



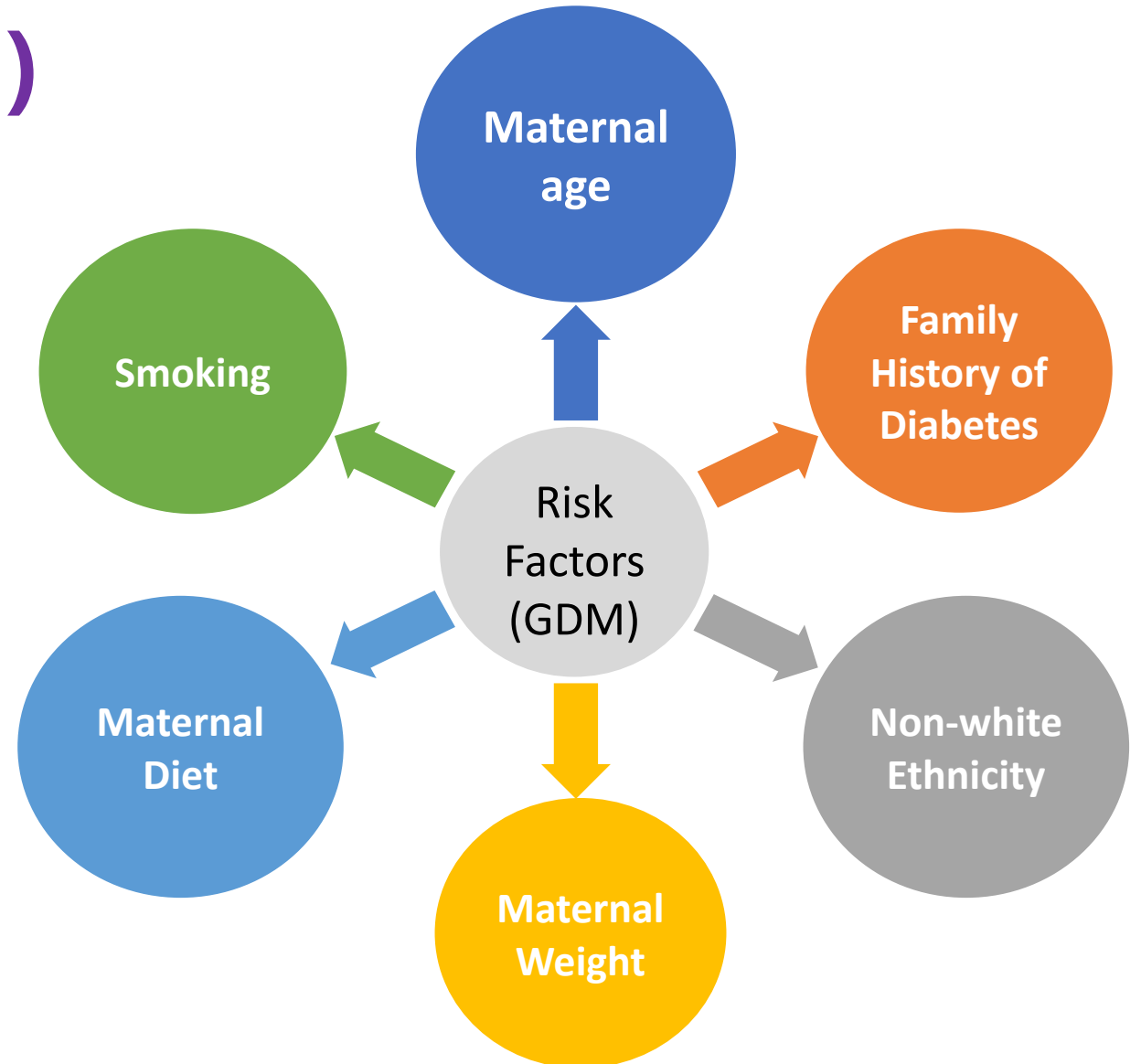
Genetic contribution to Gestational Diabetes in South Asian Women: Analysis from the START-Canada Birth Cohort study

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Supervisor: Dr. Sonia Anand

Background (Cont'd)

