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Predicted DRD4 prefrontal gene expression moderates snack intake and stress perception in response to the environment in adolescents

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Abstract

Body weight is substantially determined by eating behaviors, which are themselves driven by biological factors interacting with the environment. Previous studies in young children suggest that genetic influences on dopamine function may confer differential susceptibility to the environment in such a way that increases behavioral obesity risk in a lower socioeconomic status (SES) environment but decreases it in a higher SES environment. We aimed to test if this pattern of effect could also be observed in adolescence, another critical period for development in brain and behavior, using a novel measure of predicted expression of the dopamine receptor 4 (DRD4) gene in prefrontal cortex. In a sample of 76 adolescents (37 boys and 39 girls from Baltimore, Maryland/US, aged 14-18y), we estimated individual levels of DRD4 gene expression (PredDRD4) in prefrontal cortex from individual genomic data using PrediXcan, and tested interactions with a composite SES score derived from their annual household income, maternal education, food insecurity, perceived resource availability, and receipt of public assistance. Primary outcomes were snack intake during a multiitem ad libitum meal test, and food-related impulsivity assessed using a food-adapted go/ no-go task. A linear regression model adjusted for sex, BMI z-score, and genetic ethnicity demonstrated a PredDRD4 by composite SES score interaction for snack intake (p = 0.009), such that adolescents who had lower PredDRD4 levels exhibited greater snack

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intake in the lower SES group, but lesser snack intake in the higher SES group. Exploratory analysis revealed a similar pattern for scores on the Perceived Stress Scale (p = 0.001) such that the low PredDRD4 group reported higher stress in the lower SES group, but less stress in the higher SES group, suggesting that PredDRD4 may act in part by affecting perceptions of the environment. These results are consistent with a differential susceptibility model in which genes influencing environmental responsiveness interact with environments varying in obesogenicity to confer behavioral obesity risk in a less favorable environment, but behavioral obesity protection in a favorable one.

Introduction

We are amidst an obesity epidemic [1] but not everyone becomes obese [2]. Part of this variability is attributable to environmental factors. For example, we know that individuals with lower socioeconomic status (SES), are generally more prone to obesity [3, 4], but there is still great heterogeneity in how individuals respond to the distinct environmental conditions that promote obesity. Some of this variation is likely due to genetic and related downstream biological factors that influence behavioral responses to the food environment [5–8]. A potential biological moderator of environmental influences is the mesocorticolimbic dopamine system. Dopamine is known to play a role in modulating general perceptual sensitivity, where extensive dopaminergic innervation of brain regulatory systems in ascending limbic-frontal circuits as well as descending and reciprocal striatal-thalamocortical circuits [9], may be especially sensitive to environmental changes [10].

In studies of young children, we have found evidence suggesting that genes influencing brain dopamine function may moderate environmental responses. For example, we previously demonstrated that 4-year old girls who were carriers of a hypofunctional polymorphism of the Dopamine Receptor 4 (7 tandem repeat of 48-base-pair region, in the third exon of the DRD4 gene, or DRD47R [11] showed greater sensitivity to environmental conditions such that they had a higher preference for fat when living in a low SES environment, but a diminished preference when living in a high SES environment as compared to non-carriers of the 7-repeat polymorphism^[12]. In line with this finding, we have shown that carriers of this variant had increased likelihood of developing obesity at 4 years of age if exposed to lower levels of maternal sensitivity as toddlers [6]. Recently we have demonstrated that genetically regulated expression of the DRD4 gene (predDRD4) in prefrontal cortex interacts with the postnatal environment to predict emotional eating in 4yo, and desire to drink in 5yo children in two independent cohorts[13]. The above results may be thought of as an extension of Belsky's Differential Susceptibility Hypothesis [14, 15] into the obesity realm, helping to explain individual differences in food preferences and food choices in response to different environments[5]. According to the Differential Susceptibility Hypothesis, genes previously thought of as "vulnerability" genes are in fact developmental plasticity genes that promote greater individual responsiveness to *both* positive (e.g. healthy fetal environment, warm/sensitive maternal care, high socioeconomic status) and negative (e.g. altered fetal environment, low maternal sensitivity, low socioeconomic status) environmental contexts [15].

Adolescence is a critical period for obesity development [16–18], and for the development of brain systems serving reward seeking behaviors and cognitive control [19]–processes that may underpin excessive consumption of palatable high fat and high sugar "junk" foods. Consistent with the Differential Susceptibility Hypothesis, candidate plasticity genes (such as

DAT1, *DRD2*, *DRD4* 5HTTLPR, *COMT* and *MAOA*) have been shown to moderate the link between parenting quality and male adolescent self-regulation and impulsivity [15]. However, the Differential Susceptibility Hypothesis has yet to be tested within a male and female adolescent population in the context of obesity and associated behavioral factors, the latter of which may be most informative for targeted prevention.

