Integrating polygenic scores and family history for type 2 diabetes prediction in East Asians: Insights from the Taiwan Biobank

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Background: Type 2 diabetes is a complex disease influenced by both genetic and environmental factors. While polygenic risk scores (PRS) and family history (FH) are established predictors, their combined utility in East Asian populations remains unclear.

Methods: We analyzed 111,899 participants from the Taiwan Biobank, linking genetic data to Taiwan's National Health Insurance Research Database. We used inpatient and outpatient claims data from 1998 to the date of death or until the end of 2023 to identify type 2 diabetes (ICD-9: 250 (excluding 250.x1, 250.x3); ICD-10: E08, E09, E11, E13). We constructed trans-ancestry, East Asian-specific, and European-derived PRSs for type 2 diabetes and assessed their associations with type 2 diabetes using logistic regression models. We used the covered insurance relationship to infer pedigree relationships; FH in the father, mother, and sibling(s) was examined.

Results: The trans-ancestry PRS improved the explained variance in disease risk compared to ancestry-specific PRSs and FH. FH, particularly sibling history, also showed a strong association with type 2 diabetes. When combined, PRS and FH contributed independently and additively, improving predictive performance.

Conclusions: These findings demonstrate that PRS and FH are independent yet complementary risk indicators and support the application of trans-ancestry PRS models in East Asian populations. Incorporating both genetic and familial risk factors may enhance early detection and facilitate more personalized prevention strategies for type 2 diabetes.