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Dietary habits and advanced imaging/laboratory markers in multiple sclerosis: An exploratory cross-sectional study

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Abstract

Introduction: Diet is increasingly recognized as a potential factor influencing MS pathophysiology.

Objective: To examine associations between diet and clinical/imaging/laboratory biomarkers of MS-related burden.

Methods: In this cross-sectional study, daily nutrient intake was quantified in 112 MS patients using the French MetaCardis food frequency questionnaire. Participants underwent matched serum and 3T brain magnetic resonance imaging (MRI), including brain volumetrics, brain-predicted age, cortical lesions (CL), central vein sign (CVS), paramagnetic rim lesions (PRLs), and enlarged perivascular space (EPVS) assessments. *p*-values were false discovery rate corrected (pFDR), and regression models adjusted for energy intake and potential confounders.

Results: Participants (66% women, 72% relapsing-remitting MS) had a median age of 42 years (interquartile range (IQR) = 20), disease duration of 9 years (20), body mass index (BMI) of 22.8 (5.3) kg/m², and expanded disability status scale (EDSS) of 2 (2.5). Saturated and trans-fatty acids intake were positively associated with anxiety symptoms ($\beta = 0.39$, pFDR = 0.02; $\beta = 13.09$, pFDR = 0.03, respectively). Alcohol intake was positively associated with EPVS score ($\beta = 0.02$, pFDR = 0.01), whereas trans-fatty acid intake was positively associated with CL count ($\beta = 17.50$, pFDR = 0.04) and PRL volume ($\beta = 3251.37$, pFDR = 0.04).

Conclusion: Higher intake of saturated and trans-fatty acids and alcohol was associated with biomarkers of chronic inflammation and neurovascular dysfunction, suggesting a potential role in MS progression. Longitudinal and interventional studies are needed to establish causality.

Keywords: Diet, multiple sclerosis, magnetic resonance imaging, paramagnetic rim lesion, cortical lesion, glial fibrillary acidic protein

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Introduction

Recent years have seen growing interest in nutrition as an environmental factor in multiple sclerosis (MS) pathogenesis and progression. Food may affect MS by modulating inflammation, inducing oxidative stress, and contributing to neuroaxonal loss.[1] Diet can also affect the gut microbiota, potentially disrupting immune responses and contributing to central nervous system (CNS) inflammation.[2]

Pro-inflammatory foods are of particular interest in MS research, as evidence shows a link between these foods and disease activity and progression.[1] Historically, it has been suggested that low-saturated fat diets may slow disability accumulation and reduce mortality in MS.[3] More recent studies have reported that a pro-inflammatory diet is associated in MS with increased anxiety and depression scores,[4] a greater relapse risk, and higher brain magnetic resonance imaging (MRI) T_2-lesion load.[5] Consumption of ultra-processed foods (UPF), known to promote chronic inflammation, has also been associated with greater clinical disability in MS.[6]

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Although not unequivocally pro-inflammatory, alcohol intake has been associated with MS disease progression,[7] potentially through its effects on immune regulation and glymphatic clearance.[8]

New MRI biomarkers—including paramagnetic rim lesions (PRL), cortical lesions (CL), brain-predicted age, and enlarged perivascular spaces (EPVS)—have gained considerable attention in recent years for their potential to depict key pathological processes in MS, such as chronic inflammation, neurodegeneration, and microangiopathic disease.[9] In parallel, serum biomarkers such as serum neurofilament light chain (sNfL) and serum glial fibrillary acidic protein (sGFAP) are now well-established indicators of neuroaxonal damage and astrocytic activity in MS, respectively.[10] Together, these imaging and serum measures not only capture subtle signs of disease activity but also provide insight into the mechanisms driving MS progression. However, these biomarkers remain largely unexplored in MS nutritional research.

To address this gap, we evaluated the association between the dietary intake of pro-inflammatory foods and several advanced MRI, laboratory, and clinical measures in a cohort of MS patients. We aimed to explore how patients' dietary habits may relate to biomarkers reflecting different aspects of MS pathophysiology.