Traditional candidate gene and genome-wide association studies probing human brain and behavior responses to environment have been very useful to understand gene-environment relationships relevant to many complex behaviors. However, since genetic data reflects code that is present in all cells of an organism, it conveys limited information regarding the genetically-driven biological mechanisms that influence each cell, tissue and system and ultimately determine phenotypes of interest[20]. This organ/tissue specificity is especially important for the study of phenotypes resulting from the functions of specific brain areas. Therefore, the aim of this study was to use a novel genomic approach that imputes the gene expression of DRD4 in prefrontal cortex using individual level genomic information^[21] to evaluate how genetically-influenced prefrontal brain dopamine function interacts with environmental obesity risk (captured by SES) to influence indices of behavioral (multi-item ad libitum meal intake) and neurobehavioral (food go no go task performance) obesity risk in adolescents. Also, because eating behavior and adiposity can be influenced by stress [22, 23], and because plasticity genes may indirectly impact eating behavior by altering the general perception of the environment, we conducted an exploratory analysis of differential susceptibility using perceptions of environmental stress as a secondary outcome.

Methods

Participants and procedures

Participants were part of a larger study investigating the neurobehavioral basis of obesity and familial obesity risk. Adolescents and their mothers were recruited via flyers posted at the Johns Hopkins Hospital in Baltimore, MD and online advertisements. For adolescents, exclusion criteria included being outside our target age range of 14–18 years old, current diagnosis of a significant health problem (e.g. eating disorder, learning disability), use of medication affecting appetite and body weight (e.g. stimulants, anti-depressants), participation in a structured weight loss program, medical contraindications to MRI (e.g. metal implants), and food allergies. For mothers, exclusion criteria included current pregnancy, and excessive smoking, recreational drug use or alcohol intake. Adolescent-mother dyads were required to speak English fluently. The sample was balanced based on current weight status and familial obesity risk of the adolescents, resulting in 3 groups: i) a lean low-risk group (adolescent <85th BMI centile, mother BMI <25), ii) a lean high-risk group (adolescent <85th BMI centile, no requirement for maternal weight group).

Potential participants completed an initial telephone screening and eligible participants were then tested in a fed and fasted condition (counterbalanced across subjects). For the fed condition, participants consumed 474 ml/480 kcal Boost c.3.30pm, completed an MRI scan c.4pm, then underwent a multi-item ad libitum buffet meal test c. 5pm. For the fasted condition, participants consumed 474 ml/0 kcal water before the MRI scan and meal test. During the initial consultation, a total of 98 adolescents were consented/assented (parental consent and child assent for <18 y, self-consent for 18y or over). Fifteen completed neither test day and were excluded from further analysis. Of the remaining 83 participants, we excluded adolescent-mother pairs with incomplete socioeconomic information or missing meal intake data, resulting in a final sample of 76 adolescent-mother pairs who completed the initial

consultation and at least one of the test days (no data were imputed). Baseline characteristics are given in Table 1. Demographic characteristics (child age, child sex, child race, child BMI z-score, and household income) were similar between the entire consented (n = 98) and final (n = 76) samples. However, maternal education was significantly lower in the entire sample (n = 98) compared to the final sample (p = 0.015), i.e. 14.4% had less than high school education in the entire sample vs. 11.8% in the final sample. This study was approved by the Johns Hopkins University School of Medicine Institutional Review Board.

Measures

Anthropometric measures. Body weight and fat percentage were assessed at the initial consultation using a SC-331S Total Body Composition Analyzer (TANITA Corp., Tokyo), which measures body weight and estimates fat percentage via Bio-Impedance Analysis. Height was assessed using a wall-mounted stadiometer after shoe removal. BMI values (kg/m²) were calculated, and BMI z scores and percentiles were derived for adolescents, based on Center for Disease Control (CDC) growth charts from 2000 [24]. For adolescents, those under the 85th percentile were classified as normal-weight, those between the 85th and 95th percentiles as overweight, and those at the 95th percentile or above as obese.

	Mean (or N)	SD (or %)
Age (years)	16.1	(1.2)
Female	39	(51.3)
BMI	24.2	(6.3)
BMI z-score	0.54	(1.23)
BMI percentile	63.1	(33.3)
Weight Group		
Lean	45	(59.2)
Overweight	13	(17.1)
Obese	18	(23.7)
Familial Risk Group		
Lean-LR	22	(28.9)
Lean-HR	23	(30.3)
Overweight	31	(40.8)
Race		
White	42	(55.3)
Black/African-American	25	(32.9)
Asian	2	(2.6)
More than one race	6	(7.9)
Other/Unknown	1	(1.3)
Annual Household Income		
0-49,999	26	(34.2)
50,000-79,999	20	(26.3)
80,000 or more	30	(39.5)
Maternal Education Level		
High school graduate or less	9	(11.8)
College or equivalent training	42	(55.3)
Post graduate	25	(32.9)
Food Security		
Yes	58	(76.3)

