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The genomics of childhood eating behaviors

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Abstract

Eating behaviors may be expressions of genetic risk for obesity and are potential antecedents of later eating disorders. However, childhood eating behaviors are heterogeneous and transient. Here we show associations between polygenic scores for body mass index (BMI-PGS) and anorexia nervosa (AN-PGS) with eating behavior trajectories during the first ten years of life using data from the Avon Longitudinal Study of Parents and Children (ALSPAC), N=7,825. Results indicated

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Competing interests

C.M.B. is a Scientific Advisory Board Member for and grant recipient from Shire Pharmaceuticals Ltd. (Takeda Pharmaceuticals Ltd); a consultant for Idorsia Pharmaceuticals Ltd; and author and royalty recipient from Pearson Plc. All others authors declare no competing interests.

Author contributions

M.H., C.M.B., B.D.S., R.L., R.B-W., and N.M. and devised the research. M.H., M.A., C.H., and B.D.S. analyses the data. All authors (M.H., M.A., C.H., D.S.F., R.L., R.B-W., C.M.B, B.D.S, N.M.) interpreted the data and drafted the manuscript. All authors approved the submitted version and have agreed to be personally accountable for author's own contributions.

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that one standard deviation (SD) increase in the BMI-PGS was associated with a 30-37% increased risk for early- and mid-childhood overeating. In contrast, one SD increase in BMI-PGS was associated with a 20% decrease in risk of persistent high levels of undereating and a 15% decrease in risk of persistent fussy eating. There was no evidence for a significant association between AN-PGS and eating behavior trajectories. Our results support the notion that child eating behavior share common genetic variants associated with BMI.

Introduction

The rise of obesity is well documented, with ~23% of children and ~37% of adults classified as having overweight or obesity[1]. Higher weight has been associated with health consequences such as increased risk of diabetes and mental health problems found across populations[1]. The importance of genetic risk for obesity has been supported by large-scale genome-wide studies, detecting more than 100 associated genetic loci[2]. Despite this evidence, genetic differences cannot account for the rapid rise of obesity over the past decades, and changes in the food environment such as increased portion sizes, availability of energy dense foods, and sedentary work and leisure activities have been suggested as driving this increase[3]. However, despite this obesogenic environment, considerable variability in body size still exists in the population. The behavioral susceptibility theory of obesity attributes the joint contribution of genetic and environmental factors by proposing that eating behaviors, which regulate our food intake, such as overeating, are the behavioral expressions of genetic risk for obesity[4]. Evidence from previous research indicates that eating behaviors in childhood are associated with later higher BMI[5], increased food intake[6], and are heritable in childhood[7] and adulthood[8]. Furthermore, twin analyses revealed a shared genetic etiology between eating behaviors and BMI[9]. In addition, pathway analyses have indicated that genetic loci associated with BMI are primarily expressed in the brain, emphasizing the behavioral component of obesity[10]. We have recently derived longitudinal trajectories of childhood eating behaviors during the first ten years of life. These trajectories highlight the heterogeneity of eating behaviors and emphasize that only a small proportion of children show persistent and elevated levels of overeating, undereating and fussy eating[11] (for an illustration including number of classes, class description, and class size per parent-reported eating behavior see Figure 1 and Supplement Table 1).

Readily available polygenic scores (PGS) afford testing of the hypothesis that genetic variants associated with BMI are also associated with eating behaviors. PGS are derived from aggregating effect sizes of associated common variants across the genome into a single variable that measures genetic liability to a disorder or a trait[12]. In children, one study showed that increased genetic risk for obesity was associated with decreased sensitivity to internal satiety cues[13]. This finding that was not replicated in a smaller subsequent study[14]. In adults, genetic variants associated with BMI were also associated with eating behaviors, such as uncontrolled eating, emotional eating, and responsiveness to external food cues[15–17]. In addition, fussy eating has been identified as another key eating behavior. Childhood fussy eating captures the tendency of children to only eat specific foods, based on flavor, texture, or other reasons as well as an aversion to trying new foods[18]. Fussy eating during childhood and in prospective analyses has been associated with childhood underweight[19] and lower

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vegetable and fruit intake[20]. Fussy eating in childhood has been found to be moderately heritable (46%)[21], but whether fussy eating and BMI share genetic risk is unknown.