Methods

Study population

Patients with a diagnosis of relapsing–remitting MS (RRMS), secondary progressive MS (SPMS), or primary progressive MS (PPMS) according to the 2017 McDonald criteria[11] were recruited between February 2021 and August 2024 from Saint-Luc University Hospital (Belgium).

Patient eligibility criteria included (1) age ⩾18 years, (2) completion of the food frequency questionnaire (FFQ), and (3) availability of 3-Tesla (3T) T_2-weighted turbo spin echo (TSE), and three-dimensional (3D) segmented T_2*-weighted echo planar imaging (EPI), double inversion recovery (DIR), and T_1-weighted magnetization prepared rapid gradient echo images (MPRAGE).

Participants were excluded if: (1) they lacked a matched imaging, laboratory, and clinical assessment (including the FFQ evaluation) within 30 days, (2) more than 15 responses were missing from the FFQ, (3) the estimated daily energy intake was biologically implausible (<500 or >5000 kcal/day), or (4) if the MRI image quality was suboptimal.

The study received approval from the hospital's ethical standard committee, and written informed consent was obtained from all participants prior to their study inclusion.

Dietary assessment

Included participants completed a validated MetaCardis FFQ.[12] Participants were asked to report the average quantity and frequency of food intake in the previous 12 months. As previously described,[12] each FFQ item referred to a single food, a combination, or a food type with examples (e.g. apple; waffles and pancakes; fatty fish like salmon). Portion sizes were given in units, standard servings (e.g. 1 slice of bread), or household measures (e.g. cup, teaspoon). Intake frequency ranged from "never or <1/month" to "6 or more/day."

A nutrition researcher (M.F.) processed the data using NubelPro (https://www.nubel.be/pro). Reported foods, amounts, frequencies, and preparation methods were manually entered and standardized. NubelPro, using a validated database, estimated daily energy and nutrient intake and flagged missing or implausible data.

In this study, we focused on food components with established pro-inflammatory properties based on the current literature and quantifiable in the NubelPro database. Specifically, we examined total fat and total saturated-fatty acids, as well as specific saturated-fatty acids (lauric (C12:0), myristic (C14:0), and palmitic (C16:0)), trans-fatty acids, omega-6/omega-3 fatty acid ratio, carbohydrates, salt, and daily alcohol intake.[13–15] Food items were categorized using the NOVA classification: group 1—unprocessed/minimally processed (e.g. fruits, vegetables); group 2—processed culinary ingredients (e.g. oils, sugar); group 3—processed foods (e.g. canned produce, cheeses); group 4—UPF (e.g. soft drinks, packaged snacks). We calculated the percentage of total energy intake from UPF for each participant.

Clinical and laboratory data

Demographic and clinical data were recorded for all patients. The MS disability (expanded disability status scale (EDSS)) and severity (multiple sclerosis severity scale (MSSS)) scales were assessed by experienced MS clinicians. Anxiety and depression were assessed using the Beck anxiety inventory

(BAI)[16] and Beck depression inventory (BDI) short form.[17] Weight and height measurements were also obtained for body mass index (BMI) calculation. Information on presence/absence of MS relapses during the past year, as well as disease-modifying therapy (DMT) use was obtained from the patients' medical records. Furthermore, the presence/absence of the following additional vascular risk factors (VRFs) was recorded for each patient: (1) arterial hypertension (AHT), that is, established diagnosis and treatment with at least one antihypertensive drug; (2) type 1 or type 2 diabetes (diabetes), that is, established diagnosis and treatment with at least one antidiabetic drug; (3) smoking, current or former; (4) hypercholesterolemia, that is, established diagnosis and treatment with at least one hypolipemic drug. A cumulative VRFs score was then calculated.

To ensure temporal consistency, MRI-matched blood samples were collected on the same day as the clinical assessment or, whenever this was not feasible, within a tightly scheduled window of 30 days. sNfL levels were measured using the Atellica Immunoassay System (Siemens Healthineers Atellica® IM). sGFAP levels were quantified using the newly launched LumiPulse (Fujirebio LumiPulse® G GFAP) assay.