Table 1.	Sample	baseline	characteristics	(N = 76).	
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Food go/no-go task. To assess food-related impulsivity, a food go/no go task was administered. This task was adapted from an existing simple go/no go task[25]. Participants were instructed to press a button as quickly as possible in response to a picture of a low energy-density food (broccoli; 'go' trial) but to inhibit pressing the button in response to a picture of a high energy-density food (French fries or ice cream, depending on preference as stated on day of testing; 'no-go' trial). Stimuli were presented for 300 ms, followed by a fixation cross (1,500 ms). The task was divided into two 4-min 7 sec runs, each with 78 go and 26 no-go trials. 'Go' trials were presented in consecutive groups of 1–6, while 'no-go' trials never appeared more than twice in a row. Thus, 'no-go' stimuli were effectively jittered, with a varying number of preceding go stimuli. Each run began and ended with a 10-s rest period; four 10-s rest periods also occurred at irregular intervals during each run. Reaction times (RTs) were recorded during the entire trial length.

Multi-item ad-libitum buffet meal. To assess eating behavior in response to an environmental challenge, a multi-item ad libitum buffet meal was administered. Adolescents were brought into a room in which they were presented with an ad-libitum buffet meal, including three 12" pizzas cut in 12 slices [plain cheese (c. 790 g, 2009 kcal), vegetable (c. 940 g, 2050 kcal), pepperoni (c. 825 g, 2199 kcal)], hummus (c. 283 g, 700 kcal), ranch dressing (c. 224 g, 880 kcal), vanilla ice cream (c. 250 g, 530 kcal), chocolate chip cookies (c. 200 g, 970 kcal), fudge brownies (c. 350 g, 1200 kcal), M&Ms (c. 200 g, 1000 kcal), Ruffles potato chips (c. 200 g, 1143 kcal), Cheetos (c. 250 g, 1339 kcal), baby carrots (c. 250 g, 103 kcal), cherry tomatoes (c. 300 g, 55 kcal), celery sticks (c. 200 g, 32 kcal), grapes (c. 600 g, 414 kcal), water (20 fl oz, 0 kcal), regular Coke (20 fl oz, 240 kcal) and diet Coke (20 fl oz, 11 kcal). Adolescents were instructed to eat as much as they wanted. They were informed that they would be left alone for 30 minutes to eat but they could step out of the room if they were finished sooner or could request for extra time. To encourage ad libitum eating, participants were asked to "imagine this meal is your regular dinner" and "imagine not eating for 4-5 hours following this meal". Each food was weighed separately prior to and following the meal (out of sight of the participant) to determine amount consumed. The ad libitum meal was preceded and followed by verbal appetite and stress ratings (e.g. hunger, fullness, stress) on 0-100 VAS scale.

For the purposes of the current report we focus on task and meal data from the fed condition only. Our rationale was that fasting could mask gene-by-environment interactions by inducing a homeostatic hunger state across all participants, thus reducing individual variation in dependent variables of interest. The neuroimaging data are the subject of a separate investigation and will be reported elsewhere.

SES composite score. To assess socioeconomic environment, we used a combination of variables collected as part of the larger study. Mothers completed a demographic questionnaire in which they reported their education level (Less than high school, High school graduate or GED, Post high school training other than college, Some college, Graduated from college, Post graduate), annual household income (10 categories between \$0–19,000 and \$100,000 or more), and their own and their child's ethnicity. They also completed the Household Food Security Survey [26], a questionnaire assessing perceived resource availability [27], and the Project F-EAT survey, which contained a question assessing whether families receive public assistance [28]. Variables used for the composite score were: annual household income, maternal education, food insecurity, perceived resource availability, and receipt of public assistance (see below for details). These variables were selected a priori and represented the entirety of the variables assessing socioeconomic status in our sample.

Perceived stress. The Perceived Stress Scale (PSS) [29], a widely used psychological instrument assessing the degree to which situations in one's life are perceived as stressful, was administered. The PSS is a 10-item questionnaire using 5-point ratings (0 = Never, 1 = Almost

Never, 2 = Sometimes, 3 = Fairly Often, 4 = Very Often). Responses across the 10 PSS items were summed to create a total score such that higher values indicated more perceived stress in daily life (Cronbach's alpha = 0.868).