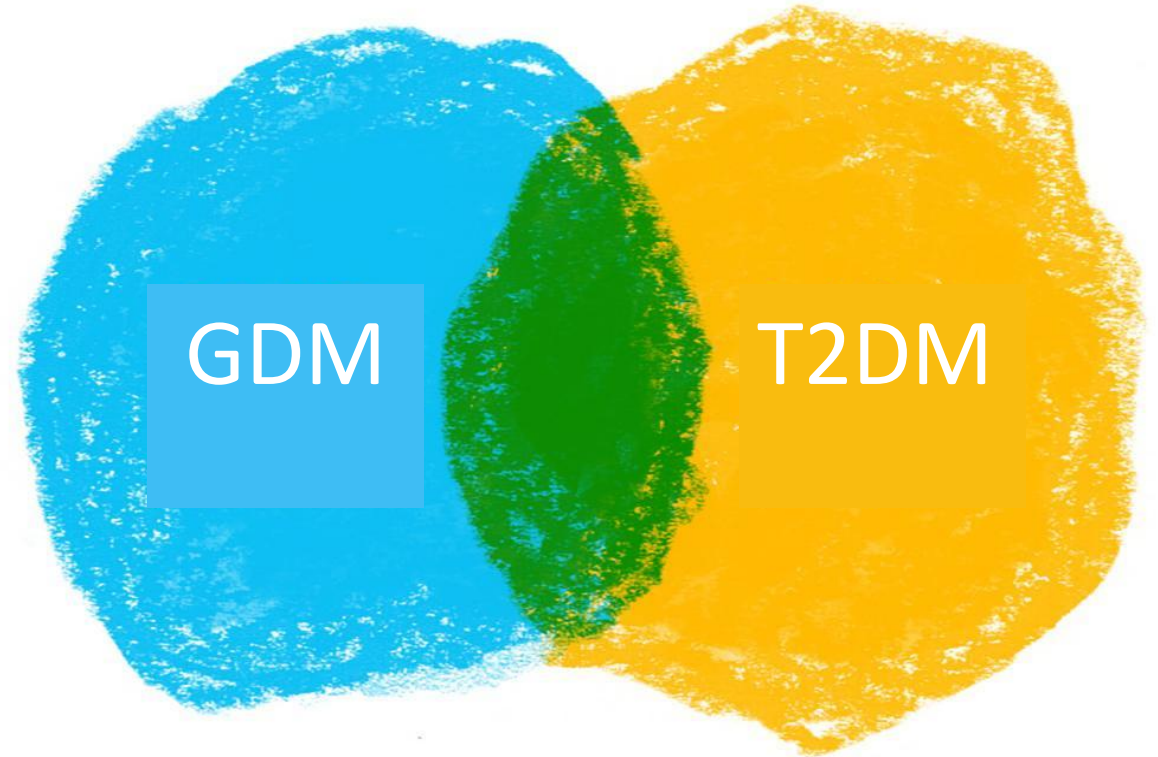
Previous analysis (Anand et. al., CMAJ open)

- Pre-pregnancy weight
- Low diet quality
- Advanced maternal age
- Maternal height
- Family History of T2DM



Background (Cont'd)

- Family history of T2DM may be a crude surrogate for the genetic component of GDM
 - Large GWAS and GWAMA studies have confirmed more than 1500 loci associated with glycemic traits
 - A) MAGIC, B) DIAGRAM
 - Several T2DM loci have been shown to be associated with GDM



