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eat & move

Diet and Gut Microbiome Diversity for Multiple Sclerosis Patients - results from a cross-sectional case-control study with 125 participants

LB-28

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AIM

The aim of this study is to **compare dietary intake as well as identify differences of gut microbiome diversity** between patients with multiple sclerosis (MS) and healthy controls (HCs).

Furthermore, we **investigate if markers of a healthy diet and/or a high gut microbiome diversity are inversely associated with MS disease severity.**

Lastly, we **explore the association between diet and the gut microbiome diversity** in patients with MS and HCs to identify the most promising dietary modifications to be tested in future MS trials.

CONCLUSION

A high intake of saturated fatty acids were associated with a high disease severity and differences in gut microbiome diversity between multiple sclerosis patients and healthy controls were found

Patients with MS and HCs had similar dietary intakes (I), and the majority of the study participants did not comply with the current Danish Official Dietary Guidelines and Nordic Nutritional Recommendations. A high intake of saturated fatty acids (SFA) were associated with a high disease severity (II). Differences in gut microbiome diversity between MS patients and HCs were found in β-diversity (III), but not in α-diversity. A higher abundance of the phyla *Verrucomicrobia* was observed in MS patients compared to HCs (IV). Furthermore, a high disease severity could possibly be associated with an altered gut microbiome diversity (V). Dietary intake might be differently associated with gut microbiome diversity in patients with MS compared to HCs (VI). We suggest future MS trials to further examine the effects of a low SFA intake on disease severity, as well as the effects of a diet high in fruit and vegetables (FV) and fiber in relation to gut microbiome diversity.

BACKGROUND

Multiple Sclerosis (MS) is a neurodegenerative, currently incurable, autoimmune disorder of the central nervous system. An altered gut microbiome composition has been observed in MS patients. Even though diet constitutes a main factor in shaping the gut microbiome composition, the interactions between diet and gut microbiome diversity in MS have yet to be explored. In healthy people a diet rich in dietary fibers has shown to increase gut microbiome diversity. And a diet high in fruits, vegetables and whole grain, and low in saturated fat has been associated with a less severe disease course of MS.

METHODS

A cross-sectional case-control study including 125 Danish participants, (78 MS patients, 47 HCs). Dietary intake was assessed using weighed dietary records (MyFood24®) and a food frequency questionnaire. Gut microbiome diversity was assessed using amplicon sequencing of the V3 region of the 16S ribosomal RNA gene. α-diversity was measured with Shannon-Wiener diversity index and Observed features. β-diversity was measured with Bray-Curtis and weighted UniFrac distance. Disease severity was assessed using MS Severity Score (MSSS), Fatigue Severity Scale (FSS), and SymptoMScreen. Anthropometric measurements and questionnaires were performed.

