

M30. HIGH HERITABILITY OF TELOMERE LENGTH IN FAMILIES WITH BIPOLAR DISORDER

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Background Bipolar Disorder (BD) is a highly debilitating mental illness and its etiology and pathophysiology are not completely known yet, despite the evidence of an important genetic component from twin and adoption studies. More recently, BD has been related to a process of accelerated aging, with some studies showing shortened leukocyte telomeres in this population. The purpose of the present study was to investigate genetic and environmental influences on telomere length trait in families with BD, using a variance component approach, by estimating the heritability of this trait as well as co-variate effects.

Methods Telomere length (T) was estimated in a sample of 144 individuals, including 60 BD patients from 18 Brazilian families, which was measured in relation to the single copy gene (S) – β -globin gene (HBB) – using a singleplex real time PCR, providing a ratio of number of copies of T by S (T/S). Heritability estimate was obtained by a polygenic mixed model.

Results Before adjustment for sex, age and status of disease (null model), the polygenic heritability of telomere length was 0.58. When adjusted for sex, age and status of disease, the heritability continues as 0.58, but when adjusted only for sex and age, it increases to 0.68. Only p value of the effect of age is significant (<0.05) in all models.

Discussion To our knowledge, this is the first study evaluating heritability of telomere length in families with several members affected by bipolar disorder. The heritability estimation for telomere length in those Brazilian families was high (0.68). When calculation for the heritability of this trait was adjusted for the co-variate “status of disease” (bipolar dichotomous co-variate), it decreased a little to 0.58 (as null model). Mapping efforts to identify genetic loci associated with telomere length and other genetic variants on this population are warranted.

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