Association between miR-137 polymorphism and risk of schizophrenia: a meta-analysis

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ABSTRACT. miR-137, a brain-enriched microRNA, is involved in the control of neuronal proliferation, differentiation, and dendritic arborization, all of which are important for proper neurogenesis and relevant to schizophrenia. miR-137 is also known to regulate many genes implicated in schizophrenia risk. Although reports have associated the miR-137 polymorphism rs1625579 with this disease, their results have been inconsistent. The aim of this meta-analysis was to evaluate the relationship between rs1625579 and schizophrenia. Data were obtained from an electronic database, and pooled odds ratios (ORs) with 95%
confidence intervals (95%CI) were used to test the association using the RevMan 5.3 software. Twelve case-control studies comprising 11,583 cases and 14,315 controls were included. An estimated lambda value of 0.46 was recorded, suggesting that a codominant model of inheritance was most likely. A statistically significant association was established under allelic (T vs G: OR = 1.15, 95%CI = 1.10-1.21, P < 0.001) and homogeneous codominant models (TT vs GG: OR = 1.32, 95%CI = 1.13-1.54, P < 0.001), but no such relationship was detected using the heterogeneous codominant model (GT vs GG: OR = 1.14, 95%CI = 0.97-1.34, P = 0.11). This meta-analysis demonstrates that the rs1625579 miR-137 genetic variant significantly increases schizophrenia risk.

**Keywords:** Schizophrenia; miR-137; Single nucleotide polymorphism; Meta-analysis; Fixed-effect analysis