MRI acquisition protocol and biomarker assessment

MRI studies were performed using a 3T General Electric Signa Premier scanner (GE Healthcare, USA). The MRI protocol included a 3D T_2-fluid-attenuated inversion recovery (FLAIR) sequence for the identification of T_2-hyperintense white matter lesions, a submillimeter isotropic 3D-segmented T_2*-weighted EPI sequence for the detection of PRL and the proportion of central vein sign (CVS)-positive lesions,[18,19] a 3D-DIR and 3D-MPRAGE sequences for the assessment of CL,[19,20] and an axial T_2-weighted TSE sequence for the EPVS evaluation. Additional MRI methods are detailed in the Supplementary Methods section and Supplementary Table 1.

Given that raters were partially involved in the recruitment of cases, all images were de-identified before analysis. The PRL, CVS, CL, and EPVS assessments were conducted as previously described (see Supplementary Methods for details).[9,19] For the PRL analysis, each rater manually identified and evaluated all PRL for each subject following published guidelines.[21] Subsequently, the manually identified PRL were matched with automatic segmentations on 3D-FLAIR images using FLAMeS,[22] and post-processed using an in-house algorithm to determine the total PRL lesion volume for each subject. For the CVS assessment, the proportion of perivenular lesions across all eligible brain lesions was determined in each participant.[19,23] For CL analysis, lesions were identified on 3D-DIR images as hyperintensity compared to adjacent normal-appearing gray matter and confirmed on 3D-MPRAGE sequences as hypointense signal relative to the surrounding cortex, following published guidelines.[20,24] The total number of CL was used for CL analysis. For EPVS, the total score was computed by summing the scores from assessments at the level of the basal ganglia and centrum semiovale.

In each individual, EPVS, PRL, CVS, and CL analysis were independently assessed by two trained investigators (S.B. and F.G. for EPVS and CVS assessments, A.S. and S.B. for PRL and CL assessments), and in case of discrepancies, the scans were jointly reviewed to reach a consensus.

Brain volumetric measures, normalized to intracranial volume, were computed using FreeSurfer v7.2.0 (surfer.nmr.mgh.harvard.edu)[25] after lesion filling on MPRAGE images. Automated lesion segmentation was performed using 3D-FLAIR images with FLAMeS,[22] yielding a total (T_2-hyperintense) lesion volume.

Brain-predicted ages were calculated using BrainageR software v2.1 (https://github.com/jamescole/brainageR) as previously described.[9] Based on the brain-predicted age, the brain-predicted age difference (brain-PAD) was calculated by subtracting the chronological age from the brain-predicted age for each subject.[9]

Statistical analysis

Statistical analyses were performed with IBM SPSS Statistics (v29.0.1.0) and RStudio (v2023.06.1 + 524). A p-value of <0.05 was considered statistically significant.

In a subset of patients, the inter-rater reliability for EPVS, CVS, CL, and PRL assessment was explored on a per-patient level using the one-way random model intraclass correlation coefficient (ICC).[26]

For univariable analyses, nutrients were energy-adjusted using the residual method,[27] to control for total energy intake. These adjusted nutrients were then used as predictors of clinical, MRI, and laboratory markers.

Spearman's rank correlation coefficients were used to assess associations between the NOVA score or the percentage of UPF and clinical, MRI, and laboratory measures, as these indices represent relative measures of diet quality and therefore do not require energy adjustment.

To account for multiple comparisons, *p*-values within each nutrient were corrected using the Benjamini–Hochberg false discovery rate (FDR) method. Associations that remained significant after FDR correction were further examined in multivariable linear regression models. These models included the energy-adjusted nutrient as a predictor[27] and were further adjusted for total energy intake, age, sex, BMI, VRFs score, DMT use, presence of a recent relapse (in the year prior to inclusion), and EDSS.