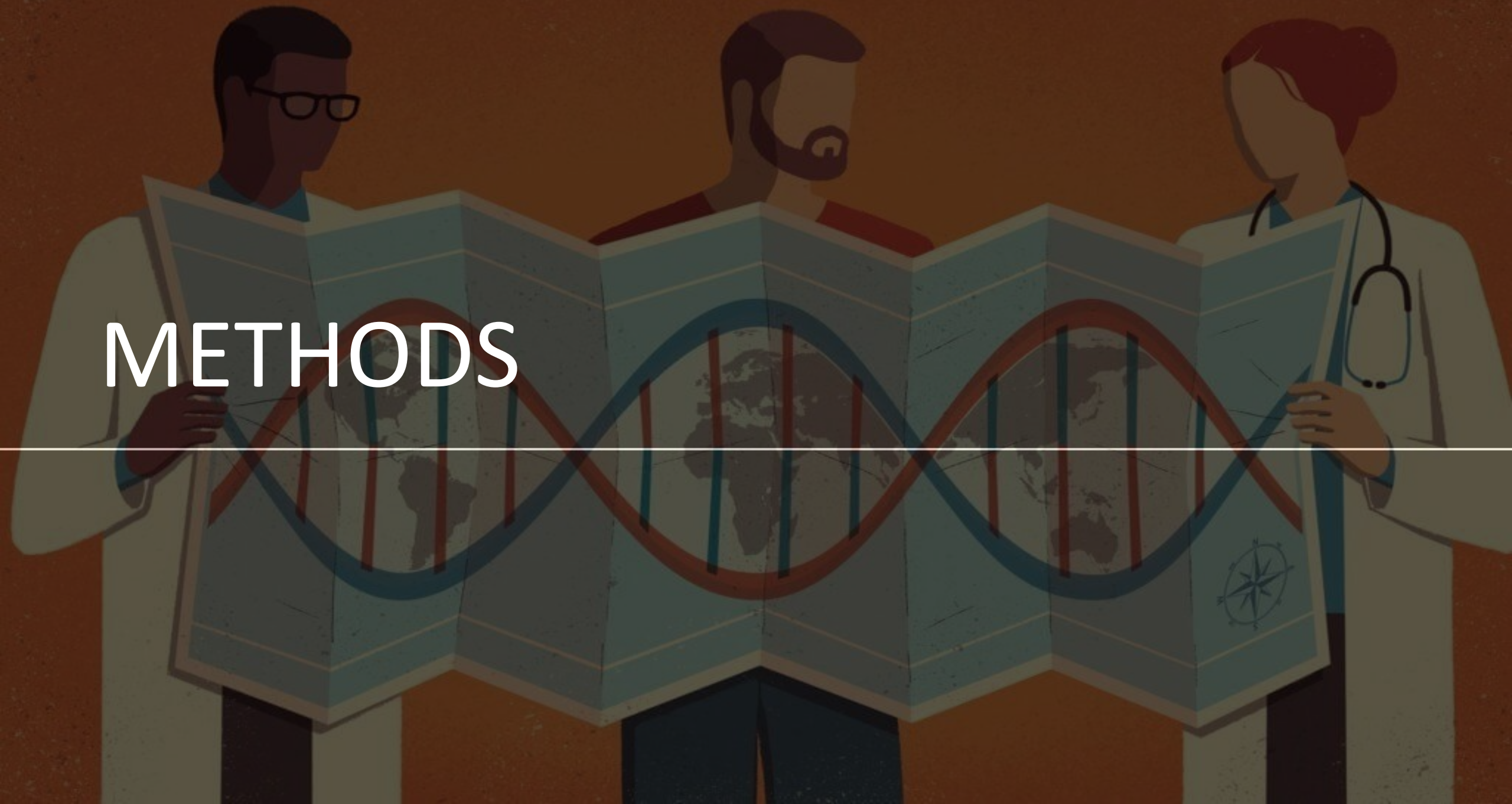
Purpose/Objective

- 1) Test the association of a T2DM GRS with GDM in South Asians
- 2) Determine the extent of the contribution of our GRS in explaining the family history of T2DM (association with GDM)

Research Question

Among South Asian pregnant women part of START, is maternal GRS a significant predictor of GDM and to what extent does it change the effect size of family history of T2D as a predictor of GDM in this population

METHODS



Study design -

START

- Longitudinal prospective birth cohort
- examines early determinants of health in South Asians
- conducted among 1012 SA pregnant women from the Peel Region.

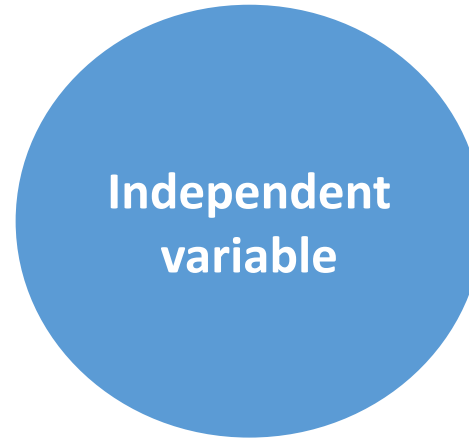
Ref: Anand, S. S., Gupta, M., Teo, K. K., Schulze, K. M., Desai, D., Abdalla, N., . . . Gerstein, H. (2017). Causes and consequences of gestational diabetes in South Asians living in Canada: results from a prospective cohort study. *CMAJ Open*, 5(3), 604-611. doi:10.9778/cmajo.2017002



