

# Infant Growth as an Effect Modifier of Genetic-Lipid Associations: Evidence From a Chilean Infancy Cohort

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## Introduction

- Early infancy serves as a window of time in which environmental exposures are associated with chronic disease risk factors in adulthood.
  - Extensive studies support functional association between genetic regions and lipid levels.
  - Infant growth may influence genetic mechanisms and subsequent metabolic programming of lipid metabolism.
- Hypothesis** Infant growth influences the strength of association between selected genetic variants and adverse lipid levels for children.

## Aim

- Assess SNP-lipid additive association across latent early infancy growth classes for 20 candidate genetic variants underlying lipid metabolism and fasting lipid profiles assessed at average 17 years of age.

## Sample

### Santiago Longitudinal Study (SLS)

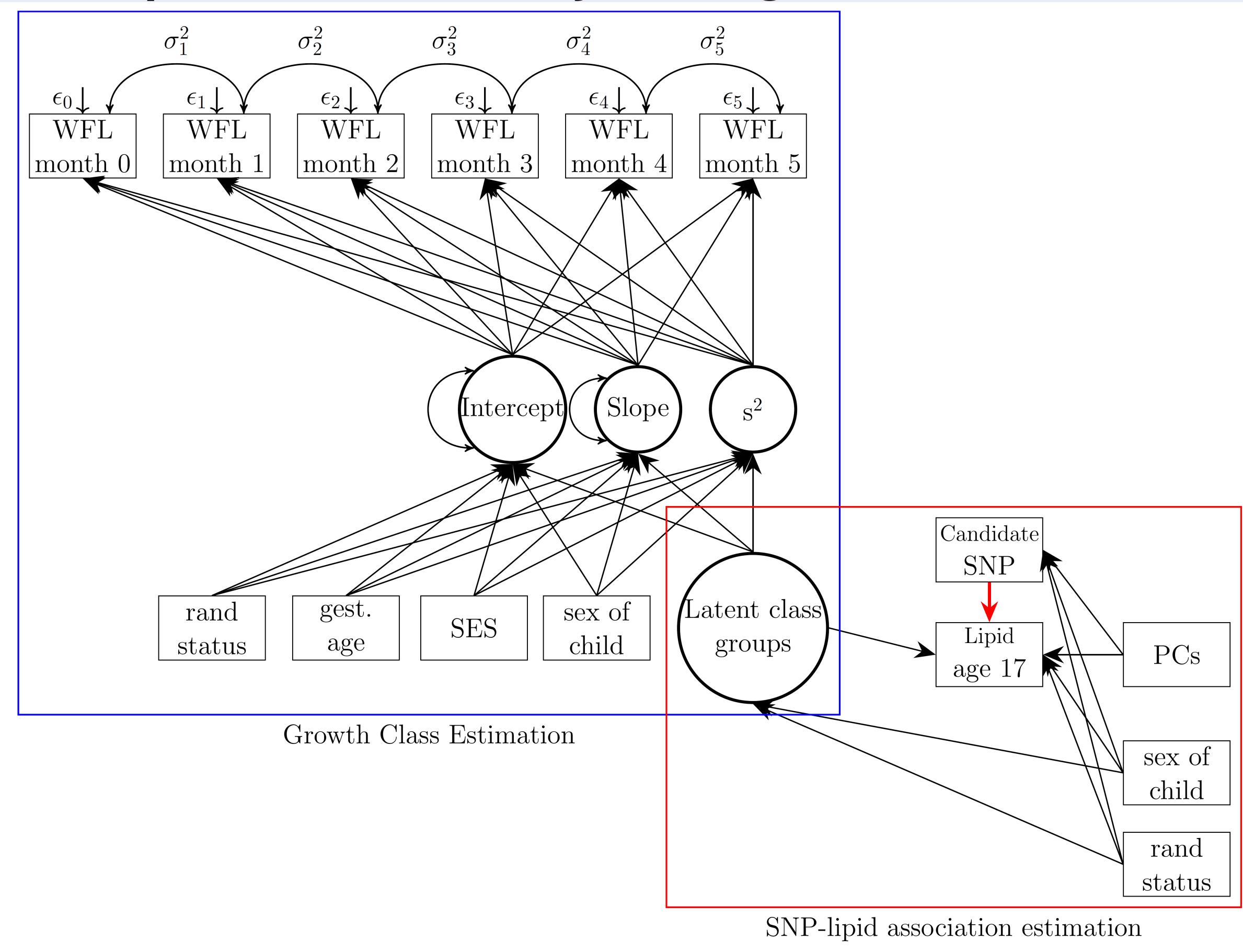
- 1,645 infants were enrolled in SLS between 1991-1996 from low- to middle-income neighborhoods in Santiago, Chile.
- Started as a randomized preventive trial for iron deficiency anemia.
- Participants are from admixed Latino families.
- Analysis includes participants (n=546) with genotyped data and measures during infancy and adolescence.
- Lipid traits measured after overnight fasting at mean age 17 years.