Predicted prefrontal DRD4 expression. DNA for the adolescents was extracted from saliva samples, obtained using Oragene OG500 (DNAGenotek, Ottawa, Canada) saliva collection kits. Expression of DRD4 in prefrontal brain regions was computed using a machine learning prediction method (PrediXcan) [21] that estimates tissue-specific gene expression based on individual-level genotype data. Genotyping for this cohort was conducted using the genome-wide Illumina Infinium Multi-Ethnic Global Array (MEGA), with clusters for the SNPs being defined using GenomeStudio version 2011.1 and GenTrain 1.0. Quality control on the genotyping calls has been previously described [30]. SNPs were verified for a genotyping rate \geq 95% and no deviation from Hardy–Weinberg equilibrium (P < 0.001), and minor allele frequency >0.05, using PLINK [31, 32]. After quality control procedures and imputation, 1,767,525 SNPs were available for use in PrediXcan. Details on how the PrediXcan method creates prediction models of gene expression can be found elsewhere [33]. In brief, PrediXcan uses a machine learning approach to generate algorithms to estimate the genetically determined component of gene expression in specific brain regions at the individual level from the subject's genotype. The algorithm was built using a reference dataset from deceased human brain donors, being therefore tissue-specific. This reference dataset is composed of data from the GTEx project (version 7) [34], GEUVADIS [35] and DGN [36] containing both genotype and gene expression levels. The PrediXcan method was executed according to methods available in [21], and using GTEX version 7 frontal cortex eQTL model [34].

Statistical analysis

Food go/no-go. Guidelines for exclusions as described in Patros et al [37] were followed. No participants needed to be excluded due to the proportion of go trials with RTs <200 ms exceeding .30, or omission error rate exceeding .50 (n = 0), indicating adequate attention during task presentation. Our primary outcome measure was number of commission errors for no-go stimuli (fGNG commission error), which reflects inhibitory control, with larger number of errors indicating poorer inhibitory control. Variables of interest were computed in MATLAB version 7.1 (The Mathworks, Inc., Natick, MA).

Multi-item ad-libitum buffet meal. For the analysis of meal intake, we created three primary variables: *snack intake* (included vanilla ice cream, chocolate chip cookies, fudge brownies, M&Ms, Ruffles potato chips, and Cheetos), *pizza intake* (included cheese, vegetable, and pepperoni pizzas), and *fruit and vegetable intake* (included baby carrots, cherry tomatoes, celery, and grapes) by summing the weights of each of the foods consumed within each group. In addition, nutrition facts labels for each food item were used to calculate total macronutrient (carbohydrate, sugar, fat, protein) intake for each participant.

SES composite score. To ensure that the 5 socioeconomic variables described above reflected the same underlying theoretical structure (SES) and to derive a composite score reflecting multiple dimensions of SES, we conducted a principal component analysis (PCA) [38–40] with Promax rotation. All variables loaded on a single component with loadings ranging from 0.678 to 0.891, supporting our choice to create a composite score. This component explained 59.1% of variance. Each of the socioeconomic variables was standardized and weighted by its factor loading to create an SES composite score in which a higher score indicates higher SES. A detailed description of the variables and PCA factor loadings is given in Table 2.

	Туре	Mean (SD)	Component 1 Loading
Annual Household Income	Ordinal	6.2 (3.2)	0.891
Maternal Education Level	Ordinal	4.6 (1.4)	0.772
Receiving Public Assistance (positive direction)	Dichotomous	0.8 (0.4)	0.793
Food Security	Dichotomous	0.8 (0.4)	0.690
Perceived Resource Availability	Continuous	12.1 (5.3)	0.678

Table 2. Detailed variable description for SES composite score and PCA factor loadings.

KMO Measure of Sampling Adequacy = 0.796.

Bartlett's Test of Sphericity: p<0.001.

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General statistical methods and differential susceptibility analysis

To test for differential susceptibility, linear regression models using continuous DRD4 predicted gene expression values for the prefrontal cortex (Z variable), SES composite score (X variable) and the interaction term between these two variables (X*Z) were run for ad libitum intake (kcal) of snacks, pizza, and fruit and vegetables (primary outcomes), and ad libitum intake (grams) of carbohydrates, sugar, fat, and protein. To ensure that differences in ad libitum intake were not driven by differences in key demographic and anthropometric variables, the models were adjusted for BMI z-score, age, sex, and two principal components reflecting population stratification (PC1, PC2). These components were used as covariates to account for differences in ancestry and geographic origins in place of self-reported race, which can be inaccurate for genetic studies [41]. Following Roisman et al's recommendations [42], to ensure that any observed differential susceptibility effects are not an artifact of imposing a linear model on nonlinear relationships, additional linear regression models, including X^2 and Z^*X^2 as predictors, were created to verify that neither of these two terms were statistically significant. This step was performed only for models with a significant X*Z interaction term. Post hoc analysis for the interaction terms included analysis of Proportion of Interaction (PoI) (i.e. the proportion of the total area represented in the interaction plots uniquely attributable to differential susceptibility), and proportion affected (PA) (i.e. the proportion of the population that is differentially affected by the moderator-Z variable) [42]. The regions of significance (RoS) analyses were conducted using a Web-based program developed by Fraley (http://www.yourpersonality.net/interaction). Preliminary analysis showed no interaction with sex, therefore in the main analysis boys and girls were analyzed together. Data were analyzed using the Statistical Package for the Social Sciences (SPSS) version 25.0 software (SPSS Inc., Chicago, IL, USA) and R software [43-45]. Significance levels for all results were set at p < 0.05. Results were corrected for multiple comparisons across all the linear regression models with False Discovery Rate (FDR) correction, using the Benjamini–Hochberg method (threshold set at q = 0.15) [46].