In addition to childhood weight and obesity, eating behaviors are of great interest due to their potential role in the development of adolescent eating disorders and their modifiability. Eating disorders are debilitating and complex illnesses that commonly emerge in adolescence and importantly affect individuals across the entire weight spectrum[22]. Eating disorders are characterized by disordered eating behaviors, such as prolonged caloric restriction or binge eating episodes. Hence, the hypothesis has been proposed that childhood eating behaviors, as well as premorbid BMI might be antecedents of adolescent eating disorders[23,24]. We have previously found that sustained fussy eating and undereating in childhood are associated with increased risk of later anorexia nervosa[25]. These data are in accordance with previous findings from smaller studies[26,27]. So far, eight genome-wide significant common genetic variants for anorexia nervosa have been identified[28]. The authors of this GWAS reported a shared genetic etiology of anorexia nervosa and metabolic phenotypes, including glycemic traits, supporting the notion that childhood risk factors affecting the former may also affect the latter[29]. In addition, a polygenic score based on the anorexia nervosa GWAS, has been successfully used to predict symptoms of obsessive-compulsive disorder[30].

For all eating behaviors, the majority of previous research relies on single time point measures of eating behaviors, failing to capture the considerable heterogeneity across developmental stages[31]. Here, we present an exploration of the association between PGS for BMI and anorexia nervosa and longitudinal patterns of eating behaviors in childhood using data from a prospective population-based cohort, ALSPAC. We hypothesize that BMI-PGS will be positively associated with persistent overeating trajectories and negatively associated with trajectories marked by persistent undereating and fussy eating. Conversely, we hypothesize that AN-PGS will be positively associated with undereating and fussy eating, but negatively associated with overeating.

Results

Overall, BMI-PGS was significantly positively associated with overeating (R^2 = 0.014, p <0.001) and negatively associated with undereating (R^2 = 0.004, p<0.001) and fussy eating (R^2 = 0.007, p<0.001), when treated as continuous outcomes (see Supplement Table 2a). The distribution of the standardized BMI-PGS and AN-PGS in each eating behavior group is shown in Figure 2. As hypothesized, higher mean BMI-PGS values were found for children characterized by higher rates of overeating, and lower means for trajectories with high levels of under and fussy eating. The trajectories are illustrated in Figure 1a-c, and the following associations are expressed as relative risk ratios in comparison to a reference trajectory (gray lines). These reference categories were chosen as they represent the most normative behavior, with children rated never to engage in the target behavior. Specifically, one standard deviation increase in BMI-PGS was associated with a 16% (relative risk ratio (RRR) = 1.16, 95%CI 1.08-1.24, p<0.001) increase in the probability of belonging to the low transient overeating trajectory (light blue-colored line Figure 1a, Supplement Table 3). Further, one standard deviation increase in BMI-PGS was associated with a 37%

(RRR=1.37, 95%CI; 1.27-1.47, p<0.001) increase in the probability of belonging to the late increasing group as well as a 30% (RRR=1.30, 95%CI:1.19-1.43, p<0.001) increase in belonging to the early increasing overeating group (green and pink lines in Figure 1a). These two trajectories are characterized by progressively increasing rates of overeating during childhood. This also fits with previous research suggesting a potential feedback loop between child eating behaviors and child weight, whereby children rated to be highly susceptible to food cues in early life have higher weight, which in turn may predict higher food cue susceptibility later[32].

In line with our hypotheses, the BMI-PGS was negatively associated with undereating. A one standard deviation change in BMI-PGS was associated with a 16% (RRR=0.84, 95%CI: 0.78-0.91, p<0.001) decreased risk of belonging to the high transient group (light blue line in Figure 1b, Supplement Table 3) relative to the low stable group (gray line). Additionally, a higher BMI-PGS was associated with 20% (RRR=0.80, 95%CI: 0.68-0.95, p=0.012) lower risk of persistently high levels of undereating (pink line in Figure 1b). The two groups, high decreasing and high stable undereating, stand out as they include the highest probabilities of undereating overall, especially during the first three years of life. These results are in line with our previous findings suggesting that children in these two trajectories had a lower BMI at age 11 years[11]. Furthermore, satiety responsiveness has been shown to be linked to smaller meals sizes in childhood[6], which is a predictor of childhood weight gain[33]. In contrast to overeating, low appetite and strong satiety sensitivity, might be a protective factor, shielding children from the obesogenic environment.

