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REVIEWS: CURRENT TOPICS

Epigenetics and neurodegeneration: role of early-life nutrition

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Abstract

Neurodegeneration represents a global problem due to the progressive increase in the aging population all over the world. The quality of life in aging and the cost for the health care system require actions to promote healthy aging. In this regard, several risk factors associated with the development of neurodegeneration can be identified, and programs to educate people on the key role of prevention could significantly ameliorate the future picture of the aging population. Here we describe the key role of the pre- and postnatal period of life during the first 1000 days of life, focusing on the importance of nutrition and a healthy lifestyle of mother and offspring for the prevention of neurodegeneration later in life. Environmental risk factors (i.e., nutrition, stress, xenobiotics, alcohol, drugs, smoking, etc.) mediate the genetic and epigenetic signature of offspring which may have long-term effects on the onset of neurodegeneration.

Keywords: Epigenetics; Early-life nutrition; Nutrigenomics; Neurodevelopment; Neurodegeneration

Contents

1. Introduction

It is now well recognized that the environmental effects experienced during the first 1000 days of life, represented by the 9 months of pregnancy plus the first 2 years of life and as early as preconception, are transmissible to offspring and to subsequent generations. Animal studies using rats and mice appear to indicate that the predisposition to cardiovascular (CV), metabolic and neurological diseases may originate *in utero* and is associated with inheritance of epigenetic alterations to gene expression. This in turn is partly associated with the early life experiences of the mother and to the offspring's nutrition, especially during its first 2 years of life in the case of humans [1,2]. Some of the environmental risk factors which shape the genetic and epigenetic signature of offspring range from nutrition, stress, xenobiotics to alcohol, drugs and smoking. While plenty of studies have focused on the association between nutrition in early-life (prenatal and postnatal period) and the risk of CV and metabolic diseases later in life, the link with neurodegenerative diseases is however still not clear. Since diet influences every organ and body system, which can in turn affect brain health, the question arises as to whether nutrition in the early stages of life may affect neurodevelopment and predispose for the onset of neurodegeneration in the long term. This is of interest considering that the field of epigenetics is

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emerging as an important and novel mechanism in neurodegenerative diseases. This review summarizes the major breakthroughs and discoveries that have been mainly made over the last 5 years and discusses the evidence for the possible connections and mechanisms involved between early-life nutrition during the 1000 days of window of plasticity and predisposition for neurodegeneration later in life. In other words, our brain's health and mental well-being throughout our life span are not just influenced by "what we eat" but probably also by "what our mothers ate during our early life" and "what our mothers fed us in the first 2 years of life."

2. C1 metabolism, DNA methylation and early-life programming of adult health

Early life represents a key period for the programming of adult health. During the first 1000 days of life, the differentiation process leading to specialized cells from the pluripotent ones is mediated by epigenetic remodeling required for switching off genes that do not have to be expressed in a particular tissue while maintaining active those that do [3,4]. In this context, DNA methylation and posttranslational modifications work to differentiate cells properly. DNA methylation depends on the activity of DNA methyltransferases (DNMTs) which catalyze the methylation of CpG islands at the gene's promoter leading to a progressive switching off of the gene. The obstruction of the interaction between the transcription factors and the promoter region due to methyl groups limits binding with RNA-polymerases required for gene expression to begin (Fig. 1A). At the same time, methylation of regulatory regions contributes to an additional control of gene expression (Fig. 1B), likewise for histone methylation which is however more complex (Fig. 1C). The methylation process is strongly dependent on the availability of methyl group donors during pregnancy and through life via the one-carbon metabolism (folate) pathway (Fig. 1D) [4]. The availability of methyl groups is associated with a folate-rich diet (i.e., green leaves, asparagus, beans, lentils, peas, liver, etc.) and to supplementation of folic acid during pregnancy, together with the availability of B6 and B12 vitamins. Methylenetetrahydrofolate reductase (MTHFR) catalyzes the transfer of a methyl group to folate, leading to 5-methyl tetrahydrofolate and finally to homocysteine which is then converted into methionine by 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR). For this step, the presence of B12 is necessary, and because it is present only in animal food (i.e., meat, fish, eggs), in vegans, a synthetic one can be taken orally through sublingual treatment to avoid its hydrolysis by the liver. Methionine adenosyltransferase (MAT) catalyzes the synthesis of *S*-adenosylmethionine (SAM), which is the key factor for methylation, because DNMTs employ its methyl groups to methylate DNA. Alcohol intake, for example, can interfere with SAM synthesis and for this reason should be avoided during pregnancy and breast-feeding, likewise deficits of folic acid and folate from food (Fig. 1D).

The epigenetic mechanisms associated with a healthy/unhealthy phenotype include not only DNA methylation that plays a key role during the first 1000 days of life but also posttranslational modifications, like histone modifications. In this context, histone methylation,

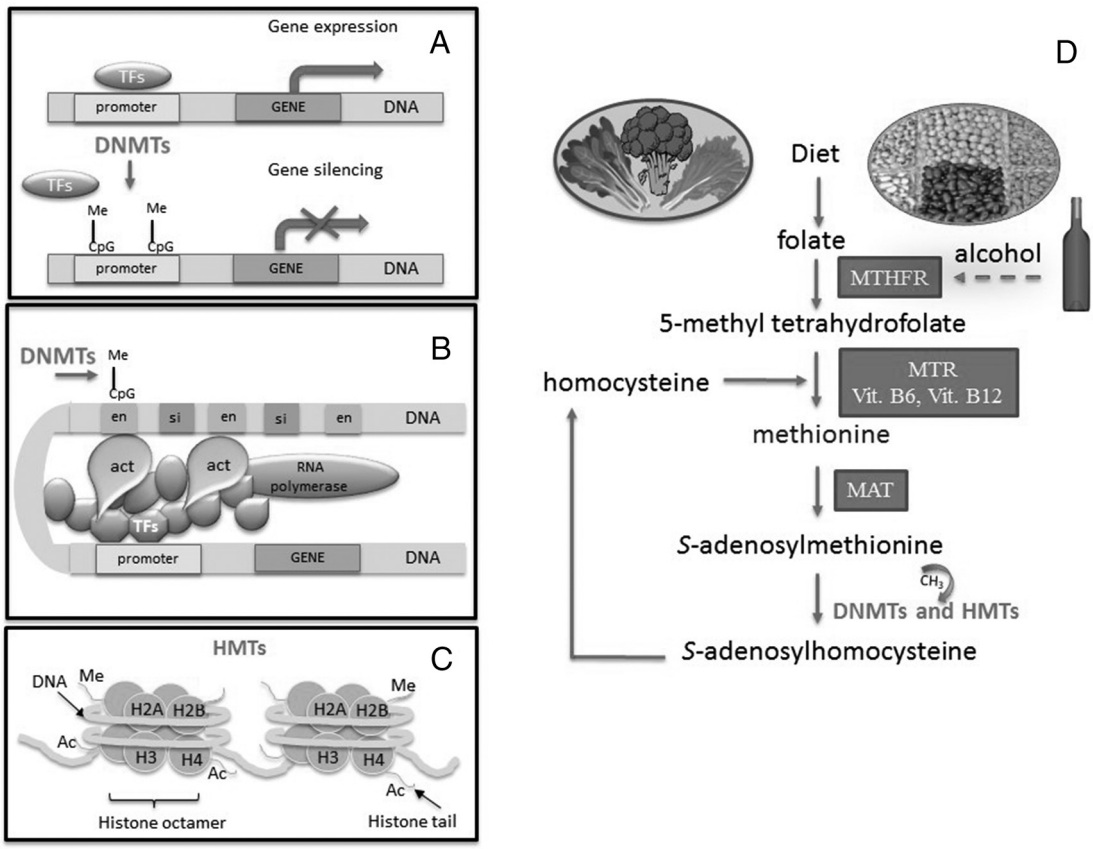

Fig. 1. Simplified folate pathway and connection with DNA/histone methylation. (A) Cytosine methylation hampers gene expression by limiting binding of TFs and RNA polymerases. (B) Gene expression controlled by methylation of regulatory regions. (C) Methyl groups from the folate pathway are used by histone methyltransferases (HMTs) for modifying chromatin structure and finally regulating gene expression. (D) Simplified folate pathway leading to methyl groups useful for DNA and histone methylation. TFs: transcription factors; MTHFR: methylenetetrahydrofolate reductase; MTR: 5-methyltetrahydrofolate-homocysteine methyltransferase; MAT: methionine adenosyltransferase; en: enhancer; act: activator; si: silencer.

acetylation, phosphorylation, ubiquitinization, sumoylation and glycoylation can work with opposing effects leading to chromatin remodeling associated with activation or inhibition of gene expression (Fig. 1C). Every time that a gene is expressed, chromatin remodeling represents the first step required to permit the start of gene expression. In the modulation of this process, nutrition plays a key role because supply precursors are required for histone-methyltransferases, which need the methyl group donor SAM to methylate histones (Fig. 1C); moreover, the methylation process depends also on the FAD/$FADH_2$ ratio which is always related to the quantity and the quality of nutrient intake. Acetylation of lysine's positive charge in histones is a fundamental event promoting histone-DNA remodeling necessary to support gene transcription; to this aim, acetyl groups deriving from the oxidative glucose pathway or beta-oxidation of fatty acids are used by histone acetyltransferases (HATs) which need coenzyme A as cofactor. The flexible process is reversed when chromatin is stabilized by deacetylation catalyzed by histone deacetylases (HDACs) that require NAD+ as cofactor [5]. Phosphorylation instead depends mainly on the activity of histone kinases, which transfer a phosphate group to the hydroxyl group of threonine and serine in histone H3. Overall, ATP-dependent remodeling complexes require the energy of ATP hydrolysis to achieve nucleosome structure required for transcription [6].

Reduced folate intake during early life has been associated with incorrect DNA methylation that leads to long-term effects, as observed during the Dutch famine where low nutrients intake by mothers during pregnancy has been associated with a decrease in promoter methylation of the insulin growth factor 2 (IGF2) of the maternal allele in the offspring. The long-term consequences of this imbalance in the maternal IGF2 promoter methylation associated with deficits in nutrient intake have been correlated with the development of overweight in men at 20 years old and glucose intolerance when they reached 50 years old, and to an increase in body mass index (BMI) in females at the same age [7]. Despite these outcomes, Lumey et al. did not find any significant correlation between prenatal famine and global DNA methylation on 350 births with prenatal exposure to the Dutch famine [8]. Recently, Tserga et al. [9] studied the correlation between folate supplementation and IGF2 methylation in cord blood of 90 mothers–children which resulted in a complex picture depending on the MTHFR genotype. Tobi et al., in a recent work on 60 individuals with periconceptional famine exposure and genetic variation within the IGF/H19 region, suggested that both famine and genetic factors can alone or together be responsible for DNA methylation at the same regulatory site [10]. Overall, there are various aspects that can modify the DNA methylation of the imprinted IGF2 gene, and the absence of an epigenome-wide association study of DNA methylation in humans contributes to delineate a heterogeneous picture. Furthermore, Tobi et al. found differences in offspring in DNA methylation of genes involved in growth, development and metabolism only when famine exposure was during the first 10 weeks of gestation of their mothers [11]. In agreement with this is the work of Stein et al. on 923 individuals affected by depressive symptoms in adulthood that were born from mothers exposed to famine prior to conception [12]. Similarly, 360 offspring from prenatally undernourished fathers, but not mothers, were heavier and more obese than offspring from parents receiving a normocaloric diet before conception [13].

The association between birth weight and obesity, coronary heart disease (CHD) and glucose intolerance later in life was first discussed by Barker [14] who observed a correlation between low birth weight and CHD death rates. Furthermore, low birth weight has also been associated with impairment of neurocognitive development later in life, and maternal smoking during pregnancy seems to promote this phenotype [15,16]. Additionally, studies on monozygotic and dizygotic twins revealed a nongenetic negative association between birth weight and insulin resistance and glucose intolerance, and it was estimated that the genetics associated with birth weight were 38% [17]. The mechanisms linked to the long-term effects of prenatal and postnatal dietary nutrients on obese phenotype seem to be mediated by the early-life programming of appetite regulatory hormones [18]. Studies on animal models showed that a protein-restricted diet or a high-fat diet during pregnancy is associated with decreased beta-cells in the pancreas, early or reduced leptin source, increased orexigenic peptide, resistance to glucose, hypertrophic adipocytes and finally development of the obese phenotype [19].

