Prognostic Value of Clinical and Genomic Data on Predicting Major Adverse Cardiovascular Events (MACE)

Background
Atherosclerotic cardiovascular disease (ASCVD) has an estimated heritability of 40-60% (1,2). Application of genomic risk scores (GRS) may provide additional benefit in the identification of patients at high risk of CVD and allow for early intervention (3,4). However, use of genomic risk scores is not routinely used to predict cardiovascular outcomes.

This study aims to determine whether genomic risk prediction of CVD confers prognostic value when compared with conventional clinical risk prediction models.

Method
Patients in the Genetics of Diabetes Audit and Research Tayside Scotland (GoDARTS) database had their clinical risk score for ASCVD calculated using the Pooled Cohort Equation (PCE). The GRS for each patient was obtained from previously published data. Cox Regression and Kaplan-Meier analysis were applied to evaluate the independent association between GRS and major adverse cardiovascular events (MACE), and to determine if there is significant association between clinical and genetic risk scores.

Results
19,709 patients in the GoDARTS database were evaluated in this study, of which 4502 (22.8%) had suffered a MACE. Both GRS and ASCVD risk score independently predicted MACE ($p < 0.001$). However, GRS was evaluated to be a better predictor of MACE compared with ASCVD risk score (AUC 0.665 vs 0.623 respectively, $p < 0.001$).

Conclusion
Risk stratification based on patient's GRS in conjunction with traditional methods of CV risk assessment has prognostic value and may allow for earlier detection and management of CVD.

References

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