Results

A total of 112 predominantly White/Caucasian participants were included in the analysis. The median age was 42.0 years (Q1–Q3: 32.2–52.6), and two-thirds of the patients were women (66%). The median BMI was 22.8 kg/m^2 (20.8–26.1), with the majority (61%) classified as having normal weight. Most participants had an RRMS phenotype (72%), and nearly half (46%) were on DMT. Clinical, nutrient, and biomarker characteristics are reported in Table 1.

The ICC inter-rater agreement for EPVS, CVS, CL, and PRL assessment was 0.877 ($p < 0.001$), 0.995 ($p < 0.001$), 0.998 ($p < 0.001$), and 0.986 ($p < 0.001$), respectively.

Association of diet with clinical, MRI, and laboratory features

After adjusting food intake for total energy and applying FDR correction within each dietary component, several significant associations emerged between specific nutrients and clinical, MRI, and laboratory biomarkers (Figure 1(a) and Supplementary Tables S2):

- *Clinical features:* Higher intake of saturated and trans-fatty acids was positively associated with disability and severity scores and anxiety symptoms. Specifically, higher consumption of saturated-fatty acids was associated with greater EDSS (β=0.08, 95% confidence interval (CI)=0.03–0.13, pFDR=0.02) and MSSS (β=0.11, 95% CI=0.04–0.18, pFDR=0.02) as well as with higher BAI scores (β=0.39, 95% CI=0.13–0.65, pFDR=0.02). Similarly, trans-fatty acid intake was positively related to both EDSS (β=2.10, 95% CI=0.48–3.73, pFDR=0.04) and MSSS (β=3.31, 95% CI=0.92–5.69, pFDR=0.04) and with higher BAI scores (β=13.09, 95% CI=5.09–21.09, pFDR=0.03).
- *MRI features:* Higher alcohol intake was positively associated with EPVS total score (β=0.02, 95% CI=0.01–0.03, pFDR=0.01) and brain-predicted age (β=0.30, 95% CI=0.09–0.50, pFDR=0.03), whereas trans-fatty acid intake was associated with a higher number of CL (β=17.50, 95% CI=3.90–31.10, pFDR=0.04; Figure 2) and increased PRL volume (β=3251.37, 95% CI=787.98–5714.75, pFDR=0.04; Figure 2).
- *Laboratory features:* Higher alcohol intake was positively associated with sGFAP levels (β=1.16, 95% CI=0.40–1.92, pFDR=0.03).

In contrast, after FDR correction, no significant associations were found between the NOVA score or the UPF% and any clinical, MRI, or laboratory features tested (Supplementary Tables S3).

Multivariable regression models adjusted for confounders

In multivariable linear regression models adjusted for age, sex, BMI, and VRFs score, all previously observed associations remained statistically significant except the association between alcohol intake and brain-predicted age, which was no longer significant (Figure 1(b) and Supplementary Table S4). When DMT use was added as a covariate, the association between alcohol intake and sGFAP levels also lost significance, whereas the other associations persisted (Supplementary Table S5). The presence of a recent relapse (in the year prior to inclusion) did not influence the results (Supplementary Table S6). Further adjustment for EDSS category (0–3, 3.5–6, 6.5–10) confirmed that higher saturated and trans-fatty acid intake remained positively associated with BAI scores, and, for MRI outcomes, that alcohol intake remained significantly associated with EPVS total score, and trans-fatty acids with PRL volume and CL count (Figure 2; Supplementary Table S7).

Discussion

In this cross-sectional study of individuals with MS, we found that pro-inflammatory dietary factors—such as saturated-fatty acids, trans-fatty acids, and alcohol—were associated with clinical, MRI, and laboratory markers of neuroinflammation, neurodegeneration, and neurovascular dysfunction.

Table 1. Clinical, nutrient, and biomarker characteristics of participants.