3. Risk factors associated with neurodevelopment and neurodegeneration

Exposure to unhealthy environmental factors in early life and during the life span has been associated with neurodevelopmental disorders and neurodegeneration later in life [20]. An unbalanced diet negatively modulates gene expression, leading to reversible epigenetic signatures that are responsible for various features later in life. Other environmental factors that contribute to epigenome remodeling associated with early and long-term neurobehavioral deficits are smoking, alcohol, stress and exposure to pesticides during pregnancy. In this review, we focus on food, alcohol and food pesticides.

A general consensus based on several evidences on human and animal models supports the hypothesis that the development of idiopathic neurodegenerative diseases is strongly associated with the quality of lifestyle starting from prenatal age. Alcohol and food intake modulates the epigenome, but another important environmental risk factor is the presence of pesticides and metal residues in food because these xenobiotics are associated with promoting neurodegeneration in the long term.

Pesticides are required to respond to the increasing demand of food by the population and to guarantee the absence of microorganism contamination in fresh and long-term stored food (i.e., mycotoxins). However, the main concern regarding risks linked to food pesticides should take into account not only the presence of single chemicals over the authorized limits but also the presence of mixtures of pesticides that are within the maximum residue levels permitted by the legislation. Pesticides can modulate gene expression later in life by early remodeling of the epigenome. Exposure to these hazard factors is associated with genetic and epigenetic modifications, leading to oxidative stress, mitochondrial damage, change in calcium homeostasis, reduction of overall brain volume, loss of dopaminergic neurons in substantia nigra, shortened fetal telomere length, microbiota imbalance promoting proinflammatory cytokine release and finally altered brain development which has long-term effects on the onset of the more common neurodegenerative disorders like Alzheimer's disease (AD) and Parkinson's disease (PD) [21–24].

Worthy of note are the studies on animal models where the long-term effects of early life exposure to pesticides, herbicides and metals, identified as residues in food, can be demonstrated. Neonatal exposure to permethrin pesticide during brain development promotes a progressive neurodegeneration characterized by the typical features of PD with behavioral and dopamine deficit, and a worrisome intergenerational effect [25,26]. Permethrin is able to induce a progressive PD-like neurodegeneration if administered in early life because it can cross the blood–brain barrier (BBB) and remains long after the exposure [26–32]. In particular, permethrin binding to sodium channels induces neuron depolarization that seems to modulate DNMT activities responsible for DNA methylation [31]. Accordingly, changes in DNMTs have been demonstrated in the striatum of animals exposed to permethrin during brain development [32]. Furthermore, permethrin is able to decrease global DNA methylation in mothers exposed to the food pesticide during early life as well as in their untreated offspring, underlining the intergenerational effect of the pesticide [26]. This effect seems to be mediated

by reactive oxygen species production induced by the pesticide that leads to up-regulation of DNMTs [33].

Of particular concern are the recent data obtained by the CHAMACOS cohort in the USA on the association between increased biomarkers of organophosphate exposure in urine of farmworker mothers and abnormal mental development in their children [34]. Other studies support the capacity of organophosphates to act as endocrine disruptors underlining their possible involvement in promoting neurodevelopmental toxicity in early life [35,36]. Dialkyl phosphates (DAPs) and 3-phenoxybenzoic acid (3-PBA), the urine metabolites of organophosphate and pyrethroids, respectively, are increased in urine of children affected by attention-deficit/hyperactivity disorder (ADHD). The risk of developing ADHD increases by 55% when the level of urine's DAPs is increased 10-fold compared with controls, while the risk of developing ADHD may be twice when children have detectable concentrations of 3-PBA with respect to the undetectable metabolite [37]. The PELAGIE cohort in France has associated urine 3-PBA levels with a decline in verbal and memory functions in children of age 6 years [38]. The mechanisms associated with these effects might be mediated by both genetic and epigenetic modulation. Recently PON1, a detoxifying enzyme for organophosphate and pyrethroid pesticides, has been shown to modulate DNA methylation [39].

Low levels of heavy metals in early life and higher levels later in life identified in the food chain (i.e., fish and molluscs) also represent risk factors associated with the promotion of neurodegenerative diseases [40]. High levels of cadmium in food has been linked to global DNA methylation [41], and aluminum, a metal present in water, can cross the BBB, promoting chromatin remodeling associated with oxidative stress, inflammation, mitochondrial dysfunction, impairment of glutamate transport and finally neuronal death [42].

Iron deficit in early life has been connected with permanent deficits in recognition memory and procedural memory in adult age; at the same time, an excess of maternal iron or during adult age might lead to poor developmental consequences and long-term effects mediated by epigenetic and neuroinflammatory processes, respectively [43,44]. Studies on animal models have demonstrated that deficit of iron during neonatal age is associated with neurodevelopmental dysfunction that is a consequence of altered hippocampal DNA methylation and to changes in expression of genes involved in the regulation of the BBB permeability, hypoxia and angiogenesis [45]. Furthermore, iron deficiency has been related to changes in histone deacetylase 3 which modifies hepcidin expression involved in the regulation of systemic iron homeostasis [46]. Deficiencies in two other metals, copper and zinc, during pregnancy and in early life have been associated with decreased fetal neurogenesis due to impairment of DNA methylation [47], and both can promote amyloid-β peptide production typically present in the plaques of patients with AD [48].

Concerning alcohol as a risk factor for neurodegeneration later in life, several studies on human and animal models have indicated that maternal alcohol consumption during pregnancy and lactation is associated with a decrease in DNA methylation, [49]. Alcohol interferes with the methyl donor transfer to methylenetetrahydrofolate (Fig. 1D), and the coadministration of the methyl donor betaine was effective in contrasting DNA hypomethylation due to ethanol intake [50] Furthermore, chronic alcohol intake perturbs folate homeostasis due to decrease in folate absorption in the small intestine, abnormal uptake and low folate storage in the liver [51]. Overall, mother alcohol consumption inhibits the one-carbon metabolism pathway affecting the DNA methylome. This in turn influences several genes associated with brain development, oxidative stress and proinflammatory cytokine production [52,53]. Physical and cognitive abnormalities known as fetal alcohol spectrum disorder have in fact been observed in children following mother alcohol intake [54].

These risk factors exert their impact differently on people according to their own genetic profile: the individual responses to the exposome, which includes all external and internal factors interacting with humans, lead to a healthy or unhealthy phenotype according to the genetic polymorphism differences, ultimately mediating the onset of PD and AD neurodegeneration. Of particular interest is the hypothesis that the incidence of neurodegeneration is mainly increased when a secondary exposure to toxicants occurs in adult age. This hypothesis known as the "two hits" model is in agreement with studies on PD where occupational and nonoccupational exposure to toxicants has been associated with the increased incidence of neurodegeneration [55–58]. Table 1 summarizes some of the epigenetic modulators treated in this section, with the possible outcomes, while the others will be discussed in the subsequent sections.

4. Strategies for prevention: maternal diet during pregnancy

Maternal diet is a major determinant of offspring health. Most studies have focused on the metabolic consequences of perinatal nutrition, but very few have addressed those concerning neurodegenerative diseases. There are now several indications in the literature demonstrating that neurodevelopmental health and cognitive deficits of offspring are also associated with maternal obesity, and an association between increased BMI in healthy mothers and decreased cerebellar growth in offspring has been observed [59–62]. The link between obesity and neurodegeneration appears to be in part associated with inflammation. Systemic inflammation is a common consequence of obesity and high-fat diet (HFD) consumption; hence, it is logical to question whether a maternal inflammatory diet may have adverse outcomes in offspring in both early life and later life that could predispose to neurodegenerative diseases and whether correction of a high-fat maternal diet might prevent this.

The source of the low-grade systemic inflammation characteristic of obesity is believed to derive from lipopolysaccharide (LPS), a potent trigger of the innate immune system. LPS is an endotoxin naturally present in the intestinal lumen as a component of the cell wall of Gram-negative bacteria, and it enters the circulation along with other nutrients following a meal, initiating a transient postprandial endotoxemia. Under normal conditions, the immune system responds normally to this acute endotoxin stimulus, and once the toxin is neutralized and removed, the state of inflammation returns to baseline levels. However, frequent consumption of high-fat meals chronically elevates LPS in circulation, contributing to the low-grade inflammatory state observed in the obese phenotype [63,64]. This is exemplified by a recent study in which pregnant and lactating mice regardless of whether they were fed on an HFD or continuous infusion of LPS had similar outcomes in their offspring: obese phenotype and greater inflammatory response in adulthood even if they consume normal diets throughout adulthood [65]. This prenatal inflammation has been associated not only with an obese phenotype but also with long-term impaired adult neurogenesis and hypothalamic inflammation [66,67].

Neuroinflammation is mediated by microglia which are resident macrophages and are the first line of active immune defense in the central nervous system (CNS), and systemic inflammation has been shown to induce long-lasting neuroinflammation via TNFα and inflammatory cytokines that cross the BBB. In fact, microglia abundantly express TLR-4, a signal-transducing receptor that responds to saturated fats through the IKKβ/NFκB pathway releasing proinflammatory cytokines (such as IL-6 and TNF-α) [68]. Obesity has been demonstrated to induce the expression of cytokines and the proinflammatory transcription factor NFkB in the hypothalamus [69], and since TNFα and inflammatory cytokines can cross the placenta and BBB as they have been measured in the uterus, fetal circulation and the fetal brain, it is expected that maternal-diet-induced inflammation may directly influence the developing fetus' CNS and brain with far-reaching consequences [70–72]. Maternal dietary fatty acids have in fact been found to induce hypothalamic inflammation via

Table 1
Time frame for epigenetic remodeling by diet/environmental factors and outcomes during the first 1000 days of life (early life) and overall life span

Epigenetic modulators	Period of exposure	Outcomes	References
Exposure to food and food pesticides/metals	Pregnancy Early life Adult age	Inflammation Neurodevelopmental /neurological disorders	[20,22,25,27,29,34,35,38,40,41]
Alcohol	Pregnancy Early life	Reduction in folate absorption	[49–54]
Low folate intake	Pregnancy	Decrease in methyl groups	[51,103,105,106]
Low B12 intake	Pregnancy	Decrease in methyl groups	[4,10]
High fats intake	Pregnancy	Inflammation	[63–68,73,75]
High meat intake	Adult age	TMA-N-oxide mediates inflammation	[90]
High vegetables intake	Pregnancy Adult age	Inhibition of inflammation	[80,106,164,175]
Intake of whole cereals	Pregnancy Adult age	Inhibition of inflammation (SCFA)	[116]
Intake of phytochemicals	Pregnancy Adult age	Inhibition of inflammation and oxidative stress	[107,163–179]

TLR4/NFκBp65 signaling in adult offspring, but also normolipidic diets with unbalanced quantities of different fatty acids (trans-fats, palm oil and interesterified fats) have led to inflammatory responses on the hypothalamus (increased TLR-4 expression) in the offspring of dams [73–75].

Inflammation caused indirectly via LPS administration, and not through diet during gestation, has also been shown to increase TNFα and IL-1β mRNA in the fetal brain and alter the glial cell population, thus impairing neuronal differentiation and neurogenesis [76]. Interestingly, Graciarena et al. found that prenatal and adult LPS treatments in Wistar rats reduced adult neurogenesis and provoked specific microglial activation in the dentate gyrus (DG), but more importantly, that only prenatal inflammation-mediated effects were long-lasting (>60 days). In fact, only prenatal LPS treatment reduced the local levels of TGF-β1 mRNA in the DG of offspring, and it exerted its proneurogenic effects via the Smad 2/3 pathway in a neural stem cell culture [66]. These data highlight the importance of the consequences that prenatal immune programming has on CNS physiology compared to the limited response observed in the adult brain. Others have also led to similar conclusions using mouse models and LPS that accurately mimic intrauterine inflammation in humans: exposure to intrauterine inflammation during pregnancy results in postnatal brain injury, with chronic inflammation, presence of macrophages in the adult cortex, activation of microglia and long-term EEG biomarkers of neurodegeneration, setting the stage for development of neurodegenerative diseases in adulthood [77–79].

