1	Epigenetic dysregulation of dopaminergicsystem by maternal cafeteria dietduring
2	early postnatal development
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34

35 Abstract:

36 Dopamine is a neurotransmitter crucial for motor, motivational, and reward-related 37 functions. Our aim was to determine the effect of a palatable maternal diet on the 38 transcriptional regulation of dopaminergic-related genes during perinatal development of 39 the offspring. For that, female offspring from dams fed with a control (CON) or a cafeteria 40 (CAF) diet were sacrificed on embryonic day 21 (E21) and postnatal day 10 (PND10). 41 Using micropunch techniques, ventral tegmental area (VTA) and *nucleus accumbens*(NAc) 42 were isolated from brain's offspring. Bioinformatic analysis of the promoter regions, 43 mRNA quantification and methylation studies were done. The increase in tyroxine 44 hidroxylase (TH), dopamine receptor (DRD) 1 and ghrelin receptor (GHSR) expression in 45 VTA and NAc from E21 to PND10 was correlated with changes in DNA methylation of 46 their promoter regions. Maternal diet did not affect the expression patterns in E21.At 47 PND10, maternal CAF diet decreased the transcription of TH, GHSR, DRD2 and dopamine 48 transporter (DAT) in VTA. Interestingly, the changes in TH, DRD2 and DAT expression 49 were related to the methylation status of their promoters. In NAc, maternal CAF diet 50 reduced DRD1, DRD2 and DAT expression in the offspring at PND10, although 51 alternations in the methylation patterns were only detected in DAT promoter. These results 52 show the importance of maternal nutrition and provide novel insights into the mechanisms 53 through which maternal junk-food feeding can affect reward system during development 54 and early postnatal life. Particularly important is the expression decline of DRD2 given its 55 physiological implication in obesity and addiction.

56

57 Highlights

- Maternal cafeteria diet decreased the transcription of TH, DRD2 and DAT in the
 ventral tegmental area of neonatal offspring.
- 60 2. In *nucleus accumbens*, maternal cafeteria diet reduced DRD1, DRD2 and DAT
 61 expression at postnatal day 10.
- 62 3. The methylation status of dopaminergic gene promoters was affected by maternal63 diet.

64	Abbreviations
65	ACT: activator
66	AP: activator protein
67	C/EBP: CCAAT/enhancer-binding protein
68	CAF: cafeteria
69	CRE: cAMP response element
70	CREB: cAMP response element-binding protein
71	DA: dopamine
72	DAT: dopamine transporter
73	DRD: dopamine receptor
74	E: embryonic day
75	GHSR: ghrelin receptor
76	GRE: glucocorticoid response element
77	HFD: high fat diet
78	INH: inhibitor
79	NAc: nucleus accumbens
80	NF-1: nuclear factor 1
81	NF-AT: nuclear factor of activated T cells
82	Sp1: selective promoter factor 1
83	TH:tyrosine hydroxylase
84	VTA: ventral tegmental area
85	

86 Introduction

87 Obesity represents one of the major public health problems in the world and it is mainly 88 caused by overeating and physical inactivity. Palatable, or high-fat, high-sugar, foods 89 activate the dopaminergic signaling pathways within the mesolimbic reward system 90 (Berthoud, 2006; Fulton, 2010). Dopamine (DA) is a neurotransmitter crucial for motor, 91 motivational, and reward-related functions of the central nervous system(Cragg and Rice, 92 2004) and is also associated with the gratifying effects of sex and drugs of abuse (Nestler 93 and Carlezon, 2006). This neurotransmitter is produced in the dopaminergic neurons of the ventral tegmental area (VTA)by the action of the tyrosine hydroxylase (TH) (Baik, 2013a, 94

95 2013b). Interestingly, it was shown that there is a high degree of co-expression of TH and 96 ghrelin receptor (GHSR) in VTA in adults (Zigman et al., 2016a, 2016b). It is well known 97 that ghrelin impairs VTA by inducing DA release and stimulating food intake (Fulton, 98 2010); thus, GHSR-TH coexistence suggests a possible coordinated regulation of DA 99 levels. VTA dopaminergic neurons project to the *nucleus accumbens* (NAc), where DA is 100 released and binds to specific DA receptors (DRD1 and DRD2). This nucleus receives 101 sensitive information from various regions, and then projects to the hypothalamic and 102 midbrain areas that contribute to the motor action of food (Valdivia et al., 2014). NAc 103 mediates reward effects in response to natural stimuli and is where termination of DA 104 signaling occurs through reuptake by the active DA transporter (DAT)(Cragg and Rice, 105 2004). Prolonged exposure to palatable food in adult rodents is associated with behavioral 106 and neurophysiological adaptations comparable to those seen in drug addicts. In particular, 107 desensitization of the central reward pathway, which then drives continued 108 overconsumption(Ong and Muhlhausler, 2011).

109 Several epidemiological and experimental studies have demonstrated that susceptibility to 110 obesity can have its origins early in life and can be influenced by the nutritional experience 111 during critical periods of fetal and early postnatal development. In rodents, an experimental 112 model used to reproduce the characteristics of the Western obesogenic food is the cafeteria 113 diet (CAF) (Sampey et al., 2011).Numerous authors reported that exposure to a maternal 114 diet dominated by palatable food and/or high-fat diet before and during pregnancy and 115 throughout lactation, disturb glucose and lipid homeostasis, predispose to adiposity, modify 116 food preference, alter the development of the central reward circuitry and modify the 117 expression of brain genes such as DAT, DRD1 and DRD2 in the offspring after birth and 118 later in life (Akyol et al., 2009; Bayol et al., 2007; Bayol et al., 2008; Chen et al., 2008; 119 Ong et al., 2012; Ong and Muhlhausler, 2011; Sarker et al., 2018; Vucetic et al., 2010). 120 However, there are no prior reports about the effects of these maternal diets on the 121 dopaminergic reward system during perinatal periods.

