

Influence of *PON1* gene variants and enzymatic activity on the risk of coronary artery disease: a meta-analysis of case-control studies

Sana Ashiq^{1*}, Kanwal Ashiq²

¹Centre for Applied Molecular Biology, University of the Punjab, Lahore-Pakistan, ²Faculty of Pharmaceutical Sciences, Superior University, Lahore-Pakistan

Introduction and Aim

Non-communicable diseases (NCDs), including coronary artery disease (CAD), is responsible for high mortality and morbidity rate in developed or developing countries. It is a multifactorial disease that involves a complex relationship between either gene-environment or gene-gene. The paraoxonase 1 (*PON1*) gene encodes a paraoxonase enzyme that plays an essential role in atherosclerosis due to its antioxidative properties. This meta-analysis study aimed to analyze the association between *PON1* gene polymorphisms (rs662 and rs854560) in coronary artery disease.

Methodology

This study was conducted according to PRISMA guidelines. The relevant literature was searched using various keywords through various electronic databases. The pooled odd ratios (ORs) were used to evaluate the role of variants in the *PON1* gene and CAD. Begg’s and Egger’s test was used to assess the publication biasness. Data analysis was performed by the MetaGenyo program.

Study Registration: PROSPERO CRD42020202278

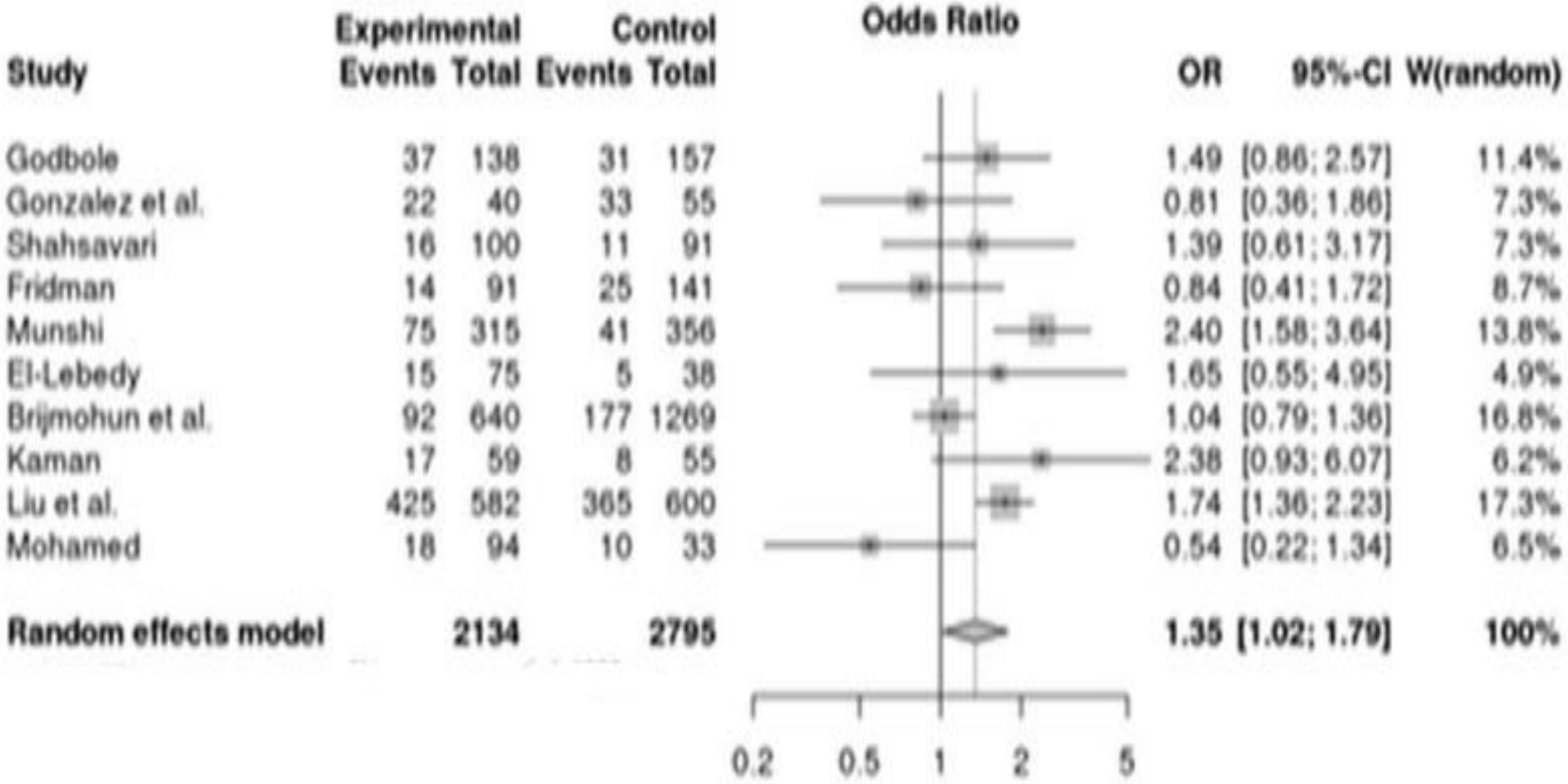
References

1. Ashiq S, Ashiq K. The role of paraoxonase 1 (PON1) gene polymorphisms in coronary artery disease: a systematic review and meta-analysis. *Biochemical Genetics*. 2021 Aug;59:919-39.
2. Ashiq S, Ashiq K, Shabana SU, Qayyum M, Sadia H. Prevalence and role of different risk factors with emphasis on genetics in development of pathophysiology of coronary artery disease (CAD). *Pakistan Heart Journal*. 2019;52(4).
3. Ashiq S, Ashiq K. In-silico analysis of PON1, PON2 and PON3 genes role in coronary artery disease. *International Journal of Computational Biology and Drug Design*. 2020;13(4):415-23.