The already well-established link between diet and inflammatory biomarkers in the nonpregnant population also persists in pregnant mothers, particularly in those that are obese [80,81]. This is particularly worrisome considering that the sharp rise in obesity over the last 25 years is reflected in the increasing trend of obesity during pregnancy [82]. Increased adiposity associated with an HFD also increases the number of resident macrophages in white adipose tissue, the major type of immune cells in this tissue involved in the development of chronic inflammation [83]. These secrete inflammatory cytokines and chemokines and inhibit the production of anti-inflammatory adiponectin, further exacerbating an inflamed state. A maternal HFD is not the only contributor to chronic inflammation. Intrauterine growth restriction in which maternal under/poor nutrition is one of the principal causes also leads to an inflammatory response in pregnant mothers and fetuses which is reflected by elevated serum concentrations of inflammatory markers, including TNFα, IL-6 and C-reactive protein (CRP) [84]. Prenatal protein restriction in maternal diet has also been associated with a proinflammatory state in offspring since increased expression of the proinflammatory genes IL-6 and IL1β in white adipose tissue macrophages of Sprague–Dawley rat offspring was observed [85].

In a recent cohort study, an inflammatory diet was associated with small-for-gestational age infants among mothers with prepregnancy obesity and with high levels of the inflammatory marker CRP [86]. Evidence from cell models suggests that cytokines such as IL-6 released by an inflammatory state may influence the epigenome by altering DNMT1 expression patterns which could result in disruption of epigenetic programming. [87]. This is in accord with accumulating evidence showing the association between maternal obesity (an inflammatory condition) and offspring methylation. Nomura et al. showed that maternal obesity was associated with placental global hypermethylation, which was also linked to infant length and head size. Although their findings did not reach significant levels, maternal obesity could potentially affect fetal programming of development, including neurodevelopment. This study was conducted on a small sample size; therefore, the results would need to be reconfirmed on a greater sample size [88]. In another epigenetic study, maternal prepregnancy BMI was associated with offspring DNA methylation of the CpG sites in genes involved in a broad array of chronic diseases, including inflammation-mediated disorders and lipid metabolism, suggesting that maternal-BMI-induced alteration in DNA methylation may be one of the mechanisms underlying fetal origins of adult diseases, comprising neurodegeneration [89]. However, because of some pitfalls in this study regarding sample size, possible inadequate techniques that had low coverage of CpG sites for each gene as well as a lower coverage of genes in the genome (~15k genes, <50% known human genes), small DNA methylation differences across BMI categories for the top hits found and possible misclassification of maternal prepregnancy BMI, future studies in a larger sample and using denser chips would be required to strengthen these findings.

Recently, in a nonhuman primate model, maternal overnutrition via *in utero* exposure to an HFD led to developmental programming of obesity and to proinflammatory gene signatures along with alterations in DNA methylation in key developmental genes in the offspring. Significant changes in gut microbiota were also observed [90]. In HFD-fed rats, Reynolds et al. were able to demonstrate that the dietary anti-inflammatory nutrient, conjugated linoleic acid (CLA), a lipid commonly found in beef and dairy produce, was effective in reversing the increased expression of the immunomodulatory cytokines TNFα and IL-1β in the gut of offspring. In the same offspring, they also observed that CLA was able to partially reverse the altered expression of the gut taste receptors Tas1R1 and Tas1R3 which are linked to metabolic diseases [91].

The hypothesis that a proinflammatory diet leads to elevated concentrations of cytokines and other inflammatory molecules that alter the regulation of key genes in the developing fetus, mediated by epigenetic mechanisms, was recently investigated by McCullogh et al. They found consistent inverse associations between maternal inflammatory cytokine concentrations (IL-12, IL-17, IL-4, IL-6 and TNFα) and lower methylation at the MEG3 regulatory sequence in offspring, but

their results failed to support the link between a maternal inflammatory diet and circulating cytokines. However, they did observe that women with proinflammatory diets had elevated rates of preterm birth among female offspring but not male ones and higher rates of cesarean delivery among obese women. Based on their findings, they concluded that other factors may be more important contributors to inflammation than diet in the pregnant population. There are many sources of inflammatory molecules in pregnant women which could make it more difficult to observe than the contribution of diet alone [92].

In rodents, several relationships have also been established between inflammation, iron homeostasis and neurobehavioral changes induced by a maternal HFD [93]. Hepcidin is a critical hormone in iron homeostasis and is primarily stored in oligodendrocytes. It is increased following inflammation, causing subsequent decreases in ferroportin expression and the available iron needed for myelination [94]. Therefore, disruptions in these interconnected processes may have deleterious effects on neurodevelopment by reducing myelination. Evidence is the decrease in myelination in the medial cortex recently observed in male pups (but not in females) born to maternal HFD-fed dams at PN21 with resulting changes in behavior at 4 months [95].

Vitamin D is an anti-inflammatory nutrient, and its role in maternal diet and consequent systemic inflammation in offspring has recently been investigated. Low maternal vitamin D status is associated with systemic low-grade inflammation, assessed via serum LPS in mouse offspring at adulthood [96]. However, when mothers were fed a diet enriched with vitamin D before pregnancy and during lactation, this was shown to be reversed in male offspring only. Long-lasting benefits to the metabolic, gut and bone health of C57BL/6J adult male mouse offspring exposed to an obesogenic diet were observed along with lower intestinal permeability and lower circulating levels of LPS [97,98]. At present, an understanding of the specific mechanisms responsible for the sex-specific alterations in offspring born to obese dams, and whether the same occurs in humans, is not known. However, if it were to be confirmed, it would be an area of investigation worth pursuing for developing preventive and treatment strategies.

In summary, maternal dietary-induced inflammation appears to directly affect the developing fetus and offspring including neurodevelopment, and this may have a long-term impact on the onset of neurodegenerative disease later in life. Since most studies have focused on intervention in early life as a possible effective strategy for preventing developmental programming of metabolic dysfunction, this could also be valuable for preventing neurodegenerative diseases later in life since they share a common denominator: inflammation. Controlling and preventing maternal obesity which is linked to inflammation would be beneficial not only to expectant mothers but also to their offspring in the long run. Epigenetic modifications that control genes involved in inflammation, together with oxidative stress, may provide a mechanistic link between obesity and the promotion of neurodegeneration [99]; therefore, epigenetic markers may in the future be used for assessing the effects of intervention.

5. Strategies for prevention: folate intake and microbiota during pregnancy

In the previous sections, we have mentioned how epigenetic marks are determined by nutrition, and this cannot be better exemplified than in the Agouti mouse model. Female mice fed on a high-methyl supplemented diet (folic acid, vitamin B12, choline, betaine) deliver offspring that are brown in color and healthy as opposed to controls which are yellow in color and obese. This is associated with increased DNA methylation and silencing of the Agouti viable yellow (A^{vy}) gene [100].

There are specific micronutrients that act as cofactors and methyl donors which are responsible for mediating epigenetic processes in response to the maternal diet. Both prenatal iron and zinc deficiencies [101,102] have been reported to affect histone modifications and DNA methylation, likewise maternal folate and choline [103]. Offspring of rats fed on a maternal diet poor in the methyl donors folate, choline and methionine showed increased anxiety behavior and altered methylation of neurontin, an essential gene in neonatal brain development [104]. Severe maternal folate deficiency also results in neural tube defects (NTDs) where brain and spinal cord fail to develop normally and in other congenital defects [105]. Early pregnancy is a critical period with rapid cell division, growth and proliferation, as well as high responsiveness to external influences; therefore, optimal maternal folate concentrations are vital. However, the ideal concentrations are frequently not achieved through regular dietary folate intake (leafy green vegetables, beans and pulses), and deficiencies can lead to compromised epigenetic programming associated with long-term health consequences [106]. Because of this risk, women are advised to increase folate intake during pregnancy, and a red blood cell folate level of greater than approximately 900 nmol/L is considered sufficient to reduce the risk of NTDs [107]. A recent study has highlighted the importance of folic acid supplement during the vulnerable periconception period (14 weeks before and 10 weeks after conception) on embryonic growth. A negative association was found between inadequate maternal folic acid supplementation and embryonic growth as well as growth rate during the first trimester [108]. In rodents, folic acid supplementation to pregnant rats prevents epigenetic and phenotypic effects on offspring [109], while paternal folate dietary deficiency is associated with increased birth defects in the offspring. Genome-wide DNA methylation analysis and the subsequent functional analysis showed differential methylation in sperm of genes implicated in development and chronic diseases, suggesting that epigenetic transmission may involve sperm histone H3 methylation or DNA methylation and that adequate paternal dietary folate is essential for offspring health [110]. However, in this study, overlap between genes that were identified as being differentially methylated in sperm and differentially expressed in placenta was limited to only two genes which moreover did not show methylation differences in the placenta. This suggests that mechanisms other than DNA methylation are involved such as histone methylation. Although the study demonstrated that paternal environment can influence offspring phenotype by transfer of epigenetic information through sperm, at present, no definitive convincing mechanism has been established either in this study or in other similar studies. Both diet and stress are common examples for rodent models of intergenerational transfer of information about paternal conditions that have key metabolic outcomes in future generations, and these have been recently reviewed in Refs. [111,112].

Folic acid is recommended prior to and during the first trimester of pregnancy. However, because of folic acid food fortification programs in many parts of the world for ensuring sufficient intakes in women approaching pregnancy and because many women continue to take folic acid supplements beyond the recommended first trimester, there has been an overall increase in folate intakes. This has raised concerns on the consequences of this for the developing fetus, recently reviewed by McStay et al. [113]. Based on several human studies, they bring into question the role of folic acid intake in late pregnancy in the development of allergic disease in children, after the critical period of time for protection against NTDs. In animal studies, folic acid has been found to modify gene expression linked to the development of allergic disease in offspring, which strengthens their findings [114].

Since maternal dietary folates and other micronutrients are involved in epigenetic programming of offspring and because they all pass through the gut in order to be metabolized and absorbed, the role of a healthy gut and microbiome is thus of vital importance [115,116]. The gut microbiota with its variability and complexity modulates gastrointestinal functions because it works actively on the degradation of products derived from food intake, releasing active

metabolites able to exert local and systemic effects even on the brain, through the gut–brain axis (GBA) [117]. Food intake plays an essential part in the gut microbiota composition and metabolite's production: fibers can actively promote the production of short-chain fatty acids (SCFAs) like butyric acid, propionic acid and acetic acid which have systemic effects. In particular, butyric acid can promote anti-inflammatory and antiapoptotic effects in the colorectal region by promoting inhibition of TNF-α and IL6 production and encouraging IL10 release [116]. At the same time, SCFAs work actively to promote glucose production and ATP synthesis in the colonocyte, with systemic effects on the hypothalamic hunger–satiety center, insulin production and lipid synthesis [117]. Of particular relevance are recent elegant studies on human and animal models that underline the key role of microbiota composition in the mediation of gut inflammatory cytokines promoting neuroinflammation in PD and AD diseases [118–124]. The control of inflammation represents a key factor in the prevention of neurodegeneration: intrauterine infection has been suggested to inhibit microglial-derived growth factors which are associated with deficit in brain development and promotion of neurodegeneration in adulthood [125,126]. A well-designed recent study on 43 neonates born before 28 weeks of gestation showed the association between placental indicators of inflammation and mRNA expression of 445 genes in umbilical cord tissue, six of which were correlated with cognitive deficit later in life [127].

In the previous section, we discussed how an obese phenotype contributes to inflammation and how this is believed to arise in the gut following an HFD that induces increased circulatory LPS. It follows therefore that changes in the maternal gut microbiome and intestinal permeability consequent to inflammation may alter folate levels, thus affecting epigenome programming in the offspring with long-term consequences. Indeed, a significant role of gut microbiota as an epigenetic factor that influences DNA methylation and other epigenetic signatures has been speculated. Microbes within the human gut are important in the regulation of various elements of the GBA via immunological, endocrine and direct neural mechanisms [128,129]. Therefore, it is plausible that neurodegenerative disorders may partly derive from dysregulation of this axis associated with gastrointestinal manifestations. This, for example, has been postulated for PD where dysregulation of the gut–brain–microbiota axis may significantly contribute to the pathogenesis of the disease, reviewed in Ref. [130]. Indeed, a mechanistic hypothesis has been advanced indicating the gut as the gateway in neurodegenerative disease [131]. A wide gut microbial diversity represents a fundamental aspect associated with a healthy phenotype required to guarantee the maintenance of gut permeability in order to avoid any absorption of toxic compounds (i.e., lead, pesticides and other xenobiotics), and the release of proinflammatory cytokines that could reach the brain via the GBA and promote neuroinflammation associated with neurodegeneration (Fig. 2) [132].

