# Prefrontal cortex VAMP1 gene network moderates the effect of the early environment on cognitive flexibility in children

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### **Abstract**

During development, genetic and environmental factors interact to modify specific phenotypes. Both in humans and in animal models, early adversities influence cognitive flexibility, an important brain function related to behavioral adaptation to variations in the environment. Abnormalities in cognitive functions are related to changes in synaptic connectivity in the prefrontal cortex (PFC), and altered levels of synaptic proteins. We investigated if individual variations in the expression of a network of genes co-expressed with the synaptic protein VAMP1 in the prefrontal cortex moderate the effect of early environmental quality on the performance of children in cognitive flexibility tasks. Genes overexpressed in early childhood and co-expressed with the VAMP1 gene in the PFC were selected for study. SNPs from these genes (post-clumping) were compiled in an expression-based polygenic score (PFC-ePRS-VAMP1). We evaluated cognitive performance of the 4 years-old children in two cohorts using similar cognitive flexibility tasks. In the first cohort (MAVAN) we utilized two CANTAB tasks: (a) the Intra-/Extradimensional Set Shift (IED) task, and (b) the Spatial Working Memory (SWM) task. In the second cohort, GUSTO, we used the Dimensional Change Card Sort (DCCS) task. The results show that in 4 years-old children, the PFC-ePRS-VAMP1 network moderates responsiveness to the effects of early adversities on the performance in attentional flexibility tests. The same result was observed for a spatial working memory task. Compared to attentional flexibility, reversal learning showed opposite effects of the environment, as moderated by the ePRS. A parallel ICA analysis was performed to identify relationships between whole-brain voxel based gray matter density and SNPs that comprise the PFC-ePRS-VAMP1. The early environment predicts differences in gray matter content in regions such as prefrontal and temporal cortices, significantly associated with a genetic component related to Wnt signaling pathways. Our data suggest that a network of genes coexpressed with VAMP1 in the PFC moderates the influence of early environment on cognitive function in children.

**Keywords**: spatial short-term memory; MAVAN; GUSTO; synaptic proteins; neuroplasticity; neuroimaging.

### Introduction

James McGaugh was one of the first neuroscientists to point to the important influence of stress hormones on memory consolidation (Mcgaugh, Gold, Van Buskirk, & Haycock, 1975). He and others considered that hormones released by stressful experiences could enhance memory consolidation, indicating particularly the hormones epinephrine and glucocorticoids as memory modulators (McGaugh & Roozendaal, 2009). It was suggested that several brain regions work in synergy to assure that emotionally significant experiences are well-remembered, and this could prepare the organism for future experiences by inducing long-term behavioral changes (Bahtiyar, Karaca, Henckens, & Roozendaal, 2020; McGaugh, 2013). However, whereas moderate acute stress may facilitate later retrieval, chronic stress can impair cognitive functions, depending on factors such as type, duration and intensity of the stressor, and type of cognitive function evaluated.

One of the brain structures impacted by stress exposure is the prefrontal cortex (PFC), which mediates multiple behavioral responses, including planning, accounting for the demands of a changing environment. Many studies, both in animals and humans, have described stress-induced effects upon executive functions related to this area, such as working memory, cognitive flexibility, and attentional set-shifting (e.g., (Bondi, Rodriguez, Gould, Frazer, & Morilak, 2008; Jett, Bulin, Hatherall, McCartney, & Morilak, 2017; Conor Liston et al., 2006; Merz & McCall, 2011). In these studies, different types of chronic stressors were shown to be able to affect specific prefrontal cognitive functions: for example, several studies reported that chronic stress disrupts extradimensional set-shifting (Jett et al., 2017; Conor Liston et al., 2006; Moench, Breach, & Wellman, 2020; Nikiforuk & Popik, 2014; Xu et al., 2016; Zhang, Shao, Wang, Xie, & Wang, 2017), while physical stressors, such as chronic intermittent cold stress, may affect reversal learning (Bondi et al., 2008; Danet, Lapiz-Bluhm, & Morilak, 2010; Lapiz-Bluhm, Soto-Piña, Hensler, & Morilak, 2009). The inability to adapt to an unanticipated environment by changing behavioral strategies may have detrimental consequences for an organism (Clark, Cools, & Robbins, 2004; Graybeal, Kiselycznyk, & Holmes, 2012; Tremblay & Schultz, 1999; Wellman, Bollinger, & Moench, 2020), and this is why the study of stress-induced disruption of PFC functions is a subject of increasing interest.

Stress effects on behavior and executive functions are associated with altered plasticity in specific sub-regions of the PFC, such as, for example, changes in the arborization or the spine density at the apical dendrites of pyramidal neurons, particularly in the mPFC (Cerqueira et al., 2005; Cook & Wellman, 2004; Dias-Ferreira et al., 2009; Conor Liston et al., 2006; Michelsen et al., 2007; Radley et al., 2006; Silva-Gomez, Rojas, Juarez, & Flores, 2003), and effects upon the morphology and imbalanced activation patterns of the mPFC have also been reported in stressed humans (Soares et al., 2012). Consistently, it is known that experiences during sensitive periods of development - periods of maturation and intense plasticity - have a long-term impact on brain function (Folha et al., 2017; Lazzaretti et al., 2018; Sarabdjitsingh, Loi, Joëls, Dijkhuizen, & Van Der Toorn, 2017). One of the best studied examples of early life stress-induced brain function alteration is the life-long modified control of stress-related hormones release (McGowan et al., 2009; Weaver et al., 2004).

Studies both in humans(Harms, Shannon Bowen, Hanson, & Pollak, 2018; Romero-Martínez, Lila, Catalá-Miñana, Williams, & Moya-Albiol, 2013) and in animal models (Baudin et al., 2012; Lazzaretti et al., 2018; Xu et al., 2016) have shown that early adversities have long-term influence upon cognitive flexibility. The high vulnerability of PFC to the effects of early-life stress

(Chocyk, Majcher-Maślanka, Dudys, Przyborowska, & Wędzony, 2013; Sarabdjitsingh et al., 2017) might be explained by the fact that this is one of the last brain regions to mature during development (Fuster, 2015; Hoops & Flores, 2017; Reynolds et al., 2018). It is reasonable to expect that early adversities may lead to reductions in PFC-based cognitive functions, which include the impairment of children's ability to adapt to different conditions in their environment through adequate stress and emotional responses (Hostinar, Stellern, Schaefer, Carlson, & Gunnar, 2012).

Notwithstanding the above-mentioned effects on cognitive flexibility, several other lines of evidence suggest that the quality of the early life environment induces changes in synaptic plasticity within the PFC(Folha et al., 2017; Lazzaretti et al., 2018; Lesuis, Lucassen, & Krugers, 2019; Xu et al., 2016), which might underlie the distinct cognitive-behavioral responses verified. The Soluble N-ethylmaleimide-sensitive factor Attachment Protein Receptor (SNARE) complex, for instance, which is involved in synaptic plasticity by enabling membrane fusion during neurotransmitter release (Cupertino et al., 2016), is a strong target candidate. SNARE is composed by three distinct proteins, all with an important role in neurodevelopment (Cupertino et al., 2016; Halim et al., 2003), and one of them, VAMP 1 (vesicular associated membrane protein 1), is a highly conserved synaptic molecule in evolution (Südhof, Baumert, Perin, & Jahn, 1989). Certain pathologies which result in abnormal cognitive functions, such as attention and/or working memory deficits, were also shown to have altered synaptic connectivity in the PFC, and among them, altered VAMP levels have been observed (Halim et al., 2003).

Our general hypothesis is that the early interaction between the environment and the genetic background results in changes in brain plasticity and neurotransmission, which may influence cognitive flexibility, among other functions. In recent years, studies covering the interface between genetics and behavioral outcomes have made use of polygenic risk scores (PRS) in order to detect vulnerability to neurological or psychiatric diseases (Guo et al., 2018; Mistry, Escott-Price, Florio, Smith, & Zammit, 2019; Morgan et al., 2017; Palk, Dalvie, De Vries, Martin, & Stein, 2019), and recent reports have focused on gene networks integrated by genes related to certain characteristics (Hari Dass et al., 2019; Miguel et al., 2019). These latter reports propose the use of biologically-informed genetic scores, which could aggregate a potential array of genes coexpressed with a known gene relevant to the outcome under question (expression-based polygenic risk score or ePRS), operating in a specific brain region. In this way, variations in the ePRS could be interpreted as reflecting variations in the function of the network. This analysis includes individual variations and allows to compare behavioral outcomes according to the environment.