Similarly, BMI-PGS was negatively associated with fussy eating (see Figure 1c). A one standard deviation increase in BMI-PGS was associated with a 14% decrease in risk (RRR=0.86, 95%CI: 0.80-0.93, p<0.001) of belonging to the high decreasing fussy eating trajectory as well as a 15% decrease (RRR=0.85, 95%CI: 0.78-0.93, p<0.001) in risk of belonging to the persistently high fussy eating, relative to the low stable class (Figure 1c, light blue and pink lines; Supplement Table 3). These two trajectories differ from the others, as they are characterized by high levels of fussy eating in early life. In contrast, fussy eating behavior later in childhood might be associated with other genetic variants or a response to exposures to new flavors and textures as part of an expanding diet. We have previously shown that fussy eating during the first 3 years of life is associated with lower BMI at age 11 years[11]. However, the association between fussy eating and measures of body size in childhood has been debated, as fussy children might have limited variety, but could still overconsume their favored foods. A recent review concluded no strong evidence for the impact of child fussy eating on growth or body weight in either direction[34].

The AN-PGS was not statistically significantly associated with eating behavior trajectories (see Supplement Table 2b). However, inspecting Figure 2, the pattern of mean scores of AN-PGS differed across the eating behavior trajectories, with differences being as expected in opposite directions for overeating and fussy eating. A one standard deviation change in AN-PGS was associated with a 8% decrease in likelihood of being assigned to the low transient group of overeating (RRR=0.92, 95% CI: 0.86- 0.98, p=0.011), marked by overeating in early life (light blue line, Figure 1a). In contrast, one standard deviation increase in AN-PGS was suggestive of an 8% increase (RRR=1.08, 95%CI: 0.99-1.18, p=0.097) in belonging to

the persistent high stable fussy eaters (Figure 1c, pink line). These results are in line with our previous study highlighting the association between persistent fussy eating in childhood and increased risk for AN in adolescence[25]. We also examined the joint associations of BMI-PGS and AN-PGS with the eating behavior trajectories (Supplement Table 4). Results did not differ from the primary analyses that treated them separately. The explanatory power of PGS is dependent on the sample size of the discovery GWAS[35]. For BMI, due to its straightforward and routine collection, GWAS sample sizes have exceeded 700,000 individuals[2], whereas for AN the most recent GWAS included ~17,000 cases and 55,000 controls[28]. This difference in sample size might explain the largely null associations between the AN-PGS and the eating behavior trajectories in these analyses. As discovery GWAS sample sizes continue to grow, future analyses will have increased power to detect the underlying associations between genetic liability for AN and associated eating behaviors.

Discussion

In addition to genetics, environmental factors, such as parental feeding behaviors and parental eating behaviors, are proposed to be involved in the etiology of childhood eating behaviors. Parents engage in specific feeding strategies to regulate their child's eating and weight, as well as model eating styles. However, the direction of effect between parental feeding and child eating is not straightforward. Parental feeding strategies have been posited to be a consequence of the child's eating behavior[36], causal to later child eating[37], and reciprocally related[38]. An exploration of the origins of parental feeding using genetically informative methods, suggested that parental feeding in childhood was moderately heritable, and that the child's BMI-PGS was positively longitudinally associated with parental restrictive feeding.[39]. These results are consistent with an evocative gene-environment correlation, whereby the genetic liability for higher BMI in the child elicits parental restrictive feeding. In addition, it is important to note that parental feeding strategies have been found to vary across cultural backgrounds, potentially contributing to differences in obesity risk across cultures[40,41]. Recent evidence has suggested that children from poorer families showed greater increases of emotional eating and food responsiveness between 16 months and five years[42]. In context with our findings, it becomes apparent that child eating behaviors are influenced by genetic and environmental factors, and future research should aim to investigate should aim to investigate the manner in which they act and co-act. Additionally, future research is needed to elucidate the specific mechanisms, by which genetic liability influences child eating behavior. One potential mediating factor could be birthweight, which could lie on the causal pathway from genetic liability and early life eating behaviors.