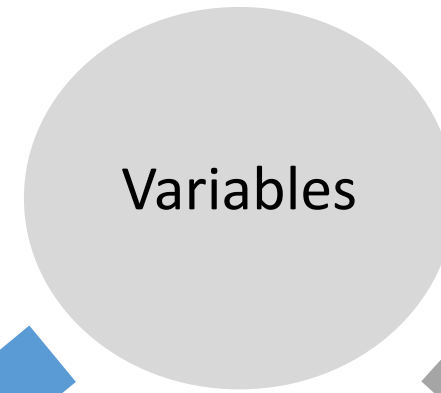
Derived Variables

n = 832 mothers with known GDM status

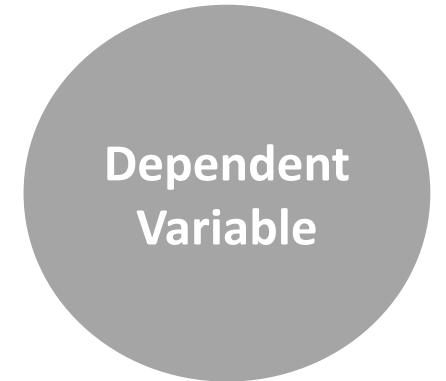
Predictor of interest



- Maternal GRS (contin /categ)



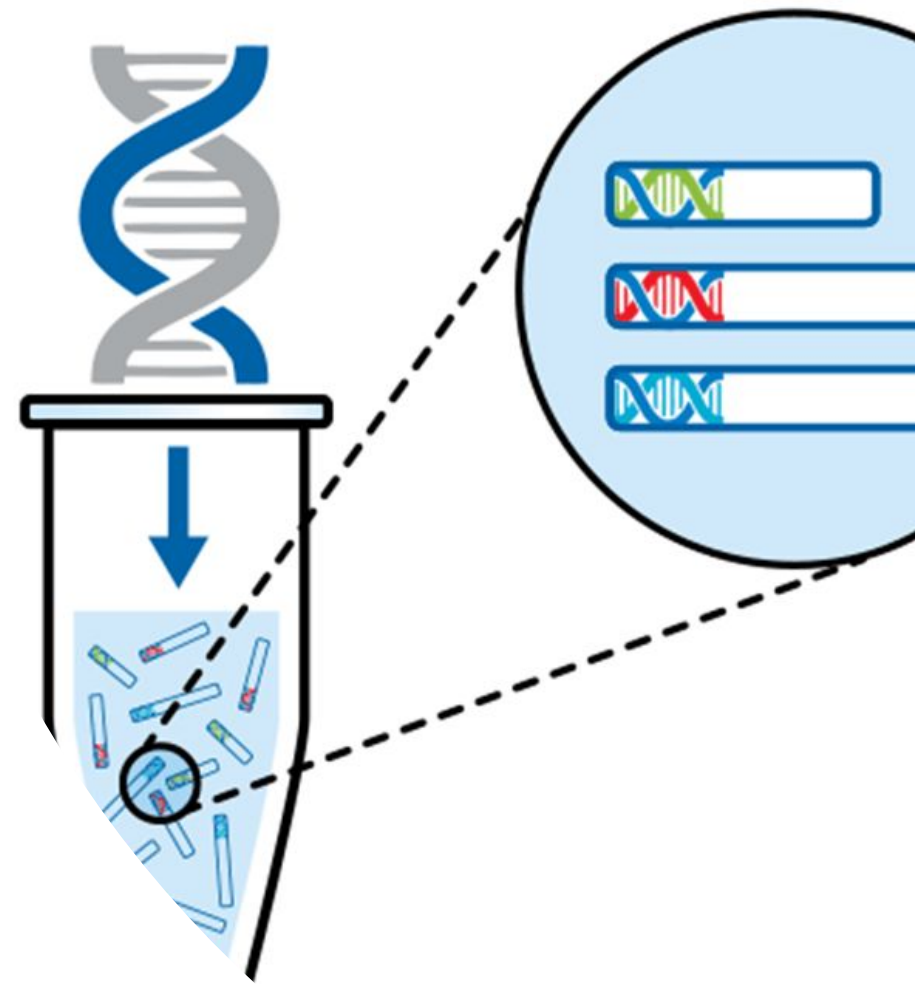
- Fam hx (cat)
- Maternal age (years)
- Prepregnancy weight (kg)
- Prepregnancy height (cm)