We thus hypothesize that VAMP1 and its entourage of co-expressed proteins constitutes an interesting heuristic guide to investigate PFC-mediated behavioral-cognitive changes putatively based on stress-induced local plasticity changes, including those resulting from stressful events in early life. We therefore investigated whether individual variations in the expression of a gene network co-expressed with the gene encoding for the synaptic protein VAMP1 in the prefrontal cortex is somehow correlated with the causal effect of early life stress on the performance of children in cognitive flexibility tasks, spatial working memory, as well as brain gray matter density in childhood, analyzing data from two different cohorts.

# Materials and methods

# Subjects.

Discovery sample: MAVAN is a community-based birth cohort study of Canadian women and their offspring. Pregnant women aged 18 years and above were recruited in Montreal (Quebec) and Hamilton (Ontario), Canada. Eligibility criteria for mothers included singleton gestation, and

fluency in French or English. Severe chronic illness, placenta previa, and history of incompetent cervix, impending delivery, or a fetus/infant affected by a major anomaly or born at a gestational age of less than 37 weeks or had birth weight less than 2,000 g were exclusion criteria. Approval for the MAVAN project was obtained from McGill University, Université de Montréal, Royal Victoria Hospital, Jewish General Hospital, Centre Hospitalier de l'Université de Montréal, Hôpital Maisonneuve-Rosemount, St Joseph's Hospital and McMaster University. The study was conducted in accordance with the rules and regulations of the University ethics committees and informed consent was obtained from all participants. A total of 132 children had the necessary data (information on early life adversities/buffering conditions, genotype, and the score on at least one of the cognitive flexibility tasks at 48m), and this sample is described in Table 1. From these children, 106 completed stage 7 of IED task at 48 months and 103 completed stage 8 and were included in the behavioral analyses related to these stages. One hundred twenty-nine children performed the SWM task (4 boxes) at this age. A total of 43 children had complete data (genotype, information on early life adversities/buffering conditions, and imaging data) and were included in the imaging study.

Replication Sample: Growing Up in Singapore Towards Healthy Outcomes (GUSTO)(Soh et al., 2014): Pregnant women aged 18 years and above were recruited at the National University Hospital and KK Women's and Children's Hospital from Singapore. The pregnant women included Chinese, Malay, or Indian ethnicity with homogeneous parental ethnic background. Mothers receiving chemotherapy, psychotropic drugs or who had type I diabetes mellitus were excluded. The study was approved by the National Healthcare Group Domain Specific Review Board (NHG DSRB) and the Sing Health Centralized Institutional Review Board (CIRB). Informed written consent was obtained from each participant. A total of 140 children had complete data (genotype, information on early life adversities/buffering conditions, age, and scores on a cognitive flexibility task at 54 months of age) and were included in the study.

Demographic information for MAVAN and GUSTO cohorts is provided in Table 1.

### **Procedures**

*Genotyping:* 

MAVAN. **SNPs** genotyped using genome-wide autosomal were (PsychArray/PsychChip, Illumina) according to the manufacturer's guidelines with 200 ng of genomic DNA derived from buccal epithelial cells. Participant samples with a low call rate (< 90%) were removed, as well as SNPs with a low call rate (< 95%), a minor allele frequency less than 5% or a low p-value on Hardy-Weinberg equilibrium test (p  $< 10^{-40}$ ), resulting in 242,211 SNPs. PLINK 1.951 (Purcell et al., 2007) was used for quality control procedures. The remaining SNPs were submitted for imputation to Sanger Imputation Service using a Haplotype Reference Consortium (release 1.1) panel (McCarthy et al., 2016) and post-imputation quality control, resulting in 20,790,893 SNPs with imputation accuracy greater than 0.80. We recoded imputed dosage genotypes to hard-called genotypes using posterior genotype probability greater than 0.90. Polygenic scores were calculated based on hard-called genotypes

In GUSTO, genomic DNA was extracted from frozen umbilical cord specimens. Samples were genotyped on Illumina Omni Express Exome arrays, following the manufacturer's instructions

(Expression Analysis Inc). SNPs with call rates < 95%, minor allele frequencies < 5% and Hardy-Weinberg equilibrium of  $p \le 10^{-6}$  were removed. Variants discordant with their respective subpopulation in the 1000 Genomes (1000 Genomes Project Consortium, 2015) reference panel were removed. More precisely, variants with different allele coding than 1000 Genomes Project as well as SNPs with frequencies that differ more than the threshold specified for the reference population (Chinese: EAS with a threshold of 0.20; Malay: EAS with a threshold of 0.30; Indian: SAS with a threshold of 0.20) were excluded. The resulting data were pre-phased using SHAPEIT v2.837 with family trio information. The genotyping data were then sent to Sanger Imputation Service (https://www.sanger.ac.uk/tool/sanger-imputation-service/) for imputation, choosing 1000 Genomes Project Phase 3 as the reference panel and imputed using the Positional Burrows Wheeler Transform (PBWT) algorithm (Durbin, 2014).

# Population structure

The population structure of the MAVAN and GUSTO cohorts were evaluated using principal component analysis (Patterson, Price, & Reich, 2006) of all autosomal SNPs that passed quality control. Genotyped SNPs with high linkage disequilibrium (r2 < 0.20) were pruned with a sliding window of 50 kilobases in increments of 5 SNPs using PLINK 1.9. We performed principal component analysis using SMARTPCA on this pruned data set and generated a scree plot. Based on the inspection of the scree plot, the first 3 principal components were the most informative of population structure and were included in all analyses as covariates.

# Construction of the PFC-VAMP1 gene network

Discovery sample

# Genes co-expressed with VAMP1 in the PFC and ePRS calculation

The expression-based polygenic risk score was created considering genes co-expressed with the *VAMP1* gene (ePRS- *VAMP1*) in the PFC, according to the protocol described previously (Silveira et al., 2017). This ePRS was generated using several resources: (a) GeneNetwork (http://genenetwork.org) (b) BrainSpan (http://www.brainspan.org), (c) NCBI Variation Viewer (https://www.ncbi.nlm.nih.gov/variation/view) and (d) GTEx (https://www.gtexportal.org/home).

The ePRS was constructed in several stages: (i) GeneNetwork (http://genenetwork.org) was used to generate a list of genes co-expressed with Vamp1 in the PFC in mice. Only genes with absolute value of the co-expression correlation r higher or equal to 0.5 were kept; (ii) Brainspan (http://www.brainspan.org) was used to identify transcripts from this list with enrichment within the human PFC from the last gestational weeks until mid-childhood (25 to 38 post-conception weeks and first 5 years of life). We selected autosomal transcripts that were differentially expressed in PFC at 1.5-fold during this period of development as compared to adult samples (http://brainspan.org; Miller et al., 2014) due to our interest in gene networks with higher activity in the period considered for the environmental index. The resulting list consisted of 33 genes. (iii) Based on their functional annotation in the National Center for Biotechnology Information, U.S. National Library of Medicine (NCBI Variation Viewer), using GRCh37.p13, we gathered all the existing SNPs from these genes, and merged this list with SNPs from the Genotype-Tissue Expression (GTEx) project (Lonsdale et al., 2013) data in human PFC, and from our study sample. The list of common SNPs was subjected to linkage disequilibrium clumping (r<sup>2</sup><0.25). It resulted in 276 independent functional SNPs that (iv) were weighed using the SNP-gene expression association slope from the GTEx. Number of effect alleles at a given cis-SNP was weighed by the estimated effect of the genotype on gene expression from the GTEx. The sum of these values over the total number of SNPs provided the PFC-ePRS-VAMP1 score. Our final list of genes included 32 genes (one of the original genes had no common SNPs when considering NCBI, GTEx and the samples) (Supplementary Table S1). The standardized PFC-ePRS-VAMP1 score was used as a continuous variable.