Our study is subject to limitations. First, childhood eating behaviors were parent-reported, raising the potential of reporter bias. This bias could be particularly evident in older children, who eat a substantial number of meals away from parental oversight. However, young children are not able to report their own eating behaviors reliably and behavioral observations are not feasible in large-scale data collections, like this study, whose sample size exceeds many other investigations using PGS. Therefore, for large population cohorts like ALSPAC, parent-reported questionnaires of child eating behaviors remain the most efficient and pragmatic solution. Second, it is important to acknowledge that derived

trajectories using latent class growth analysis, or any similar method, are descriptive and population specific. The latent class growth models used to identify the trajectories only included measures of eating behavior. It is possible to fit more complex specifications, including other factors and time-varying confounders such as school performance. However, this is out of scope for the analyses presented here. In addition, future research should aim to replicate this work using independent samples for, respectively, the calculation of the PGS and the derivation of the eating behavior trajectories. Apart from BMI and AN-PGS, other psychiatric and metabolic traits might be implicated in the development of eating behaviors. However, we chose a theoretical and hypothesis driven approach, focusing only on genetic liability for BMI and AN for the present study. Future work might broaden the scope by including polygenic scores for other phenotypes, likely to be relevant to eating behaviors such as anxiety or schizophrenia. Due to limitations of the polygenic scoring software, we needed to fit linear models, treating the trajectories as continuous variables in the first instance, with values corresponding to the intercept of the trajectories. Of course, this is not an ideal solution, as the trajectories cross over time, and just focusing on their starting point does not represent severity. However, we respected their unordered nature in the second step, treating them as distinct categories in the main analyses. This two-step approach was taken, as it was the most pragmatic and feasible solution; however, a potential misspecification of the models might have resulted in some bias. Finally, the power of polygenic scores is dependent on the sample size of their underlying discovery GWAS. In this case, the sample size of the BMI and AN GWAS differed substantially, and the comparatively smaller sample size for AN is likely to have led to underpowered AN-PGS. In order to quantify the difference in power between the AN-PGS and BMI-PGS we have estimated their statistical power using the AVENGEME package[43] at different expected levels of genetic covariance between the discovery and target sample, see Supplement Table 5 and Supplement Figure 1.

In summary, this study provides evidence that common genetic variants associated with BMI are also associated with eating behaviors trajectories in childhood, supporting the behavioral susceptibility theory of obesity[4]. Our study improves on previous work, due to its large sample size and its use of longitudinal trajectories, capturing the transitional nature of eating behaviors across development in childhood. The findings highlight that individuals characterized with a genomic propensity for higher BMI may be more vulnerable to an obesogenic environment, as they are more likely to overeat persistently and increasingly during the first 10 years of life. This link between genetic risk and overeating in childhood might be specifically powerful, given the current obesogenic environment that is defined by substantially larger portion sizes and increased availability of low-cost highly palatable food creating an environment for children to overeat[3]. This overconsumption allows a child's underlying genetic propensity for a higher BMI to be fully expressed and contributes to the development of an obese phenotype[3]. The link between genetic liability for AN and eating behavior trajectories is less clear, but our results are indicative of a potential shared genetic etiology of AN and persistent fussy eating in childhood.

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Methods

Participants

Data were from ALSPAC, a population based, longitudinal cohort of mothers and their children born in the southwest of England[44]. All pregnant women expected to give birth between the 1st April 1991 and 31st December 1992 were invited to enroll in the study. From all pregnancies (n = 14,676), 14,451 pregnant women decided to take part, and 13,988 of their children were alive at 1 year. In order to guarantee for independence of data, only one child per multiple birth per family were included (N=203 sets). Please note that the study website contains details of all the data that is available through a fully searchable data dictionary and variable search tool. (www.bristol.ac.uk/alspac/researchers/our-data). Ethical approval for the study was obtained from the ALSPAC Ethics and Law Committee and the Local Research Ethics Committees. Consent for biological samples has been collected in accordance with the Human Tissue Act (2004).

Measures

The following characteristics of the sample are presented in Supplement Table 1, alongside the distribution of eating behavior groups, (i) socioeconomic position of the family, approximated by maternal education status (A-Levels or higher, lower than A-Levels; A-Levels are needed to enroll in university in the UK); (ii) maternal age at birth; (iii) size at birth (gestational age and birthweight).

