Spinal cord involvement in multiple sclerosis is highly predictive of disability and disease phenotype

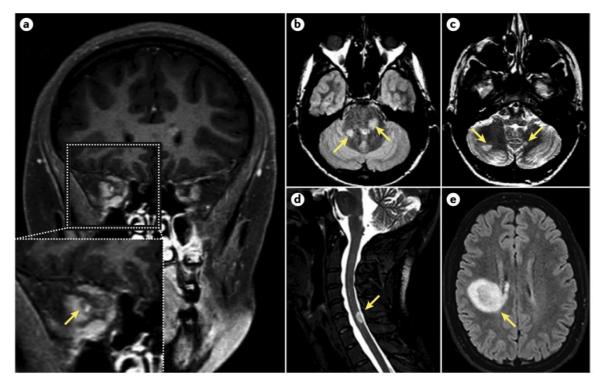
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Background

- Multiple sclerosis is a chronic, inflammatory, demyelinating and neurodegenerative disease of the central nervous system
- The **pathological hallmark** of MS is the accumulation of **demyelinating lesions** in the white matter (WM) and grey matter (GM) of the brain and spinal cord (SC), but MS pathology is highly complex and heterogenous

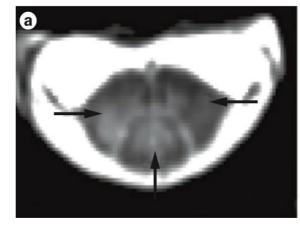
- Spinal cord (SC) pathology:
 - Common
 - Likely to be clinically relevant
 - Precise anatomical organization

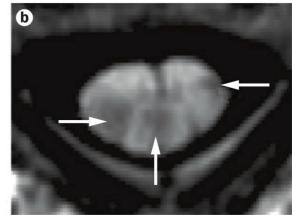


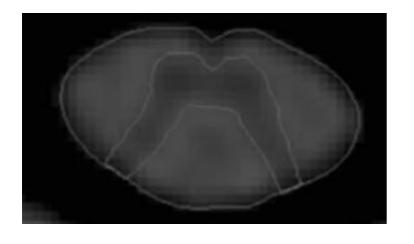
Background

Cervical SC lesion load:

- Correlated with EDSS score on single 2D slices at C2-C3 vertebral level
- Axial 3D T_2 -weighted superior accuracy compared to sagittal
- No study with SC axial 3D lesion volumes (LV) in MS performed yet







Cervical cord atrophy:

- Correlated with EDSS score
- GM atrophy: strongest predictor of EDSS in multivariate models including brain lesion load and atrophy measures

Aims

 To investigate cervical SC damage in MS by combining several wellestablished MRI measures

 To assess the role of SC involvement in explaining the severity of clinical disability in MS

 To investigate the contribution of SC involvement in explaining the heterogeneity of disease clinical phenotypes in MS

Methods

Subjects: 57 relapsing-remitting (RR) MS, 54 progressive MS (PMS) patients and 32 healthy controls (HC)

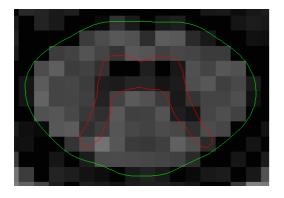
Neurologic assessment: rating of the EDSS score + general & clinical Hx

- MRI acquisition (3.0 T scanner):
 - Brain 3D T_1 —weighted, T_2 —weighted and FLAIR images
 - Cervical SC 3D T_1 —weighted, T_2 —weighted, diffusion-weighted and sagittal 2D STIR images
 - Cervical SC axial PSIR at C2-C3 vertebral level

MRI analysis

Spinal cord

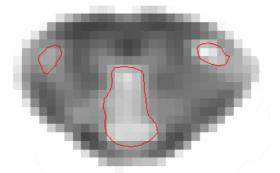
PSIR C2-C3 level



Green – global SC cross-sectional area

Red – GM cross-sectional area

 $3DT_2$



DTI

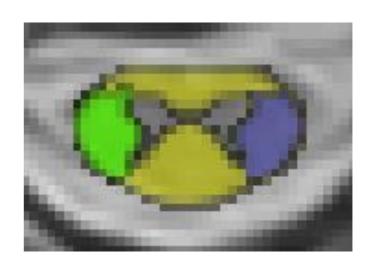


Brain

- T₂-hyperintense LV
- SIENAX 2.0 for quantification of normalized WM, GM and total brain volumes

Statistical analysis

• Deformation of **template and atlas of SC WM** regions on the T_2 -weighted image



Statistical analysis:

- Group comparisons
- Associations of MRI variables with EDSS explored by age-, sex- and phenotypeadjusted linear models
- Multivariable linear models with step-wise variable selection to identify independent predictors of EDSS

Results

	HC (n=32)	MS (n=111)	MS vs HC p value	RRMS (n=57)	PMS (n=54)	PMS vs RRMS p value
Men/Women	15/17	47/64	0.650	24/33	23/31	0.900
Mean age (SD) [years]	40.1 (14.4)	45.3 (10.6)	0.13+	40.5 (9.6)	50.3 (9.2)	<0.001+
Median disease duration (IQR) [years]	-	14 (4-22)	-	8 (2-16)	19 (11-24)	<0.001*
Median EDSS score (IQR)	-	4.0 (1.5-6.0)	-	1.5 (1.0-2.5)	6.0 (5.0-6.5)	<0.001*