RESULTS

I – Dietary Intake

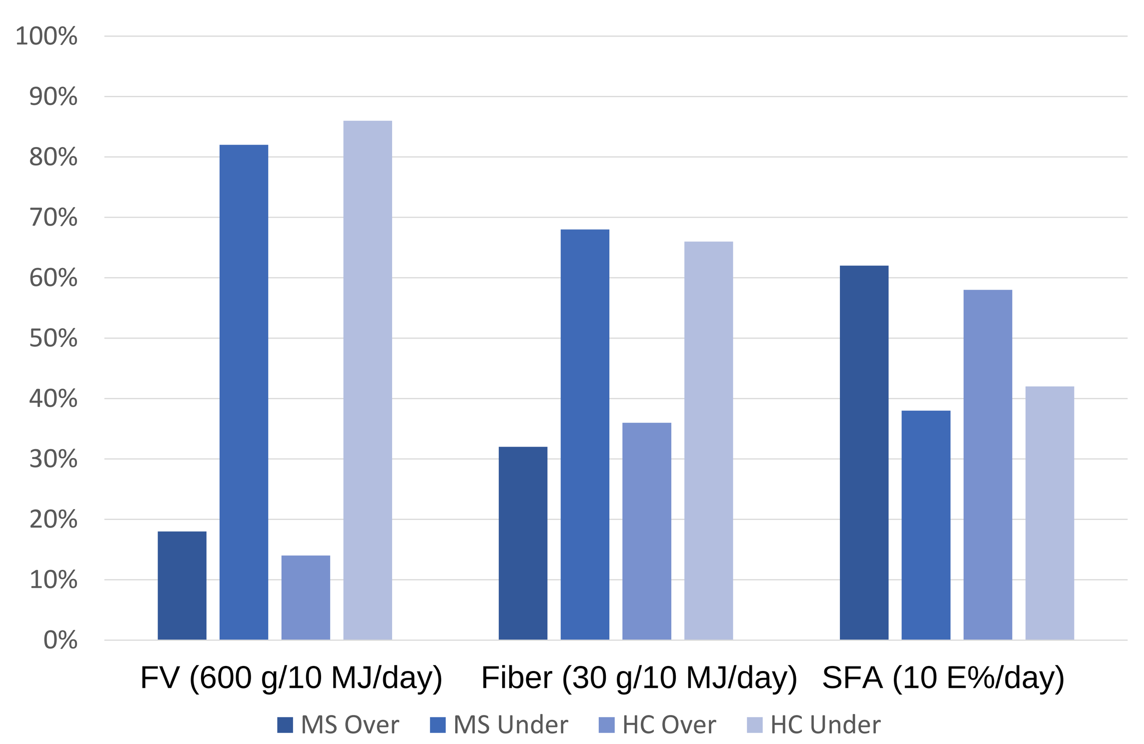

Figure 1: Dietary intake comparisons between the MS group and the HC group according to the Danish Official Dietary Guidelines and the Nordic Nutrition Recommendations

III - Differences in Gut Microbiome Diversity

A significant difference was found between the MS group and the HC group when comparing their β-diversity at OTU level measured using weighted UniFrac distance (p = 0.021) and Bray-Curtis dissimilarities (p = 0.047).