Characteristic	$N = 112$[a]
Age (years)	42.0 (32.2, 52.6)
Sex (women)	74 (66%)
BMI	22.8 (20.8, 26.1)
BMI category	
Underweight	7 (7.0%)
Normal weight	61 (61%)
Overweight	21 (21%)
Obese	11 (11%)
VRFs cumulative score	0 (0, 1)
MS phenotype	
PPMS	16 (14%)
RRMS	81 (72%)
SPMS	15 (13%)
On treatment (DMT)	48 (46%)
With recent relapse (in the year prior the inclusion)	32 (29%)
EDSS	2.0 (1.5, 4.0)
MSSS	4.7 (2.8, 6.8)
BAI score	9.5 (5, 16)
BDI score	5 (2, 10)
Nutrients	
Total energy intake (kcal/day)	1694.5 (1372.0, 2184.5)
Total saturated-fatty acids (g/day)	23.6 (14.4, 34.1)
- Lauric acid (C12:0)	0.6 (0.3, 1.3)
- Myristic acid (C14:0)	1.8 (1.0, 3.1)
- Palmitic acid (C16:0)	11.0 (6.1, 14.8)
Trans-fatty acids (g/day)	0.6 (0.4, 0.9)
Omega-6 to omega-3 fatty acid ratio	5.0 (3.7, 6.6)
Carbohydrates (g/day)	196.4 (141.8, 250.2)
Alcohol (g/day)	0.0 (0.0, 8.4)
Salt (g/day)	3.7 (2.4, 4.8)
NOVA score	2.1 (1.8, 2.4)
UPF (% of total diet)	24.4 (14.4, 34.6)
MRI and laboratory biomarkers	
Total lesion volume (mm^3)	3836 (1356, 8823)
Brain volume (normalized)	0.741 (0.724, 0.760)
Gray matter volume (normalized)	0.409 (± 0.025)
White matter volume (normalized)	0.297 (0.280, 0.308)
Thalamic volume (normalized)	0.009 (± 0.001)
Brain age (years)	50.6 (± 14.4)
Brain-predicted age difference (years)	7.5 (2.0, 11.5)
Proportion of CVS-positive lesions	87 (67, 100)
Number of PRL	1.0 (0.0, 3.0)
Total PRL volume (mm^3)	0.0 (0.0, 823.4)
Number of CL	4.0 (2.0, 8.0)
EPVS total score	2.0 (2.0, 3.0)
sNfL (pg/mL)	12.7 (9.9, 18.9)*
sGFAP (pg/mL)	30.3 (24.5, 40.5)*

[a]Median (Q1, Q3); mean (± SD); *n* (%).
*Available for 103 participants.
BMI: body mass index; VRFs: vascular risk factors; PPMS: primary progressive multiple sclerosis; RRMS: relapsing–remitting multiple sclerosis; SPMS: secondary progressive multiple sclerosis; DMT: disease-modifying treatment; EDSS: expanded disability status scale; MSSS: multiple sclerosis severity score; BAI: Beck Anxiety Inventory; BDI: Beck Depression Inventory; UPF: ultra-processed foods; CVS: central vein sign; PRL: paramagnetic rim lesions; CL: cortical lesion; sNfL: serum neurofilament light chain; sGFAP: serum glial fibrillary acidic protein; EPVS: enlarged perivascular spaces.