Specificity of the findings: In order to test the specificity of the PFC-ePRS-VAMP1 score, we also investigated the ability of other scores to moderate the effect of early life environment on the outcome (cognitive flexibility): (i) We calculated a score considering genes co-expressed with the VAMP2 gene in prefrontal cortex (PFC-ePRS-VAMP2). VAMP2 is also a protein of the VAMP family which is highly expressed in PFC (Uhlén et al., 2015) (<a href="https://www.proteinatlas.org">https://www.proteinatlas.org</a>); (ii) We calculated the score considering genes co-expressed with the VAMP1 gene in a different brain region, the hippocampus (HPC-ePRS- VAMP1). These scores were calculated with the same premise and using the same methods described above for the PFC-ePRS-VAMP1. The final list of co-expressed genes included 184 genes for PFC-ePRS-VAMP2 (Supplementary Table S2), and 92 genes for HPC-ePRS-VAMP1 (Supplementary Table S3). These scores were tested for the interaction ePRS x environmental index on cognitive flexibility, as was the PFC-ePRS-VAMP1.

### Replication sample.

In order to replicate and test the generalizability of our findings in a different cohort, we conducted the same analyses in the GUSTO cohort. For that, ePRS was created following the same steps as above, starting from the 33 genes.

### Characterization of early life environment

Discovery sample.

Environmental score: The following tools were used to calculate a early life environmental index combining adversity and positive experiences in MAVAN: The Health and well-being questionnaire is a composite of validated short versions of multiple measures (Kramer, Goulet, et al., 2001): a) a subscale from the Daily Hassles is used to measure how often, and to what degree, the woman has lacked money for basic needs such as food, heating and electricity, since the beginning of pregnancy (Kanner, Coyne, Schaefer, & Lazarus, 1981); b) The Marital Strain Scale of Pearlin and Schooler is used to assess chronic stress with the romantic partner (Pearlin & Schooler, 1978); c) The Abuse Assessment Screen is used to assess conjugal violence. This fiveitem instrument assesses the frequency, severity, perpetrator, and body sites of injury (Newberger et al., 1992; Parker, McFarlane, Soeken, Torres, & Campbell, 1993); d) Questions about anxiety during pregnancy (Lobel & Dunkel-Schetter, 1990; Lobel, Dunkel-Schetter, & Scrimshaw, 1992). Smoking during pregnancy was simply scored as a binary outcome. Household gross income was assessed according to the Institut de la statistique du Québec (Daveluy & Québec, 2001). Birth weight and gestational age were assessed using birth records obtained directly from the birthing unit. Birth weight percentiles were calculated using the Canadian reference (Kramer, Platt, et al., 2001). Besides, the following tools were also used: Child Health Questionnaire: Includes questions on acute and chronic conditions, as well as hospitalizations (Plante, Courtemanche, & Groseilliers, 2002). Attachment: The Preschool Separation - Reunion Procedure (PSRP) was applied at 36 months. The PSRP is a modified and developmentally appropriate version of the Ainsworth Strange Situation used to measure attachment security in preschool-aged children (Cassidy & Marvin, 1992; Moss, Bureau, Cyr, Mongeau, & St-Laurent, 2004). The task consists of a baseline interaction, followed by two separation and reunion episodes lasting 5 minutes; scoring was based on video coding (reliability k=0.83). Four categories were assessed: secure, ambivalent, avoidant and disorganized. Family Assessment Device (FAD): The FAD is a 60-item self-report instrument developed to assess the six dimensions of the family functioning outlined in

the McMaster Model of Family Functioning (Epstein, Baldwin, & Bishop, 1983). The first six scales assess problem solving, communication, roles, affective responsiveness, affective involvement and behavior control. A general functioning scale assesses overall health-pathology (Kabacoff, Miller, Bishop, Epstein, & Keitner, 1990). *Breastfeeding Questionnaire*: This is a maternal self-report that queries the age of the baby (in weeks) when she or he was fed for the first time with something other than breast milk and the age of the baby (in weeks) when mothers stopped nursing (or giving breast milk). Women were provided the option of responding that they never breastfed or provided breast milk to their baby (Adedinsewo et al., 2014). See Table 2 for factors included in the environmental score. A combined score was calculated, giving negative points to adverse exposures and positive points to supportive/enriching events, and therefore ranging from more negative (adverse environment) to more positive values (positive scenarios). *Replication sample*.

In GUSTO, the tools applied for the calculation of these scores were similar to MAVAN (see description above), except for the absence of the following components: attachment, domestic violence, lack of money, pregnancy anxiety, and marital strains information (see Table 2).

### **Behavioral outcomes**

Discovery sample.

Intra-/Extra-dimensional Set Shift (IED) (Downes et al., 1989) The IED task from the CANTAB battery comprises rule acquisition and reversal (set shifting) throughout nine stages with increasing difficulty. There are two dimensions used in the task (color-filled shapes, introduced in the first stage, and white lines, introduced in the third stage). In the first 7 stages, shape remains the relevant dimension. At stage 6 new stimuli are presented, still with the same 2 dimensions, and subjects are required to learn which of the new exemplar is correct (intra-dimensional shift). An extra-dimensional shift occurs at stage 8, when subjects are required to shift attention to the previously irrelevant dimension (i.e., lines). At stages 2, 5, and 7, contingencies are reversed, so that the previously incorrect stimulus is now correct (reversal learning). We focused on the sum of errors for stages 2, 5 and 7 as a measure of reversal learning, and on the errors during stage 6 and stage 8 as the measures of attentional flexibility (intra and extradimensional shifts, respectively). This task was applied in MAVAN children at the age of 48 months (mean±S.D.: 4.10±0.08 years).

Spatial Working Memory (SWM): This is a self-ordered task, also from the CANTAB battery, which measures the ability to retain information and manipulate items in working memory, being related to frontal lobe executive function (Owen, Downes, Sahakian, Polkey, & Robbins, 1990). Participants were shown a group of boxes on a computer screen. They were asked to search for a token hidden beneath one of the boxes by touching a box to discover whether or not a token was there. After the token was found, the procedure was repeated, and the participants were told that a token would never be hidden beneath the same box. Thus, participants needed to remember which of the boxes had previously hidden a token within a set of trials. Performance on the test was evaluated by quantifying number of (a) between errors (i.e., revisiting a box in which a token had been found in a previous trial); (b) within errors (i.e., searching a box already found to be empty during a single trial); (c) double errors (errors categorized as both between and within errors); and (d) total errors (i.e., between errors + within errors – double errors).

# Replication sample.

For the evaluation in the replication cohort (GUSTO), we used the *Dimensional Change Card Sort* (DCCS). The DCCS is test of executive functioning and, like the attentional flexibility in IED, measures the ability to learn and apply new rules while refraining from using old rules (Zelazo,

2006). DCCS was applied at 54 months, as described in Pang et al. (Pang et al., 2020). In this test, children were asked to sort pictures according to color and then subsequently by spatial orientation or emotional expression. The order in which the children received the two versions of the test was counterbalanced. In the present study, we used the non-emotional condition, in order to maintain comparability of the dataset to the discovery sample. The test was administered on a computer with press pad, using E-Prime version 2.0. Children were first asked to sort bivalent pictures according to one rule for an entire block of 5 trials, and then according to a different rule for an entire block of 5 trials. One of the rules included "sort by color", and the other rule was to sort by spatial orientation. That is, children saw neutral colored faces that were either upside down or right side up. An additional block was added for children who passed the simpler conditions. In this last "mixed trials" block consisting of 30 trials, an instruction word and sound cue preceded each trial and indicated the rule for sorting the test stimuli in that trial. We considered the ability of the children to perform (% of accuracy) in the mixed trials block, since it was more relevant to replicate the findings in the extradimensional shift for the discovery sample.

### **Gray matter volume**

Parallel-independent component analysis (p-ICA):

Structural MRI acquisition was performed when children were 8-11 years-old. High-resolution T1-weighted images for the whole brain were acquired using a 3T trio Siemens scanner available at Cerebral Imaging Center, Douglas Mental Health Institute (Montreal, Canada) and a GE MR750 Discovery 3T MRI scanner at the Imaging Research Centre, St Joseph's Healthcare (Hamilton, Canada). The following parameters were used: 1 mm isotropic 3D MPRAGE, sagittal acquisition, 256 x 256 mm matrix, TR=2300ms, TE=4ms, FA=9degrees (Montreal); a 3D inversion recovery-prepped, T1-weighted anatomical data set, fSPGR, axial acquisition, TE/TR/flip angle = 3.22/10.308/9, 512 x 512 matrix with 1mm slice thickness and 24cm FOV (Hamilton). Computational Anatomy Toolbox (CAT12) from the Statistical Parametric Mapping software (SPM12; Welcome Department of Cognitive Neurology, London, UK) was used to process the T1-weighted images. In the preprocessing step, the images were normalized and segmented into gray matter and white matter. After a high-dimensional Diffeomorphic Anatomical Registration Through Exponentiated Lie Algebra (DARTEL) normalization, a smoothing process was applied using 8mm full width half maximum kernel.