Metabolic and eating disorders are associated with alterations in the DNA methylation pattern of particularly genes, such as TH and DAT(Vucetic et al., 2012). DNA methylation represents one of the most important epigenetic mechanisms for blocking gene expression and implicates the addition of methyl groups to CpG dinucleotides. A CpG island is a DNA sequence generally greater than 250 bp that is rich in CpG sitesand, thus,
ithas a key role in transcriptional control(Deaton and Bird, 2011). In this context, DNA
methylation provides a mechanism by which maternal diet can modify the predisposition of
the offspring to obesity-associated disordersor other pathologies.

130 In the present study, we hypothesized that maternal CAF diet is associated with alterations 131 in the epigenetic control of dopaminergic system of the reward pathway in early postnatal 132 development. Thus, the objective of our work was to analyzed the transcriptional regulation 133 of dopamine-related genes in the brain of female offspring (F1), from dams fed with 134 standard chow and CAF diet, at embryonic day 21 (E21) and postnatal day 10 (PND10). 135 The study was performed in two discrete brain reward areas, NAc and VTA, using 136 microdissection techniques. This experimental model allowed us to study the individual 137 and combined effects of age (E21 vs. PND10) and maternal diet (CON vs. CAF) on the 138 mRNA expression of dopaminergic genes and the DNA methylation mechanisms that are 139 involved in their control.

140

141 Experimental Procedures

142

143 Animals an experimental design

Wistar female rats were obtained from the Department of Human Physiology of the School
of Biochemistry and Sciences (UNL). All animals' procedures were approved by the
Ethical Committee of the School of Biochemistry and Biological Sciences (UNL, Santa Fe,
Argentina) and designedin accordancewith the Guide for the Care and Use of Laboratory
Animals issued by the U.S. National Academy of Sciences (Commission on Life Sciences,
National Research Council, Institute of Laboratory Animal Resources, 1996).

Rats were housed two per cage, at 22 ± 2 °C and with a 12-h light–dark cycle, and fed with either standard chow (CON) or a cafeteria diet (CAF) (N= 10/group) from weaning. The standard chow (Cooperación, ACA Nutricion Animal, Buenos Aires, Argentina) provided 12.55 KJ/g, 5% energy as fat, 23% protein and 72% carbohydrate. The CAF diet was composed of standard chow and food that reflects variety, palatability, and energy density (parmesan cheese, cheese flavored snacks, crackers, sweet biscuits, pudding, and chocolate). This diet provided an average of 20.29 KJ/g, 49% of energy as fat, 7% as protein, and 44% as carbohydrate, in addition to that provided by the standard chow.Dietary composition and treatment procedure are described in Lazzarino et al. (2017).

159 On the 14th week of treatment, when CAF animals were significantly heavier of that than

the CON, females were mated with male rats that were housed under standard laboratory conditions during all the experiment $(22 \pm 2 \,^{\circ}C, 12$ -h light–dark cycle, fed with standard chow). After mating, each dam was single caged and continued with the respectively diet. Five dams per diet groupwere euthanized on embryonic day 21(E21). The rest of the

- animals (N=5/group) were maintained and at day 1 after delivery each litter was adjusted to
 8 pups per dam. At postnatal day 10 (PND10), pups were euthanized.During all the
- 166 experimental period, dam body weight and energy intake were recorded weekly and litter
 167 weight was measured daily. After euthanization, female fetus and pups brains (named as
 168 E21-CAF, E21-CON, PND10-CAF and PND10-CON) were removed, frozen on dry ice
- 169 and stored at -80 °C until sectioning for RNA and DNA analysis.
- 170

171 Micropunches of VTA and NAc

172 Following the procedure of microdissection technique described by Palkovits (Palkovits 173 and Brownstein, 1988), embryo and pup brains were cut in a cryostat at -12 °C (serial 174 coronal sections of 150µm). To identify and punch VTA and NAc regions, theatlas of the 175 developing rat nervous system(Paxinos et al. 1994) and atlas of the postnatal rat brain in 176 stereotaxic coordinates(Khazipov et al. 2015) were used. Both areas were removed 177 bilaterally using a 0.5 mm stainless steel micropunch needlesand the reproducibility was 178 checked analyzing the topography of the holes under a stereo microscope (Stemi 305, 179 Zeiss, Oberkochen, Germany). Samples were stored at -80 °C until RNA and DNA 180 isolation.

181

182 Reverse transcription and real-time quantitative PCR analysis (qRT-PCR)

VTA and NAc areas(N=8/group) were homogenized in TRIzol (Invitrogen, Carlsbad, CA, USA), and total RNA was isolated. 1 µg of RNA were reverse-transcribed into cDNA with Moloney Murine Leukemia Virus reverse transcriptase (10 units; Promega, Madison, WI, USA) as previously described(Rossetti et al., 2015) and final product was diluted with nuclease-free water to a final volume of 60 µl. Reverse-transcribed products were combined with HOT FIRE Pol Eva Green qPCR Mix Plus (Solis BioDyne; Biocientífica, Rosario, Argentina) and 10 pmol of each primer (Invitrogen) and further amplified in duplicate using Real-Time DNA Step One Cycler (Applied Biosystems Inc., Foster City, CA, USA).The primer pairs used are detailed in Table 1 and the protocol for real-time quantitative PCR is described byRossetti et al. (2015).