Results

RRMS vs HC

- SC lesions (HC had no SC lesions)
- Lower WM and global SC crosssectional areas
- Similar global and regional fractional anisotropy (FA)
- Higher brain T₂-LV
- Lower NBV and WMV

PMS vs RRMS

- Lower GM and global SC crosssectional areas
- Higher global and regional SC nT₂-LV
- Lower global and regional FA
- Higher brain T₂-LV
- Lower NBV, WMV and GMV

Univariate associations

		RRMS patients Beta (p value)	PMS patients Beta (p value)	
Brain [mL]	T ₂ -LV	0.382 (<0.001)	0.152 (<0.01)	
	GMV	-0.315 (0.001)	-0.216 (<0.01)	
	WMV	-0.191 (0.02)	-0.051 (0.46)	
	NBV	-0.298 (<0.001)	-0.191 (0.02)	
SC cross- sectional areas [mm ²]	GM	-0.111 (0.32)	-0.219 (0.02)	
	WM	-0.056 (0.46)	-0.091 (0.23)	
	Global	-0.147 (0.12)	-0.050 (0.45)	
SC nT ₂ -LV	GM	0.195 (0.02)	0.052 (0.47)	
	WM	0.190 (0.01)	0.030 (0.71)	
	Dorsal columns	0.056 (0.48)	-0.082 (0.28)	
	Lateral funiculi	0.260 (<0.001)	0.046 (0.55)	
	Global	0.196 (0.01)	-0.023 (0.78)	
SC FA	GM	-0.216 (<0.01)	-0.172 (0.01)	
	WM	-0.352 (<0.001)	-0.152 (0.02)	
	Dorsal columns	-0.225 (0.02)	-0.134 (0.05)	
	Lateral funiculi	-0.394 (<0.001)	-0.167 (<0.01)	
	Global	-0.362 (<0.001)	-0.158 (<0.01)	
	Lesions	-0.153 (0.13)	-0.113 (0.07)	

Univariate associations

		RRMS patients Beta (p value)	PMS patients Beta (p value)	Heterogeneity among phenotypes p value	MS Patients phenotype-adjusted Beta (p value)
Brain [mL]	T ₂ -LV	0.382 (<0.001)	0.152 (<0.01)	0.04	0.207 (<0.001)
	GMV	-0.315 (0.001)	-0.216 (<0.01)	0.40	-0.254 (<0.001)
	WMV	-0.191 (0.02)	-0.051 (0.46)	0.19	-0.110 (0.04)
	NBV	-0.298 (<0.001)	-0.191 (0.02)	0.35	-0.241 (<0.001)
SC cross- sectional areas [mm²]	GM	-0.111 (0.32)	-0.219 (0.02)	0.45	-0.177 (0.01)
	WM	-0.056 (0.46)	-0.091 (0.23)	0.75	-0.074 (0.17)
	Global	-0.147 (0.12)	-0.050 (0.45)	0.40	-0.083 (0.12)
	GM	0.195 (0.02)	0.052 (0.47)	0.20	0.111 (0.04)
	WM	0.190 (0.01)	0.030 (0.71)	0.04	0.094 (0.09)
SC nT ₂ -LV	Dorsal columns	0.056 (0.48)	-0.082 (0.28)	0.21	-0.015 (0.78)
	Lateral funiculi	0.260 (<0.001)	0.046 (0.55)	0.04	0.166 (<0.01)
	Global	0.196 (0.01)	-0.023 (0.78)	0.04	0.099 (0.08)
SC FA	GM	-0.216 (<0.01)	-0.172 (0.01)	0.66	-0.191 (<0.001)
	WM	-0.352 (<0.001)	-0.152 (0.02)	0.07	-0.217 (<0.001)
	Dorsal columns	-0.225 (0.02)	-0.134 (0.05)	0.43	-0.164 (<0.01)
	Lateral funiculi	-0.394 (<0.001)	-0.167 (<0.01)	0.03	-0.246 (<0.001)
	Global	-0.362 (<0.001)	-0.158 (<0.01)	0.05	-0.225 (<0.001)
	Lesions	-0.153 (0.13)	-0.113 (0.07)	0.74	-0.125 (0.02)

Multivariate analysis

Independent predictors of EDSS in RRMS patients (R²=0.53):

- SC lateral funiculi n T_2 -LV (B=0.56; p<0.001)
- NBV (B=-0.41; p<0.01)

Independent predictors of EDSS in PMS patients (R²=0.49):

- SC lesion-free dorsal column FA (B=-0.52; p<0.01)
- SC GM atrophy (B=-0.36; p=0.03)

Best predictors of phenotype with logistic multiple regression analysis (AUC=0.97):

- SC GM atrophy (OR=0.23; p=0.001)
- SC global nT_2 -LV (OR=2.35; p=0.05)

Conclusions

- Cervical SC suffers from macroscopic and microscopic damage in MS, more severe in PMS compared to RRMS
- Cervical SC involvement in MS is highly correlated with disability
- Different MRI measures contribute to explain disability in RRMS and PMS:
 - SC lateral-funiculi T₂-LV and brain atrophy in RRMS
 - SC dorsal-column FA and GM atrophy in PMS
- Cervical SC MRI involvement is an accurate predictor of MS phenotype: cross-sectional GM atrophy and T_2 -LV are the main predictors