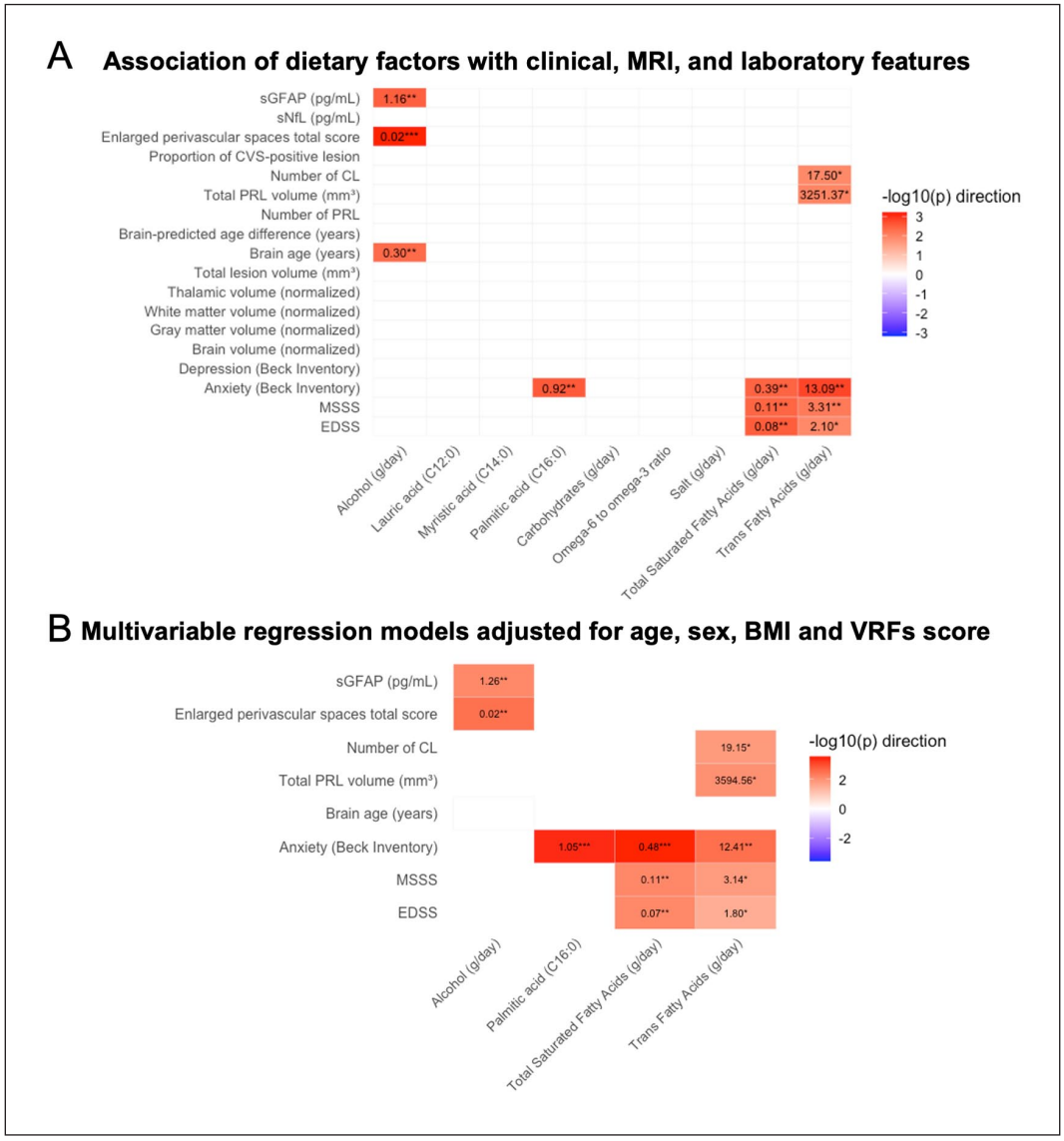

Figure 1. (a) Linear regression analyses of selected nutrient intakes, adjusted for total energy intake. Non-significant associations are shown in white. (b) Multivariable regression models adjusted for total energy intake and relevant confounders (age, sex, body mass index (BMI), and vascular risk factors (VRFs) cumulative score), showing only statistically significant results.
Significant associations with clinical, laboratory, and MRI biomarkers are highlighted: negative in blue, positive in red, with color intensity reflecting *p*-value strength.
Please refer to the online version of the article to view this figure in colour.

In particular, trans-fatty acids showed strong associations with MS disability, severity, CL, and PRL burden. Notably, the association with CL and PRL persisted even after adjusting for the EDSS, suggesting that the link between trans-fatty acid intake and chronic compartmentalized inflammation is independent of physical disability—which itself may influence a patient's ability to access or prepare healthy food. Saturated-fatty acids were associated with MS disability, severity, and with increased anxiety symptoms. Alcohol consumption was associated with higher sGFAP levels and increased EPVS scores, suggesting a potential connection between alcohol, astrocytic activation, and neurovascular dysfunction in MS.