GDM status (BiB cutoffs - cat)

Building the GRS

- Summary statistics from DIAGRAM (Mahajan 2014)
 - SNPs tested in South Asians only
 - SNPs tested in $\geq 95\%$ of samples only
- Genotyped data from 867 samples from START was used
- 837 samples passed QC
- Variants with an info score of ≥ 0.7 were kept for analysis
- A pruning and thresholding (PT) method was used to build the optimal GRS
 - START data use as LD template
 - P value threshold = 0.2



Statistical Analysis

- Analyses were conducted using SPSS v.24.
- Continuous GRS was transformed into a dichotomous category (T1 vs T2+T3)
- Binomial logistic regression: Single and multivariable models (including previously identified predictors of GDM)
- IRAP: calculate the population attributable risks (PAR) – frequency and disease exposure
 - Age was divided into categories (29-31, 32-43, vs 19-28)
 - BMI was divided into 3 categories (<18.5, 18.5-23, >23)

RESULTS

regression

independent

outcome

Multiple

risk factors

stratified

equation

coefficient

Y-intercept

weighted

simple

taking

association

average

bo

dependent

squares

logistic

Multiple

Factors

dumming

adjusting

Correlation

Linear

stratum

Logistic

primary

coefficients

estimates

least

bi

stratum

Logistic

primary

association

average

bo

dependent

squares

logistic

multiple

analysis

effect

variables

Regression

correlation

Cochran-Mantel-Haenszel

adjusted

modification

Analysis

effect

variables

Regression

correlation

Cochran-Mantel-Haenszel

adjusted

modification

Table 1: Characteristics of START participants

	No GDM (n=531)	GDM (n=301)	p value
Maternal Age, yr	30 (4)	31 (4)	<0.001
Genetic Risk Score, cont.	0.01353	0.01356	<0.001
Maternal Height, cm	162.71 (6.22)	161.50 (6.18)	0.007
Pre-pregnancy weight, kg	61.38 (11.71)	64.89 (12.19)	<0.001
Pre-pregnancy BMI, kg/m ²	23.17 (4.21)	24.89 (4.61)	<0.001
Low diet quality, n (%)	123 (23.5%)	96 (32.2%)	0.006
Family history of diabetes, n (%)	180 (34.0%)	154 (51.2%)	<0.001
Maternal Genetic Risk Score, n (%)			
Tertile 1	118 (22.2%)	41 (13.4%)	0.002
Tertile 2+3	413 (77.8%)	260 (86.4%)	



Univariable model - odds for GDM

- Continuous GRS: **OR = 1.09**, [95% CI: 1.06-1.13, $p = <0.001$]
- Categorical GRS (T1 vs T2+T3): **OR = 1.82**, [95%CI: 1.23-2.67, $p = 0.003$]

