

STRESS REGULATES GLUCOCORTICOID-RESPONSIVE GENES EXPRESSION IN PREFRONTAL CORTEX BY ALTERING DNA METHYLATION: IMPLICATION FOR LURASIDONE TREATMENT

Paola Brivio¹, Giulia Sbrini¹, Letizia Tarantini², Chiara Favero², Mariusz Papp³, Marco Andrea Riva¹, Valentina Bollati², Francesca Calabrese¹

¹Department of Pharmacological and Biomolecular Sciences, Università degli Studi di Milan, Milan - Italy, ²EPIGET-Epidemiology, Epigenetics and Toxicology Lab, Department of Clinical Sciences and Community Health, Università degli Studi di Milan, Milan - Italy, ³Institute of Pharmacology, Polish Academy of Sciences, Cracovia - Poland

Introduction: Stress represents one of the main factors that contribute to the development of mental illness. Recently, epigenetics has been hypothesized as a potential mechanism by which environmental factors can contribute to psychiatric disorders, including major depression. In particular, DNA methylation can result in long-lasting changes that may modulate neurobiological processes, as well as the neuroendocrine systems. Hence, the purpose of our study was to investigate the effect of chronic stress exposure on the functional activity of the hypothalamic pituitary adrenal (HPA) axis, by focusing on the DNA methylation of genes containing the glucocorticoid responsive element (GRE), namely *Gadd45b*, *Sgk1* and *Gilz*. Furthermore, we evaluated the long-lasting effect of prolonged stress after a period of recovery. In this scenario, we assessed the possible role of the pharmacological intervention with the multimodal antipsychotic lurasidone (LUR) in modulating the epigenetic alterations induced by stress.

Material and methods: Adult male rats were exposed to 7 weeks of chronic mild stress (CMS) and treated with lurasidone (3mg/kg/day) starting from the second week of stress for the five subsequent weeks. Another batch of animals was exposed to 4 weeks of chronic restraint stress (CRS), treated with LUR starting from the second week of stress while continuing the CRS procedure and then left undisturbed in the homecage for other 3 weeks. Gene expression and DNA methylation analyses were conducted in rat prefrontal cortex, a brain area mainly involved in stress response.

Results: CMS produced a downregulation of the expression of *Gadd45b* and *Gilz*, whereas *Sgk1* mRNA levels were not altered by stress exposure. LUR normalized the stress-induced alteration of *Gadd45b*. The reduction of *Gadd45b* at transcriptional level was sustained by alterations at epigenetic level. Indeed, chronic stress induced an increased DNA methylation specifically in the GRE, effect that was reversed by chronic LUR treatment. By contrast, *Gilz* and *Sgk1* methylation was not altered either by CMS or by the pharmacological treatment.

Furthermore, stress has long-lasting consequences on the expression of these genes. Indeed, after a period of washout from stress, *Gadd45b* and *Gilz* were still downregulated, while no changes were observed for *Sgk1*. LUR was able to normalize only the reduction observed on *Gilz* expression. According to the persistent effect of the stress on the mRNA levels, after the washout, the CGs in the GRE of *Gadd45b* and *Sgk1* were hypermethylated in stressed rats in comparison to control animals. Interestingly, lurasidone treatment was not able to counteract the modulations induced by stress at methylation level.

Discussion and conclusion: Our results indicate that chronic stress mainly affects the expression and the methylation status of *Gadd45b*, effects that are prolonged over time. In conclusion, these data highlight that stress exposure leads to persistent changes in DNA methylation of specific genes related with glucocorticoids signaling, even after a period of washout, and that lurasidone acts as a modifier of such mechanisms, pointing out its potential properties as "epigenetic modulator".