194

195	Table 1. Sec	uences of pri	mer oligonu	cleotides for	PCR amplification.

Target	Primer sense	Primer antisense	Temperature of annealing (°C)
L19 (housekeeping)	5'- AGCCTGTGACTGTCCATTCC -3'	5'- TGGCAGTACCCTTCCTCTTC -3'	60
TH	5'-TACCAAGATCAAACCTACCAGCC-3'	5'-GGTCAAACTTCACAGAGAATGGG-3'	58
DRD1	5'-TCCAAGGTGACCAACTTCTT-3'	5'-GTTACAAAAGGACCCAAAGG-3'	55
DRD2	5'-CCCAGCAGAAGGAGAAGAAA-3'	5'-CAGGATGTGCGTGATGAAGA-3'	55
DAT	5'-CATCACCACCTCCATTAACTCC-3'	5'-CATTGTGCTTCTGTGCCATG-3'	56
GHSR	5'-GCTCTGCAAACTCTTCCA-3'	5'-AAGCAGATGGCGAAGTAG-3'	56

196

197 **Bioinformatics**

198 TH, DRD1, DRD2, DAT and GHSR promoters were analyzed for: a) CpG islands using 199 MethPrimer program (http://www.urogene.org/cgi-bin/methprimer/methprimer.cgi; 200 RRID:SCR_010269); b)restriction sites for Smal (New England BioLabs, Beverly, MA, 201 USA), BstUI(New England BioLabs) or Mae II (Roche Applied Science, Indianapolis, IN, 202 USA); and c) potential binding sites for transcription factors with the bioinformatic tool 203 (http://alggen.lsi.upc.es/cgi-bin/promo_v3/promo/promoinit.cgi?dirDB=TF_8.3; PROMO 204 RRID: SCR_016926) (Messeguer et al., 2002). PCR primers were designed with the online 205 software NCBI **Primer-BLAST** (National for Biotechnology; Center 206 https://www.ncbi.nlm.nih.gov/tools/primer-blast/; RRID: SCR 003095; Table 2).

Table 2. Sequences of primer oligonucleotides for PCR amplification to evaluate methylation sensitive sites inpromoters.

Target	Primer sense	Primer antisense	Temperature of annealing (°C)
ТН ІС	5'- CCATCAGATTTACCTAGAAGC-3'	5'-TGAGACTATGAAGGGACATTG-3'	51.5

TH-Maell	5'-ACAGCAGGCGTGGAGAGGAT-3'	5'-TGGTGGTCCCGAGTTCTGTC-3'	60
TH-MaeII b	5'-CCTTAGGAAATCCAGCATGG-3'	5'-ATTGCATCCACTGTCACAGG-3'	57.7
TH-Maell c	5'-CATGTGGCTGCTCCTATGTA-3'	5'-GAGAGAGATTGGCACACACA-3'	52.6
DRD1 IC	5'-GTGGTGAGAATCCCCTCAGG-3'	5'-AGTTCCACAGGCGGAGAACC-3'	55
DRD1-MaeII	5'-CAGGCAAAGAGGTTCACAAG-3'	5'-CCGCCATCTAAACAGTTACC-3'	54.6
DRD1-BstUI	5'-AGCAGGAAACCACAGGCACC-3'	5'-GCTTCTGCGGTCAACTCACG-3'	60
DRD2 IC	5'-AATTCTGTGGTGCCTTCTCCT-3'	5'-ATGGGGTCAATCCAGAGTAGA-3'	55
DRD2-BstUI	5'-AGTGCAGAGATAGTTCTGGG-3'	5'-AGAAGCCACAGACTGTCGTT-3'	63
DAT IC	5'-TTTGGGGTCTCAACTAGAAA-3'	5'-TAAGACCTTTTCAGAACCCA-3'	55
DAT- BstUI (a)/MaeII	5'-CTTCTGACAACCTCGCTGGA-3'	5'-GGGGCTTGACAGGAGTCTTT-3'	60
DAT- BstUI (b)/SmaI	5'-CGTACAACACCGAAGGAAGA-3'	5'-CGAGGTTGTCAGAAGCAGAT-3'	57.7
GHSR IC	5'-TCCAGCATACTCCTTATCCA-3'	5'-TGGCAATCTTAGAACACACC	54.6
GHSR- BstUI(a)/SmaI	5'-TACGCCACGGTCCTCACCAT-3'	5'-ACGCTGGACACCCACACCAT-3'	61
GHSR- <i>BstUI</i> (b)/ <i>MaeII</i>	5'-TCTCCCTTTCCTCTCCAAGC-3'	5'-TTCGTCAGGCAGTGAGTCGT-3'	61

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212 Methylation-sensitive analysis

213 Genomic DNA from VTA and NAc areas (N=8/group) was isolated using the 214 phenol/chloroform/isoamyl alcohol extraction and digested with 1 unit of SmaI/Mae II or 215 10 units of BstUI and 1X enzyme buffer for 1 h at 25°C, 60 °C or 50 °C, respectively. After 216 purification with the Wizard SV gel and PCR Clean-Up System Kit (Promega, Madison, 217 WI), an optimized qRT-PCR protocol was used to analyze the relative methylation levels of 218 various regions of the TH, DRD1, DRD2, DAT and GHSR promoters (Table 2). The 219 procedure for DNA amplification was previously described by our group in several studies 220 (Lazzarino et al., 2017; Rossetti et al., 2018; Rossetti et al., 2016; Rossetti et al., 2015).