Table 2: Multivariable model with all risk factors associated with GDM

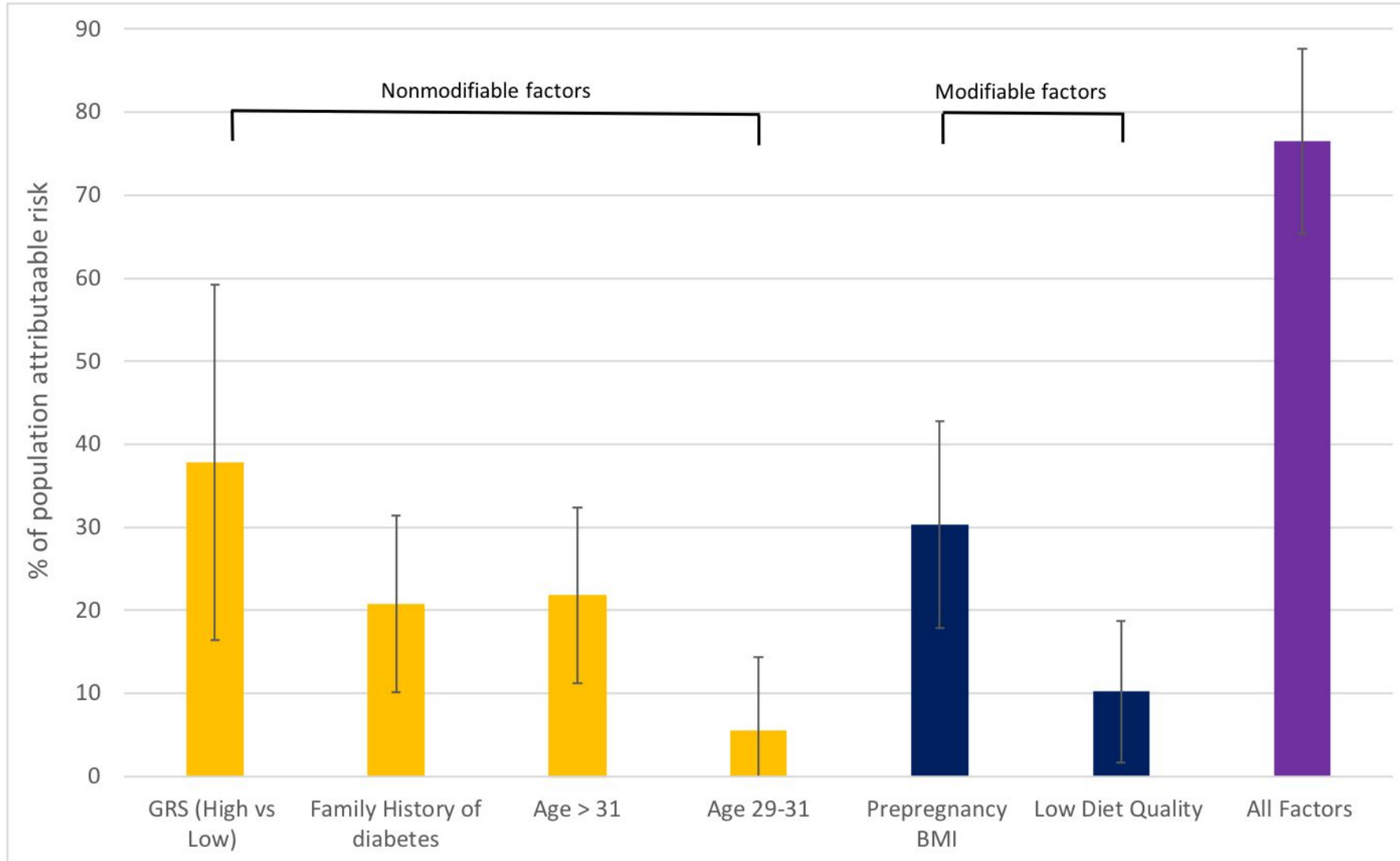
Risk Factor	OR [95%CI] *	P-value*
GRS		
Continuous	1.002 [1.001- 1.003]	7.67e ⁻⁰⁸
Tertile 2 + 3	1.71 [1.14 - 2.57]	0.01
Maternal Age	1.08 [1.04 - 1.12]	<0.001
Pre-pregnancy weight, kg	1.03 [1.01 - 1.04]	<0.001
Maternal Height, cm	0.96 [0.94 - 0.99]	0.004
Diet quality (low vs medium + high)	1.44 [1.04 - 2.01]	0.03
Family history of diabetes	1.65 [1.21 - 2.23]	0.001



Table 3: PARs for maternal GDM risk factors

Risk Factor	OR (95%CI) from multivariable model	Prevalence %	Population attributable risk % (95% CI)
GRS Tertile 2 + 3 vs 1	1.77 (1.18 to 2.67)	80.1	37.8 (16.4 to 59.2)
Age 32-43 yr v. < 29 yr	1.89 (1.32 to 2.70)	36.6	21.80 (11.2 to 32.4)
Age 29-31 yr v. <29 yr	1.27 (0.86 to 1.87)	27.7	5.6 (-3.2 to 14.4)
Body Mass index >23 v. ≤ 23	1.90 (1.40 to 2.58)	48.2	30.3 (17.9 to 42.8)
Low diet quality	1.46 (1.05 to 2.04)	26.7	10.2 (1.7 to 18.7)
Family history of diabetes	1.68 (1.24 to 2.28)	40.4	20.8 (9.7 to 31.9)
All factors			76.5 (65.5 to 87.5)