Results and Conclusion

Final analysis was performed on the ten eligible studies. In the coding region, SNPrs662 significantly increased the risk of CAD (OR 1.16, CI 1.00–1.33). However, the results were non-significant for the second polymorphism rs854560. Further, compared to healthy subjects, PON1 enzyme levels were much lower in CAD patients. However, in the future, there is a need to conduct large sample-size genetic association studies, which can provide us better understanding of the association or effect of these variants with the risk of coronary artery disease.

rs662



rs854560

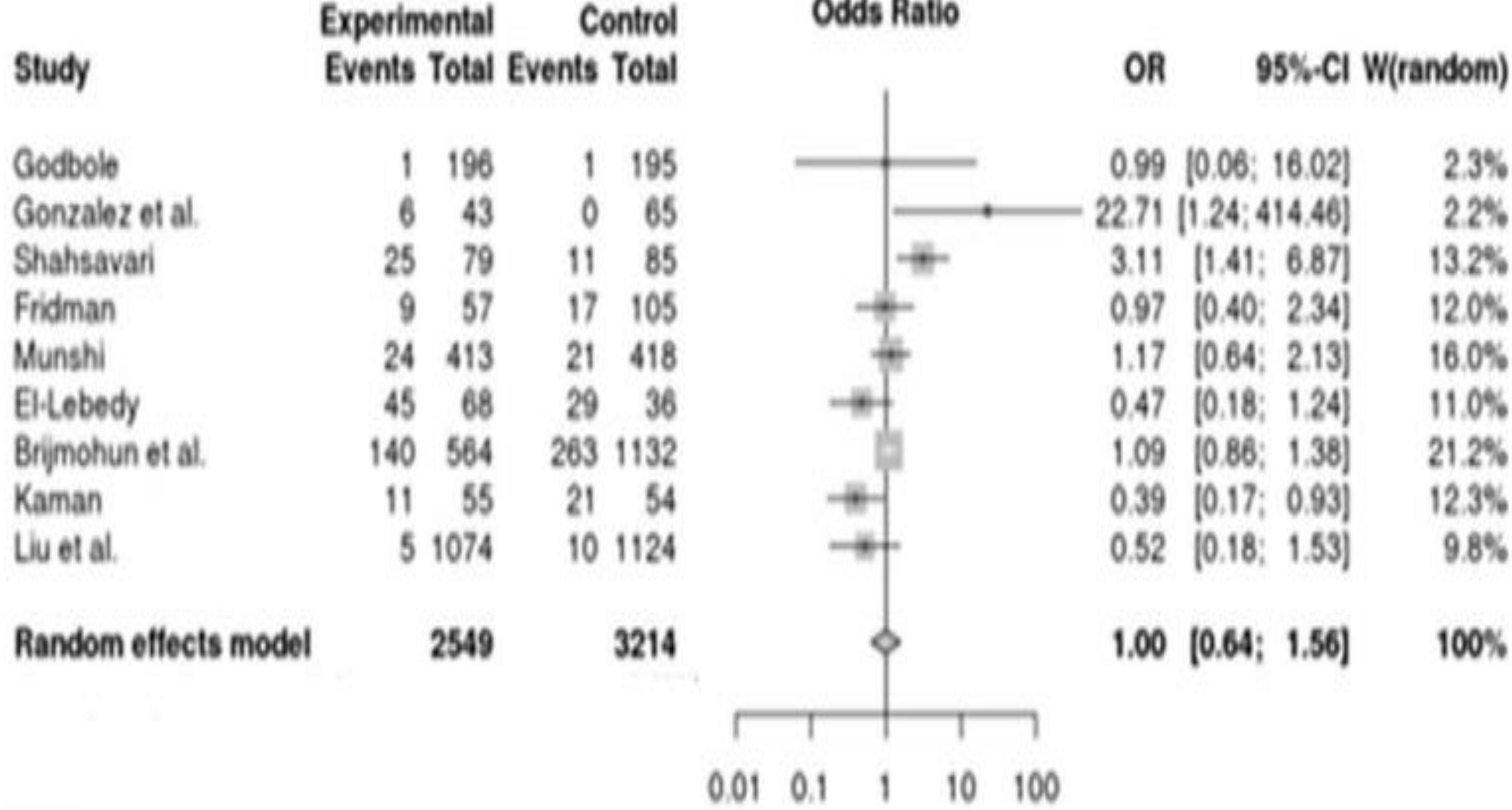


Figure: Genetic model comparison between rs662 and rs854560