A multivariate parallel independent component analysis (pICA) was applied to identify relationships between two different data modalities (SNPs and brain gray matter density) in a data-driven manner (Khadka et al., 2016). This analysis estimates the maximum independent components within each data modality separately while also maximizing the association between modalities using an entropy term based on information theory (Liu & Calhoun, 2014; Pearlson, Calhoun, & Liu, 2015). We sought the relationship between the SNP based PFC-ePRS-*VAMP1* (or genotype \* GTEx gene expression slope at each SNP that compose the PFC-ePRS-*VAMP1* score) and the voxel based gray matter in the whole brain. Weighted SNPs were aggregated with the most significant principal components from population stratification for adjustment (ethnicity). T1 gray matter weighted images were adjusted by age and sex using the R package RNifti (https://cran.r-project.org/web/packages/RNifti). The early environment defined the groups for comparison (21 children high environmental score, meaning low adversity or high buffering environment, 22 children low environmental score, meaning more adversity). The Fusion ICA Toolbox (http://mialab.mrn.org/software/fit/) within MATLAB® R2014 was used to run the analysis. The number of independent components estimated using minimum description length

criteria (Calhoun, Adali, Pearlson, & Pekar, 2001; Pearlson et al., 2015) was 8 for MRI data. SNP dimensionality inside the toolbox was used for the genetic modality resulting in 16 estimated independent components. Components for both modalities were converted to z-scores and a threshold at |Z| > 3.5 was used to identify significant brain regions and |Z| > 2.5 for SNPs that contributed the most for the component overall pattern. Significant components associations p-value was adjusted for multiple comparison (128 comparisons) by Bonferroni. To identify the anatomical classification of brain areas included in the significant MRI components, Talairach coordinates were used (Talairach & Tournoux, 1988.). The SNPs from the significant genetic components were analyzed using Metacore® and Panther (http://pantherdb.org/), to identify associated underlying biological processes. Loading coefficients, which describe the presence of the identified component across subjects (Liu et al., 2012), were extracted for each component, modality and subject. The mean subject-specific loading coefficients of these components between children from high and low early environment index groups were compared using Student's t-test.

# Characterization of the prefrontal VAMP1 co-expression network

Gene ontology (GO) enrichment analysis: Enrichment analysis of the genes comprising PFC-ePRS-VAMP1 was performed using Metacore® (<a href="https://portal.genego.com">https://portal.genego.com</a>) for molecular functions.

Gene interaction network analysis: GeneMANIA (<a href="https://genemania.org/">https://genemania.org/</a>; (Warde-Farley et al., 2010) was used to analyze functional interactions between the genes from our list of PFC-VAMP1 co-expressed genes. The topological properties (Neves de Oliveira, Dalmaz, & Zeidán-Chuliá, 2018; Yu, Kim, Sprecher, Trifonov, & Gerstein, 2007) of the network (such as degrees and betweenness) were considered using Cytoscape software (Saito et al., 2012). The data were retrieved from the GeneMania database and the network constructed in Cytoscape. Degrees are calculated by summing the number of adjacent nodes, giving information about the local topology, while betweenness considers the number of shortest paths linking two nodes and passing through a node n. Nodes with degrees higher than +1SD above the mean were considered hubs, and nodes with betweenness higher than +1SD above the mean were considered bottlenecks (Neves de Oliveira et al., 2018), and were identified as central nodes within the network.

In order to obtain insight into possible biological mechanisms related to this gene network, we used the *FUMA* (Watanabe, Taskesen, Van Bochoven, & Posthuma, 2017) (<a href="http://fuma.ctglab.nl">http://fuma.ctglab.nl</a>) GENE2FUNC process. Age specific expression patterns based on Brainspan (Miller et al., 2014) for each gene were visualized as a heatmap. Overrepresentation in sets of differentially expressed genes (DEG; sets of genes which are more (or less) expressed in a specific age in brain compared to other ages) was also obtained. The proportions of overlapping genes, against gene sets obtained from MsigDB and WikiPathways, enrichment *P*-value, and which input genes are overlapping with the present gene list were also visualized using FUMA (Watanabe et al., 2017).

### **Statistical Analysis**

The data were analyzed using the IBM Statistical Package for the Social Sciences (SPSS) version 24.0 (Armonk, NY: IBM Corp.) and R (R Core Team, 2014).

Descriptive statistics: Baseline characteristics of the samples according to ePRS categories (median split) are shown in Table 1. Low and high ePRS groups were compared using Student's t-test for independent samples for means and Chi-square test for percentages (for categorical variables). In the main (MAVAN) cohort, differences between low and high ePRS groups were

not statistically significant for birth weight, gestational age at birth or maternal age at birth, socioeconomic status, or environmental index. In the replication (GUSTO) cohort, no differences were observed in these parameters, except for birth weight. Therefore, we included birth weight as one of the covariates in the model. Student's t-test was also applied to compare mean subject-specific loading coefficients between children from high and low environment score in p-ICA.

Analysis: For all behavioral outcomes in both main and replication cohorts, we applied linear regression analysis to examine the effect of interaction between genetic scores (PFC-eRPS-VAMP1, as well as PFC-eRPS-VAMP2 and HPC-ePRS-VAMP1 when testing the specificity of the score) and the environmental index on cognitive flexibility and spatial working memory. Simple slope analysis was conducted to analyze the post-hoc differences between low and high ePRS groups. In the replication cohort, one subject was identified as an influential point and was excluded from the analyses. All analyses were adjusted for sex, age, three genetic PCs, and site for MAVAN cohort.

### Results

PFC-ePRS-VAMP1 score created from co-expressed genes in the PFC moderates the effect of the environmental index on cognitive flexibility and spatial working memory in 4 years-old children

A Poisson regression showed a significant effect of ePRS and environmental index interaction in predicting reversal learning ability (evaluated as the sum of errors in the reversal stages of IED task, stages 2, 5, and 7) in MAVAN 4 years-old children ( $\beta$  = -0.12, p = 0.003; see Figure 1A). To investigate the specific effects in the low and high ePRS groups we performed simple slopes analysis, that showed that the effect of environmental index on the number of errors in reversal learning stages was larger with the increase of PFC-ePRS-*VAMP1*: for low ePRS score (-1 SD) the estimated effect of the environmental score on the outcome was  $\beta$ =0.11, p = 0.06 and for the high ePRS score (+1 SD) the estimated effect was  $\beta$ =-0.13, p = 0.01. This suggests that children from the high ePRS group had less ability to show reversal memory when exposed to an adverse environment.

There was also a significant interaction effect between ePRS and environmental index in predicting attentional flexibility in the extradimensional set shift (evaluated as the number of errors in the 8<sup>th</sup> stage, where extradimensional shift occurs in the IED task) ( $\beta = 0.04$ , p = 0.03; Figure 1B). A simple slopes analysis showed that the effect of environmental index on the number of errors in attentional flexibility increased with the decrease of PFC-ePRS-*VAMP1*: for low ePRS score (-1 SD);  $\beta$ =-0.05, p = 0.08 and for the high ePRS score (+1 SD)  $\beta$ =0.03, p = 0.16. Therefore, attentional flexibility for extradimensional shift may be influenced by the quality of the environment, and individual differences are expected according to the ePRS. No significant differences were observed for the interaction between environmental index and PFC-ePRS-*VAMP1* in predicting errors in the intra-dimensional shift ( $\beta$ =-0.12, p=0.14).

A linear regression analysis of the performance in the spatial working memory task (SWM) showed a significant effect of ePRS x environmental index interaction on total errors in the 4 boxes stage of the task (Figure 1C;  $\beta = 0.34$ , p = 0.02). Simple slope analysis showed that the effect of environmental index on the number of Total errors changes with the PFC-ePRS-*VAMP1*: for low ePRS score (-1 SD);  $\beta$ =-0.33, p = 0.11 and for the high ePRS score (+1 SD)  $\beta$ =0.32, p = 0.08. This suggests that this ePRS influences the way the individual responds to the environment, when evaluating spatial working memory at this age.

