

# Nature versus nurture of the puberty: a combined clinical and polygenic risk score to predict pubertal timing in girls



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## Background

Precocious or late puberty are common causes of referral to pediatric endocrinology.

## Methods

#### **STUDY COHORT : ALSPAC<sup>2</sup>**

- British birth cohort with genotypic and clinical data
- 8,799 children of European ancestry/3,140 girls  $\bullet$
- Median AAM : 12.7 years (SD 1,15)
- Most of these cases are idiopathic and do not require extensive work-up.
- Pubertal traits are highly heritable.
- Epidemiological risk factors (obesity, socio-economic status etc) have also been linked to pubertal timing.

<u>Objective 1</u>: to evaluate the impact of genetic and epidemiological factors on age at menarche (AAM) and age at peak height velocity (APHV)

Objective 2: to develop a predictor of early or late AAM

- Mean APHV : 11.8 years (SD 0,82)
- 1.9 % girls with BMI  $\geq$  25

## **POLYGENIC RISK SCORE (PRS) for AAM**

- Developed from a GWAS in UK Biobank on AAM using LDpred2 (Privé F et al., 2022<sup>1</sup>).
- 854,735 single-nucleotide polymorphims (SNPs) included in the PRS
- 699,499 SNPs (after QC) used to calculate the AAM PRS in ALSPAC

## PHENOTYPIC DATA

- Exposure of interest: PRS
- Outcomes:

- AAM as a continuous outcome
- Early menarche (AAM  $\leq$  10.4y); Late menarche (AAM  $\geq$  15y)
- APHV evaluated by serial height measurements between ages 8y and 20y
- Covariates : BMI at age 8y, birthweight, gestational age, emotional difficulties score, mother's AAM, BMI and SES, fathers' BMI.

#### **STATISTICAL METHODS**

- Linear regression models in univariate and multivariate analyses
- All models with PRS were adjusted for 10 principal components (PC)
- Metrics of performance of each model : R<sup>2</sup> (continuous outcomes), AUROC (binary outcomes)

## Results

#### **UNIVARIATE MODELS**



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## Discussion

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- We demonstrates the advantage to combine PRS with clinical risk factors to predict pubertal timing, in agreement with a Chinese study<sup>3</sup>.
- Such predictors could help clinicians diagnose idiopathic forms of early puberty and avoid unnecessary investigations.
- Next step: replication of our findings in larger cohorts, various ancestries and in boys.

Fig. 4: Comparison of the AUROC of the PRS, clinical predictors, and their combination

## Conclusion

A combined clinical and polygenic risk score could be proposed as a tool to predict (at no risk and low cost) which girls with extreme presentations of their pubertal timing do not warrant further investigations.

#### References

<sup>1</sup>Privé, F., et al. Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. Am J Hum Genet. 2022 Jan 6;109(1):12-23. PMID: 34995502 <sup>2</sup>Fraser, A., et al. Cohort Profile: the Avon Longitudinal Study of Parents and Children: ALSPAC mothers cohort. Int J Epidemiol. 2013; 42, 97-110.

<sup>3</sup>Zhao, W., et al. Associations between polygenic risk score for age at menarche and serum hormone levels in multiple race/ethnic groups. Menopause. 2021 Apr 19;28(7):819-828.