Confirming differential susceptibility. Following Roisman et al. [42], to verify differential susceptibility, when the RoS analyses are performed to determine whether the moderator (Z variable) and the outcome variable are correlated at the low and high ends of the distribution of the predictor (X variable), results should be considered significant only within a certain range of interest that is ± 2 SD of the observed predictor variable. Additionally, the PoI index should be roughly within 0.40 and 0.60 and the PA index should be close to 0.50.

Results

Descriptive statistics for baseline characteristics can be found in <u>Table 1</u>. Linear regression beta coefficients and significance levels for the effect of the predictor variables ([*DRD4*

Variables		Snack Intake		Pizza Intake			Fruits & Vegetables Intake			
R ² (p-ANOVA)	0	0.241 (p = 0.017)			0.226 (p = 0.027)			0.229 (p = 0.885)		
	β	Р	P _{FDR}	β	Р	P _{FDR}	β	Р	P _{FDR}	
DRD4 predicted expression (Z)	0.049	0.680	0.868	-0.029	0.810	0.868	0.097	0.463	0.847	
SES composite score (X)	0.125	0.438	0.847	-0.037	0.818	0.868	0.004	0.981	0.981	
Z*X	0.407 [¶]	0.009	0.083	0.051	0.739	0.868	0.077	0.653	0.868	
Age	-0.118	0.303	0.747	0.171	0.142	0.506	-0.052	0.682	0.868	
Sex	-0.297	0.011	0.089	-0.456	<0.001	0.003	0.043	0.737	0.868	
BMI z-score	0.058	0.606	0.868	0.192	0.092	0.391	0.059	0.638	0.868	
PC1	0.186	0.163	0.533	-0.053	0.693	0.868	-0.144	0.332	0.747	
PC2	-0.129	0.258	0.743	-0.046	0.685	0.868	-0.126	0.322	0.747	

Table 3. Linear regression analyses results for caloric intake.

PC1: Principal Component 1 for population stratification; PC2: Principal Component 2 for population stratification.

⁹ Effect size attributable to interaction, R-Square change = 0.084 (p=0.009 for R-Square change). FDR threshold set at q=0.15

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predicted gene expression], [SES composite score], [*DRD4* predicted gene expression*SES composite score]) on the outcome variables, caloric intake and macronutrient intake, are displayed in Tables 3 and 4. *DRD4* predicted gene expression and the SES composite score had no significant main effects on the outcome variables when investigated separately from their interaction term, with the exception of the ad-libitum fat intake, where low SES composite score was associated with increased fat intake ($\beta = -0.258$, p = 0.040) (see S1 Data).

DRD4 predicted gene expression moderated the relationship between the SES composite score and ad-libitum snack intake ($\beta = 0.407$, p = 0.009). Furthermore, RoS analysis for the *DRD4* predicted gene expression effect revealed lower and upper bounds of significance within the observed predictor variable (for lower bound: SES composite score = -1.696; for higher bound: SES composite score = 0.736; simple slopes were significant outside this region). Finally, the proportion of interaction and the proportion affected/percentage above indices

Variables	C	arbohydrate	es		Sugar Fat			Protein					
R ² (p-ANOVA)	0.	0.300 (p=0.002)			0.236 (p=0.020)			0.313 (p=0.001)			0.248 (p=0.013)		
	β	Р	P _{FDR}										
DRD4 predicted expression (Z)	-0.005	0.967	0.	-0.037	0.756	0.868	0.	0.	0.868	0.028	0.811	0.868	
SES composite score (X)	0.088	0.569	0.868	0.176	0.	0.747	-0.097	0.529	0.868	-0.024	0.882	0.907	
Z*X	0.295	0.047a	0.251	0.318¶	0.041	0.251	0.249	0.089	0.391	0.087	0.567	0.868	
Age	0.035	0.751	0.868	-0.019	0.868	0.906	0.061	0.576	0.868	0.173	0.131	0.506	
Sex	-0.499	<0.001	0.001	-0.388	0.001	0.014	-0.487	<0.001	0.001	-0.479	<0.001	0.002	
BMI z-score	0.218	0.046	0.251	0.166	0.142	0.506	0.206	0.056	0.268	0.222	0.049	0.251	
PC1	0.103	0.418	0.837	0.193	0.148	0.506	0.038	0.764	0.868	-0.	0.	0.868	
PC2	-0.101	0.352	0.768	-0.083	0.468	0.847	-0.	0.307	0.747	-0.082	0.	0.868	

Table 4. Linear regression analyses results for macronutrient intake (grams).