Pearson correlations to check interrelationships between performances in the distinct CANTAB tests were performed. No correlations were found between (i) spatial working memory

(total errors) and IED (errors in stage 8) (-0.00259), (ii) spatial working memory and reversals (0.0425), or IED (stage 8) and reversals in the IED test (-0.102).

In order to test the region-specificity of the PFC-ePRS-VAMP1 findings, we calculated ePRS scores considering genes co-expressed with the VAMP1 gene in the hippocampus (HPC-ePRS-VAMP1); we tested the protein-specificity considering genes co-expressed with the gene coding for VAMP2 (VAMP2) in the prefrontal cortex (PFC-ePRS-VAMP2). No significant interaction effects between ePRS (hippocampal ePRS-VAMP1 score and prefrontal ePRS-VAMP2 score) and environmental index were observed on all the outcomes. More specifically, linear regression analysis for reversal learning (errors in stages 2, 5, and 7 of the IED task) including HPC-ePRS-VAMP1,  $\beta$ =-0.07, p=0.21, and including PFC-ePRS-VAMP2,  $\beta$ =-0.03, p=0.47; for attentional flexibility (errors in stage 6 and stage 8 of the IED task), for HPC-ePRS-VAMP1,  $\beta$ =0.004, p=0.97 for errors in the 6th stage, and  $\beta$ =0.02, p=0.37 for errors in the 8th stage, and for PFC-ePRS-VAMP2,  $\beta$ =0.007, p=0.94 for errors in the 6th stage, and  $\beta$ =0.004, p=0.82 for errors in the 8th stage; and for total errors in the SWM task, for HPC-ePRS-VAMP1,  $\beta$ =-0.24, p=0.12, and for PFC-ePRS-VAMP2,  $\beta$ =0.11, p=0.44.

# Replication sample

We then aimed at replicating our findings, exploring whether the PFC-ePRS-VAMP1 would interact with early life environmental index to predict attentional flexibility in children in the GUSTO cohort (at 54 months of age). A linear regression analysis was conducted to investigate if percentage of accuracy in the orientation mixed trials of the DCCS task, which involves attentional flexibility, is associated with the ePRS x environment interaction. A significant interaction effect between PFC-ePRS-VAMP1 and environmental index was observed (Figure 2;  $\beta$  = -0.622, p = 0.05). As was observed for the MAVAN cohort, accuracy decreases with increased adversity in the lower ePRS group. A simple slopes analysis showed that the effect of environmental index on the accuracy changes with the PFC-ePRS-VAMP1: for low ePRS score (-1 SD);  $\beta$ =1.00, p = 0.03; and for the high ePRS score (+1 SD)  $\beta$ =-0.183, p = 0.68. Since this sample had shown some effect of high or low ePRS on birth weight, we repeated the analysis adjusting the model for birth weight (using birth weight as a covariate). The same results were obtained (an interaction between PFC-ePRS-VAMP1 and environmental index was observed:  $\beta$  = -0.624, p = 0.05). Simple slopes analysis also remained similar: for low ePRS score (-1 SD);  $\beta$ =1.03, p = 0.03; and for the high ePRS score (+1 SD)  $\beta$ =-0.15, p = 0.73.

# Characterization of the prefrontal VAMP1 co-expression network

Figure 3A shows the connected network (related mainly by coexpression of the genes). Data were retrieved from the Genemania database and the network constructed in Cytoscape. Centralities measures are displayed in Supplementary Table S4. RFNG, IGFBP4, and SGTA had high centrality values for both degrees and betweenness. *Enrichment analyses* of the genes comprising the PFC-ePRS-*VAMP1* were performed using Metacore® (<a href="https://portal.genego.com">https://portal.genego.com</a>) for molecular functions (Figure 3B), and point to the Wnt signaling pathway and actin monomer binding, which is involved in synaptic assembly and neurotransmission. Figure 3C shows overlapping genes from this network, against gene sets obtained using FUMA (Watanabe et al., 2017); many of the gene sets related to the genes in our ePRS are related to inflammation.

Figure 4 displays a heatmap (Figure 4A) of age-specific expression patterns based on Brainspan (Miller et al., 2014) and obtained from FUMA for each gene, and sets of differentially expressed genes (DEG; Figure 4B), whose expression is up or down regulated in the brain

according to the age. It may be observed the presence of sets of genes up-regulated during infancy and childhood. This result suggests distinct co-expression patterns of these genes in adulthood.

MRI Gray matter density and the PFC-ePRS-VAMP1

A multivariate p-ICA identified imaging/genetic significant associations, correlating regional gray matter density and SNP-based PFC-ePRS-VAMP1 data. Significant relationships were found between three phenotype-genotype component pairs (Table 3). When comparing the mean loading coefficients of these components between children from high and low environmental index groups using Student's t-test, we observed statistically significant differences for MRI components 4 (t = -3.388, p = 0.001) and 7 (t = -2.149; p = 0.037) and for genetic component 11 (t= 2.556, p=0.014). This suggests that the quality of the environment influences gray matter density and SNP-based PFC-ePRS-VAMP1 relationship in these components. Since MRI component 4 and genetic component 11 association was significant after multiple comparison correction by Bonferroni and both had a significant difference in its loading coefficient according to the environment, it was of primary interest in the present study, and it will be further considered. Figure 5 illustrates the relationship for the chosen linked components (genetic component 11 and MRI component 4). Active regions are listed in Supplementary Table S5. Many regional variations contribute to this component, located in distinct portions of PFC, parietal cortex, cingulate gyrus, and temporal gyrus.

In the genetic component 11, from the 281 SNPs used, we found 7 significant SNPs with contribution weights above 2.5 (Supplementary Figure S1). An enrichment analysis pointed to GO processes Wnt-signaling (adjusted p = 0.046) and extracellular matrix-cell signaling (adjusted p = 0.046). The genes related to these SNPs are also significantly enriched in a gene set of the Hallmarck P53 pathway (adjusted p = 0.016).

### **Discussion**

In this study we considered individual differences in the expression of a gene network that might explain some observed susceptibilities to environmental changes, and the influence of these factors on cognitive flexibility in children. A scheme of potential effects is illustrated in Figure 6. We observed interactions between the quality of the environment in which the individual was raised and the PFC-ePRS-*VAMP1* score on attentional flexibility in the extra-dimensional shift, spatial working memory, and reversal learning in young children. Our results are in line with reports from the literature, that show that these functions are dissociated (e.g., Birrell & Brown, 2000; Conor Liston et al., 2006; McAlonan & Brown, 2003; Rogers, Andrews, Grasby, Brooks, & Robbins, 2000), to such an extent that early environment interacted with the genetic score distinctly when considering different modalities of executive functions. We also observed an association between extracted data components of this gene network and data from gray matter density components.

Regarding the effect of the early environment, the present findings are consistent with previous studies, both in animal models and in humans, that have pointed to the susceptibility of cognitive flexibility to the milieu in which the individual is raised (Harms et al., 2018; Lazzaretti et al., 2018; Romero-Martínez et al., 2013; Sakhai, Saxton, & Francis, 2016; Xu et al., 2016). Our gene network was built around a select set of genes co-expressed with VAMP1, a SNARE complex protein, whose functionality in human cortex has been related to some cognitive abilities (Ramos-Miguel et al., 2018). In addition, early stress leads to altered synaptic morphology and function (Arcego et al., 2016; Folha et al., 2017; Lazzaretti et al., 2018; Lesuis et al., 2019; Xu et al., 2016;

Zimmermann, Richardson, & Baker, 2019), and changes in synaptic connectivity in the PFC have also been observed concomitantly with altered working memory or attention (e.g., Halim et al., 2003; Hansel & Mato, 2013; Morris et al., 2016).

Four years-old children from MAVAN cohort showed a performance somehow better in the CANTAB tasks than that reported by Luciana and Nelson (Luciana & Nelson, 1998), who studied children with different ages. This could be due to differences in the sample, but possibly another factor to consider would be the fact that our study is more recent, and children have become more used to perform tests in computer screens in the last decades. We also used the site of data collection (Hamilton or Montreal) as a variable in the regression analysis, and no effect was observed comparing these two sites.

An interesting, yet somehow expected finding was that the quality of the early environment had opposite effects upon reversal learning and attentional flexibility in terms of *PFC-ePRS-VAMP1* effect as a moderator. These two functions have distinct requirements since they operate at different moments of cognitive information processing: While attentional flexibility demands the ability to shift attention to a distinct stimulus, reversal learning requires the individual to be able to make a context discrimination and, then, learn that the opposite becomes true.

