTERFERON-ALPHA INDUCED DEPRESSION

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Background/aims: Chronic hepatitis C infection (CHC) represents a public health problem that affects around 3% of population worldwide. Pegylated Interferon-alpha (PegIFN-α) and Ribavirin (RBV) is the recommended treatment reaching about 40-80% of sustained virological response. However, a common treatment side-effect is induced-depression that impairs patient's quality of life and treatment adherence (1,2). This paper showed polymorphisms in HTR1A, NCR1, TPH2 genes as predictive variables of IFN-induced depression.
Material/methods: 396 consecutive, euthymic, CHC outpatients treated with PegIFN-α/RBV were included. Patients were assessed at baseline, 4, 12, 24 and 48 weeks of treatment using PHQ and MINI-DSM-IV-R interview to diagnose depression. Survival analysis was performed. In the univariated analysis functions were compared using logrank test. Significative variables (0.1 level) were extracted for the multivariated model, using a Weibull regression model.
Results: The incidence of induced-depression along the treatment was 39.4%. Polimorphisms on HTR1A (P=0.0104), TPH2 (P=0.0231) and NRC1 (P=0.0702) genes predicted IFN-induced depression.
Conclusions: Genes related with serotonine and inflamation system may play an important role in the pathogenesis of IFN-induced depression. Knowledge of predictive variables for IFN-induced depression may help to better manage patients at risk.
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