Eating behaviors

Parents rated their children's eating behavior when their children were 1.3 yrs, 2 yrs, 3.2 yrs, 4.6 yrs, 5.5 yrs, 6.9 yrs, 8.7 yrs and 9.6 yrs old. Parents answered five questions at each wave indicating how worried they were about their child's overeating, undereating, and three questions on fussy eating (being choosy, refusing food, and general feeding difficulties). Response options for all questions were: "did not happen", "happened, but not worried", "a bit/greatly worried". Latent class growth analyses were used to derive longitudinal trajectories of child eating behavior[11]. Briefly, trajectories were derived using latent class growth analyses using full information maximum likelihood. Data were parent-reported child eating behaviors measured at 8 time points between 1.3 and 9 years. Latent class growth analyses included covariates indexing the social class of the families (maternal age at birth, maternal education, and manual or non-manual labor of the highest earner of the family). Model fit of increasing number of assumed classes were compared against each other using following indicators: Akaike's Information Criterion, Bayesian Information Criterion, adjusted for sample size Bayesian Information Criterion. Entropy, class size and interpretability were also taken into consideration when selecting the best fitting model. This process identified 4 classes of overeating and 6 classes for undereating and fussy eating, which were then carried over for the analyses presented here (Figure 1a-c). The trajectories were named to reflect their shape, e.g. "low stable" indicating that parents consistently rated that the behavior was not present, whereas "high stable" indicated that parents consistently rated that they were worried about their children's' eating behavior across time. Trajectories that were characterized by changes in parental report across time were summarized by describing their start point at first measurement followed by their shape, e.g. "high

decreasing" describes a trajectory in which parents initially reported the presence of the eating behavior, as well as being very worried about their child's eating behavior but this decreased over time. In contrast, "low increasing" describes a trajectory a low starting point and an increase over time. This study included participants who had data on eating behavior trajectories and were genotyped (N=7,825).

Genotyping

Genotype data were available for 9,915 children out of the 15,247 ALSPAC participants. Participants were genotyped on the Illumina HumanHap550 quad chip. Individuals with >3% individual missingness, insufficient sample replication (identity by descent < 0.1), where sex was mismatched, and non-European ancestry defined by multi-dimensional scaling using the HapMap Phase II release 22 reference populations were excluded. SNPs with a minor allele frequency (MAF) <1%, call rate < 95%, or a departure from the Hardy–Weinberg equilibrium (P value < 5 x 10^{-7}) were removed. Imputation was carried out with Impute3 using the Haplotpye Reference Consortium 1.0 reference panel with prior phasing using ShapeIT (v2.r644). Post-imputation SNPs with MAF <1%, INFO score <0.8, and not confirming to Hardy-Weinberg equilibrium (P < 5 × 10-7) were removed. After data cleaning, 8,654 individuals (4,225 females and 4,429 males) and 4,054,653 SNPs remained for analyses.

Polygenic score (PGS) calculations and multinomial regression models

The BMI-PGS was calculated based on summary statistics from the GIANT consortium (https://portals.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium). We used the updated Meta-analysis Locke et al + UKBiobank 2018. We used the corrected sumstats, which were published on the website after June 25, 2018. The AN-PGS was based on the summary statistics of the second PGC-ED GWAS of AN[29]. The calculation, application, and evaluation of the PGS was carried out with PRSice (2.1.3 beta; github.com/choishingwan/PGSice/)[45]. PRSice relies on PLINK to carry out necessary cleaning steps prior to PGS calculation[45,46]. Strand-ambiguous SNPs were removed prior to the risk scoring. A total of 1,488,001 SNPs were present in both the discovery and in the target cohort. Clumping was applied to extract independent SNPs according to linkage disequilibrium and P-value: the SNP with the smallest P-value in each 250 kilobase window was retained and all those in linkage disequilibrium (r^2 > 0.1) with this SNP were removed. Furthermore, individuals that are closely related to each other defined as a phi hat > 0.2 (calculated using PLINK v1.90b3y 64-bit, 4 Nov 2015) were removed; this meant removal of any duplicates or monozygotic twins, first-degree relatives (i.e. parent-offspring and full siblings), and second-degree relatives (i.e., half-siblings, uncles, aunts, grandparents, and double cousins). Only one individual of each pair of related individuals was removed at random. This resulted in the removal of 75 individuals. The following analyses were conducted in two stages: (1) PGS were calculated using the high-resolution scoring (e.g., across a large number of P-value thresholds) option in PRSice, treating the eating behavior trajectories as continuous outcomes to identify the p-value threshold at which the PGS is optimally associated with the outcome. (2) Then the derived PGS were used as independent variables in the multinomial regression models. The models were fitted to estimate the association between BMI-PGS, AN-PGS, and membership of eating behavior trajectory.