PC1: Principal Component 1 for population stratification; PC2: Principal Component 2 for population stratification. ⁹ Effect size attributable to interaction, R-Square change = 0.084 (p=0.009 for R-Square change). FDR threshold set at q=0.15

PC1: Principal Component 1 for population stratification; PC2: Principal Component 2 for population stratification;

a: Significance level drops to 0.906, when both nonlinear terms X^2 , Z^*X^2 are included in the model (X^2 : p=0.090, Z^*X^2 : p=0.026), indicating a nonlinear relationship between the predictor (carbohydrate intake) and SES composite score.

⁹ Effect size attributable to interaction, R-Square change = 0.091 (p=0.041 for R-Square change). FDR threshold set at q=0.15

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(PoI = 0.59, PA = 0.563) complied with a differential susceptibility model. Post hoc analysis for simple slopes for higher and lower predicted prefrontal *DRD4* gene expression levels (mean split) showed statistical significance only for the lower group (simple slope at Z = 0: -99.09, t (65) = 2.59, p = 0.012; simple slope at Z = 1: 52.25, t(65) = 1.21, p = 0.229), suggesting that only the low *DRD4* predicted expression group showed plasticity to the environmental conditions, such that lower SES composite score was associated with greater ad-libitum snack intake. Results can be seen in Fig 1.

Additionally, *DRD4* predicted gene expression levels moderated the relationship between the SES composite score and ad-libitum sugar intake ($\beta = 0.318$, p = 0.041). However, the RoS analysis for *DRD4* predicted gene expression revealed lower and upper bounds of significance outside the observed predictor variable meaning that the significance of the difference can only be observed in extreme values of SES, beyond the observed values as shown in Fig 2 (for lower bound: SES composite score = -2.690; for higher bound: SES composite score = 4.113) and the proportion of interaction and the proportion affected/percentage above indices (PoI = 0.43; PA = 0.439) were not compatible with a differential susceptibility effect. Results can be seen in Fig 2.

DRD4 predicted gene expression level did not moderate the relationship of the SES composite score with the other intake variables, or with commission errors on the food go/no go task ($\beta = 0.130$, p = 0.403).

Using a sub-sample of adolescents with available data (n = 71), we also conducted an exploratory analysis using Perceived Stress Scale scores. For initial exploration of relationships between stress and eating behavior, we used the SES composite score median to split our sample in two groups (higher SES with n = 36; lower SES with n = 35). Pearson's correlations indicated that in the lower SES group, total PSS score positively correlated with ad-libitum sugar intake in the fed condition (r = 0.399, p = 0.022) and showed a positive trend with ad-libitum snack intake (r = 0.304, p = 0.086). In the higher SES group, total PSS score did not correlate with either sugar or snack intake (r = -0.081, p = 0.637; r = -0.047, p = 0.785, respectively).

Subsequently, using the differential susceptibility framework method described above, we found that *DRD4* predicted gene expression moderated the relationship between SES composite score and PSS score ($\beta = 0.552$, p = 0.001). As for the eating behavior results described above, RoS for *DRD4* predicted gene expression revealed lower and upper bounds of



Fig 1. Effects of interaction between SES Composite Score and *DRD4* predicted gene expression on Ad-Libitum Snack Intake (kcal). The vertical lines depict the region of significance. The interaction occurs within the regions of significance providing evidence of differential susceptibility, such that lower predicted prefrontal (PFC) *DRD4* expression is associated with greater ad-libitum snack intake in adolescents with lower socioeconomic (SES) composite score.

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significance within the observed predictor variable (for lower bound: SES composite score = -1.024; for higher bound: SES composite score = 0.397; simple slopes were significant outside this region), and the proportion of interaction and the proportion affected/percentage above indices (PoI = 0.60, PA = 0.578) complied with prototypical differential susceptibility. Post hoc analysis for simple slopes for the higher and lower predicted prefrontal *DRD4* gene expression levels showed statistical significance for the lower group only (simple slope at *Z* = 0: -3.15, t (62) = 2.79, p = 0.007; simple slope at *Z* = 1: 1.61, t(62) = 1.30, p = 0.200), suggesting that only the low *DRD4* group demonstrated plasticity to the environmental conditions, such that lower SES composite score was associated with greater PSS score. Results can be seen in <u>Table 5</u> and Fig 3. Supporting the differential susceptibility framework, *DRD4* predicted gene expression and SES composite score had no main effect on PSS score when investigated separately from their interaction term (see S1 Data).