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222 Statistical analysis

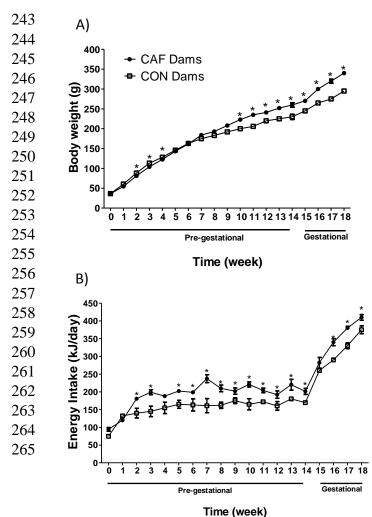
G Power software (http://www.gpower.hhu.de/; RRID:SCR_013726)was used to determine the sample size (Faul et al., 2007). To confirm the normal distribution of the data and variance homogeneity,Shapiro–Wilk test and Levene's test were performed. Weekly body weights,nutrient intake and energy intakewere analyzed using Student's T test; while a twoway ANOVA followed by Bonferroni post-test was implemented to study the ageand diet effects on mRNA and DNA methylation.All the datais expressed as the means \pm SEM and was statistically analyzed using the IBM SPSS Statistics 19 software (IBM Inc.; RRID:SCR_002865), considering significant differences at p<0.05.

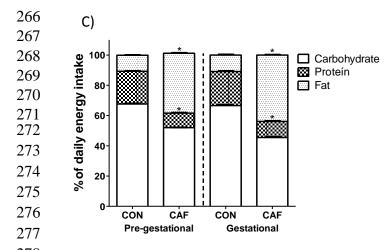
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232 **Results**

233 Effects of CAF diet on dams body weight, nutrient intake and energy intake.

234 The body weights of dams fed with CAF diet increased from week 10 of dietary 235 intervention and on the 14th week of treatment (CAF: 266.5±2.92 g; CON: 240.5±3.1 g; 236 p<0.05) females were mated with male rats. During pregnancy, CAF dams significantly 237 increased gestational weight gain in comparison with those fed the control diet (Fig 1a). In 238 addition, energy intakes over the pre-pregnancy (Week 2 to 14) and pregnancy (Week 16 to 239 18) period remained significantly higher in CAF rats when compared with CON animals 240 (Fig. 1b). Moreover, CAF ratsconsumed a significantly greater percentage of their daily 241 energy intake as fat, and significantly less as protein than CON rats (Fig 1c), during all the 242 experiment.

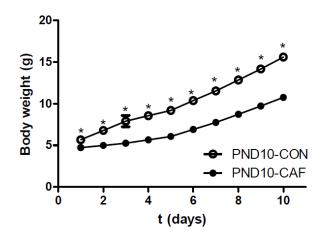




278Fig 1. Body weight (A), energy intake (B) and nutrient intake (C) of dams fed with a control (CON) or a cafeteria279(CAF) diet during pre-gestation (Week 1 to 14) and gestation (Week 15-18) periods(N=10/Group). * indicates280significant differences at p < 0.05 vs. CONgroupby Student's T test.</td>

282 Effects of CAF diet on the body weight of the offspring.

Pups of dams fed with a CAF diet had a significantly lower weight (p<0.05) than those from a CON diet from birth to PND10 (Fig. 2). It is interesting to note that during this period no apparent differences were detected in maternal behavior between CON and CAF groups. At E21no significant differences were detected (data not shown).



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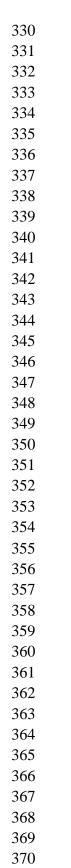
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Fig 2. Body weight pups from dams fed with a control (PND10-CON) or a cafeteria (PND10-CAF) diet from
 birth up to post-natal day 10 (PND10). Values are means, with standard errors represented by vertical
 bars(N=16/Group). * indicates significant differences at p < 0.05 vs. CON groupby Student's T test.

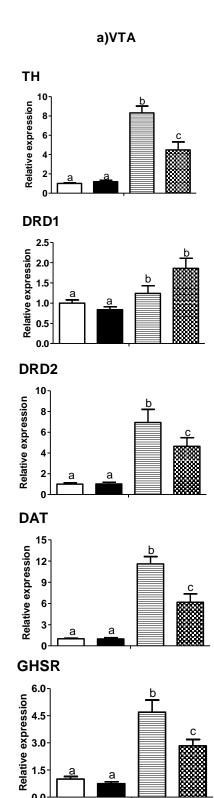
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293 Maternal CAF diet modifies the mRNA expression of dopamine-related genes in the 294 reward brain system of the offspring at early postnatal development. To analyze the effect of maternal CAF diet on dopaminergic reward system in the offspring before and during gestation and lactation periods, we analyzed the expression of molecules that are involved in the synthesis, transport and reuptake of DA in two key regions of the reward system, VTA and NAc, at E21 and PND10.

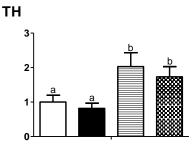
- In VTA, the two-way ANOVA revealed interactions between age and maternal diet for the expression of TH (p <0.01, F = 8,804), DRD2 (p <0.05, F=4.875), DAT (p<0.01, F=13.93) and GHSR (p<0.001, F=8.458) (Fig 3A). Maternal CAF diet decreased the expression of these genes in the offspring in PND10 (DPN10-CAF vs DPN10-CON, p <0.05), without affecting expression in E21 (E21-CAF vs E21-CON, p >0.05). In addition, the increase in age generated an increase on their transcription (E21 vs DPN10, p<0.05). Related to DRD1, mRNA levels were not found to be modified by maternal diet in VTA, but age increased
- 306 the expression in the offspring (E21 vs PND10, p < 0.01, F = 48.86, Fig 3A).
- 307 In NAc, the expression of DRD1 (p<0.05,F=7.369), DRD2 (p<0.01,F=10.01) and DAT
- 308 (p<0.01, F=15.29)was affected by the interactions between age and maternal diet (Fig 3B).
- 309 Their expression decreased in the offspring of dams fed with CAF diet in PND10 (DPN10-
- 310 CAF vs DPN10-CON, p <0.05); however, no expression changes were observed in E21.
- 311 Age generated an increase in the transcription of these genes (E21 vs DPN10, p<0.05). TH 312 and GHSR mRNA levels were not found to be modified by maternal diet in NAc, but age 313 improved the expression in the offspring (E21 vs PND10, p <0.05, $F_{TH} = 10.31$,
- 314 F_{GHSR} =5.29, Fig 3B).
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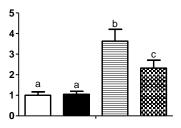
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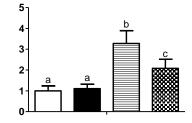