Hence, the microbiota of a pregnant mother may shape neurodevelopment of her offspring and predispose her child to neurodegeneration later in life. Maternal microbiota, obesity and dietary intake are known to influence the composition of the infant gut microbiota. This is particularly relevant since the mother plays a direct role in initial colonization of the infant microbiota depending on whether infants are born vaginally or by cesarean section [133]. Furthermore, microbiota of pregnant obese women is different from that of normal pregnant women: the former have significantly higher *Staphylococcus*, Enterobacteriaceae and *Escherichai coli* and fewer *Bifidobacterium*, *Bacteroides* and *Akkermanisa muciniphila* [134]. These differences could influence microbial colonization of the infant with important metabolic consequences in adulthood, recently reviewed in Refs. [135,136]. Could similar associations between obese mothers and their offspring predispose towards increased risk of developing neurodegenerative diseases later in life? A recent review by Contu and Hawkes who investigated the impact of maternal obesity on the cognitive function and mental health of offspring points in this direction [137]. In fact, a few animal studies have reported disrupted DNA methylation patterns and altered clearance of the β-amyloid peptide, marker of AD, in the brains of adult offspring exposed to an HFD during the prenatal period. However, no work has been done yet to determine epigenetic changes in the brains of human offspring born to obese mothers for obvious ethical reasons, although alterations in the extent of DNA methylation in cord blood and microRNA in amniotic fluid have been reported in human studies of maternal obesity, supporting the above hypothesis [138,139].

6. Strategies for prevention: postnatal nutrition on differences between breast-fed and formula-fed

The importance of early-life feeding patterns is vital since it shapes the early pioneering bacteria in the new-born, setting the stage for gut function and immune system development. This in turn may influence susceptibility to intestinal inflammatory disorders and other health and disease risks and, in the context of this review, possibly neurodegenerative disorders too later in life. The immune system of neonates is immature and requires the exposure of gut bacteria to develop properly, and this is particularly important within the early days of life [140,141]. Other functions such as vitamin biosynthesis, energy retention and intestinal permeability essential for human health also develop in parallel with gut microbe expansion. Initially, the infant gut is colonized by facultative anaerobes such as *Enterobacteriaceae* and *Lactobacillus*, followed by *Bifidobacterium*, *Bacteroides* and *Clostridium* [142]. Subsequently, milk-feeding practices play an essential role in microbiota composition. Compared to formula-fed milk, breast milk in healthy women contains a wider variety of viable and more beneficial bacteria, including *Staphylococcus*, *Streptococcus*, *Lactobacillus* and *Bifidobacterium*, the latter two known to stimulate the developing immune system and improve intestinal barrier function [143–145]. The source of this diverse population of bacteria in breast milk is unclear, but it appears to derive from bacteria residing in the mother's gut. Human milk also contains secretory IgA, antimicrobial peptides, cytokines, immune cells and over 200 nondigestible oligosaccharides (HMOs) which provide nutrients to the microbes colonizing the infant gut that produce specific SCFAs [146]. The HMOs and sIgA present in human milk are involved in preventing the colonization of pathogenic Proteobacteria during establishment of the early gut flora. Proteobacteria are believed to be important contributors to inflammation associated with metabolic disease in adults, and their role in infant immunity is critical for early priming of the innate and adaptive immune system [147–149]. Recently, differences in HMOs composition in mother's milk have also been associated with infant growth and body composition [150].

The gut microbiome of formula-fed infants is instead dominated by members of the Enterobacteriaceae, *Streptococcus*, *Bacteroides*, *Clostridium* and *Bifidobacterium* families [151]. The SCFA profiles of formula-fed infants are also different to those that are breast-fed, the latter being characterized by high proportions of acetate and lactate and a lower proportion of propionate [152]. Since SCFAs play essential roles in host-immune regulation and have anti-inflammatory effects, considered important to protect against obesity and metabolic syndrome, it follows that the differences found between SCFAs consequent to the two types of milk-feeding will lead to different outcomes in terms of health risks later in life. For instance, the different gut microbial community of formula-fed infants which have significantly higher levels of *Bacteroides* than breast-fed infants has been linked to the possible risk of celiac disease [153].

Overall, breast-feeding compared to formula feeding which is more calorie-dense is widely recognized to provide significant health benefits to infants, particularly in reducing the risk of pediatric obesity [154,155], and this risk is inversely related to the duration [156]. Since

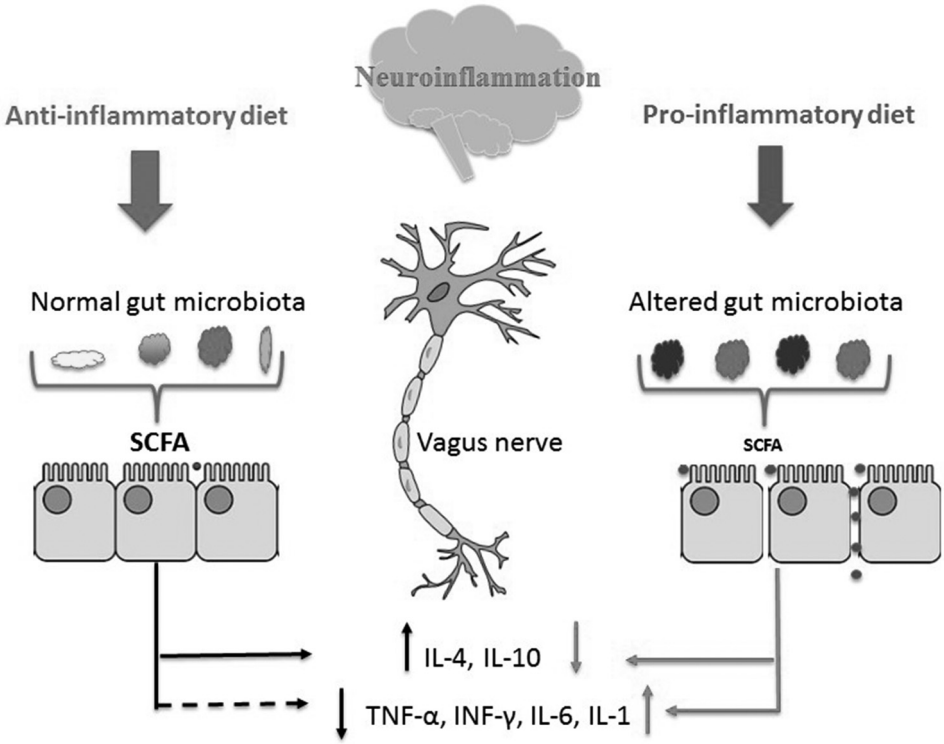

Fig. 2. Simplified scheme on how diet modifies cytokine production by gut microbiota and its connection with neuroinflammation.SCFAs: short-chain fatty acids.

obesity is linked to inflammation and this in turn to neuroinflammation, then the risk of developing neurodegenerative diseases later in life may also be reduced by breast-feeding. Worthy of note is that breast milk from obese mothers has been shown to harbor a different and less diverse and beneficial bacterial community than that of normal-weight subjects, such as higher levels of *Staphylococcus* and *A. muciniphila* and lower levels of *Bifidobacterium* [157], along with a different composition of hormones, cytokines and oligosaccharides [158]. In fact, infants born to obese mothers are exposed to higher levels of the hormones leptin and insulin present in mother's milk, and these appear to be correlated with changes in the composition and characteristics of the neonatal microbiome [159]. Whether the early effects of human milk from obese mothers on changes in the microbiome contribute to future disease risks in their infants remains to be explored.

7. Strategies for prevention: what can be done in adult age?

Strategies for prevention could be defined mainly in three phases: the first includes nutrigenomic dietary interventions for the mother during pregnancy, the second is defined during the postnatal age in a different way by breast- or formula -feeding, both described above, while the last one includes both nutrigenomics and supplements useful to counterbalance the progression of neurodegeneration. It is important to mention that all these approaches exhibit common mechanisms of action: the first and the second might be useful for avoiding or delaying the development of neurodegeneration, while the third in adult age may be useful to also counterbalance/inhibit the alterations that have already initiated.

An anti-inflammatory diet might represent a key strategy to prevent the risk factors associated with the development of neurodegeneration later in life. To this aim, the daily diet should include food able to promote an active modulation on genes involved in the control of inflammation and in the maintenance of a balanced redox state starting from toddlers which should be educated on their importance and use throughout their whole life. Food containing phosphatidylcholine (i.e., red meat, fish, egg and other animal products) should be controlled in adult age because they can promote microbiota-mediated trimethylamine (TMA) which is converted into trimethylamine-oxide (TMA-N-oxide) after hepatic metabolism, and that can be accumulated inside the vascular wall, leading to atherosclerosis and promoting macrophages proinflammatory responses [90]. A high-fat diet also should be avoided because it modifies the inflammatory responses via NFkβ stimulation and proinflammatory cytokines that may change intestinal permeability. The latter can also be regulated by the level of *A. muciniphila*, a mucin-degrading bacterium that has been reported to be positively associated with a reduction in adipose tissue inflammation, insulin resistance and restoration of the gut barrier [160–162].

Foods such as green/white/red/orange vegetables, red fruits, broccoli, curcuma and tea represent an important source of bioactive compounds able to protect against neurodegeneration [163]. Broccoli, kale and radish of the Brassicaceae family contain sulforaphane, an isothiocyanate which becomes active only after myrosinase-mediated degradation of glucosinolate precursors such as glucoraphanin. However, the myrosinase contained in the Brassicaceae is inactivated by high temperatures (>60°C). Recently, it has been observed that gut microbiota can exert a myrosinase-like activity, giving the possibility to produce sulforaphane even after cooking of vegetables [164]. The protective effect of sulforaphane is linked to its modulation of anti-inflammatory and antioxidant pathways. Several reports have demonstrated that sulforaphane is able to inhibit COX-2 while promoting the Nrf2/ARE pathway, an indicator and modulator of oxidative stress in neurodegeneration [165,166]. Moreover, sulforaphane has been reported to improve behavioral cognitive impairments and attenuated brain Aβ burden in an AD animal model [167].

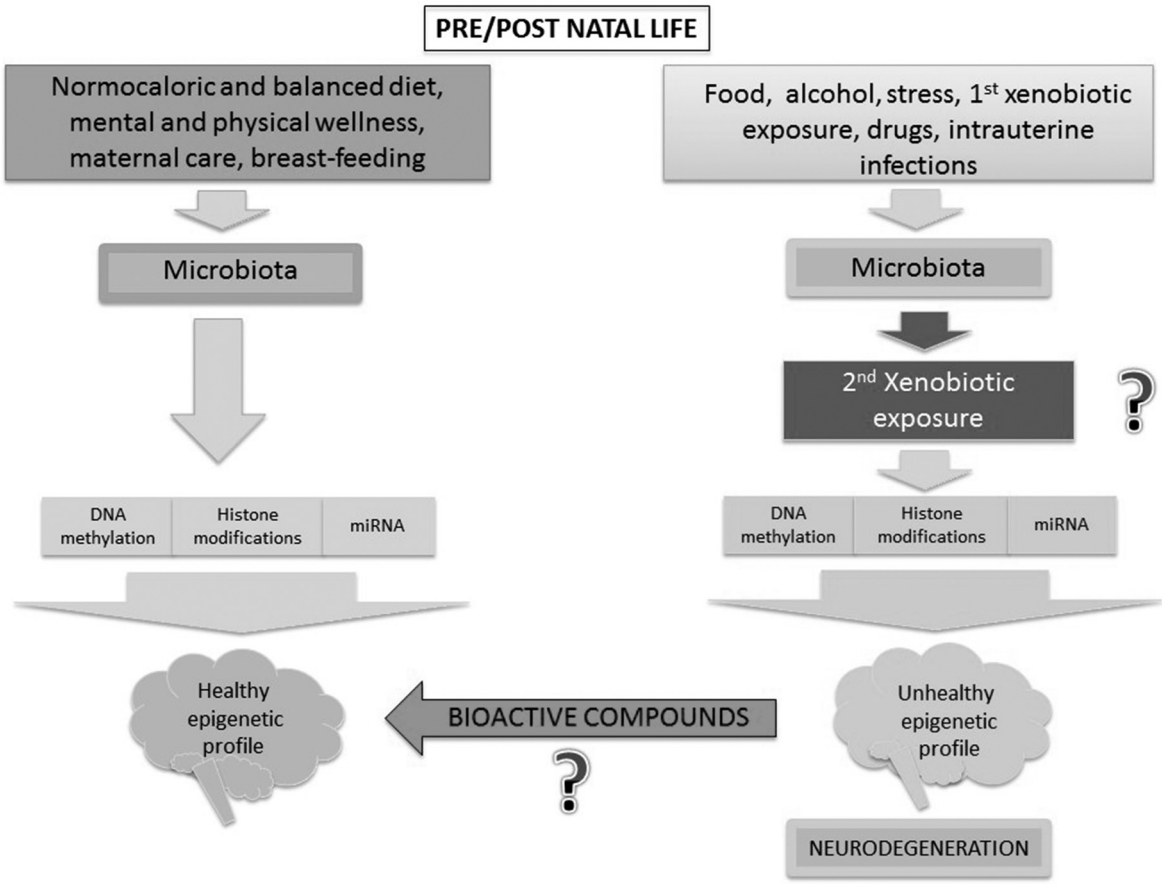

Fig. 3. Risk factors for neurodegeneration and possible prevention strategies.