Variables	PSS						
R ² (p-ANOVA)	0.219 (p=0.042)						
	β	Р	P _{FDR}				
DRD4 predicted expression (Z)	0.084	0.492	0.863				
SES composite score (X)	0.207	0.206	0.617				
Z*X	0.552 [¶]	0.001	0.009				
Age	0.035	0.768	0.868				
Sex	0.064	0.588	0.868				
BMI z-score	0.037	0.752	0.868				
PC1	-0.135	0.324	0.747				
PC2	-0.054	0.649	0.868				

Table 5. Linear regression analysis results for Perceived Stress Scale (PSS) score.

PC1: Principal Component 1 for population stratification; PC2: Principal Component 2 for population stratification. ⁹ Effect size attributable to interaction, R-Square change = 0.164 (p=0.001 for R-Square change). FDR threshold set at q=0.15

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Fig 3. Effects of interaction between SES Composite Score and *DRD4* **predicted gene expression on total PSS score.** The vertical lines depict the region of significance. The interaction occurs within the regions of significance providing evidence of differential susceptibility, such that lower predicted prefrontal (PFC) *DRD4* expression is associated with greater Perceived Stress Scale (PSS) score in adolescents with lower socioeconomic (SES) composite score.

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Discussion

In the current study, we describe the moderating effect of genetically predicted prefrontal *DRD4* gene expression on responses to the environment such that low frontal cortex expression of *DRD4* was associated with a higher environmental response, whereas a higher expression of *DRD4* was associated with no significative response to the environment. This effect of differential plasticity in response to environmental variation was observed across two different domains, with one outcome representing an actual eating behavior relevant to obesity development (snack intake in a buffet meal challenge), and the other a subjective rating of how stressful an individual perceives situations in his or her life to be. Importantly, our findings pertain to adolescence. This life period is crucial for investigation, since adolescents with obesity are more likely to maintain this phenotype through to adulthood than adolescents of normal weight [47]. Adolescence is a period especially vulnerable to psychological comorbidity in relation to obesity [48, 49]. Adolescence is also a critical period for prefrontal cortex development, including its dopamine innervation [19, 50–52], making it a sensitive window for the effects we observed here.

Specifically, in terms of eating behavior, adolescents with lower predicted prefrontal *DRD4* expression showed greater snack intake at an ad libitum meal test if they were of lower socioeconomic status (SES). Neighborhoods inhabited by lower SES populations have been shown to exhibit higher availability of calorie-dense food choices and associated food cues[53, 54], and such environmental forces have been associated with the rising trends in overconsumption and associated obesity over recent decades [55, 56]. SES also serves as a more general proxy of the quality of the surrounding environment, capturing factors including stress exposure [57] and lower opportunities for physical activity [58], as well as poorer access to nutritional foods [59]. Our results are therefore consistent with a differential susceptibility model whereby individual variations in dopamine-mediated openness to the environment affect the likelihood of unfavorable responses (i.e. snack intake) to unfavorable conditions (i.e. low SES), and might therefore also determine responses to improvements in such conditions [60].

This study also confirms findings on environmental plasticity from our previous research using the same genomic methodology (predicted prefrontal DRD4 expression). In that paper,

Barth et al [13] demonstrated differential susceptibility effects on eating behavior in two ethnically distinct cohorts of children [13]. The present study extends these findings to an older age group, and provides support for perceived stress as an additional feature showing modulation by this gene by environment interaction.

Notably, analysis of macronutrients consumed during the meal test revealed a tendency toward a similar interaction effect for sugar calories consumed, although this variable did not show a formal differential susceptibility effect. Nevertheless, this pattern of results provides further support for the possibility that that prefrontal dopamine function may be specifically affecting behaviors towards palatable food. This is in accordance with a wealth of literature implicating the dopamine system in addictive like eating behavior [61], behavioral risk for obesity [62] and obesity itself [63].

The modulation of environmental responsiveness by *DRD4* gene expression that we observed here is consistent with well-established general functions of *DRD4*. *DRD4* functionally produces inhibitory effects, and is expressed in brain regions playing a role in planning, executive function and reward [64]. The *DRD4* exon III VNTR polymorphism (hypofunctional polymorphism), for instance, has been implicated in both planning/executive function effects and in heightened susceptibility to environmental influences [15], as well as with reduced inhibitory effects on postsynaptic neurons [65–67]. Such effects could be due to differential modulation of signal-to-noise ratio in subpopulations of mPFC neurons [68–71]. For example, afferent signals may be amplified relative to spontaneous basal firing (noise), thus affecting the signal to noise ratio and therefore consequent behavioral responses [69].

Our findings also build on previous literature demonstrating the role of dopamine function on responsiveness to food cues. For example, functional magnetic resonance (fMRI) imaging in response to imagined intake of palatable foods shows that future increases in body mass can be predicted by weaker brain activation of specific brain areas, particularly in individuals carrying low functioning variants of dopamine receptor genes, such as the *DRD2 TaqIA A1* allele or the *DRD47R* allele [72, 73]. The *DRD47R* polymorphism has been associated with markedly decreased affinity for dopamine and impaired intracellular signaling in comparison to other exon III alleles [74]. Our group has studied the *DRD47R* allele in several disorders characterized by increased eating that are most prevalent in females [7, 75, 76]. *DRD47R* carriers also report significantly more craving for food in a cue-elicited food-craving test [77].

