Approaching to the Essence of Major Depressive Disorder

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Background of Major Depressive Disorder

Major Depressive Disorder (MDD) is a serious neuropsychiatric disease. It destroys people’s family relationship and social connections seriously. Latest WHO investigation disclosed nearly 4.4% of the population worldwide (approximately 322 million people) were being affected by MDD extensively [1]. While in China, Dong M, et al. reported the occurrence rate of suicide attempt during hospitalization and after the onset of MDD were 17.3% (95% CI: 12.4-23.7%) and 42.1% (95% CI: 26.1-60.0%) respectively [2]. Another research made by Grupta S, et al. announced MDD in urban China might be under-diagnosed and untreated [3].

Gene-Related Antidepressant Studies

Currently MDD is often resistant to standard antidepressant treatment. Venlafaxine is norepinephrine reuptake inhibitor and widely used to cure MDD for many decades [4]. It presents lower rate of dizziness [5], more acceptability and tolerability [6], better efficacy [7]. Recently, 2018 Olgiati P, et al., compared treatment effect between Anti-Depressant (AD) naturalistic studies and Treatment-Resistant Depression (TRD, Venlafaxine). They pooled the publications from 2000 to 2017 and concluded that the nature of TRD is complicated and different with other subtype of MDD [8]. In the same year, Cipriani, A et al pooled 522 trials comprising 116477 participants, found that venlafaxine, amitriptyline, mirtazapine, escitalopram, paroxetine, agomelatine and vortioxetine presented better than placebo in efficacy and acceptability [9].

System Biology Expand our Horizon on MDD

Early in 2010, de la Fuente A announced the disease-associated gene may be involved in the specific regulatory network. Therefore transcriptional profiles under the disease state may disclose the facts of interaction between gene and environment [15]. With the rapid developing of system biology, several novel approaches for uncovering the mechanism of MDD have emerged. For example in 2018, Akil H discussed the possibility and feasibility of multi-scale framework to disclose the relationship between disease-related gene expression to brain circuit, further by using of neuroimaging technique to identify the candidate circuits and molecules [16].

In 2016, Miyata S employed the transcriptomic biomarkers from blood in patients with late-onset MDD and testified the CIDECK (Cell Death-Inducing DFFA-Like Effector C) has the tremendous potential discriminant validity (specificity 87.5%, Sensitivity 91.3%) [17]. Moreover, in 2015, Malik K discovered some convergent genes participated in the pathogenesis of MDD in an integrative rat-human study. 8% of these genes were functionally linked with stress response signaling cascade, involving nuclear factor kappa-light-chain-enhancer of activated B (NF-κB) cells, activator protein 1 (AP-1) and ERK/MAPK pathway, which has correlated with MDD’s neuroplasticity and neurogenesis systematically [18].

Also, 2014 Powell TR validated the putative transcriptomic biomarkers differentiates MDD significantly in the inflammatory cytokine pathway [19]. Several studies as to the dysmetabolism of MDD presented novel perspectives of MDD. In 2010, Oxenkrug GF emphasized that Tryptophan kynurenine pathway presents a significant gathering point of metabolic disturbance in MDD, which correlated with the kynurenine pathway inflammatory cytokine profile of MDD patients. Recent meta-analytic studies have shown that several cytokines are increased in MDD [20, 21].

In 2015, Fan X et al. cross-experimented on the differential expression and regulation analyses reveal different mechanisms underlying major depressive disorder and subsyndromal symptomatic depression in patients with major depressive disorder in the Han Chinese population (2017) BMC Bioinformatics 16: 133.

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