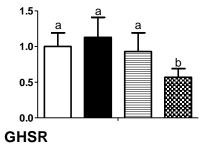




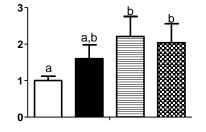












□ E21-CON
 ■ E21-CAF
 □ PND10-CON
 ∞ PND10-CAF

371 Fig 3. Analysis of relative mRNA levels of dopaminergic related-genes and ghrelin receptor in ventral tegmental

372 area (VTA, A) and nucleus accumbens (NAc, B) of the offspring in embryonic day 21 and on post-natal day 10

373 from dams fed with control (E21-CON and PND10-CON, respectively) or cafeteria (E21-CAF and PND10-CAF,

374 respectively) diet.Relative amounts of mRNA in E21-CAF, PND10-CON and PND10-CAF are showed as fold changes
375 from those of E21-CON. The means ± SEM (N=8/group) are represented by columns and error bars. Significant
376 differences at p < 0.05 by Bonferroni's test after two-way ANOVA are denoted by different letters. TH: tyrosine
377 hydroxylase, DRD1: dopamine receptor 1, DRD2: dopamine receptor 2, DAT: dopamine transporter, GHSR: ghrelin
378 receptor.

379

380 Transcriptional regulation of dopaminergic-related genes by DNA methylation in the 381 reward brain system during development and in response to the maternal diet.

382 To determine if the changes observed in the transcript levels of those genes are related to

383 DNA methylation modifications, we analyzed *in silico*the promoter regions of TH, DRD1,

384 DRD2, DAT and GHSR and we determined the methylation state in the E21-CON, E21-

385 CAF, PND10-CON and PND10-CAF groups (Fig. 4 and 5).

- In VTA, DNA methylation levels of TH-MaeII c (p <0.05, F =5.545, Fig 4A), DAT-SmaI
- 387 (p < 0.05, F = 6.943, Fig 4D) and GHSR-Smal (p < 0.05, F = 26.91, Fig 5) sites were affected
- 388 by the interactions between age and maternal diet. In TH-MaeII c and DAT-SmaIsites,
- 389 maternal CAF diet increases methylation in the offspring in PND10 (DPN10-CAF vs
- 390 DPN10-CON, p <0.05); in GHSR-Smal this occurs in E21 (E21-CAF vs E21-CON, p
- 391 <0.05); and in DRD2-BstUI this arises at both stages (E21 and PND10, p<0.05, F=21.95, ,
- Fig 4C). On the other hand, age decrease methylation levels of TH-*MaeII* c site in the offspring of dams fed with CON diet in PND10 (E21-CON vs DPN10-CON, p<0.05). In addition, age decrease methylation levels of DRD1-*BstUI* and GHSR-*MaeII* sites in the offspring of dams fed with both CON and CAF diet in PND10 (E21 vs DPN10, p<0.0001,
- F_{DRD1} = 42.35 and F_{GHSR} =68.51, Fig 4B and 5). No differences were observed in methylation in the others studied sites (data not shown).
- In NAc, DNA methylation levels of DAT-*SmaI*(p < 0.05, F = 15.17), TH-*MaeII* b(p < 0.05, F = 23.66) and DRD1-*MaeII* (p < 0.05, F = 29.88) siteswere affected by the interactions between age and maternal diet. In the first site, maternal CAF diet increased methylation in the offspring in PND10 (DPN10-CAF vs DPN10-CON, p < 0.05). Age also increased methylation levels in this site in the offspring from dams fed with CAF diet (E21-CAF vs
- 403 DPN10-CAF). Contrary, age decreased DNA methylation levels of TH-MaeII b (p <0.005,

404	F = 13.26) and DRD1-MaeII (p <0.0001, F = 33.07) sites in the offspring from dams fed
405	with CON diet (E21-CON vs DPN10-CON). No differences were observed in methylation
406	of DRD2, DAT and GHSR sites (data not shown).
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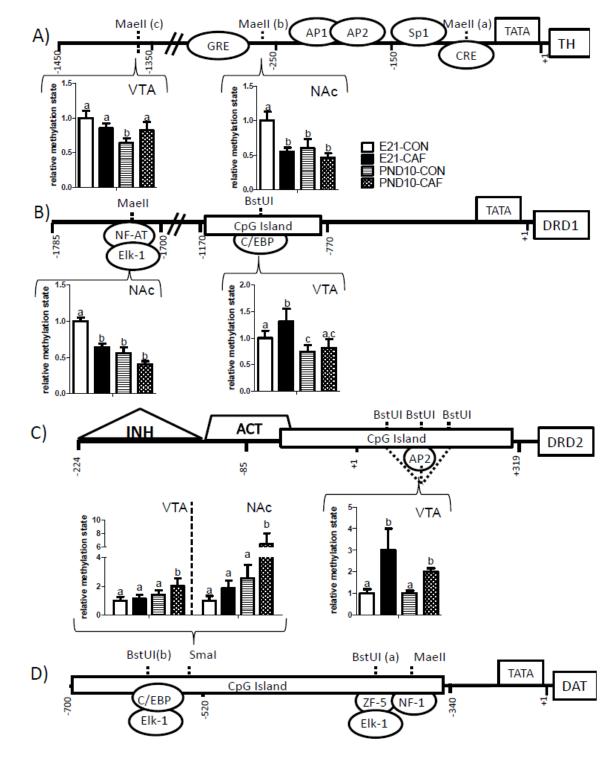