Both cortical and subcortical brain regions control cognitive and behavioral responses to food cues, and food intake [78–81]. The balance between involuntary stimulus-driven processes (bottom-up, in response to stimulus exposure) and reflective goal-driven processes (top-down, related to information processing and cognition) determine cognitive representations of the reward value of food cues, attentional responses to such cues, and impulsive behaviors [81, 82], with combined perturbation of these processes likely to underlie the predisposition to overeat [83]. Moreover, adolescence is a period associated with poor inhibitory control resulting from ongoing maturation of neural systems subserving these functions [50, 84]. Therefore, the extent to which people show enhanced selective attention to food cues in tasks such as a food go/no go (i.e. attentional bias) provides a neurobehaviorally-informed index of individual differences in reactivity to food reward, as determined by this integrated system. In the present study, we did not find any association or interaction between predicted prefrontal DRD4 expression and SES composite score on food go/no go performance. This negative finding contrasts with predictions based on other studies which have shown that alterations of dopaminergic pathways can impact both sensitivity to reward and impulsivity [85-87], that can lead to poor decision-making processes and maladaptive behaviors such as altered eating behavior and addiction [88-90]. Impulsive subjects show an inability to refrain from a stimulus-driven action, as measured by response inhibition paradigms such as the go/

no-go task[91] and impulsivity has been associated with functional polymorphisms of dopamine-related genes [92]. These negative results suggest that, in this sample, behavioral inhibitory control did not play a critical role in the response to environment [93–95].

In addition to effects on food intake, we here demonstrated that predicted prefrontal DRD4 gene expression moderated the effects of SES on stress perception. Only the low DRD4 group reported higher perceived stress. In contrast there was no effect of low SES on perceived stress in those with higher expression of DRD4, suggesting that higher expression may confer a higher resilience or what could be called a higher "internal buffering capacity" to environmental conditions [96]. We also demonstrated greater intake with higher perceived stress within lower SES participants. This exploratory result requires replication but is consistent with an overall alteration in environmental perception among individuals with blunted dopamine function with potential impacts on eating behavior, rather than a specific effect on eating behavior responses to the food environment. Our finding is consistent with literature in healthy adults demonstrating that dopamine function is associated with perceptual experiences including sensitivity to pain [97] and responsivity to acute psychosocial stressors [98]. Also, in accordance with our finding, pre-clinical studies have demonstrated that diminished presynaptic dopamine regulation and function in DRD4 deficient mice can produce increased sensitivity to aversive [99] as well as reward cues [100]. Further, human studies also found that diminished dopamine inhibitory feedback in DRD47R carriers is linked to weaker physiological dopamine signaling compared to non-carriers [101]. Human imaging studies have also suggested that DRD47R variations might impact neural reactivity to both aversive as well as rewarding cues, with alcohol cue-triggered reactivity in the OFC, anterior cingulate cortex (ACC), and striatum being greater in DRD47R carriers [102], and DRD47R carriers showed greater neural responsivity to unpleasant images [103].

Limitations

This study contained only a small proportion of very low-income individuals in this study sample. Nevertheless, we were able to observe interactions with SES here, arguing for the existence of effects even at higher income ranges. This is consistent with other research demonstrating health effects of SES that are not restricted to conditions of poverty but distributed across a whole range of wealth [104]. A further cause for caution in interpreting these results is that the generalizability of the PrediXcan method to non-Caucasian populations is unclear [105], necessitating further validation and replication work, although we were able to find similar effects using the same methodology in a cohort of predominantly Asian individuals[13, 105]. PrediXcan is an imputation technique with some limitations inherent to its method, which aims to predict only the genomic-related proportion of gene expression, not real expression or associated protein levels or functional activity. The real expression of DRD4, and its biological function, could still be subject to variation between subjects due to gene-environment interactions. Indeed the actual differential susceptibility phenotype could even be causally related to other indirect mechanisms, such as network polygenic effects, where DRD4 could work as a hub gene, or relate to genes adjacent to DRD4. The association between the predicted DRD4 and differential susceptibility phenotype we show here is, though, in line with findings in two different cohorts with heterogeneous populations in terms of age and ethnic background [13], and findings on the DRD4-7R polymorphism from previous literature[6, 12, 106–111]. Notwithstanding the limitations described, the results we present here are consistent with a nonlinear moderating effect of dopamine function on neural responses [112, 113], such that low predicted DRD4 expression in prefrontal cortex was associated with a more plastic

phenotype, conferring obesity risk in more adverse environments, and obesity protection in predominantly favorable environments.

Supporting information

S1 Data. (DOCX)

S2 Data. (ZIP)

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