Studies on mitochondria from human neuroblastoma SH-SY5Y cells treated with hydrogen peroxide show that sulforaphane is able to protect mitochondrial membrane against lipid and protein oxidation; moreover, it can also protect against loss of ATP 168]. For these reasons, its use against particular signs and symptoms of AD has been suggested [169].

Green tea for its high content of the flavonoid epigallocatechin gallate (EGCG) exerts a significant antioxidant and anti-inflammatory activity. In a mouse model of dopaminergic oxidative damage induced by the prodrug 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine, EGCG was shown to regulate the iron-export protein ferroportin, reducing oxidative stress in the brain [170]. In neonatal mice, EGCG inhibited the damage induced by exposure to sevuflurane, a toxicant used to induce neurodegeneration, and improved learning and memory by acting on the activation of the CREB/BDNF/TrkB-PI3K/Akt signaling pathway [171]. Quercetin, another flavonoid widely distributed in nature, has also been associated with a reduced risk of development of neurodegenerative disorders because it may mitigate oxidative stress and mitochondrial dysfunctions [172].

Resveratrol and curcumin, found in the skin of red and blue berries and in turmeric powder respectively, have anti-inflammatory properties due to their ability to decrease the expression of inflammatory genes (i.e., NFκB, AP1, COX-2 and iNOS); it has been suggested that histone acetylation by activated NFκB can be repressed by resveratrol [173]. The numerous reports on the positive effects of resveratrol and curcumin against the production of anti-inflammatory cytokines underline their key protective role against neurodegeneration. A recent review that has summarized the data on curcumin in the last 5 years highlights the neuroprotective role of curcumin which is able to cross the BBB and exert anti-inflammatory, antioxidant, and anti-protein-aggregating roles [174,175].

Melatonin, produced by the pineal gland in animals but also produced in plants, has been suggested as a strategic compound for its long-term effect on neuroprotection. Studies on LPS-treated animals show that melatonin can stimulate the SIRT1/Nrf2 pathway reducing reactive oxygen species production [176]. Similarly, a protective effect against the neurotoxin polychlorinated biphenyls on motor coordination and anxiety-like behavior was observed when animals were co-treated with melatonin [177]. In a rat model of AD, melatonin improved the neurotoxicity and astrocyte activation due to β-amyloid1-42 (Aβ1-42) exposure in the cerebral cortex. Furthermore, melatonin was able to inhibit the reduction of Reelin and Dab1 expression stimulated by Aβ1-42 [178].

Lutein, a xanthophyll found in high quantities in green leafy vegetables, has been proposed to be useful in the protection of brain damage because of its beneficial properties during brain development. Lutein concentration has been correlated with lipid and energy metabolites, brain osmolytes and aminoacid neurotrasmitters [179].

Lastly, since a high-fat diet promotes hypothalamic inflammation and epigenetic programming, the composition and the content of fatty acids in the diet should be under control during all stages of life. At present, the main problem in early-life nutritional strategies to prevent neurodegeneration is associated with the poor knowledge on “how much” and “which” foods should be included in the diet that actually become bioavailable in order for their bioactive compounds to exert their protective effects. In dietary supplements, how much of the bioactive compounds should be present in order to achieve only long-lasting

positive effects? These are all questions which are waiting to be addressed. Further research aimed to identify the association between "quantity/quality of food" and individual metabolic responses should be promoted to finalize the data on the numerous bioactive compounds known and those still awaiting to be discovered for contrasting the development of neurodegeneration (Fig. 3).

8. Conclusion

Neurodegeneration is a complex aging process which starts as early as the intrauterine period of life. Early-life actions are here suggested to prevent and counterbalance its development: (1) mother-to-be lifestyle should be carefully monitored to guarantee the required balanced micro/macronutrients and avoidance of stress, drugs, xenobiotics or smoke exposure and finally any intrauterine infections; (2) early postnatal age of life should be under control for mother's food intake and environmental exposure if offspring is breast-fed; (3) vaginal delivery should be preferred, when possible, with respect to cesarean-section delivery particularly when the mother has a lean phenotype; (4) breast-feeding should be promoted longer because of its protective effect on offspring; (5) a diverse intake of organic fruit and vegetable should be present in the diet of both young and adult people because of their key role in the maintenance of microbiota diversity which is importantly linked with SCFA production and with their anti-inflammatory activity associated with a healthy metabolic profile; (6) moderate physical activity, equilibrated emotional status and mental wellness contribute to the maintenance of an anti-inflammatory status; and (7) intake through diet or supplements of bioactive compounds able to reduce oxidation and inflammation, thus preventing or counterbalancing progressive neurodegeneration, should be taken into account particularly in people exposed to environmental chemical and physical stressors.

References

[1] Hanson MA, Gluckman GP. Early developmental conditioning of later health and disease: physiology or pathophysiology? Physiol Rev 2014;94:1027-6.
[2] Burton T, Metcalfe NB. Can environmental conditions experienced in early life influence future generations? Proc Biol Sci 2014;281(1785) [20140311].
[3] De Rooij SR, Caan MW, Swaab DF, Nederveen AJ, Majoie CB, Schwab M, et al. Prenatal famine exposure has sex-specific effects on brain size. Brain 2016;139:2136–42.
[4] Dominguez-Salas P, Cox SE, Prentice AM, Hennig BJ, More SE. Maternal nutritional status, C(1) metabolism and offspring DNA methylation: a review of current evidence in human subjects. Proc Nutr Soc 2012;71(1):154–65.
[5] Bannister AJ, Kouzarides T. Regulation of chromatin by histone modifications. Cell Res 2011;21(3):381–95.
[6] Chatterjee N, Sinha D, Lemma-Dechassa M, Tan S, Shogren-Knaak MA, Bartholomew B. Histone H3 tail acetylation modulates ATP-dependent remodeling through multiple mechanisms. Nucleic Acids Res 2011;39(19):8378–91.
[7] Ravelli AC, van Der Meulen JH, Osmond C, Barker DJ, Bleker OP. Obesity at the age of 50 y in men and women exposed to famine prenatally. Am J Clin Nutr 1999;70:811–6.
[8] Lumey LH, Terry MB, Delgado-Cruzata L, Liao Y, Wang Q, Susser E, et al. Adult global DNA methylation in relation to pre-natal nutrition. Int J Epidemiol 2012;41(1):116–23.
[9] Tserga A, Binder AM, Michels KB. Impact of folic acid intake during pregnancy on genomic imprinting of IGF2/H19 and 1-carbon metabolism. FASEB J 2017;31(12):5149–58.
[10] Tobi EW, Slagboom PE, van Dongen J, Kremer D, Stein AD, Putter H, et al. Prenatal famine and genetic variation are independently and additively associated with DNA methylation at regulatory loci within IGF2/H19. PLoS One 2012;7(5):e37933.
[11] Tobi EW, Slieker RC, Stein AD, Suchiman HE, Slagboom PE, van Zwet EW, et al. Early gestation as the critical time-window for changes in the prenatal environment to affect the adult human blood methylome. Int J Epidemiol 2015;44(4):1211–23.
[12] Stein AD, Pierik FH, Verrips GHW, Susser ES, Lumey LH. Maternal exposure to the Dutch Famine before conception and during pregnancy: quality of life and depressive symptoms in adult offspring. Epidemiology 2009;20(6):909–15.
[13] Veenendaal M, Painter R, De Rooij S, Bossuyt P, Van der Post J, Gluckman P, et al. Transgenerational effects of prenatal exposure to the 1944–45 Dutch famine. BJOG 2013:120548–54.
[14] Barker DJ, Winter PD, Osmond C, Margetts B, Simmonds SJ. Weight in infancy and death from ischaemic heart disease. Lancet 1989;2(8663):577–80.
[15] Jones A, Osmond C, Godfrey KM, Phillips DI. Evidence for developmental programming of cerebral laterality in humans. PLoS One 2011;6(2):e17071.
[16] Stroud LR, Papandonatos GD, Rodriguez D, McCallum M, Salisbury AL, Phipps MG, et al. Maternal smoking during pregnancy and infant stress response: test of a prenatal programming hypothesis. Psychoneuroendocrinology 2014;48:29-0.
[17] Grunnet L, Vielwerth S, Vaag A, Poulsen P. Birth weight is nongenetically associated with glucose intolerance in elderly twins, independent of adult obesity. J Intern Med 2007;262:96-03.
[18] Perälä M-M, Kajantie E, Valsta LM, Holst JJ, Leiviskä J, Eriksson JG. Early growth and postprandial appetite regulatory hormone responses. Br J Nutr 2013;110:1591–600.
[19] Parlee SD, MacDougald OA. Maternal nutrition and risk of obesity in offspring: the Trojan horse of developmental plasticity. Biochim Biophys Acta 2014 Mar;1842(3):495–506.
[20] Modgil S, Lahiri DK, Sharma VL, Anand A. Role of early life exposure and environment on neurodegeneration: implications on brain disorders. Transl Neurodegener 2014;3:9.
[21] Faa G, Manchia M, Pintus R, Gerosa C, Marcialis MA, Fanos V. Fetal programming of neuropsychiatric disorders. Birth Defects Res Part C - Embryo Today Rev 2016;108:207–23.
[22] Tartaglione AM, Venerosi A, Calamandrei G. Early-life toxic insults and onset of sporadic neurodegenerative diseases — an overview of experimental studies. Curr Top Behav Neurosci 2016:29231–64.
[23] Mirzakhani H, De Vivo I, Leeder JS, Gaedigk R, Vyhlidal CA, Weiss ST, et al. Early pregnancy intrauterine fetal exposure to maternal smoking and impact on fetal telomere length. Eur J Obstet Gynecol Reprod Biol 2017;218:27–32.
[24] Tanner CM, Goldman SM, Ross GW, Grate SJ. The disease intersection of susceptibility and exposure: chemical exposures and neurodegenerative disease risk. Alzheimers Dement 2014;10(3 Suppl):S213–25.
[25] Nasuti C, Brunori G, Eusepi P, Marinelli L, Ciccocioppo R, Gabbianelli R. Early life exposure to permethrin: a progressive animal model of Parkinson's disease. J Pharmacol Toxicol Methods 2017;83:80–6.
[26] Bordoni L, Nasuti C, Mirto M, Caradonna F, Gabbianelli R. Intergenerational effect of early life exposure to permethrin: changes in global DNA methylation and in Nurr1 gene expression. Toxics 2015;3(4):451–61.
[27] Fedeli D, Montani M, Carloni M, Nasuti C, Amici A, Gabbianelli R. Leukocyte Nurr1 as peripheral biomarker of early-life environmental exposure to permethrin insecticide. Biomarkers 2012 Nov;17(7):604–9.
[28] Nephew BC, Carini LM, Sallah S, Cotino C, Alyamani RAS, Pittet F, et al. Intergenerational accumulation of impairments in maternal behavior following postnatal social stress. Psychoneuroendocrinology 2017;13:8298-106.
[29] Carloni M, Nasuti C, Fedeli D, Montani M, Amici A, Vadhana MSD, et al. The impact of early life permethrin exposure on development of neurodegeneration in adulthood. Exp Gerontol 2012;47:60–6.
[30] Miranda-Morales E, Meier K, Sandoval-Carrillo A, Salas-Pacheco J, Vázquez-Cárdenas P, Arias-Carrión O. Implications of DNA methylation in Parkinson's disease. Front Mol Neurosci 2017;10:1–13.
[31] Sharma RP, Tun N, Grayson DR. Depolarization induces downregulation of DNMT1 and DNMT3a in primary cortical cultures. Epigenetics 2008;3:74–80.
[32] Fedeli D, Montani M, Bordoni L, Galeazzi R, Nasuti C, Correia-Sá L, et al. In vivo and in silico studies to identify mechanisms associated with Nurr1 modulation following early life exposure to permethrin in rats. Neuroscience 2017;340:411–23.
[33] Kim KY, Kim DS, Lee SK, Lee IK, Kang JH, Chang YS, et al. Association of low-dose exposure to persistent organic pollutants with global DNA hypomethylation in healthy Koreans. Environ Health Perspect 2010;118:370–4.
[34] Castorina R, Bradman A, Stapleton HM, Butt C, Avery D, Harley KG, et al. Current-use flame retardants: maternal exposure and neurodevelopment in children of the CHAMACOS cohort. Chemosphere 2017;189:574–80.
[35] Slotkin TA, Skavicus S, Stapleton HM, Seidler FJ. Brominated and organophosphate flame retardants target different neurodevelopmental stages, characterized with embryonic neural stem cells and neuronotypic PC12 cells. Toxicology 2017;390:32.
[36] Roncati L, Termopoli V, Pusiol T. Negative role of the environmental endocrine disruptors in the human neurodevelopment. Front Neurol 2016;7:5–8.
[37] London L, Beseler C, Bouchard MF, Bellinger DC, Colosio C, Grandjean P, et al. Neurobehavioural and neurodevelopmental effects of pesticide exposures. Neurotoxicology 2012;33(4):887–96.
[38] Viel JF, Warembourg C, Le Maner-Idrissi G, Lacroix A, Limon G, Rouget F, et al. Pyrethroid insecticide exposure and cognitive developmental disabilities in children: The PELAGIE mother–child cohort. Environ Int 2015;82:69-5.
[39] Holland N, Lizarraga D, Huen K. Recent progress in the genetics and epigenetics of paraoxonase: why it is relevant to children's environmental health. Curr Opin Pediatr 2015;27(2):240–7.
[40] Kopp B, Zalko D, Audebert M. Genotoxicity of 11 heavy metals detected as food contaminants in two human cell lines. Environ Mol Mutagen 2017. https://doi.org/10.1002/em.22157.
[41] Nica DV, Popescu C, Draghici GA, Andrica FM, Privistirescu IA, Gergen II, et al. High-level dietary cadmium exposure is associated with global DNA hypermethylation in the gastropod hepatopancreas. PLoS One 2017;12(9):e0184221.
[42] Lukiw WJ. Evidence supporting a biological role for aluminum in chromatin compaction and epigenetics. J Inorg Biochem 2010;104(9):1010–2.

