26 September 2024

Comparison of polygenic risk scores for diabetes developed from different ethnic groups: A cross-sectional study in the Japanese population

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Background

- The Polygenic Risk Score (**PRS**), which is based on hundreds to millions of genetic polymorphisms, is expected to contribute to the prediction of disease risk and the development of tailor-made medicine.
- However, most PRS studies have been conducted in European populations, and knowledge of the specific characteristics and effectiveness of PRS in other ethnic groups is limited. (Ge T, et al. Genome Med. 2022)





Background

 In particular, many East Asians have diabetes without obesity, and the factors and mechanisms associated with diabetes might differ from those of Europeans.

(Yeyi Zhu, et al. Diabetes Care. 2019)

Objective

Compare the classification accuracy of several PRSs for diabetes developed from different ethnic groups





-MICC STUDY

Methods

[Participants]

Japan Multi-Institutional Collaborative Cohort (J-MICC) Study

J-MICC Study is a Japanese large cohort with about 100,000 participants that has been followed up to explore the relationship between lifestyle, genotype, blood composition, and the risk of developing various diseases.

Included in the analysis n = 14,083

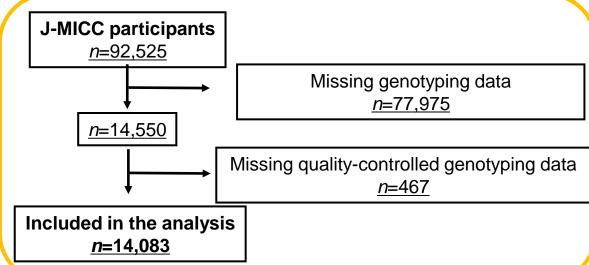
Male: 6,336 (45.0%), Female: 7,747 (55.0%)

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[Age]: 54.8 \pm 9.4 (mean \pm SD)
[Diabetes]: 926 (6.6%)
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Figure 1. Flowchart of the process for selecting study participants





Methods

[PRSs for type 2 diabetes]

PRS model information is based on the "PGS Catalog". (https://www.pgscatalog.org)

• Japanese PRS

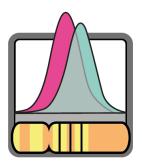
[ID: PGS002379 / Number of variants: 920,930]

• European PRS

[ID: <u>PGS002354</u> / Number of variants: **1,109,311**]

Both PRS models were developed using the same method. (Weissbrod O et al. Nat Genet. 2022)

The PRS for each participant was calculated as the weighted sum of each risk allele using previously derived weights.





Methods

[Statistical analysis]

- Association between PRS and diabetes
- Logistic regression analysis

Analyzed the odds ratio (OR) of diabetes prevalence [Outcome] : Diabetes case **[Exposure]** : **PRS** [Covariates]: age, sex, study area, top five principal components

> AUC of the ROC curve

Analyzed the classification accuracy for diabetes prevalence

Scatter plots

Visualization of diabetes prevalence per percentile of PRS



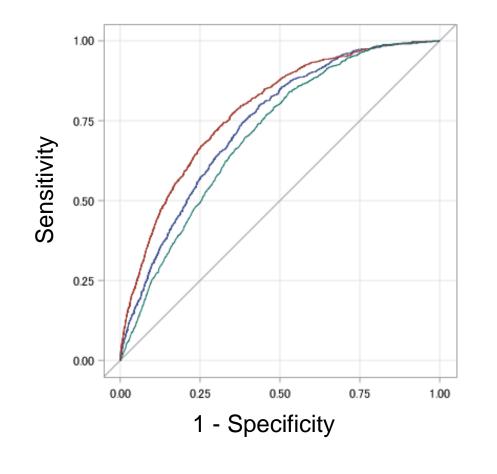


Association between PRS and diabetes by quintile or per 1 SD

PRS ID	Quintile		Per 1 SD		
		OR	95% CI	OR	95% CI
PGS002379	Q1 (Lowest)	1	(reference)		
	Q2	1.68	(1.21 - 2.33)		
	Q3	2.46	(1.81-3.34)	2.18	(2.02 – 2.35)
	Q4	4.01	(2.99-5.37)		
	Q5 (Highest)	8.08	(6.11 – 10.67)		
	Q1 (Lowest)	1	(reference)		
	Q2	1.40	(1.08- 1.83)		
PGS002354	Q3	1.92	(1.49-2.48)	1.55	(1.45 – 1.66)
	Q4	2.40	(1.87-3.07)		
	Q5 (Highest)	3.41	(2.69-4.33)		
	PGS002379	Q1 (Lowest) Q2 Q3 Q4 Q5 (Highest) Q Q1 (Lowest) Q3 Q4 Q5 (Highest) Q2 Q1 (Lowest) Q2 Q3 Q4 Q5 (Highest) Q2 Q3 Q4 Q3 Q4 Q4	OR OR Q1 (Lowest) 1 Q2 1.68 Q4 2.46 Q4 4.01 Q5 (Highest) 8.08 PGS002354 Q3 1.40 Q2 1.40 Q4 2.40	OR 95% CI Q1 (Lowest) 1 (reference) Q2 1.68 (1.21 – 2.33) PGS002379 Q3 2.46 (1.81 – 3.34) Q4 4.01 (2.99 – 5.37) (6.11 – 10.67) Q5 (Highest) 8.08 (6.11 – 10.67) PGS002354 Q3 1.40 (1.08 – 1.83) Q4 2.40 (1.87 – 3.07) (1.87 – 3.07)	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$