IV - Abundance at Phylum Level

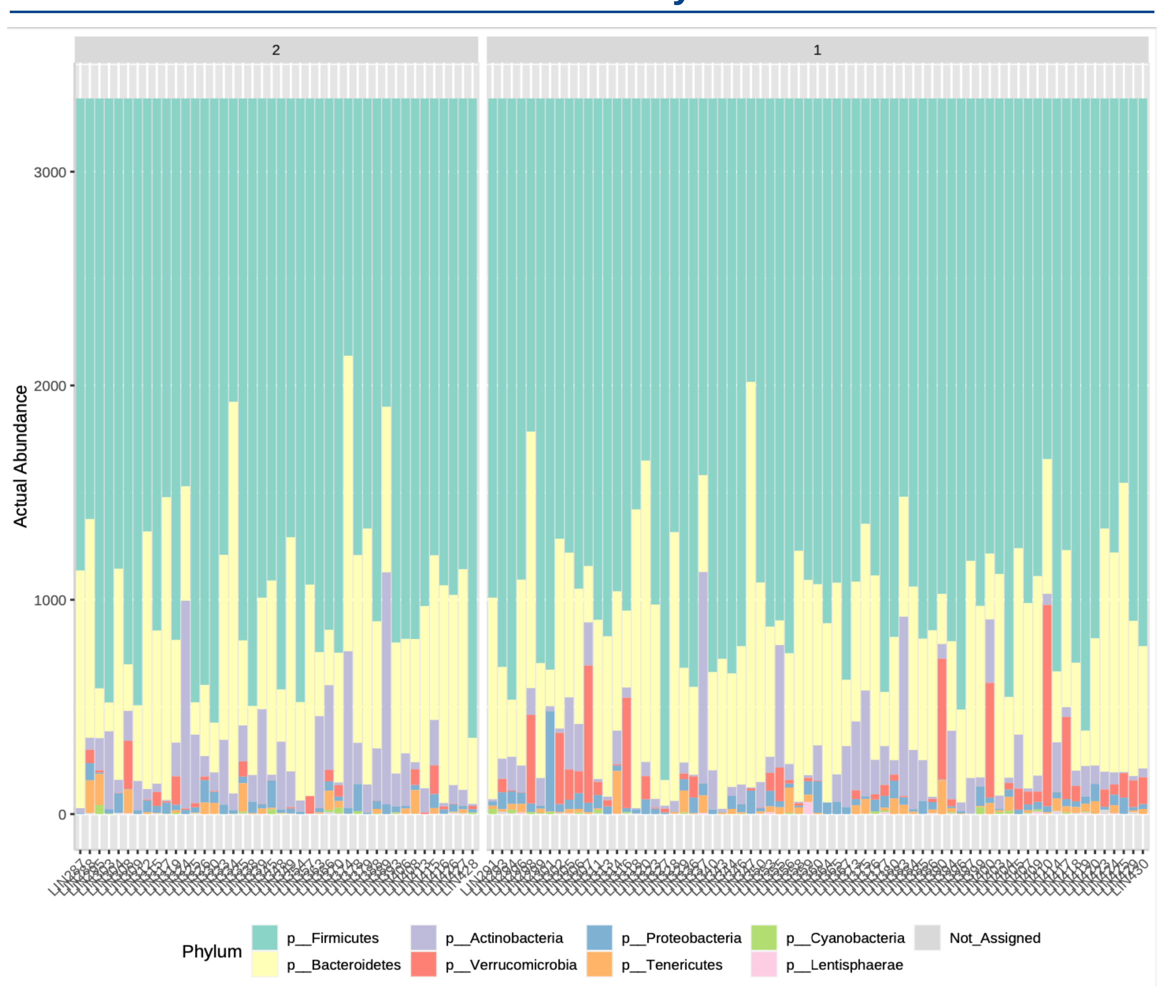

Figure 2: Plot showing the abundance at phylum level for each study participant in the HC group (2) and the MS group (1). Each colour represents a phylum. Data was rarefied to the lowest count of OTU (4000 base pairs).

II – Correlations between Dietary Intake and Disease Severity

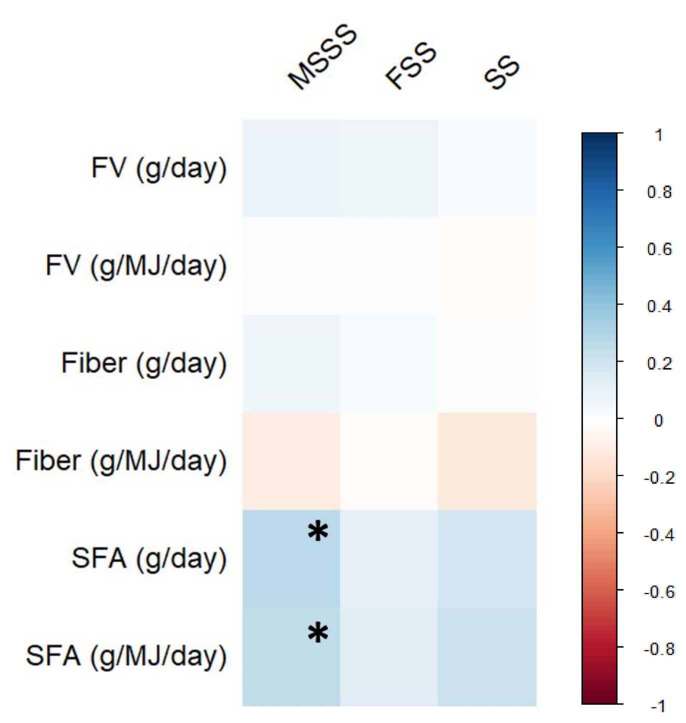

Figure 3: Correlation plot showing correlations between FV, fiber, and SFA intake in both g/day and g/10 MJ/day and FSS, SymptoMScreen, and MSSS. The colour scale shows positive correlations in blue and negative correlations in red. The deeper the colour, the larger the correlation is. FV = fruit and vegetables, SFA = saturated fatty acids, FSS = fatigue severity scale, MSSS = multiple sclerosis severity score, * = significant value.