[43] Healy S, McMahon JM, FitzGerald U. Modelling iron mismanagement in neurodegenerative disease in vitro: paradigms, pitfalls, possibilities & practical considerations. Prog Neurobiol 2017;158:1–14.
[44] Olmedo-Díaz S, Estévez-Silva H, Orädd G, Af Bjerkén S, Marcellino D, Virel A. An altered blood–brain barrier contrib to brain iron accumulation and neuroinflammation in the 6-OHDA rat model Parkinson's disease. Neuroscience 2017; 362:141–51.
[45] Schachtschneider KM, Liu Y, Rund LA, Madsen O, Johnson RW, Groenen MA, et al. Impact of neonatal iron deficiency on hippocampal DNA methylation and gene transcription in a porcine biomedical model of cognitive development. BMC Genomics 2016;17(1):856.
[46] Pasricha SR, Lim PJ, Duarte TL, Casu C, Oosterhuis D, Mleczko-Sanecka K, et al. Hepcidin is regulated by promoter-associated histone acetylation and HDAC3. Nat Commun 2017;8(1):403.
[47] Keen CL, Hanna LA, Lanoue L, Uriu-Adams JY, Rucker RB, Clegg MS. Developmental consequences of trace mineral deficiencies in rodents: acute and long-term effects. J Nutr 2003 May;133(5 Suppl 1):1477S-80S.
[48] Gerber H, Wu F, Dimitrov M, Garcia Osuna GM, Fraering PC. Zinc and copper differentially modulate amyloid precursor protein processing by γ-secretase and amyloid-β peptide production. J Biol Chem 2017;292(9):3751–67.
[49] Lussier AA, Weinberg J, Kobor MS. Epigenetics studies of fetal alcohol spectrum disorder: where are we now? Epigenomics 2017 Mar;9(3):291-11.
[50] Karunamuni G, Sheehan MM, Doughman YQ, Gu S, Sun J, Li Y, et al. Supplementation with the methyl donor betaine prevents congenital defects induced by prenatal alcohol exposure. Alcohol Clin Exp Res 2017 Nov;41(11): 1917–27.
[51] Medici V, Halsted CH. Folate, alcohol, and liver disease. Mol Nutr Food Res 2013; 57(4):596-06.
[52] Pascual M, Montesinos J, Montagud-Romero S, Forteza J, Rodríguez-Arias M, Miñarro J, et al. TLR4 response mediates ethanol-induced neurodevelopment alterations in a model of fetal alcohol spectrum disorders. J Neuroinflammation 2017;14(1):145.
[53] Nakhoul MR, Seif KE, Haddad N, Haddad GE. Fetal alcohol exposure: the common toll. J Alcohol Drug Depend 2017;5(1) [Pii 257].
[54] Ramsay M. Genetic and epigenetic insights into fetal alcohol spectrum disorders. Genome Med 2010;2(4):27.
[55] Heinemann SD, Posimo JM, Mason DM, Hutchison DF, Leak RK. Synergistic stress exacerbation in hippocampal neurons: Evidence favoring the dual-hit hypothesis of neurodegeneration. Hippocampus 2016;26(8):980–94.
[56] Berry C, La Vecchia C, Nicotera P. Paraquat and Parkinson's disease. Cell Death Differ 2010;17(7):1115–25.
[57] Moretto A, Colosio C. Biochemical and toxicological evidence of neurological effects of pesticides: the example of Parkinson's disease. Neurotoxicology 2011; 32(4):383–91.
[58] Maloney B, Sambamurti K, Zawia N, Lahiri DK. Applying epigenetics to Alzheimer's disease via the latent early-life associated regulation (LEARn) model. Curr Alzheimer Res 2012;9:589–99.
[59] Koning IV, Dudink J, Groenenberg IAL, Willemsen SP, Reiss IKM, Steegers-Theunissen RPM. Prenatal cerebellar growth trajectories and the impact of periconceptional maternal and fetal factors. Hum Reprod 2017;32:1230–7.
[60] Hinkle SN, Schieve LA, Stein AD, Swan DW, Ramakrishnan U, Sharma AJ. Associations between maternal prepregnancy body mass index and child neurodevelopment at 2 years of age. Int J Obes (Lond) 2012;36(10):1312–9.
[61] Widen EM, Kahn LG, Cirillo P, Cohn B, Kezios KL, Factor-Litvak P. Prepregnancy overweight and obesity are associated with impaired child neurodevelopment. Matern Child Nutr 2017. https://doi.org/10.1111/mcn.12481 [n.d.].
[62] Mina T H, Lahti M, Drake A J, Forbes S, Denison F C, Räikkönen K, et al. Maternal lipids in pregnancy are associated with increased offspring cortisol reactivity in childhood. Psychoneuroendocrinology, 83, 79-3.
[63] Laugerette F, Vors C, Peretti N, Michalski MC. Complex links between dietary lipids, endogenous endotoxins and metabolic inflammation. Biochimie 2011: 9339–45.
[64] Moreira AP, Texeira TF, Ferreira AB, Peluzio Mdo C, Alfenas Rde C. Influence of a high-fat diet on gut microbiota, intestinal permeability and metabolic endotoxaemia. Br J Nutr 2012;108:801–9.
[65] Dudele A, Hougaard KS, Kjølby M, Hokland M, Winther G, Elfving B, et al. Chronic maternal inflammation or high-fat-feeding programs offspring obesity in a sex-dependent manner. Int J Obes (Lond) 2017:1–7.
[66] Graciarena M, Roca V, Mathieu P, Depino AM, Pitossi FJ. Differential vulnerability of adult neurogenesis by adult and prenatal inflammation: role of TGF-f21. Brain Behav Immun 2013;34:1728.
[67] Valdearcos M, Robblee MM, Benjamin DI, Nomura DK, Xu AW, Koliwad SK. Microglia dictate the impact of saturated fat consumption on hypothalamic inflammation and neuronal function. Cell Rep 2014:92124–38.
[68] Lehnardt S, Massillon L, Follett P, Jensen FE, Ratan R, Rosenberg PA, et al. Activation of innate immunity in the CNS triggers neurodegeneration through a Toll-like receptor 4-dependent pathway. Proc Natl Acad Sci U S A 2003;100(14): 8514–9.
[69] De Souza CT, Araujo EP, Bordin S, Ashimine R, Zollner RL, Boschero AC, et al. Consumption of a fat-rich diet activates a proinflammatory response and induces insulin resistance in the hypothalamus. Endocrinology 2005;146: 4192–9.
[70] Qin L, Wu X, Block ML, Liu Y, Breese GR, Hong JS, et al. Systemic LPS causes chronic neuroinflammation and progressive neurodegeneration. Glia 2007: 55453–62.
[71] Fidel Jr PL, Romero R, Wolf N, Cutright J, Ramirez M, Araneda H, et al. Systemic and local cytokine profiles in endotoxin-induced preterm parturition in mice. Am J Obstet Gynecol 1994:1701467–75.
[72] Cai Z, Pan ZL, Pang Y, Evans OB, Rhodes PG. Cytokine induction in fetal rat brains and brain injury in neonatal rats after maternal lipopolysaccharide administration. Pediatr Res 2000:4764–72.
[73] Pimentel GD, Lira FS, Rosa JC, Oliveira JL, Losinskas-Hachul AC, Souza GI, et al. Intake of trans fatty acids during gestation and lactation leads to hypothalamic inflammation via TLR4/NFκBp65 signaling in adult offspring. J Nutr Biochem 2012;23(3):265–71.
[74] Albuquerque KT, Sardinha FL, Telles MM, Watanabe RL, Nascimento CM, Tavares do Carmo MG, et al. Intake of trans fatty acid-rich hydrogenated fat during pregnancy and lactation inhibits the hypophagic effect of central insulin in the adult offspring. Nutrition 2006;22(7-8):820–9.
[75] Magri TP, Fernandes FS, Souza AS, Langhi LG, Barboza T, Misan V, et al. Interesterified fat or palm oil as substitutes for partially hydrogenated fat in maternal diet can predispose obesity in adult male offspring. Clin Nutr 2015;34 (5):904–10.
[76] Mendes-da-Silva C, Lemes SF, Baliani Tda S, Versutti MD, Torsoni MA. Increased expression of Hes5 protein in Notch signalling pathway in the hippocampus of mice offspring of dams fed a high-fat diet during pregnancy and suckling. Int J Dev Neurosci 2015:4035–42.
[77] Adler DA, Ammanuel S, Lei J, Dada T, Borbiev T, Johnston MV, et al. Circadian cycle dependent EEG biomarkers of pathogenicity in adult mice following prenatal exposure to in utero inflammation. Neuroscience 2014;275:305–13.
[78] Dada T, Rosenzweig JM, Al SM, Firdaus W, Al RS, Borbiev T, et al. Mouse model of intrauterine inflammation: Sex-specific differences in long-term neurologic and immune sequelae. Brain Behav Immun 2014:38142–50.
[79] Leitner K, Al Shammary M, McLane M, Johnston MV, Elovitz MA, Burd I. IL-1 receptor blockade prevents fetal cortical brain injury but not preterm birth in a mouse model of inflammation-induced preterm birth and perinatal brain injury. Am J Reprod Immunol 2014;71(5):418–26.
[80] Esmaillzadeh A, Kimiagar M, Mehrabi Y, Azadbakht L, Hu FB, Willett WC. Fruit and vegetable intakes, C-reactive protein, and the metabolic syndrome. Am J Clin Nutr 2006;84(6):1489–97.
[81] McCloskey K, Ponsonby AL, Collier F, Allen K, Tang ML, Carlin JB, et al. The association between higher maternal pre-pregnancy body mass index and increased birth weight, adiposity and inflammation in the newborn. Pediatr Obes 2018;13(1):46–53.
[82] Flegal KM, Carroll MD, Ogden CL, Curtin LR. Prevalence and trends in obesity among US adults, 1999-2008. JAMA 2010;303(3):235–41.
[83] Ferrante Jr AW. Obesity-induced inflammation: a metabolic dialogue in the language of inflammation. J Intern Med 2007;262(4):408–14.
[84] Visentin S, Lapolla A, Londero AP, Cosma C, Dalfra M, Camerin M, et al. Adiponectin levels are reduced while markers of systemic inflammation and aortic remodelling are increased in intrauterine growth restricted mother-child couple. Biomed Res Int 2014;2014:401595.
[85] Xie L, Zhang K, Rasmussen D, Wang J, Wu D, Roemmich JN, et al. Effects of prenatal low protein and postnatal high fat diets on visceral adipose tissue macrophage phenotypes and IL-6 expression in Sprague Dawley rat offspring. PLoS One 2017;12(1):e0169581.
[86] Sen S, Rifas-Shiman SL, Shivappa N, Wirth MD, Hebert JR, Gold DR, et al. Dietary inflammatory potential during pregnancy is associated with lower fetal growth and breastfeeding failure: results from project Viva. J Nutr 2016;146(4):728–36.
[87] Hodge DR, Peng B, Cherry JC, Hurt EM, Fox SD, Kelley JA, et al. Interleukin 6 supports the maintenance of p53 tumor suppressor gene promoter methylation. Cancer Res 2005:654673–82.
[88] Nomura Y, Lambertini L, Rialdi A, Lee M, Mystal EY, Grabie M, et al. Global methylation in the placenta and umbilical cord blood from pregnancies with maternal gestational diabetes, preeclampsia, and obesity. Reprod Sci 2014;21 (1):131–7.
[89] Liu X, Chen Q, Tsai HJ, Wang G, Hong X, Zhou Y, et al. Maternal preconception body mass index and offspring cord blood DNA methylation: exploration of early life origins of disease. Environ Mol Mutagen 2014;55(3):223–30.
[90] Wankhade UD, Zhong Y, Kang P, Alfaro M, Chintapalli SV, Thakali KM, et al. Enhanced offspring predisposition to steatohepatitis with maternal high-fat diet is associated with epigenetic and microbiome alterations. PLoS One 2017;12(4): e0175675.
[91] Reynolds CM, Segovia S, Zhang XD, Gray C, Vickers MH. Maternal high-fat diet-induced programing of gut taste receptor and inflammatory gene expression in rat offspring is ameliorated by CLA supplementation. Physiol Rep 2015;3:1–9.
[92] McCullough LE, Miller EE, Calderwood LE, Shivappa N, Steck SE, Forman MR, et al. Maternal inflammatory diet and adverse pregnancy outcomes: circulating cytokines and genomic imprinting as potential regulators? Epigenetics 2017; 2294:00. https://doi.org/10.1080/15592294.2017.1347241.
[93] Lieblein-Boff JC, McKim DB, Shea DT, Wei P, Deng Z, Sawicki C, et al. Neonatal E. coli infection causes neuro-behavioral deficits associated with hypomyelination and neuronal sequestration of iron. J Neurosci 2013;33:16334–45.
[94] Urrutia P, Aguirre P, Esparza A, Tapia V, Mena NP, Arredondo, et al. Inflammation alters the expression of DMT1, FPN1 and hepcidin, and it causes iron accumulation in central nervous system cells. J Neurochem 2013;126:541–9.
[95] Graf AE, Lallier SW, Waidyaratne G, Thompson MD, Tipple TE, Hester ME, et al. Maternal high fat diet exposure is associated with increased hepcidin levels, decreased myelination, and neurobehavioral changes in male offspring. Brain Behav Immun 2016;58:369–78.