Fig 4. Methylation analysis of dopaminergic related genes. Tyrosine hydroxylase (TH, A), dopamine receptor 1 (DRD1, B),dopamine receptor 2 (DRD2, C) and dopamine transporter (DAT, D) promoters were studied in the ventral tegmental area (VTA) and/or nucleus accumbens (NAc).TATA box, predicted binding sites for transcription factor, CpG islands and CG target sites for digestion by the methylation-sensitive restriction enzymes are indicated.Offspring on embryonic day 21 and on post-natal day 10 from dams fed with control (E21-CON and PND10-CON, respectively) or cafeteria (E21-CAF and PND10, respectively) diet was evaluated. Methylation levels of promoters in E21-CAF, PND10-

426 CON and PND10-CAF are showed as fold changes from those of E21-CON. The means \pm SEM (N=8/group) are 427 represented by columns and error bars. Significant differences at p < 0.05 by Bonferroni's test after two-way ANOVA are 428 denoted by different letters.ACT: activator, AP: activator protein, C/EBP: CCAAT/enhancer-binding protein, CRE: 429 cAMP response element-binding protein, CREB: cAMP response element-binding protein, GRE: Glucocorticoid response 430 element, INH: inhibitor, NF-1: nuclear factor 1, NF-AT: nuclear factor of activated T cells (NF-AT), Sp1: selective 431 promoter factor 1.

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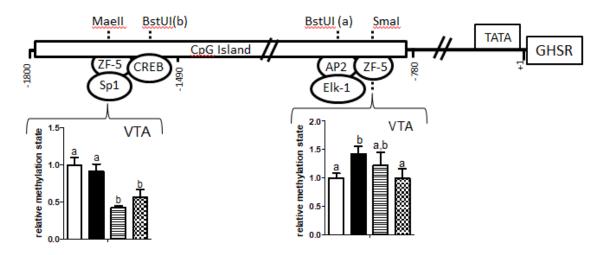




Fig 5. Methylation analysis of ghrelin receptor (GHSR) promoter in the ventral tegmental area (VTA). The offspring brain on embryonic day 21 (E21) and on post-natal day 10 (PND10) from dams fed with control (CON) or cafeteria (CAF) diet wasstudied. TATA box, activator protein (AP), cAMP response element-binding protein (CREB), selective promoter factor 1 (Sp1), CpG islands and CG target sites for*BstUI, MaeII* and *SmaI*are described.Methylation levels of promoters in E21-CAF, PND10-CON and PND10-CAF are indicated as fold changes from those of E21-CON. The means \pm SEM (N=8/group) are represented by columns and error bars. Significant differences at p < 0.05 by Bonferroni's test after two-way ANOVA are denoted by different letters.

443 DISCUSSION

444 The principal aim of the present study was to determine whether exposure to maternal CAF 445 feeding had an impact on dopaminergic reward pathways during perinatal period, selecting 446 a representative point of the embryonic stage (E21) and the lactation period (PND10). 447 Additionally, we analyzed the developmental profile of dopaminergic-related genes 448 between both stages (E21 vs. PND10). We hypothesized that epigenetic modifications may 449 be involved in the transcriptional control of these genes. To our knowledge, this is the first 450 study reporting that: 1)- increase mRNA expression of TH, DRD1 and GHSR genes from 451 E21 to PND10 in females is regulated by methylation mechanisms in VTA and/or NAc; and 2) the offspring from dams fed with CAF diet showed alterations in the transcriptionalregulation of TH, DRD2 and DAT genes in VTA and NAcat PND10.

454

455 Changes in dopamine-relatedgene expression in VTA and NAc during early 456 development are regulated by methylation mechanisms.

457

458 The development of the dopaminergic system of the striatum in the rat begins during 459 embryonic life and continues up to the 3rd postnatal week(Antonopoulos et al., 2002). The 460 first mesolimbic dopamine neurons can be identified in the rat brain in E12, although 461 dopamine axon innervations are not complete until the 3rd week of postnatal life(Ong et al., 2012). TH mRNA was found in brain tissues on early embryonic developmentE10-E12 and 462 463 its specific activity increased from gestation to adulthood(Berger et al., 1985; Burgunder 464 and Young, 1990; Marin et al., 2005). DRD1 and DRD2 receptors were detected in neural 465 tissues on E14 and on E18 their localization was already similar to that observed in the 466 adult brain. At birth, expression of mRNA for both dopamine receptor subtypes in the 467 striatum approximated that seen in mature rats(Ong et al., 2012). In addition, DAT mRNA was first detected in neurons of the ventrocaudal mesencephalon on E14. By E18, intensely 468 469 expressing neurons in the VTA and substantia nigra resembled the pattern found in adult 470 midbrain(Fujita et al., 1993; Galineau et al., 2004).GHSR mRNA was found in the brain 471 and spinal cord as early as E12 and continued to be expressed in these tissues during 472 postnatal life(Steculorum and Bouret, 2011). Along the same line, we detected the mRNA 473 presence of TH, DRD1, DRD2, DAT and GHSR in VTA and NAc areas at E21. Moreover, 474 we showed that the transcriptional levels of these genes increased from E21 to PND10, suggesting that the development of the dopaminergic system in the rat continues from 475 476 embryonic stage to the first weeks of life.