## Methods

### Statistical Methods

1. Find candidate SNPs by screening main effects.
2. Use latent growth mixture models (LGMM) to determine heterogeneous latent growth classes
3. Within each latent class estimate SNP-lipid association
4. Use Bonferroni multiple comparison correction

Figure. Structural equation model used to estimate SNP-lipid associations by latent growth class

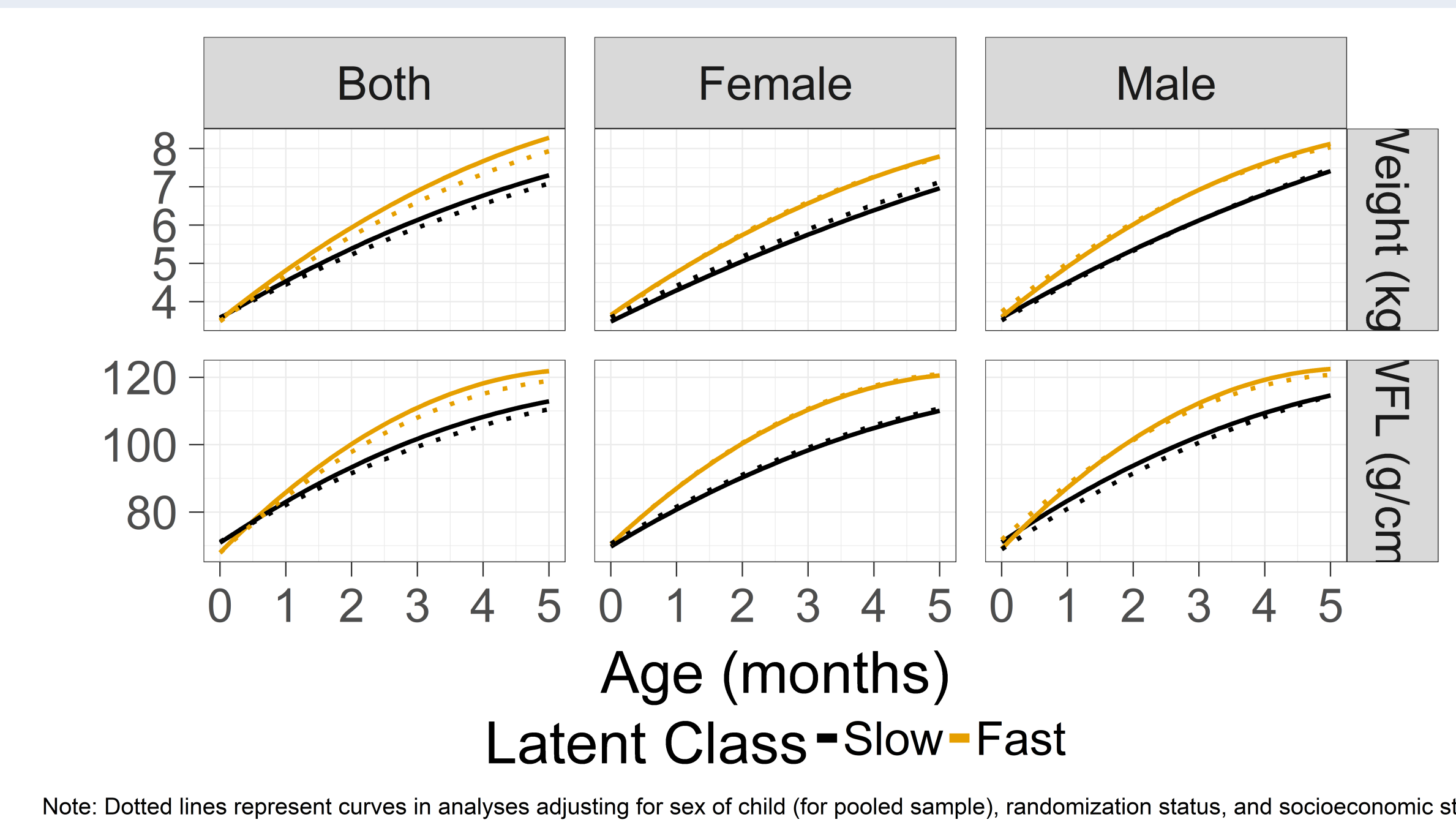


**Effect modifier:** Latent class growth group

**Outcome:** Additive association between SNP-lipid

## Results

**Growth trajectories by sample stratification status and type of trajectory**



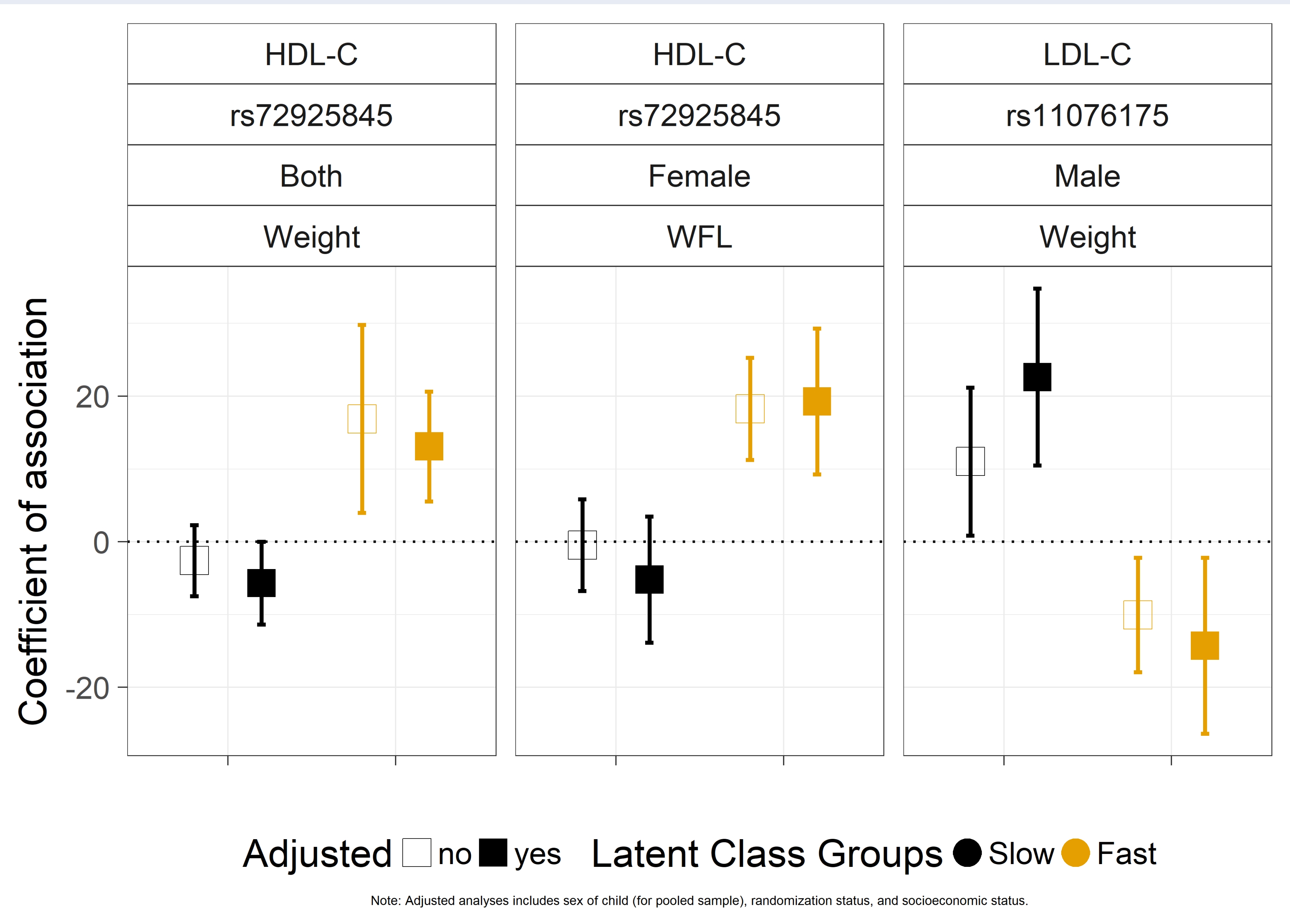
**Latent growth class pairwise differences (95% CI) in coefficient of association between distal lipid outcome (mg/dL) and candidate SNP**