[96] Jahani R, Fielding KA, Chen J, Villa CR, Castelli LM, Ward WE, et al. Low vitamin D status throughout life results in an inflammatory prone status but does not alter bone mineral or strength in healthy 3-month-old CD-1 male mice. Mol Nutr Food Res 2014;58(7):1491–501.
[97] Villa C, Chen J, Wen B, Sacco S, Taibi A, Ward W, et al. Maternal vitamin D beneficially programs metabolic, gut and bone health of mouse male offspring in an obesogenic environment. Int J Obes (Lond) 2016;40:1875–83.
[98] Villa CR, Chen J, Wen B, Sacco SM, Taibi A, Ward WE, et al. Maternal dietary vitamin D does not program systemic inflammation and bone health in adult female mice fed an obesogenic diet. Nutrients 2016;8. https://doi.org/10.3390/nu8110675.
[99] Amoako AA, Nafee TM, Ola B. Epigenetic influences during the periconception period and assisted reproduction. Adv Exp Med Biol 2017;1014:15–9.
[100] Blewitt M, Whitelaw E. The use of mouse models to study epigenetics. Cold Spring Harb Perspect Biol 2013;5:a017939.
[101] Tran PV, Kennedy BC, Lien YC, Simmons RA, Georgieff MK. Fetal iron deficiency induces chromatin remodeling at the Bdnf locus in adult rat hippocampus. Am J Physiol Regul Integr Comp Physiol 2015:308R276–82.
[102] Kurita H, Ohsako S, Hashimoto S, Yoshinaga J, Tohyama C. Prenatal zinc deficiency-dependent epigenetic alterations of mouse metallothionein-2 gene. J Nutr Biochem 2013:24256–66.
[103] Gueant JL, Namour F, Gueant-Rodriguez RM, Daval J. Folate and fetal programming: a play in epigenomics? Trends Endocrinol Metab 2013;24:279–89.
[104] Konycheva G, Dziadek MA, Ferguson LR, Krageloh CU, Coolen MW, Davison M, et al. Dietary methyl donor deficiency during pregnancy in rats shapes learning and anxiety in offspring. Nutr Res 2011:31790–804.
[105] Zhang Q, Xue P, Li H, Bao Y, Wu L, Chang S, et al. Histone modification mapping in human brain reveals aberrant expression of histone H3 lysine 79 dimethylation in neural tube defects. Neurobiol Dis 2013:54404–13.
[106] Zeisel SH. Importance of methyl donors during reproduction. Am J Clin Nutr 2009;89(2):673S-7S.
[107] Bailey LB. New standard for dietary folate intake in pregnant women. Am J Clin Nutr 2000;71(5 Suppl):1304S-07S.
[108] Van Dijk MR, Borggreven NV, Willemsen SP, Koning AHJ, Gine R, Steegers-Theunissen PM, et al. Maternal lifestyle impairs embryonic growth: the Rotterdam periconception cohort; 2017; 1–7. https://doi.org/10.1177/1933719117728801.
[109] Lillycrop KA, Phillips ES, Jackson AA, Hanson MA, Burdge GC. Dietary protein restriction of pregnant rats induces and folic acid supplementation prevents epigenetic modification of hepatic gene expression in the offspring. J Nutr 2005;135:1382–6.
[110] Lambrot R, Xu C, Saint-Phar S, Chountalos G, Cohen T, Paquet M, et al. Low paternal dietary folate alters the mouse sperm epigenome and is associated with negative pregnancy outcomes. Nat Commun 2013;4:2889.
[111] Rando OJ. Intergenerational Transfer of epigenetic information in sperm. Cold Spring Harb Perspect Med 2016;6:a022988.
[112] Rando OJ, Simmons RA. I'm eating for two: parental dietary effects on offspring metabolism. Cell 2015;161(1):93–5.
[113] McStay CL, Prescott SL, Bower C, Palmer DJ. Maternal folic acid supplementation during pregnancy and childhood allergic disease outcomes: a question of timing? Nutrients 2017;9. https://doi.org/10.3390/nu9020123.
[114] Hollingsworth JW, Maruoka S, Boon K, Garantziotis S, Li Z, Tomfohr J, et al. In utero supplementation with methyl donors enhances allergic airway disease in mice. J Clin Investig 2008;118:3462–9.
[115] Walker WA. The importance of appropriate initial bacterial colonization of the intestine in newborn, child, and adult health. Pediatr Res 2017. https://doi.org/10.1038/pr.2017.111.
[116] Louis P, Hold GL, Flint H. The gut microbiota, bacterial metabolites and colorectal cancer. Nat Rev Microbiol 2014;12(10):661–72.
[117] Sonnenburg JL, Bäckhed F. Diet-microbiota interactions as moderators of human metabolism. Nature 2016;535(7610):56–64.
[118] Sampson TR, Debelius JW, Thron T, Janssen S, Shastri GG, Ilhan ZE, et al. Gut microbiota regulate motor deficits and neuroinflammation in a model of Parkinson's disease. Cell 2016;167(6) [1469-1480.e12].
[119] Unger MM, Spiegel J, Dillmann KU, Grundmann D, Philippeit H, Bürmann J, et al. Short chain fatty acids and gut microbiota differ between patients with Parkinson's disease and age-matched controls. Parkinsonism Relat Disord 2016:3266–72.
[120] Malkki H. Parkinson disease: could gut microbiota influence severity of Parkinson disease? Nat Rev Neurol 2017;13(2):66–7.
[121] Hill-Burns EM, Debelius JW, Morton JT, Wissemann WT, Lewis MR, Wallen ZD, et al. Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. Mov Disord 2017;32(5):739–49.
[122] Parashar A, Udayabanu M. Gut microbiota: Implications in Parkinson's disease. Parkinsonism Relat Disord 2017:381–7.
[123] Nasuti C, Coman MM, Olek RA, Fiorini D, Verdenelli MC, Cecchini C, et al. Changes on fecal microbiota in rats exposed to permethrin during postnatal development. Environ Sci Pollut Res Int 2016;23(11):10930–7.
[124] Tremlett H, Bauer KC, Appel-Cresswell S, Finlay BB, Waubant E. The gut microbiome in human neurological disease: a review. Ann Neurol 2017;81(3):369–82.
[125] Fan LW, Pang Y. Dysregulation of neurogenesis by neuroinflammation: key differences in neurodevelopmental and neurological disorders. Neural Regen Res 2017;12(3):366-37.
[126] Valero J, Bernardino L, Cardoso FL, Silva AP, Fontes-Ribeiro C, Ambrósio AF, et al. Impact of neuroinflammation on hippocampal neurogenesis: relevance to aging and Alzheimer's disease. J Alzheimers Dis 2017;60(s1):S161–8.
[127] Tilley SK, Joseph RM, Kuban KCK, Dammann OU, O'Shea TM, Fry RC. Genomic biomarkers of prenatal intrauterine inflammation in umbilical cord tissue predict later life neurological outcomes. PLoS One 2017;12(5):e0176953.
[128] Alam R, Abdolmaleky HM, Zhou JR. Microbiome, inflammation, epigenetic alterations, and mental diseases. Am J Med Genet B Neuropsychiatr Genet 2017;174(6):651–60.
[129] Rhee SH, Pothoulakis C, Mayer EA. Principles and clinical implications of the brain–gut–enteric microbiota axis. Nat Rev Gastroenterol Hepatol 2009;6:306–14.
[130] Mulak A, Bonaz B. Brain-gut-microbiota axis in Parkinson's disease. World J Gastroenterol 2015;21:10609–20.
[131] Natale G, Pasquali L, Ruggieri S, Paparelli A, Fornai F. Parkinson's disease and the gut: a well known clinical association in need of an effective cure and explanation. Neurogastroenterol Motil 2008;20:741–9.
[132] Tillisch K. The effects of gut microbiota on CNS function in humans. Gut Microbes 2014;5(3):404–10.
[133] Dominguez-Bello MG, Costello EK, Contreras M, Magris M, Hidalgo G, Flerer N, et al. Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. Proc Natl Acad Sci U S A 2010;107:11971–5.
[134] Santacruz A, Collado MC, García-Valdés L, Segura MT, Martín-Lagos JA, Anjos T, et al. Gut microbiota composition is associated with body weight, weight gain and biochemical parameters in pregnant women. Br J Nutr 2010;104:83–92.
[135] Mulligan CM, Friedman JE. Maternal modifiers of the infant gut microbiota-metabolic consequences, 1 2; 2017; 1–39.
[136] Galley JD, Bailey M, Kamp Dush C, Schoppe-Sullivan S, Christian LM. Maternal obesity is associated with alterations in the gut microbiome in toddlers. PLoS One 2014;9:e113026.
[137] Contu L, Hawkes CA. A review of the impact of maternal obesity on the cognitive function and mental health of the offspring. Int J Mol Sci 2017;18:1093.
[138] Fuemmeler BF, Lee CT, Soubry A, Iversen ES, Huang Z, Murtha AP, et al. DNA methylation of regulatory regions of imprinted genes at birth and its relation to infant temperament. Genet Epigenet 2016;8:59-7.
[139] Nardelli C, Iaffaldano L, Ferrigno M, Labruna G, Maruotti GM, Quaglia F, et al. Characterization and predicted role of the microrna expression profile in amnion from obese pregnant women. Int J Obes (Lond) 2014;38:466–9.
[140] Koch MA, Reiner GL, Lugo KA, Kreuk LS, Stanbery AG, Ansaldo E, et al. Maternal IgG and IgA antibodies dampen mucosal T helper cell responses in early life. Cell 2016;165:827–41.
[141] Zeng MY, Cisalpino D, Varadarajan S, Hellman J, Warren HS, Cascalho M, et al. Gut microbiota-induced immunoglobulin G controls systemic infection by symbiotic bacteria and pathogens. Immunity 2016;4:647–58.
[142] Penders J, Thijs C, Vink C, Stelma FF, Snijders B, Kummeling I, et al. Factors influencing the composition of the intestinal microbiota in early infancy. Pediatrics 2006;118(2):511–21.
[143] Martín R, Heilig HG, Zoetendal EG, Jiménez E, Fernández L, Smidt H, et al. Cultivation-independent assessment of the bacterial diversity of breast milk among healthy women. Res Microbiol 2007;158(1):31–7.
[144] Goulet O. Potential role of the intestinal microbiota in programming health and disease. Nutr Rev 2015:7332–40.
[145] Houghteling PD, Walker WA. Why is initial bacterial colonization of the intestine important to infants' and children's health? J Pediatr Gastroenterol Nutr 2015:60294–307.
[146] Ninonuevo MR, Park Y, Yin H, Zhang J, Ward RE, Clowers BH, et al. A strategy for annotating the human milk glycome. J Agric Food Chem 2006;54(20):7471–80.
[147] Jantscher-Krenn E, Lauwaet T, Bliss LA, Reed SL, Gillin FD, Bode L. Human milk oligosaccharides reduce Entamoeba histolytica attachment and cytotoxicity in vitro. Br J Nutr 2012;10:1839–46.
[148] De Leoz ML, Kalanetra KM, Bokulich NA, Strum JS, Underwood MA, German JB, et al. Human milk glycomics and gut microbial genomics in infant feces show a correlation between human milk oligosaccharides and gut microbiota: a proof-of-concept study. J Proteome Res 2015;1:491-02.
[149] Mirpuri J, Raetz M, Sturge CR, Wilhelm CL, Benson A, Savani RC, et al. Proteobacteria-specific IgA regulates maturation of the intestinal microbiota. Gut Microbes 2014;5:28–9.
[150] Alderete TL, Autran C, Brekke BE, Knight R, Bode L, Goran MI, et al. Associations between human milk oligosaccharides and infant body composition in the first 6 mo of life. Am J Clin Nutr 2015;102(6):1381–8.
[151] Favier CF, Vaughan EE, De Vos WM, Akkermans AD. Molecular monitoring of succession of bacterial communities in human neonates. Appl Environ Microbiol 2002;68(1):219–26.
[152] Scholtens PA, Oozeer R, Martin R, Amor KB, Knol J. The early settlers: intestinal microbiology in early life. Annu Rev Food Sci Technol 2012:3425–47.
[153] Sánchez E, De Palma G, Capilla A, Nova E, Pozo T, Castillejo G, et al. Influence of environmental and genetic factors linked to celiac disease risk on infant gut colonization by Bacteroides species. Appl Environ Microbiol 2011;77(15):5316–23.
[154] Binns CLM, Low WY. The long-term public health benefits of breastfeeding. Asia Pac J Public Health 2016;28:7–14.
[155] Stettler N, Stallings VA, Troxel AB, Zhao J, Schinnar R, Nelson SE, et al. Weight gain in the first week of life and overweight in adulthood: a cohort study of European American subjects fed infant formula. Circulation 2005;111:1897–903.
[156] Ip S, Chung M, Raman G, Trikalinos TA, Lau J. A summary of the Agency for Healthcare Research and Quality's evidence report on breastfeeding in developed countries. Breastfeed Med 2009;4(Suppl. 1):S17–30.