Figure 1: PARs for individual risk factors

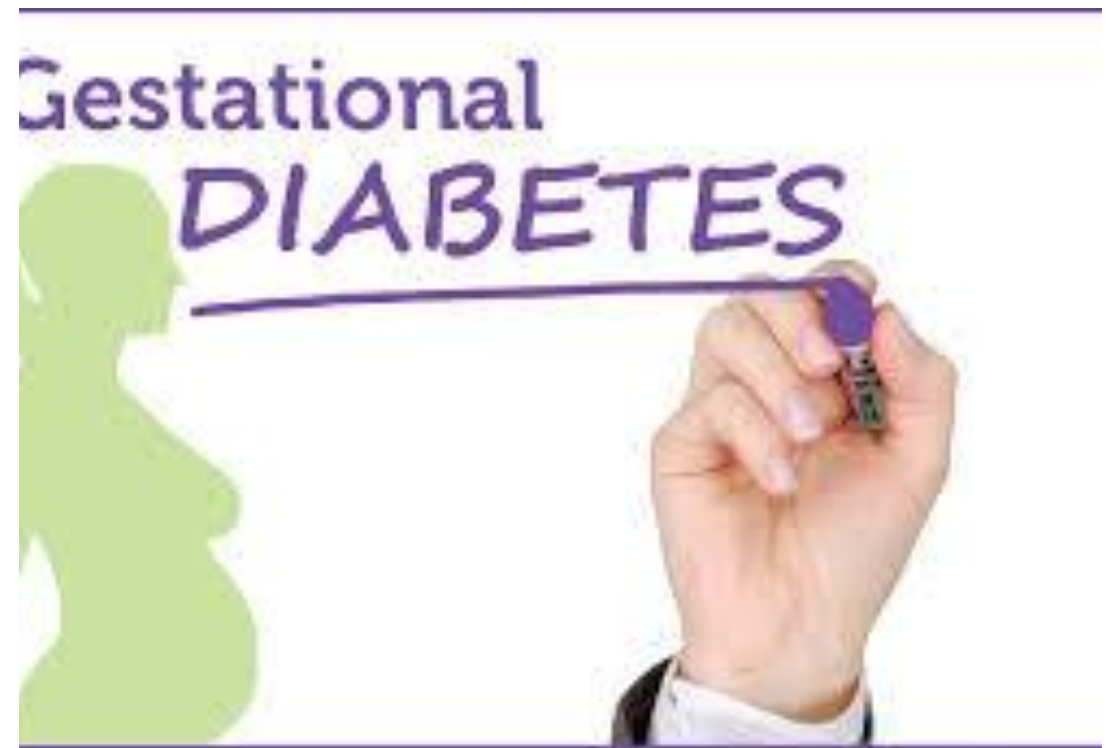


DISCUSSION



Interpretation

- Maternal GRS is an independent predictor of GDM in South Asian women
- Accounts for a substantial component of the PAR for GDM
- Family history remains significant even though GRS may be a better predictor



Interpretation and Clinical Significance

- Inquiring about family history is the only way to identify genetic predisposition to GDM
- GRS can serve as a good screening tool to identify people at risk
- Promote healthy behaviour in people with higher genetic loads



Support from other studies

T2D GRS has been associated with GDM in other populations

GRS and Family history were better predictors of colorectal cancer risk stratification – Weigl et. al., (2018)

Shared lifestyle factors involved in PH's effect on MI risk – Chow et. al., (2011)

Strengths and limitations

Strengths

- Optimized GRS to target South Asian population using a multi-ethnic GWAMA
- Used whole genome genotypes to build the GRS
- GDM status was determined using validated South Asian cutoffs and objective measures (OGTT)

Limitations

- Mahajan et. al.,'s data was not exclusive to South Asian samples (20%)
- Our GRS is based on T2D loci not GDM specific loci

Conclusion

A T2D GRS is a strong and independent predictor of gestational diabetes in South Asians



The GRS is more informative and complementary to self-reported family history of diabetes

The image features a dark blue, almost black, background. A glowing DNA double helix structure is visible, with the sugar-phosphate backbones appearing as bright orange and yellow strands. The text "THANK YOU" is centered in white, bold, uppercase letters.

THANK YOU