Our results align with previous epidemiological evidence suggesting that diets high in saturated-fatty acids and trans-fatty acids are associated with adverse MS outcomes and greater disability progression.[3,28] While mechanistic interpretations are speculative at this stage—given the cross-sectional design and the

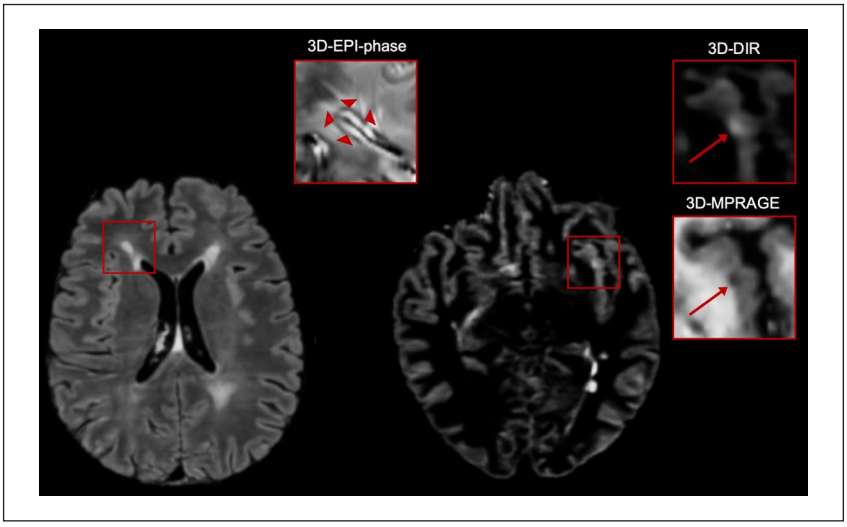

Figure 2. Representative 3T brain MRI of an adult participant with an EDSS score of 2, showing 11 paramagnetic rim lesions on 3D-EPI phase imaging and 3 cortical lesions on 3D-DIR and 3D-MPRAGE. This participant reported a daily intake of trans-fatty acids of 1.25 g (above the 75th percentile).

lack of cytokines or immune cell phenotype assessments—these dietary factors were associated in our cohort with clinical disability, lesion burden, and anxiety symptoms, supporting a link between pro-inflammatory dietary patterns and MS-related clinico-radiological outcomes.

Mechanistically, these fats may promote peripheral and central inflammation via increased production of pro-inflammatory cytokines, disruption of blood–brain barrier integrity, and modulation of gut microbiota composition, potentially leading to enhanced neuroinflammatory processes. Saturated and trans-fatty acids can activate key pro-inflammatory transcription factors such as nuclear factor-kB and activator protein-1, which are both involved in T-cell activation and upregulated in MS,[29,30] leading to overexpression of pro-inflammatory mediators.[31,32] Diet-induced gut dysbiosis may further alter the T-reg/Th17 balance, triggering inflammatory responses through molecular mimicry or microbial antigen presentation.[33]

Importantly, chronic inflammation within MS lesions is driven by persistent microglial activation and iron accumulation at lesion rims, which promotes tissue damage and ferroptosis-mediated neurodegeneration.[34] In this context, the pro-inflammatory and oxidative stress-inducing effects of saturated and trans-fats may amplify these chronic inflammatory processes, potentially exacerbating microglial activation, iron cytotoxicity, and downstream neurodegenerative mechanisms.