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ROC curves of PRS and diabetes prevalence



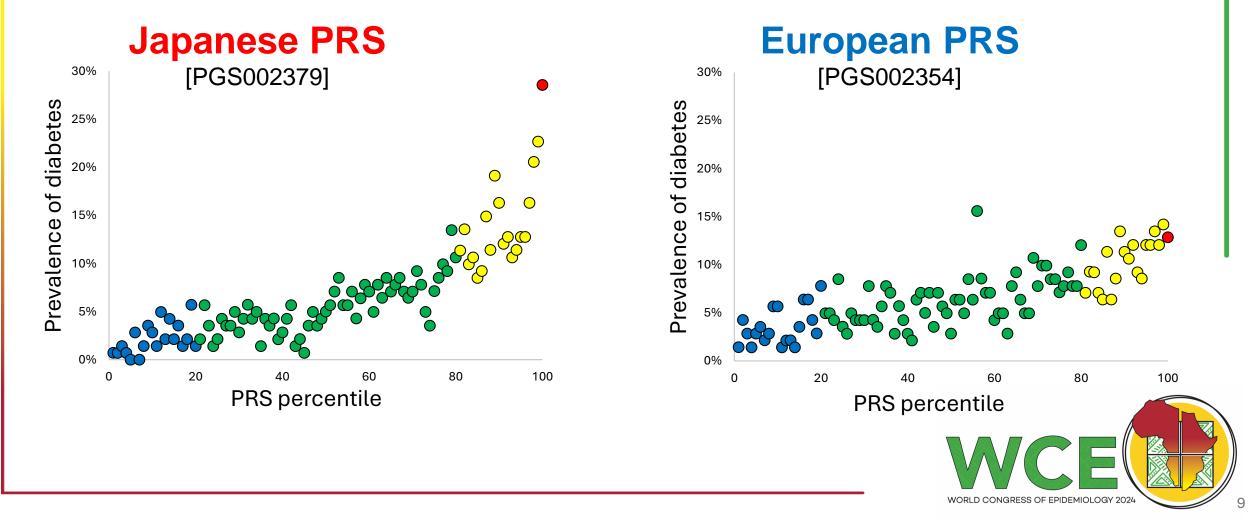
- Japanese PRS [PGS002379] AUC=0.781 (0.767–0.796)
- European PRS [PGS002354] AUC=0.738 (0.723–0.753)

Base AUC=0.706 (0.691–0.721)

P <0.001



Scatter plots of diabetes prevalence per percentile of PRS



Association between PRS and diabetes by PRS category based on diabetes prevalence

PRS developed population	PRS ID	PRS category	OR	95% CI
Japanese PRS	PGS002379	Low (1–20%)	1	(reference)
		Medium (21–80%)	2.68	(2.04 – 3.52)
		High (81–99%)	7.54	(5.69 – 9.98)
		Very High (100%)	21.82	(13.67 – 34.82)
	PGS002354	Low (1–20%)	1	(reference)
European		Medium (21–80%)	1.89	(1.52 – 2.36)
PRS		High (81–99%)	3.37	(2.65 – 4.28)
		Very High (100%)	4.11	(2.37 – 7.11)

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Discussion

The PRS developed from matched ancestry populations had higher OR and classification accuracy for diabetes

The mechanisms underlying diabetes have ethnic differences, such as insulin secretion and resistance. (Kodama K, et al. *Diabetes Care*. 2019)

Diabetes is not a monogenetic disease but rather a complex combination of many genetic and lifestyle factors. (Griffin S, et al. *Diabetologia*. 2022)

Lifestyle and physiological functions are different, suggesting that diabetesrelated variants and their weightings also differ among ancestry groups.

> Ancestry consideration would be important for diabetes PRS



Discussion

The highest category of PRS showed remarkably high OR of diabetes

Several diseases had particularly high prevalence in populations at the top 10-20% of genetic risk, including diabetes. (Khera AV, et al. *Nat Genet*. 2018)

PRS could accurately assess the risk and identify individuals with a particularly high risk of diabetes.

The PRS for diabetes developed from matched ancestry populations would be useful for

✓ Detecting particularly high-risk individuals

Early prediction and effective prevention



Conclusion

- The PRS developed from matched ancestry populations had higher ORs and classification accuracy for diabetes prevalence in the Japanese general population.
- The highest category of PRS showed remarkably high OR, detecting individuals with a particularly high risk of diabetes.
- PRSs adjusted to the characteristics of each ancestry group may enhance early prediction and effective prevention of diabetes.









Thank you for your attention