Estimates are reported as relative risk ratios (RRR), which indicate the risk of being assigned to one trajectory in comparison to the normative reference trajectory (gray lines in Figure 1a-c). Multinomial regression models are the most appropriate, as the trajectories of eating behavior are distinct categories, and cannot be assumed to be ordinal or continuous variables. Trajectories with no reported overeating, undereating, or fussy eating were used as the reference categories for the regression analyses. This way we were able to identify the extent to which a change in polygenic score was associated with the relative risk of being assigned to one of the other overeating, undereating, and fussy eating trajectories in reference to the normative trajectory. Regarding covariates, by definition polygenic scores are randomly distributed in the population at birth, and all commonly used covariates (birthweight, gestational age etc.) would conceptually lie on the causal pathway between exposure (polygenic score) and outcome (eating behavior trajectory), and hence were not included in these analyses. One possibility is that polygenic scores are not evenly distributed across different strata of socio-economic position, as the discovery GWASs were not adjusted for socio-economic status. Therefore, we conducted sensitivity analyses including maternal education as a covariate. Maternal education was a binary variable indicating if mothers had completed their A-Levels (UK requirement to attend university). Results of these sensitivity analyses are listed in Supplement Table 6. In order to, account for multiple testing (26 tests), a stringent p-value threshold of 0.002 was set, using Bonferroni correction; 0.05 / 26 = 0.002. Tests were two-tailed.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Code availability

All code associated with the analyses is available upon request.

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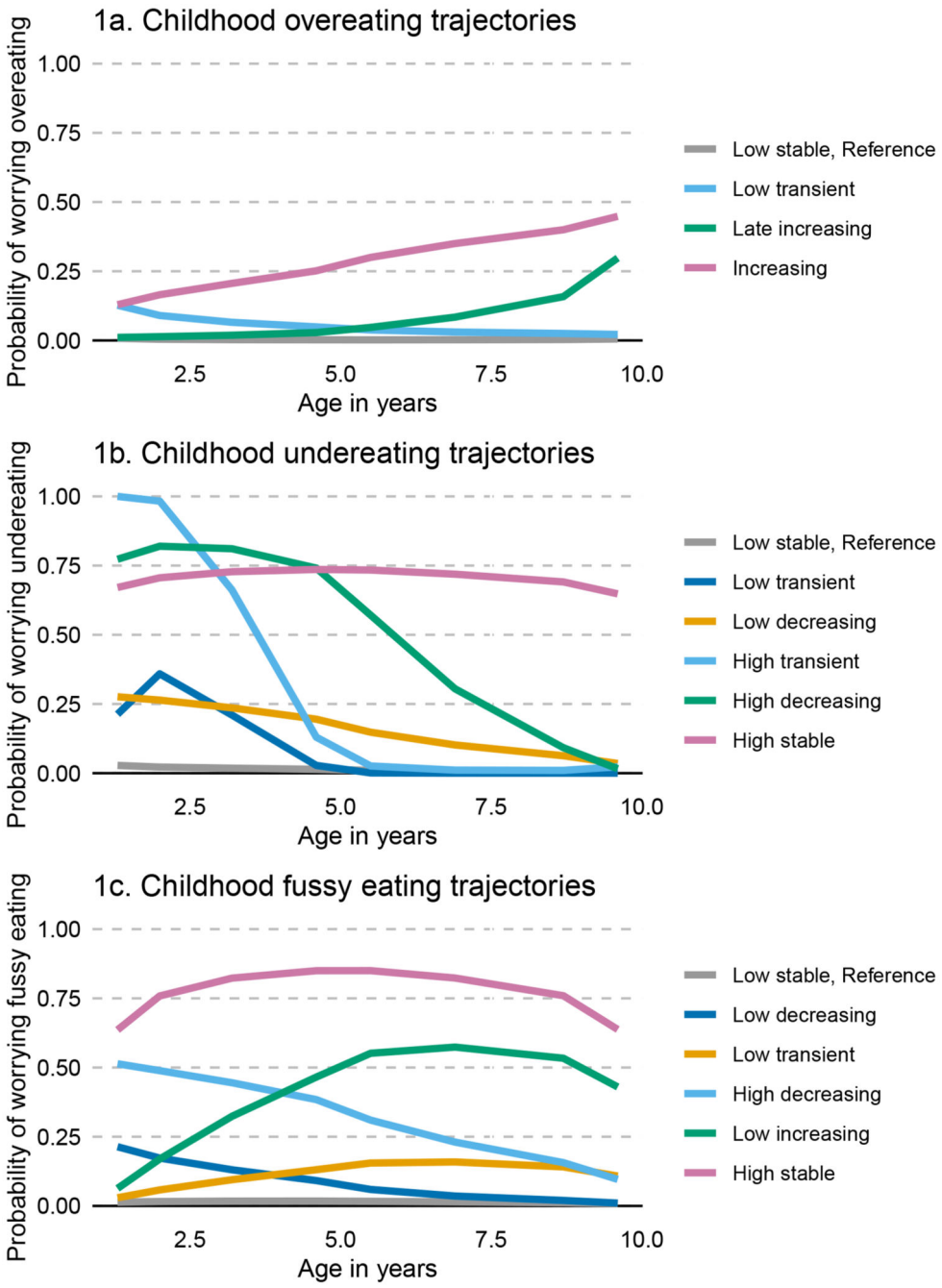