We found that early changes in gene expression of TH, DRD1 and GHSR in VTA and NAc in female rats are accompanied by alterations in promoter DNA methylation. In PND10-CON, we observed hypomethylation at the TH and DRD1 promoters (in VTA and NAc) and GHSR gene (in VTA), which may explain the increased mRNA expression of these genes, compared to E21-CON. We found that the DRD1 promoter was mostly methylated in two sites, one of it is located in a CpG Island (in VTA), while the other is a potential 483 binding site for the nuclear factor of activated T-cells (NF-AT) and for Elk-1 (in NAc). On 484 the other hand, a potential binding site for ZF5 and forselective promoter factor 1 (Sp1) was 485 predicted in the mostly methylated site within the GHSR promoter. Interestingly, these 486 binding sites have been suggested to have a role in the regulation of dopaminergic related-487 genes transcription; particularly, DRD1 and DAT (Groth et al., 2008; Lee et al., 2004; J. 488 Wang and Bannon, 2005). Moreover, changes in the methylation patterns of these sites 489 could be related to the brain area involved (as occurs in DRD1 promoter). Although the 490 increase expression of DRD1, GHSR and TH mRNA in the rat brain was previously related 491 to changes in methylation patterns (Gozen et al., 2013; Inoue et al., 2011; Vucetic et al., 492 2012); we showed for the first time a relation between changes in the expression of these 493 genes and age-associated methylations mechanisms.

494

495 Maternal CAF diet decreased body weight and affects the transcriptional regulation 496 of dopaminergic related-genesin the offspring during perinatal period.

497

498 Maternal CAF diet significantly decreased the body weight of the offspring from birth to 499 PND10.

500

501 Dams fed with a palatable diet administered from weaning to adulthood significantly 502 increased energy intakeand body weight gain compared to animals fed with the standard 503 chowduring pre-pregnancy and pregnancy periods, as was previously reported by several 504 authors(Akyol et al., 2009; Goularte et al., 2012; Lalanza et al., 2014; Lazzarino et al., 505 2017). However, maternal CAF exposure significantly reduced the body weight of the 506 pups, generating a decrease from birth (17%) to PND10 (30%). Bayol et al. (2007)found 507 similar results in the offspring of dams fed with CAF diet at PND1 and PND21; while Ong 508 and Muhlhausler (2011) observed a significant decrease in body weight at PND3. Contrary 509 to our results, the offspring from dams fed with a high fat diet (HFD) showed no body 510 weight differences at birth, while at PND 16 and PND 19 the body weight of the HFD-511 offspring was 30% higher compared to control animals (Chen et al., 2008; Purcell et al., 512 2011). These results suggest that the effects of CAF diet on the body weight of the 513 offspring is opposite tothat observed in the offspring from dams fed with other obesogenic

514 diets, such as HFD. However, both low and high birth weights have been associated with 515 the risk of diseases on adult ages, such as glucose intolerance, type II diabetes 516 mellitus, syndrome X, dyslipidemia and obesity(Gluckman et al., 2008; Reyes and 517 Manalich, 2005).

518 The decrease in the body weight of pups from dams fed with a CAF dietcould be due to the 519 excess of maternal body weight that acts as a programming agent per se or due to other 520 aspects of the CAF diet that drive the fetal responses as was previously suggested (Akyol et 521 al., 2009). In fact, the increased energy intakes of the CAF-fed dams were accompanied by a 522 significant change in the composition of their intakes: they consumed a much greater 523 proportion of their daily energy consumption from fat and less from protein, as was 524 previously reported (Akyol et al., 2009; Bayol et al., 2007; Esteve et al., 1994; Llado et al., 525 1995; Shafat et al., 2009). In this sense, Bayol et al. (2007)reported that the reduction in protein intake during gestation and lactation in CAF-fed dams would be a key factor in 526 527 explaining the reduced birth and weaning weights observed and that maternal protein intake 528 rather than overall energy intake would play a major role in regulating the offspring's body 529 mass at birth and at weaning. Importantly, the effect observed on the body weight of CAF-530 PND10 pups is similarly to those reported in the offspring of dams fed with alow protein 531 diet model(Bieswal et al., 2006; Langley-Evans and Nwagwu, 1998). On the other hand, it 532 would be possible that the limited protein intake of the CAF diet also affects the production 533 and composition of breast milk. Although this factor was not analyzed here, Rolls et al. 534 (1986)showed that the milk of CAF-fed rats contained more energy, with more fat and 535 long-chain fatty acid content but less protein and medium-chain fatty acid content than that 536 of control rats. Contrary, other authors reported that there were no differences in the protein 537 content of either the early or mid-lactation milk between CON and CAF dams, despite the 538 lower protein intake of the CAF dams during both pregnancy and lactation(Grigor et al., 539 1987; Pine et al., 1994; Vithayathil et al., 2016). It is important to note that we found no 540 differences in breeding success between the control and CAF dams, as was previously 541 suggested by Akyol et al. (2009).