Categories		Low vs High		Overall test: p-value, (Chi-sq, df)	
Sex of child	Outcome Lipid SNP	Not adjusted	Adjusted <sup>a</sup>	Not adjusted	Adjusted <sup>a</sup>
Both	Weight HDL rs72925845	-19.47 (-34.47, -4.48)	<b>-18.78 (-28.98, -8.58)</b>	0.011, (6.48,1)	0.000, (13.03,1)
	Female WFL HDL rs72925845	<b>-18.73 (-28.60, -8.85)</b>	<b>-24.47 (-36.49, -12.46)</b>	0.000, (13.80,1)	0.000, (15.93,1)
Male	Weight LDL rs11076175	21.09 (6.60, 35.57)	<b>36.92 (18.36, 55.48)</b>	0.004, (8.14,1)	0.000, (15.20,1)
	Female LDL rs4420638	-27.84 (-49.20, -6.49)	<b>-51.06 (-75.46, -26.66)</b>	0.011, (6.53,1)	0.000, (16.82,1)

**Note:** Bold values indicate Bonferroni corrected statistical significance at alpha level = 0.05.  
<sup>a</sup> Adjusted for sex of child in pooled sample, randomization status, and socioeconomic status.

## Results, cont...

**Coefficient of SNP-lipid associations by lipid, SNP, sex of child, and type of trajectory**



**SNP background information**

SNP	Chr	Gene	Type	MAF	A1/A2	Reference study	Trait
rs72925845	17	DNAH17	Intronic	0.05	A/G	Ko et al 2014	TG (OR 1.64)
rs11076175	16	CETP	Intronic	0.17	A/G	Zubair et al 2016	HDL (OR 0.36)

Note: A1=coded allele, A2=non-coded allele

- Faster weight (pooled) and WFL (female) growth groups: positive association between rs72925845 and HDL-C.  
⇒ HDL-C inversely associated with cardiovascular disease risk.  
⇒ Expect negative association with HDL-C given established positive association with TG.
- Faster weight growth group: inverse association between rs11076175 and LDL-C.  
⇒ LDL-C positively associated with cardiovascular disease risk.  
⇒ Expect positive association with LDL-C given established inverse association with HDL-C.

## Summary

- Faster growth appears to be protective against a few deleterious SNP-lipid associations.
- Heterogeneity of SNP-lipid association across growth patterns in this period suggests plasticity of response on a molecular level.