These functions are also mediated by different subregions of the PFC. Several lines of evidence derived from lesion and pharmacological studies in animals, as well as lesion and imaging studies in humans, support the idea that distinct regions of the PFC mediate different forms of cognitive flexibility (Birrell & Brown, 2000; Bissonette et al., 2008; Dias, Robbins, & Roberts, 1996; Floresco, Block, & Maric, 2008; Manes et al., 2002; McAlonan & Brown, 2003; Morris et al., 2016; Rogers et al., 2000; Rygula, Walker, Clarke, Robbins, & Roberts, 2010). It is suggested that the medial prefrontal cortex (mPFC) in rodents (Birrell & Brown, 2000; Bissonette et al., 2008; Floresco et al., 2008), or the dorsolateral PFC (dlPFC) in primates (Dias et al., 1996; Manes et al., 2002; Morris et al., 2016; Nakahara, Hayashi, Konishi, & Miyashita, 2002; Rogers et al., 2000), has a role in shifting between attentional sets or strategies. Regarding working memory, studies have also implicated parts of the mPFC, such as the prelimbic and infralimbic cortices in this function in rodents (Gisquet-Verrier & Delatour, 2006; Schwabe, Enkel, Klein, Schütte, & Koch, 2004), and the lateral PFC in humans (Manes et al., 2002; Müller, Machado, & Knight, 2002; Owen et al., 1990). On the other hand, the orbitofrontal cortex (OFC) mediates reversal learning. Lesions or pharmacological inactivation of the OFC impair reversal learning in rodents (Bissonette et al., 2008; Hervig, Piilgaard, Božič, Alsiö, & Robbins, 2020; McAlonan & Brown, 2003; Schoenbaum, Setlow, Saddoris, & Gallagher, 2006). Similar results are found in non-human primates (Dias et al., 1996; Rygula et al., 2010), and in humans (Hornak et al., 2004), and the importance of OFC for reversal learning is also shown through event-related fMRI (Hampshire & Owen, 2006). In addition, OFC lesions do not impair extradimensional shifting (Manes et al., 2002; McAlonan & Brown, 2003; but see Chase, Tait, & Brown, 2012), and conversely lesions in the medial PFC do not impair reversal learning (Birrell & Brown, 2000; Floresco et al., 2008). In humans, OFC and dIPFC also show distinct patterns of activation during performance in cognitive tasks (see Moghaddam & Homayoun, 2008 for a review). Therefore, a functional dissociation is observed between these regions.

This functional dissociation is also observed when considering stress effects on cognitive flexibility, as we pointed in the Introduction section. For example, in animal models, chronic stress impairs working memory (Barsegyan, Mackenzie, Kurose, McGaugh, & Roozendaal, 2010; Cerqueira et al., 2005; Mika et al., 2012; Mizoguchi et al., 2000), and extradimensional set-shifting (Bondi et al., 2008; Jett et al., 2017; Conor Liston et al., 2006; Moench et al., 2020; Mohamed et

al., 2020; Naegeli, O'Connor, Banerjee, & Morilak, 2013; Nikiforuk & Popik, 2014; Xu et al., 2016; Zhang et al., 2017), while reversal learning is preserved. However, some physical stressors may affect reversal learning (Bondi et al., 2008; Danet et al., 2010; Lapiz-Bluhm et al., 2009). In humans, four weeks of psychosocial stress changed the connectivity of dlPFC, and impaired attentional set-shifting (Liston, McEwen, & Casey, 2009), but not reversal learning. It has been suggested that chronic stress turns strategies towards habitual responding (Soares et al., 2012).

With regard to the opposing effects of the early environment on these functions according to the genetic scores, some studies in animal models have also pointed to distinct effects of stress according to the structure and function analyzed and according to the previous stress history. For example, (Liston et al., 2006) showed that repeated restraint stress in rats induced contrasting effects on mPFC and OFC apical dendrites: a retraction of apical dendrites in the mPFC was observed, with a corresponding selective impairment of extradimensional attentional set-shifting, while reversal learning was not affected, and an increased dendritic arborization was observed in the OFC (Liston et al., 2006). These contrasting changes in mPFC and OFC neurons morphology after stress have also been observed in their firing properties (Moghaddam & Homayoun, 2008), further suggesting that mPFC and OFC functions are differently modulated by stress exposure. In addition, Graybeal et al (2011) found that under some conditions, stress can facilitate reversal learning. Another study (Snyder, Hill-Smith, Lucki, & Valentino, 2015) has reported a dissociation of the effect of corticotropin-releasing hormone (CRH), a neuropeptide whose levels in adulthood may be affected by early adversities (Carpenter et al., 2004). CRH may facilitate set-shifting or reversal learning, depending on the stress history of the animals. The authors suggest a potential for stress history to modulate cognitive processing according to variations in CRH neurotransmission. The lack of correlation in the performance on these two tasks in our sample agrees with the literature, also suggesting that the interaction between PFC-VAMP-1 gene network and early adversity affects more than one executive function domain.

In our pICA analysis, we observed that genetic component 11 was significantly associated with MRI component 4, and that the mean loading coefficients of these components between children from high and low environmental index groups was distinct. In other words, adversity is linked to differences in processes like Wnt-signaling and extracellular matrix-cell signaling, particularly in frontal, temporal and parietal regions. It is interesting that many of the brain regions from this component, for example the superior and medial frontal gyrus (Broadmann Areas or BA 6, 10), as well as the superior parietal lobule (BA 7), show altered cerebral blood flow while subjects are performing an ID/ED shift learning task (Rogers et al., 2000). Other regions from this component such as the cingulate cortex (BA 24), demonstrate altered blood flow when the individuals are performing a task of reversal learning relative to ID shift learning (Rogers et al., 2000). Finally regions such as the medial frontal gyrus and the inferior parietal lobule show altered blood flow when the subject is performing extradimensional shifts (Nakahara et al., 2002; Rogers et al., 2000). Some of the regions positively associated with this genetic component have also been related to performance in the DCCS task, including some temporal regions (Pan, Sawyer, McDonough, Slotpole, & Gansler, 2018). These areas are mostly related to cognitive flexibility, working memory, attention and decision making (Fuster, 2015), but some of them are also related to language, as has already being pointed out in neuroimaging studies considering the performance in this type of task (Pan et al., 2018). In sum, the brain regions identified in our anatomo-functional analysis are highly involved in the behavioral outcomes investigated in our study.

MRI studies were done in middle childhood, a late critical phase of brain growth in which brain circuitry is finely tuned to support the operations of the coming adult brain (Caviness Jr,

Kennedy, Richelme, Rademacher, & Filipek, 1996). This phase is associated with significant developmental gains and a shift toward adult level functional capacities in memory (Townsend, Richmond, Vogel-Farley, & Thomas, 2010), and response inhibition (Nichelli, Scala, Vago, Riva, & Bulgheroni, 2005; Velanova, Wheeler, & Luna, 2008). The fact that environment affected associations between genetic components of this ePRS and brain morphology at this stage suggests that environment effects, observed earlier on neuropsychological tests, may leave modifications in brain morphology at this later childhood phase.

Concerning the performance variation in the ability to shift attention, it has been proposed that it could result from alterations in the working memory (Pantelis et al., 2009). In the present study, no correlations were found between these performances, in agreement with other studies (Friedman et al., 2006; Robbins et al., 1998).

The molecular functions enriched in the ePRS-VAMP1 network were especially related to Wnt signaling pathways and actin monomer binding. Wnt signaling pathways (canonical and noncanonical) are related to synaptic assembly and neurotransmission, through regulation of transcription, actin polymerization, and calcium signaling (Inestrosa & Varela-Nallar, 2014; Lie et al., 2005), and these pathways have also been reported to be important in cell proliferation, neurogenesis, and mitochondrial biogenesis (Inestrosa & Varela-Nallar, 2014; Lie et al., 2005). It should be pointed that synaptic plasticity is essential for cognitive function and for biological adaptation to changes in the environment. It involves reorganization of the cytoskeleton and synthesis of new proteins (Ehlers, 2003; Ma et al., 2017). In addition, genetic variations in Wnt signaling pathways have been related to ADHD (Grünblatt et al., 2019), and to spatial learning (Tabatadze et al., 2012). Neuroprotective effects of Wnt signaling on cognitive function in animal models of Alzheimer's disease have been reported (Cisternas et al., 2019; Oliva, Vargas, & Inestrosa, 2013), and chronic stress-induced reductions in Wnt signaling in the PFC in rats has been associated with impairment in cognitive flexibility (Mohamed et al., 2020).