Figure 1. a-c Eating behavior trajectories during the first ten years of life, total N=7,825.

(A) Childhood overeating trajectories. Low stable (N=5374), Reference trajectory;
Low transient (N=1091), BMI-PGS relative risk ratio (RRR) = 1.16 (95% CI: 1.08 – 1.23, p <0.001) and AN-PGS RRR = 0.92 (95% CI: 0.86 – 0.98, p = 0.011);
Late increasing (N=883), BMI-PGS RRR=1.37 (95%CI: 1.27-1.47, p<0.001) and AN-PGS RRR=0.94 (95%CI:0.87-1.01, p=0.072);
Increasing (N=477), BMI-PGS RRR=1.30 (95%CI: 1.19-1.43, p<0.001) and AN-PGS RRR=0.96 (95%CI: 0.87-1.05, p=0.353)

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(B) Childhood undereating trajectories. Low stable (N= 1913), Reference trajectory;
Low transient (N=2906), BMI-PGS RRR = 0.91 (95%CI: 0.87- 0.97, p=0.002) and AN-PGS RRR = 1.01 (95%CI: 0.96- 1.07, p=0.630);
Low decreasing (N=1613); BMI-PGS RRR = 0.93 (95%CI: 0.87- 0.99, p=0.027) and AN-PGS RRR = 0.96 (95%CI: 0.90-1.02, p=0.202);
High transient (N=989); BMI-PGS RRR = 0.84 (95%CI: 0.78- 0.91, p<0.001) and AN-PGS RRR = 0.95 (95%CI: 0.88- 1.02, p=0.166);
High stable (N=141); BMI-PGS RRR = 0.80 (95%CI: 0.68- 0.95, p=0.012) and AN-PGS RRR = 0.93 (95%CI: 0.79- 1.11, p=0.441)
(C) Childhood fussy eating trajectories. Low stable (N=1969), Reference trajectory
Low decreasing (N=1142); BMI-PGS RRR= 1.00 (95%CI: 0.93-1.01, p=0.993) and AN-PGS RRR = 0.99 (95%CI: 0.91- 1.06, p=0.706);
Low transient (N=2136); BMI-PGS RRR = 0.99 (95%CI: 0.93-1.06, p=0.796) and AN-PGS RRR = 0.99 (95%CI: 0.93- 1.06, p=0.826);
High decreasing (N=1112); BMI-PGS RRR = 0.86 (95%CI: 0.80- 0.93, p<0.001) and AN-PGS RRR = 1.05 (95%CI: 0.97- 1.13, p=0.218);
Low increasing (N=1040); BMI-PGS RRR = 0.93 (95%CI: 0.86- 1.00, p=0.060) and AN-PGS RRR = 0.97 (95%CI: 0.90-1.05, p=0.486);
High stable (N=699), BMI-PGS RRR = 0.85 (95%CI: 0.78- 0.93, p<0.001) and AN-PGS RRR = 1.08 (95%CI: 0.99-1.18, p=0.097)

