Author's Accepted Manuscript

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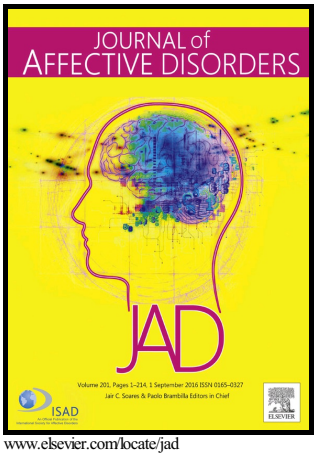

www.elsevier.com/locate/jad

PII: S0165-0327(17)31811-6
DOI: https://doi.org/10.1016/j.jad.2017.10.038
Reference: JAD9303

To appear in: *Journal of Affective Disorders*

Received date: 29 August 2017
Revised date: 18 October 2017
Accepted date: 21 October 2017

Cite this article as: H.M. van Loo, C.D. van Borkulo, R.E. Peterson, E.I. Fried, S.H. Aggen, D. Borsboom and K.S. Kendler, Robust symptom networks in recurrent major depression across different levels of genetic and environmental risk, *Journal of Affective Disorders,* https://doi.org/10.1016/j.jad.2017.10.038

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

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Accepted manuscript

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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