Among the hubs and bottlenecks detected in the network, RFNG codes for O-Fucosylpeptide 3-Beta-N-Acetylglucosaminyltransferase. This transferase modulates NOTCH1 activity (Moloney et al., 2000), which is involved in several functions, including vascular permeability (Miloudi et al., 2019) and expression of synaptic vesicle proteins (Hayashi et al., 2016). Two other nodes with high centrality indexes are the insulin-like growth factor binding protein 4 (IGFBP4), and ITGA7, that codes for integrin subunit alpha 7. Integrins mediate cell membrane interactions with the extracellular matrix, and are present at high levels at synapses, where they help shaping synapse structure and plasticity (Park & Goda, 2016). Therefore, these three central nodes code for proteins that modify plasticity.

When comparing overlapping genes from PFC-ePRS-VAMP1 network with other gene sets (using FUMA (Watanabe et al., 2017)), we observed that many of the gene sets related to the present ePRS network are from studies involving inflammation. Early life stress has been shown to predict peripheral inflammation later in life (Mondelli & Vernon, 2019; O'Connor et al., 2020; Reid et al., 2020), and Nusslock and Miller (Nusslock & Miller, 2016) have proposed a neuro-immune network hypothesis, in which early adversity would sensitize immune cells, propagating inflammation, that could spread to brain structures. That was particularly interesting, since studies both in animals (Culley et al., 2014) and humans (Lasselin et al., 2016) have related inflammation and cognitive flexibility, some of them using the same task used in the present study. Also, performance in the intra/extra-dimensional set shift (IED) test was assessed in obese and non-obese human subjects, and it was observed that low-grade inflammation was an important contributor to explain attentional flexibility performance observed in obese subjects (Lasselin et

al., 2016). In rats, the attentional set-shifting task was used to evaluate the contribution of systemic inflammation to attention impairment, and it was also observed that inflammation affects reversal learning and attentional shifts (Culley et al., 2014).

In conclusion, the network of genes whose expression was enriched in early life and that were coexpressed with *VAMP1* in the PFC seems to be acting as a moderator of early environment quality influence on cognitive flexibility and spatial working memory, both functions in which the PFC is strongly involved. These effects were verified in young children, and this finding was replicated in a different cohort, besides testing the network specificity. pICA analysis pointed to associations between genetic components of this ePRS and gray matter density in regions related to performance in the tasks observed, suggesting that the gray matter density in some of these MRI components is moderated by the quality of the environment. Overall, this study may shed light on how the quality of early environment exerts a long-lasting influence on cognition, and the individual differences in their susceptibility to changes in the environment. Also, new experimental approaches derived from these paradigms might produce empirical support for the observed effects as well as explanation for their mechanisms.

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# **Authors contributions**

CD and PPS conceived the study, participated in its design, and wrote the manuscript. BB participated in the study design, the imaging analysis and wrote the manuscript. RBS, GBCH, and MSK performed acquisition of data on neuroimaging and genotyping. SP contributed by calculating ePRSs for both cohorts. IP and ZW analyzed and interpreted the data. DMA conducted enrichment analysis, made figures, and participated in the interpretation of the data. RMSL made topological analysis and participated in the discussion. EJMF made important methodological contributions and participated in the discussion. JAQ revised important intellectual content. MM was the main person in charge for both cohorts, obtained funding, supervised the research, and reviewed the article in the neurobiological and technological aspects. All authors provided feedback and revision of the final manuscript.

The authors have no competing interests to declare.

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**Table 1**: Description of the baseline characteristics of the MAVAN and GUSTO samples according to high and low PFC-ePRS-*VAMP1*.

Cohorts	MAVAN (discovery sample)			GUSTO (replication sample)		
Characteristics	Low ePRS (n = 66)	High ePRS (n = 66)	P-value	Low ePRS (n = 70)	High ePRS (n = 69)	P-value
Males (%)	34 (51.5%)	30 (45.5%)	0.6	32 (45.7%)	28 (40.6%)	0.66
Maternal age at birth (years)	31.3 <u>+</u> 4.33	30.1 <u>+</u> 4.88	0.2	32.02 <u>+</u> 4.52	30.79 <u>+</u> 6.0	0.20
Full weeks of gestation	39.2 <u>+</u> 1.11	39.2 <u>+</u> 1.3	0.8	38.92 <u>+</u> 1.34	38.99 <u>+</u> 1.04	0.67
Birth weight (in grams)	3356 <u>+</u> 459	3264 <u>+</u> 452	0.2	3207 <u>+</u> 412	3057 <u>+</u> 425	0.03
Low SES	17 (26.6%)	15 (25%)	0.8	7 (10.0%)	9 (13.0%)	0.71
Early life environmental score	1.97 (2.17)	1.47 (2.27)	0.2	1.11 <u>+</u> 1.53	0.96 <u>+</u> 1.58	0.55
IED Total Errors Stage 8	23.8 (8.77)	24.4 (7.68)	0.7			
IED Total Errors Stages 2 +5+7	8.67 (7.67)	8.45 (8.83)	0.9			
SWM Total Errors 4 boxes	6.28 (2.97)	5.95 (3.51)	0.6			
DCCS				19.83 (6.11)	18.62 (5.71)	0.23

Data are expressed as means (± standard deviations) or number of participants (percentages). Differences between low and high ePRS groups were not significant for all variables shown (Student's t-test for means and chi-square test for percentages). Low socioeconomic status (SES) in MAVAN: maternal education is high school or less and/or monthly income under low cut off bound according to Statistics Canada

(https://www150.statcan.gc.ca/n1/en/catalogue/75F0002M2006004). Low socioeconomic status (SES) in GUSTO: maternal education attained primary school and/or monthly income <\$2000. For environmental score, see text.

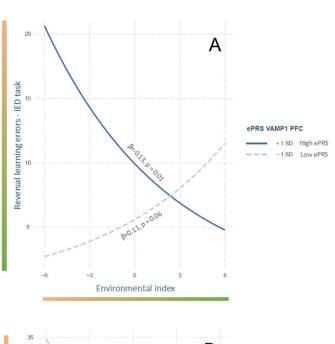
Table 2. Components included in Adversity and positive early life environment scores. The final scores ranged from negative (more adverse) to positive (buffer) values. Presence of each component (described in each bullet) yielded 1 point, and the scores represent the summation of points (see text for further details).

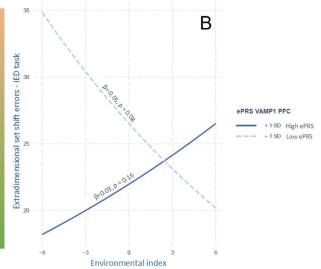
contro (bee te.	oints (see text for further details).						
Score	Component MAVAN	GUSTO					
Adversity	Hospitalization in the first 6 months	Hospitalization in the first 6 months					
Auversity	of life	of life					
	Birth size percentile below 10 <sup>th</sup> percentile or above 90 <sup>th</sup> percentile	Birth size percentile below 10 <sup>th</sup> percentile or above 90 <sup>th</sup> percentile					
	Gestational age below or equal to 37 weeks	Gestational age below or equal to 37 weeks					
	Smoking during pregnancy	Smoking during pregnancy					
	Household total gross income below 30,000\$	Household monthly income below SG\$2000					
	Lack of money score above 7						
	Presence of domestic violence (physical or sexual)						
	Disorganized attachment						
	Poor family function (score greater or equal 2.00)	Poor family function (score greater or equal 2.17)					
	Marital strain score above 3.32						
	Pregnancy anxiety greater than 1.95						
Positive	Birth size percentile greater or equal	Birth size percentile greater or equal					
	to 40% and below or equal to 70%	to 40% and below or equal to 70%					
	Gestational age between 39-40 weeks	Gestational age between 39-40 weeks					
	Household total gross income 80,000\$ and above	Household monthly income above SG\$6000					
	Still breastfeeding at 3 months	Still breastfeeding at 3 months					
	Secure attachment	<u> </u>					
	Good family function (score below 1.15)	Good family function (score below 1.35)					
	Marital strains below 1.45						

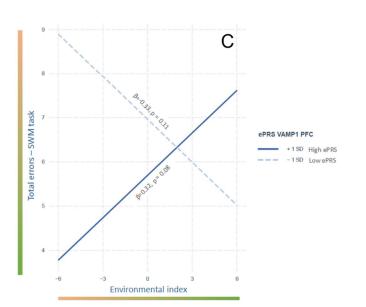
 Table 3. Significant MRI-genetic components association.