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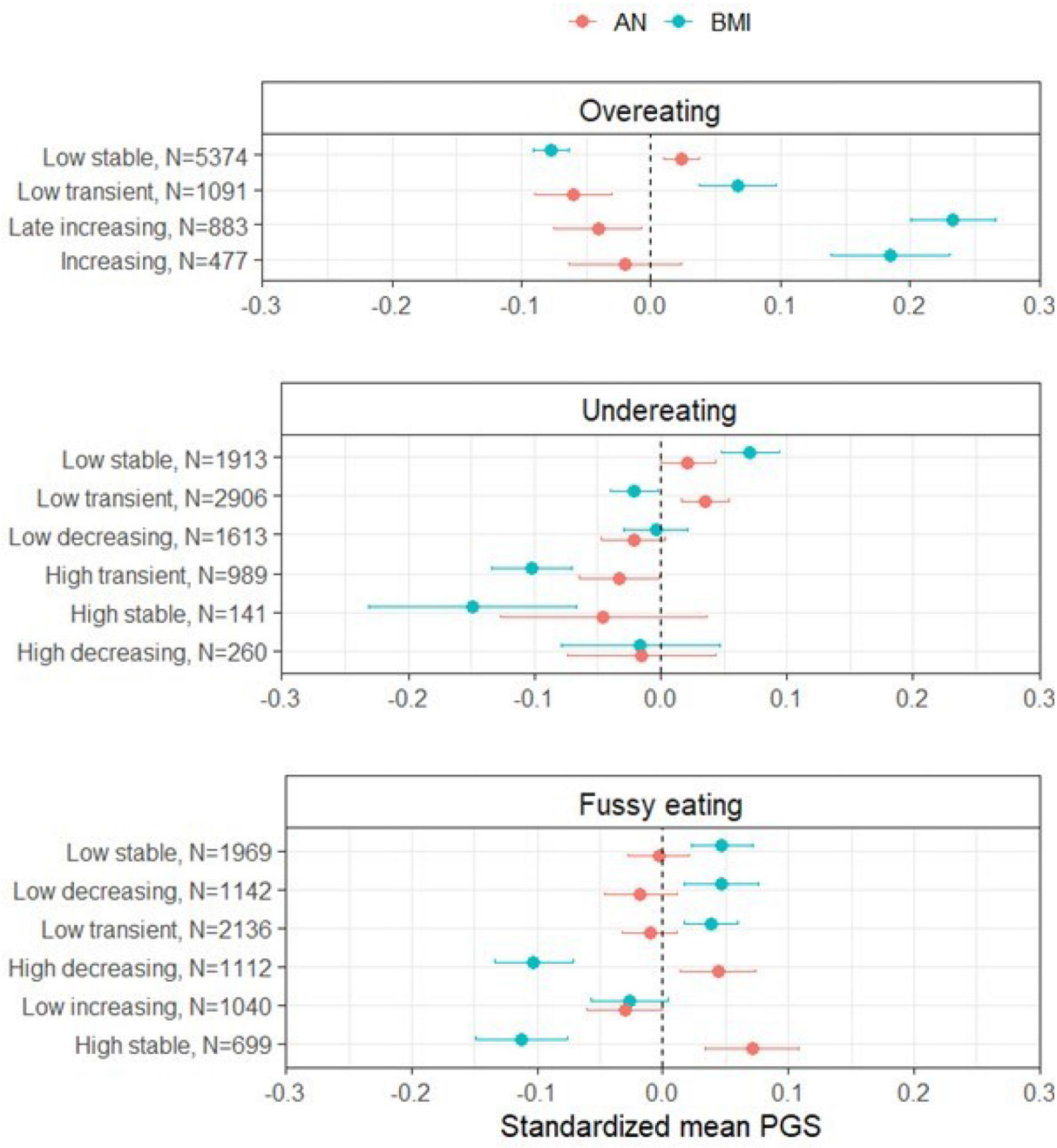

Figure 2.

Mean of standardized BMI-PGS (in blue), AN-PGS (in red), and standard error per child eating behavior group (N= 7,825)