Similarly, saturated-fatty acid intake was associated with increased anxiety symptoms in our cohort, which may broadly reflect the pro-inflammatory effects of diet. Systemic inflammation and gut immune dysregulation can influence brain function, while microglial and astrocyte activation, cytokine imbalances, and subtle blood–brain barrier alterations may propagate neuroinflammation, affecting neurotransmission and neuroplasticity.[35] Mood disturbances in MS, including anxiety, have been linked to subclinical intrathecal inflammation, with cerebrospinal fluid levels of pro-inflammatory cytokines such as interleukin (IL)-2, tumor necrosis factor (TNF)-α, and IL-1β correlating with symptom severity.[36] These findings suggest that neuropsychiatric symptoms are influenced not only by psychosocial factors but also by underlying inflammatory processes, which may be modulated by pro-inflammatory dietary patterns.

Regarding alcohol intake, our results are consistent with studies linking excessive alcohol consumption to brain atrophy and white matter changes. While moderate alcohol consumption has been associated with reduced MS risk and possibly lower disability,[37,38] this potential benefit is counterbalanced by evidence of increased lesion load in moderate drinkers[39] and worse MS outcomes in heavy alcohol users, particularly males.[40,41] High dose alcohol consumption may increase microglial activation, promotes inflammatory cytokine production, and facilitates CNS lymphocyte infiltration.[42,43] In addition, alcohol may impair glymphatic function—the brain's waste clearance system—potentially leading to accumulation of

neurotoxic proteins and contributing to neuroinflammation and neurodegeneration.[44] Interestingly, in our study, alcohol intake was associated with increased EPVS but not with a lower percentage of CVS-positive lesions nor with higher T_2 lesion load. Since in MS, higher EPVS typically reflects microangiopathic damage—evidenced by a lower percentage of CVS-positive lesions—,[9,45] our findings might reflect an alcohol-related glymphatic dysfunction eventually independent from microvascular pathology.

Nutritional imbalances in MS may also contribute to disease progression due to widespread vitamin deficiencies,[46] difficulties in weight control,[47,48] and increased prevalence of vascular comorbidities.[49,50] These comorbidities have been associated with accelerated MS progression, reinforcing the concept of a detrimental vicious cycle between metabolic and neuroinflammatory pathways.[44,51] In addition, MS-related symptoms—including fatigue and mobility limitations—may impair the ability to prepare and consume healthy meals, promoting reliance on energy-dense, nutrient-poor fast foods.[52,53] Notably, in our analysis, several dietary associations persisted even after adjusting for disability level, indicating that these relationships are not solely driven by disease-related physical limitations.

Limitations include self-reported dietary data, the cross-sectional design, the lack of a healthy control group, and possible residual confounding despite adjustments. We evaluated the average food intake over the past 12 months, while some MRI markers (PRL, CL, EPVS, and brain-predicted age) are considered to develop over a longer time period. This temporal mismatch limits causal interpretation of the observed associations, and longitudinal studies will be necessary to further explore these findings. In addition, early-life dietary patterns may influence MS pathogenesis[54] and were not assessed. Information regarding socioeconomic factors was not available in our data, which may have acted as confounders influencing nutritional intake and MS-related outcomes. Finally, the approach used to control the FDR (nutrient-specific correction) does not account for the total number of comparisons; therefore, the findings should be interpreted in the context of the exploratory nature of the study. Strengths include advanced MRI and biomarker measures of neuroinflammation and neurodegeneration, detailed energy-adjusted dietary analysis, and integration of clinical and mood outcomes.

From a clinical perspective, these findings support the potential role of dietary counseling as part of comprehensive MS management. While causal inference cannot be established due to the cross-sectional design, our data suggest that reducing the intake of saturated and trans-fats, and limiting alcohol consumption, may help mitigate the disease burden. Future research should confirm these findings in longitudinal studies, integrate metabolomic and immunologic profiling to elucidate mechanistic pathways, and evaluate whether targeted dietary interventions can modify the disease course.

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Data Availability Statement

The data that support the findings of this study are controlled by the investigation center and are not publicly available. Written requests for access to the derived data will be considered by the corresponding author. Anonymized data will be shared by reasonable request from the principal investigator.

Declaration of Conflicting Interests

The authors declared the following potential conflicts of interest with respect to the research, authorship, and/or publication of this article:
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Supplemental Material

Supplemental material for this article is available online.

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