

## Journal Article

Oluwadamilare Falola, Victor Chukwudi Osamor, **Marion Adebisi** and Ezekiel Adebisi, (2017). "Analyzing a Single Nucleotide Polymorphism (SNP) in Schizophrenia: A meta-analysis approach". *Journal of Neuropsychiatric Disease and Treatment*, Dove Medical Press, Pp 2243 – 2250. <http://dx.doi.org/10.2147/ndt.s111900>. **Impact Factor 2.198 (Indexed in Thomson Reuters and Google Scholar)**.

**Background:** Schizophrenia is a severe mental disorder affecting .21 million people worldwide. Some genetic studies reported that single nucleotide polymorphism (SNP) involving variant rs1344706 from the *ZNF804A* gene in human beings is associated with the risk of schizophrenia in several populations. Similar results tend to conflict with other reports in literature, indicating that no true significant association exists between rs1344706 and schizophrenia. We seek to determine the level of association of this SNP with schizophrenia in the Asian population using more recent genome-wide association study (GWAS) datasets.

**Methods:** Applying a computational approach with inclusion of more recent GWAS datasets, we conducted a meta-analysis to examine the level of association of SNP rs1344706 and the risk of schizophrenia disorder among the Asian population constituting Chinese, Indonesians, Japanese, Kazakhs and Singaporeans. For a total of 21 genetic studies, including a total of 28,842 cases and 35,630 controls, regression analysis, publication bias, Cochran's Q and  $I^2$  tests were performed. The DerSimonian and Laird random-effects model was used to assess the association of the genetic variant to schizophrenia. Leave-one-out sensitivity analysis was also conducted to determine the influence of each study on the final outcome of the association study.

**Results:** Our summarized analysis for Asian population revealed a pooled odds ratio of 1.06, 95% confidence interval of 1.01–1.11 and two-tailed  $P$ -value of 0.0228. Our test for heterogeneity showed the presence of large heterogeneity ( $I^2=53.44%$ ,  $P=0.00207$ ) and Egger's regression test ( $P=0.8763$ ) and Begg's test ( $P=0.8347$ ), indicating no presence of publication bias among our selected studies. In our sensitivity analysis, 10 different studies comprising of ~50% of the entire study had an impact on our final results as each leave-one-out test became insignificant. Our result suggests that genetic variant rs1344706 might be associated with the development of schizophrenia in Asians.