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Robust symptom networks in recurrent major depression across different levels of genetic and environmental risk

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Abstract

Background
Genetic risk and environmental adversity —both important risk factors for major depression (MD)— are thought to differentially impact on depressive symptom types and associations. Does heterogeneity in these risk factors result in different depressive symptom networks in patients with MD?

Methods
A clinical sample of 5,784 Han Chinese women with recurrent MD were interviewed about their depressive symptoms during their lifetime worst episode of MD. The cases were classified into subgroups based on their genetic risk for MD (family history, polygenic risk score, early age at onset) and severe adversity (childhood sexual abuse, stressful life events). Differences in MD symptom network structure were statistically examined for these subgroups using permutation-based network comparison tests.

Results
Although significant differences in symptom endorsement rates were seen in 18.8% of group comparisons, associations between depressive symptoms were similar across the different subgroups of genetic and environmental risk. Network comparison tests showed no
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