Genetic component	Image (MRI) component	Correlation	t value	p-value	Bonferroni corrected p- value
6	3	0.696	6.2149	2.14e-07	2.7392e-05
11	4	-0.653	-5.526	2.0381e-06	0.0002608768
14	7	-0.63891	5.317	4.0123 e-06	0.0005135744

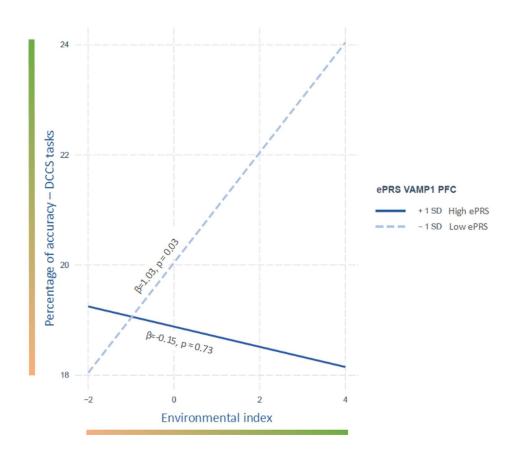
Figure 1. Interactions between PFCePRS-VAMP1 and the environmental quality affecting cognitive flexibility and working memory (4 years-old MAVAN children). A. A Poisson regression analysis showed significant effect of ePRS and environmental index interaction in predicting reversal learning ability (evaluated as the sum of errors in the reversal stages of IED task) in MAVAN 4 years-old children ( $\beta = -$ 0.12, p = 0.003 ). The effect of environmental index on the number of errors in reversal learning was larger with the increase of PFCePRS-VAMP1 (for the high ePRS score (+1 SD)  $\beta$ =-0.13, p = 0.01; simple slopes analysis). B. There was a significant interaction between ePRS and environmental index in predicting attentional flexibility in the extradimensional set shift (evaluated as the number of errors in the 8<sup>th</sup> stage of the IED task) ( $\beta = 0.04$ , p = 0.03). C. Errors in the spatial working memory task: A significant effect of ePRS and environmental index interaction for total errors in the 4 boxes stage of the task ( $\beta = 0.34$ , p = 0.02).



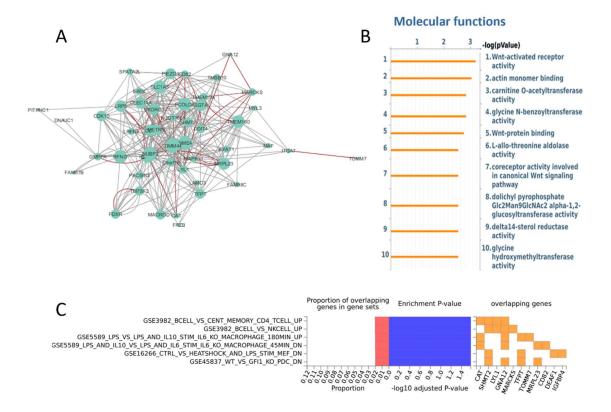




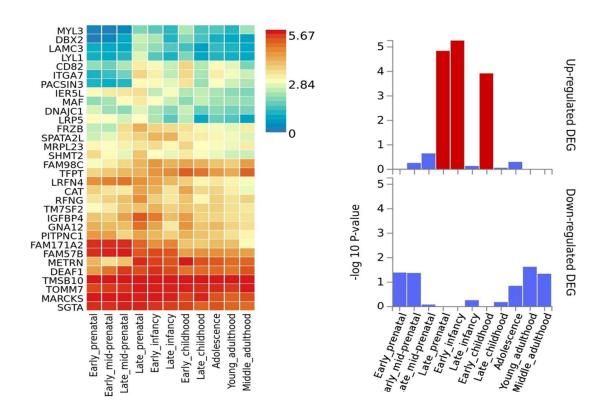
**Figure 2**. Interaction between PFC-ePRS-*VAMP1* and the environmental quality affecting cognitive flexibility (4.5 years-old GUSTO children). Results show percentage of accuracy in the orientation mixed trials of the DCCS task ( $\beta$  = -0.622, p = 0.05). The effect of environmental index on the accuracy was larger with the decrease of *PFC-ePRS-VAMP1* (for low ePRS score (-1 SD);  $\beta$ =1.00, p = 0.03).



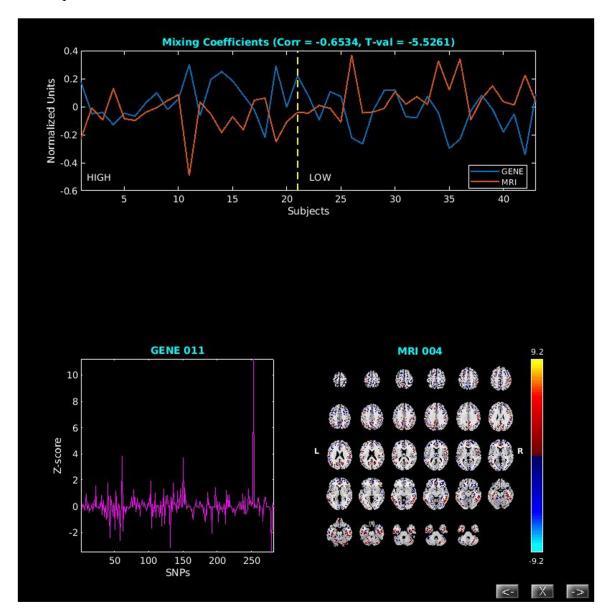
**Figure 3.** Characterization of the PFC-ePRS-*VAMP1* network. **A.** Connected network. Data retrieved from Genemania, and the network constructed in Cytoscape. Edges: gray for co-expression; red for co-localization. Sizes of the nodes are related to degrees (centrality parameter), so that the hubs are bigger. **B.** Enrichment analysis of the genes co-expressed with VAMP1 in PFC using Metacore®. The ten top molecular functions are shown. **C.** Overlapping genes from this network, against gene sets for immunological signatures obtained using FUMA (https://fuma.ctglab.nl/).



**Figure 4.** Age-specific expression patterns of the genes composing the PFC-ePRS-*VAMP1* network. **A.** Heatmap of expression pattern for each gene (based on Brainspan and obtained from FUMA). **B.** Sets of differentially expressed genes (DEG), up or down regulated in brain according to the age. Periods in this figure and Ns are as follows: Early prenatal (8-12 pcw, N=5), Early midprenatal (13-18 pcw, N=7), Late mid-prenatal (19-24 pcw, N=4), Late prenatal (25-39 pcw, N=3), Early infancy (Birth-5 months, N=2), Late infancy (6-18 months, N=3), Early childhood (19 months – 5 years, N=4), Late childhood (6-11 years, N=3), Adolescence (12-19 years, N=4), Young adulthood (20-37 years, N=5), Middle adulthood (~40 years, N=2); (<a href="http://help.brainmap.org/display/devhumanbrain/Documentation">http://help.brainmap.org/display/devhumanbrain/Documentation</a>, Donors and samples).



**Figure 5.** Relationship for genetic component 11 and MRI component 4. Upper panel (A) shows loading coefficients for gene component 11 (in blue) and MRI component 4 (in brown) for each subject in high and low environmental scores groups. (B) shows z scores for each inputted SNP for genetic component 11. (C) shows regional variations in gray matter density contributing to MRI component 4.



**Figure 6.** Summary of the findings. Expression-based PFC-ePRS-*VAMP1* moderates the effects of environmental quality on cognitive flexibility and working memory. The PFC-ePRS-*VAMP1* network is enriched in biological processes such as Wnt signaling and actin monomer binding, and the genes in this network show overlap with gene sets from studies related to inflammation. A parallel-ICA study showed that genetic component 11 was significantly associated with MRI component 4, and that the mean loading coefficients of these components between children from high and low environmental index groups was distinct. SNPs from this MRI component are enriched in processes related to Wnt signaling, P53 pathway, and integrin signaling.