V - Disease Severity and Gut Microbiome Diversity

PERMANOVA was used to test differences in β-diversity measured in Bray-Curtis and weighted UniFrac distance between high, medium, and low scores of MSSS, FSS, and SymptoMScreen scores. These disease markers were divided into tertiles (high, medium, low) with an equal number of participants. A significant difference in Bray-Curtis was found between high and low SymptoMScreen scores (p = 0.007, q = 0.021). No significant differences were observed in weighted UniFrac distance.

VI – Dietary Intake and Gut Microbiome Diversity

Table 1: Differences in β-diversity measured in Bray-Curtis and weighted UniFrac distance between high, medium, and low intakes of FV, fiber, and SFA are shown for the MS group, the HC group, and the total study population. Differences calculated by PERMANOVA are shown with the significant levels p-value and q-value. Significant p-values and q-values are shown in blue bold. B) Dietary intakes divided into tertiles: high, medium, and low with equal number of participants in each. Shown for the MS group, the HC group, and the total study population. Numbers are shown as median (IQR). MS = multiple sclerosis, HC = healthy control, FV = fruit and vegetables, SFA = saturated fatty acids.

A)	**Total Study Population** (n = 93)				**MS** (n = 60)				**HC** (n = 33)			
	Bray-Curtis		**Weighted UniFrac**		**Bray-Curtis**		**Weighted UniFrac**		**Bray-Curtis**		**Weighted UniFrac**	
	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value
FV (g/10 MJ/day)												
High - Medium	0.503	0.640	0.082	0.123	0.941	0.941	0.115	0.173	0.520	0.722	0.463	0.790
High - Low	0.414	0.640	**0.002**	**0.006**	0.299	0.897	**0.001**	**0.003**	0.722	0.722	0.790	0.790
Medium- Low	0.640	0.640	0.608	0.608	0.685	0.941	0.365	0.365	0.383	0.722	0.713	0.790
Fiber (g/10 MJ/day)												
High - Medium	0.535	0.535	0.472	0.472	0.743	0.841	0.307	0.461	0.450	0.450	0.654	0.654
High - Low	0.180	0.270	0.048	0.144	0.814	0.814	0.235	0.461	**0.0420**	0.069	**0.021**	**0.0315**
Medium- Low	0.093	0.270	0.161	0.242	0.557	0.841	0.935	0.935	**0.0460**	0.069	**0.016**	**0.0315**
SFA (g/10 MJ/day)												
High - Medium	0.111	0.333	0.553	0.553	0.123	0.329	0.733	0.733	0.874	0.874	0.155	0.321
High - Low	0.231	0.347	0.439	0.553	0.329	0.329	0.273	0.4095	0.810	0.874	0.949	0.949
Medium- Low	0.534	0.534	0.529	0.553	0.228	0.329	0.130	0.390	0.863	0.874	0.214	0.321

B)	**All participants** (n = 93)	**MS** (n = 60)	**HC** (n = 30)
FV (g/10 MJ/day)			
High	684 (526-835)	684 (526-845)	668 (540-833)
Medium	336 (304-411)	336 (310-410)	335 (298-363)
Low	127 (79.5-180)	138 (95.4-187)	113 (77.9-155)
Fiber (g/10 MJ/day)			
High	35.1 (32.1-40.7)	37.0 (32.0-42.4)	34.7 (32.9-36.0)
Medium	26.6 (24.2-28.2)	27.5 (24.6-28.6)	26.5 (23.9-27.7)
Low	18.9 (15.2-21.8)	19.6 (16.4-22.0)	15.5 (12.7-17.8)
SFA (g/10 MJ/day)			
High	39.5 (34.9-44.4)	39.6 (35.1-45.1)	36.6 (34.7-42.4)
Medium	30.3 (27.8-30.9)	30.2 (27.8-31.3)	30.3 (27.9-30.5)
Low	20.6 (18.7-23.2)	20.1 (17.8-22.5)	22.6 (21.5-23.4)

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