542

543 *Maternal CAF diet affects the transcriptional regulation of dopaminergic related-genes* 544 *in VTA and NAc regions at PND10.* 546 We found a decrease in the expression of TH and GHSR in VTA in the offspring of CAF fed-dams at PND10.The diminished expression of TH in VTA has been previously related 547 548 to a reduced DA production(Naef et al., 2008). In addition, it has been reported that ghrelin 549 impacts in VTA and induces DA release (Fulton, 2010), proposing that GHSR-TH 550 coexistence coordinates regulation of DA levels. Ghrelin is thought to incentivize food 551 intake by increasing acetyl choline levels in the VTA, increasing DA levels in the NAc, 552 activation of dopaminergic projections from the VTA to the NAc, and activation of DRD1 553 and DRD2 in the NAc(Murray et al., 2014). Contrary, in mice, absence of the GHSR gene 554 was associated with lower insulin-like growth factor 1 concentrations and lower body 555 mass, independently of food intake(Chanoine et al., 2009). Although these studies have 556 been performed in adult rats, some works suggest that ghrelin and GHSR have a role in 557 linear growth and development in early life (Chanoine et al., 2009; Steculorum and 558 Bouret, 2011). Interestingly, the decrease in mRNA expression of TH-GHSR in VTA was 559 correlated with a decreased in mRNA levels of DAT and DRD2 in VTA and reduce levels 560 of DRD1, DRD2 and DAT transcripts in NAc.The decrease in the synthesis of DA 561 accompanied by lower levels of it transporter and receptors and therefore, in the actions of 562 the DA, suggests a reduced dopamine signaling in the reward system of these animals. 563 Importantly, during this period, permanent alterations in the function of this pathway could 564 be established and could have a long-lasting effect later in life and in adulthood.

565 The effect of maternal diet on the dopaminergic reward system was not studied in embryos 566 and in early postnatal life; but it was in young and adult rats. Ong and Muhlhausler (2011) 567 reported that the offspring from dams fed with CAF diet decreased DAT expression in NAc 568 in PND42, whereas in adults the expression of DAT increased, compared to control rats. 569 No changes were found in TH, DRD1 and DRD2 expression between groups. Gugusheff et 570 al. (2013)also reported an increase preference for fat, an overall energy intake and bigger 571 fat mass in adult offspring from CAF-fed dams.In the other hand, Vucetic et al. 572 (2010)showed that the offspring from HFD-fed dams have a reduce DA signaling by 573 decreasing the expression of DRD1 and DRD2 receptors and increasing the expression of 574 DAT in adulthood.Contrary, adult offspring from HFD-fed dams displayed increased TH 575 expression in the VTA and NAc and significant increases in DA content in the NAc,

576 suggesting an elevated DA tone in this target field(Naef et al., 2011).Our results together 577 with the previously mentioned works suggest that maternal diets are critical in the 578 development of the dopaminergic pathways and the effect observed during perinatal period 579 could have a long-lasting impact in the offspring and predispose them to certain behaviors, 580 such as those related to food preferences.In this sense, it will be interesting to evaluate in

581 further studies the period (before pregnancy, during pregnancy or during breastfeeding) in

582 which changes associated with the maternal diet are more relevant.

583 Some studies showed that the maternal nutritional factors could change the offsprings' 584 epigenetic marks in association with alterations in gene expression (Glendining et al., 2018; 585 Sinclair et al., 2007; Vanhees et al., 2014). Moreover, it was reported that methylation 586 mechanisms are implicated in the transcriptional control of dopamine-related genes. For 587 example, Vucetic et al. (2010) observed global and gene-specific (DAT and Mu opioid 588 receptor) promoter DNA hypomethylation in the brains of offspring from dams that 589 consumed the HFD.In addition, epigenetic dysregulation of TH and DAT genes in a mouse 590 model of HFD-induced obesity was reported (Vucetic et al., 2012). Sanchez-Hernandez et 591 al. (2016) also reported that the male offspring from dams fed with diet with high levels of 592 vitamin A had increased levels of DNA methylation in the DRD2 promoter region 593 compared to control group. Here, we reported for the first time that maternal CAF diet 594 affects the transcriptional regulation of genes TH, DRD2 and DAT involved in 595 dopaminergic reward system by DNA methylation mechanisms in an early stage of 596 development (PND10). The fact that DRD2 and DAT promoters were mostly methylated at 597 two sites located in a CpG Island supports the idea that these methylation-sensitive sites 598 could be potential regulatory sites. To reinforce this hypothesis, it would be interesting to 599 perform further experiments using DNMT inhibitors that block the epigenetic effects of 600 maternal CAF diet in offspring.

The reduce dopamine signaling found in the offspring from CAF-fed dams is consistent with changes in the reward pathway observed in adult obese animals and in animals exposed to drugs, such as cocaine or alcohol. Particularly, several studies showed that genetic and functional alterations of the DRD2 have already been linked to the pathophysiology.Areduction in striatal density of DRD2 in overweight individuals (Stice et al., 2008; G. J. Wang et al., 2001) and rodents (Huang et al., 2006; Johnson and Kenny, 607 2010; Thanos et al., 2008)has been reported. Moreover, loss of DRD2 autorreceptors was 608 linked to drug addiction, such as cocaine intake (Bello et al., 2011; Holroyd et al., 2015). In 609 this sense, it has been shown that DRD2 plays an important role in the reward deficiency 610 syndrome, which is related to compulsive and addictive behaviors(Blum et al., 2011). In 611 VTA, a decrease in DRD2 has been linked to a greater motivation for food and the 612 development of obesity(Bello et al., 2011; Koyama et al., 2014). Here, we showed for the 613 first time a downregulation in DRD2 that is correlated with alteration in the methylation 614 levels of it promoter in the offspring of dams fed with a CAF diet at PND10. Considering 615 that these changes could have a long-lasting effect later in life, these results suggest that the 616 epigenetic dysregulation of DRD2 could be an early marker of health diseases related with 617 excessive consumption of food or drugs in adulthood. However, further studies are needed 618 to clarify the cause-effect relationship between early DRD2 dysregulation in response to 619 maternal diet and addictive behaviors in the adult offspring.

620

621 **Declaration of interest**

There is no conflict of interest that could be perceived as prejudicing the impartiality of theresearch reported.

624

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629

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