[157] Collado MC, Laitinen K, Salminen S, Isolauri E. Maternal weight and excessive weight gain during pregnancy modify the immunomodulatory potential of breast milk. Pediatr Res 2012;72:77-5.
[158] Andreas NJ, Hyde MJ, Gale C, Parkinson JR, Jeffries S, Holmes E, et al. Effect of maternal body mass index on hormones in breast milk: a systematic review. PLoS One 2014;9(12):e115043.
[159] Lemas DJ, Young BE, Baker PR, Tomczik AC, Soderborg TK, Hernandez TL, et al. Alterations in human milk leptin and insulin are associated with early changes in the infant intestinal microbiome. Am J Clin Nutr 2016;103(5):1291–300.
[160] Everard A, Belzer C, Geurts L, Ouwerkerk JP, Druart C, Bindels LB, et al. Cross-talk between Akkermansia muciniphila and intestinal epithelium controls diet-induced obesity. Proc Natl Acad Sci U S A 2013;110(22):9066–71.
[161] Schneeberger M, Everard A, Gómez-Valadés AG, Matamoros S, Ramírez S, Delzenne NM, et al. Akkermansia muciniphila inversely correlates with the onset of inflammation, altered adipose tissue metabolism and metabolic disorders during obesity in mice. Sci Rep 2015;5:16643. https://doi.org/10.1038/srep16643.
[162] Li J, Lin S, Vanhoutte PM, Woo CW, Xu A. Akkermansia muciniphila protects against atherosclerosis by preventing metabolic endotoxemia-induced inflammation in Apoe−/− mice. Circulation 2016;133(24):2434–46.
[163] Molino S, Dossena M, Buonocore D, Ferrari F, Venturini L, Ricevuti G, et al. Polyphenols in dementia: from molecular basis to clinical trials. Life Sci 2016:16169–77.
[164] Tian S, Lei P, Liu X, Zhang X, Shan Y. Microbiota: a mediator to transform glucosinolate precursors in cruciferous vegetables to the active isothiocyanates. J Sci Food Agric 2017;4. https://doi.org/10.1002/jsfa.8654.
[165] Qin WS, Deng YH, Cui FC. Sulforaphane protects against acrolein-induced oxidative stress and inflammatory responses: modulation of Nrf-2 and COX-2 expression. Arch Med Sci 2016;12(4):871–80.
[166] Tarozzi A, Angeloni C, Malaguti M, Morroni F, Hrelia S, Hrelia P. Sulforaphane as a potential protective phytochemical against neurodegenerative diseases. Oxid Med Cell Longev 2013;2013:415078.
[167] Zhang J, Zhang R, Zhan Z, Li X, Zhou F, Xing A, et al. Beneficial effects of sulforaphane treatment in Alzheimer's disease may be mediated through reduced HDAC1/3 and increased P75NTR expression. Front Aging Neurosci 2017;1:9121.
[168] De Oliveira MR, De Bittencourt Brasil F, Fürstenau CR. Sulforaphane promotes mitochondrial protection in SH-SY5Y cells exposed to hydrogen peroxide by an Nrf2-dependent mechanism. Mol Neurobiol 2017. https://doi.org/10.1007/s12035-017-0684-2.
[169] Pennisi M, Crupi R, Di Paola R, Ontario ML, Bella R, Calabrese EJ, et al. Inflammasomes, hormesis, and antioxidants in neuroinflammation: Role of NRLP3 in Alzheimer disease. J Neurosci Res 2017;95(7):1360–72.
[170] Xu Q, Langley M, Kanthasamy AG, Reddy MB. Epigallocatechin gallate has a neurorescue effect in a mouse model of Parkinson disease. J Nutr 2017;147(10):1926–31.
[171] Ding Mei-li, Ma Hui, Yi-gang Man HL. Protective effects of a green tea polyphenol, epigallocatechin-3-gallate, against sevoflurane-induced neuronal apoptosis involve regulation of CREB/BDNF/TrkB and PI3K/Akt/mTOR signalling pathways in neonatal mice. Can J Physiol Pharmacol 2017;5:1–10.
[172] Elumalai P, Lakshmi S. Role of quercetin benefits in neurodegeneration. Quercetin. Adv Neurobiol 2016;12:229–45.
[173] Bonsack F, Alleyne Jr CH, Sukumari-Ramesh S. Resveratrol attenuates neurodegeneration and improves neurological outcomes after intracerebral hemorrhage in mice. Front Cell Neurosci 2017;8:11228.
[174] Di Martino RMC, Bisi A, Rampa A, Gobbi S, Belluti F. Recent progress on curcumin-based therapeutics: a patent review (2012-2016). part ii: curcumin derivatives in cancer and neurodegeneration. Expert Opin Ther Pat 2017;27(8):953–65.
[175] Virmani A, Pinto L, Binienda Z, Ali S. Food, nutrigenomics, and neurodegeneration–neuroprotection by what you eat! Mol Neurobiol 2013;48(2):353–62.
[176] Shah SA, Khan M, Jo MH, Jo MG, Amin FU, Kim MO. Melatonin stimulates the SIRT1/Nrf2 signaling pathway counteracting lipopolysaccharide (LPS)-induced oxidative stress to rescue postnatal rat brain. CNS Neurosci Ther 2017;23(1):33–4.
[177] Bavithra S, Selvakumar K, Sundareswaran L, Arunakaran J. Neuroprotective effect of melatonin against PCBs induced behavioural, molecular and histological changes in cerebral cortex of adult male Wistar rats. Neurochem Res 2017;42(2):428–38.
[178] Hu C, Wang P, Zhang S, Ren L, Lv Y, Yin R, et al. Neuroprotective effect of melatonin on soluble $A\beta_{1-42}$-induced cortical neurodegeneration via Reelin-Dab1 signaling pathway. Neurol Res 2017;39(7):621–31.
[179] Lieblein-Boff JC, Johnson EJ, Kennedy AD, Lai CS, Kuchan MJ. Exploratory metabolomic analyses reveal compounds correlated with lutein concentration in frontal cortex, hippocampus, and occipital cortex of human infant brain. PLoS One 2015;10(8):e0136904.

Glossary

C1 metabolism: This refers to a group of metabolic reactions where there is the transfer of one-carbon groups. This one-carbon metabolism pathway is centered around folate.

DNA methyltransferases (DNMTs): Enzymes involved in the DNA methylation of cytosine at CpG sites (5'-cytosine-phosphate-guanine-3') of promoter and regulatory regions of genes, controlling gene expression.

Epigenetics: Changes in gene expression due to DNA methylation and histone modifications that change quantitatively gene expression without any modifications in the DNA sequence.

Epigenome: All DNA methylation and histone modifications in a genome of an organism.

Exposome: Includes all external and internal factors interacting with humans, leading to a healthy or unhealthy phenotype.

Gut–brain axis (GBA): It refers to the interaction between the gut and central nervous system via the vagal nerve, enteric nervous system and gut microbiota.

Gut Microbiota and microbiome: It comprises the population of microbial species (between 10 and 100 trillion microbial cells whose genes constitute the microbiome) that live in the gut (commensal bacteria, viruses and funguses).

Histone methyltransferases (HMTs): Enzymes involved in the methylation of histones.

Histone acetyltransferases (HATs): Enzymes involved in the acetylation of histones.

Histone deacetylases (HDACs): Enzymes involved in the deacetylation of histones.

High-fat diet (HFD): This refers to an abnormal content of fats and to unbalanced quantities of different fatty acids in the diet.

Lipopolysaccharide (LPS): It is a potent trigger of the innate immune system, naturally present in the intestinal lumen as a component of the cell wall of Gram-negative bacteria.

Methylome: The set of nucleic acid methylation modifications in an organism's genome or in a particular cell.

Neurodegeneration: The progressive loss of function and number of neurons.

Neural tube defects (NTDs):: Abnormal development of the brain and spinal cord due to severe maternal folate deficiency during pregnancy.

Nutrigenomics: The modulation of gene expression and the epigenome by food.

Transcription factors (TFs): Proteins involved in the promoter recognition that regulate gene expression.