MR Imaging Acquisition and Image Segmentation

MR Imaging Acquisition. An MPRAGE sequence was used to obtain T1-weighted images with TR/TE = 1540/2.34 ms, FOV = 256× 256 mm, matrix = 256 × 256, section thickness = 1 mm (with no gap), and section number = 176. T2-weighted images were acquired by using a fast spin-echo sequence with TR/TE = 2500/316 ms and the same resolution parameters as in T1-weighted images. For DTI, acquisition parameters were as follows: TR/TE = 8300/82 ms, b-value = 1000 s/mm^2, diffusion gradient directions = 42, 7 b=0 scans, FOV = 256 × 256 mm, matrix = 128 × 128, section thickness = 2 mm (with no gap), and section number = 65. A multi-gradient-echo sequence was used to estimate the apparent transverse relaxation rate (1/T2*). Six echoes with TEs ranging from 7 to 47 ms with an equal interval of 8 ms were acquired with TR = 54 ms, flip angle = 20°, FOV = 256 × 256 mm, matrix = 256 × 256, section thickness = 1.5 mm (with no gap), and section number = 64.
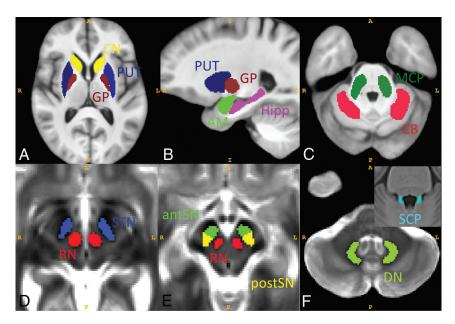
Atlas-Based Segmentation. The ROIs were obtained by using the AutoSeg package. Namely, the T1WI and T2WI were corrected by using the N4 algorithm for intensity inhomogeneity within each subject. A rigid registration was applied to roughly align an individual T1WI with the T1WI template image. A T2WI was aligned with the template image by applying the same transformation. The expectation-maximization algorithm was used for brain segmentation and skull stripping. Finally, the symmetric image normalization (SyN) algorithm was used to coregister the template T1WI (skull-stripped) to individual T1WI (skull-stripped). The generated deformable transformation was then applied to an atlas image to bring the ROIs from the template space into the individual space. Segmentation results were overlapped on T1WI/T2WI and were visually checked for potential registration failures. No severe misalignment was detected.

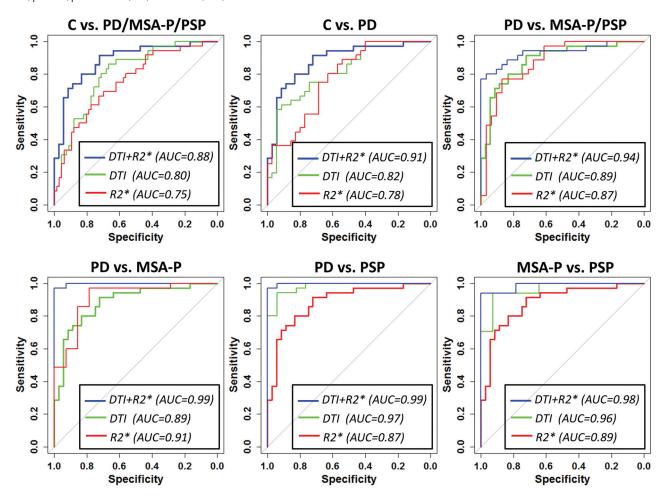**On-line Table: MRI measurements (mean and SD) for controls and patients with PD, MSA-P, and PSP[a]**

	Control	PD	MSA-P	PSP
PUT				
FA	0.332 (0.025)	0.339 (0.026)	0.325 (0.032)	0.333 (0.037)
MD	8.082 (0.633)	8.216 (0.738)	8.850 (1.376)	8.766 (0.957)
R2*	28.283 (3.572)	29.290 (5.441)	29.791 (4.124)	30.845 (6.133)
CN				
FA	0.244 (0.032)	0.245 (0.039)	0.241 (0.031)	0.251 (0.044)
MD	12.770 (1.594)	12.570 (2.239)	13.682 (2.822)	13.931 (2.316)
R2*	21.162 (3.051)	22.914 (3.532)	21.421 (4.714)	21.971 (4.332)
GP				
FA	0.395 (0.040)	0.391 (0.037)	0.379 (0.052)	0.390 (0.045)
MD	8.551 (0.562)	8.448 (0.499)	9.316 (1.292)	9.182 (0.715)
R2*	36.372 (3.974)	37.473 (6.964)	39.908 (5.026)	39.456 (5.703)
antSN				
FA	0.503 (0.075)	0.478 (0.082)	0.443 (0.077)	0.467 (0.108)
MD	7.340 (1.346)	7.897 (2.037)	8.227 (1.561)	9.057 (2.836)
R2*	41.896 (8.800)	47.688 (12.372)	49.651 (12.790)	51.381 (18.258)
postSN				
FA	0.466 (0.071)	0.407 (0.056)	0.417 (0.056)	0.434 (0.066)
MD	8.267 (0.781)	8.844 (1.043)	8.148 (1.232)	9.575 (1.257)
R2*	32.087 (4.926)	36.723 (9.573)	37.312 (9.571)	39.510 (9.785)
RN				
FA	0.448 (0.058)	0.430 (0.063)	0.402 (0.055)	0.416 (0.061)
MD	8.426 (1.099)	8.748 (1.645)	9.528 (1.483)	9.708 (1.928)
R2*	28.876 (3.622)	32.509 (5.544)	30.359 (5.116)	33.340 (5.554)
STN				
FA	0.516 (0.056)	0.495 (0.051)	0.465 (0.048)	0.490 (0.051)
MD	7.607 (1.075)	7.891 (1.251)	8.320 (1.475)	8.417 (1.409)
R2*	31.985 (5.710)	34.237 (5.030)	37.798 (5.268)	36.535 (4.875)
Hipp				
FA	0.195 (0.016)	0.192 (0.020)	0.189 (0.019)	0.180 (0.015)
MD	12.348 (1.859)	12.247 (1.623)	12.275 (1.226)	14.694 (1.636)
R2*	19.304 (3.352)	19.172 (2.607)	18.478 (2.306)	17.082 (2.960)
AM				
FA	0.208 (0.016)	0.201 (0.021)	0.197 (0.021)	0.194 (0.016)
MD	10.630 (0.912)	11.075 (1.432)	10.900 (0.846)	11.858 (1.405)
R2*	19.603 (4.226)	20.068 (3.100)	20.015 (5.454)	18.171 (3.803)
DN				
FA	0.372 (0.029)	0.364 (0.037)	0.360 (0.048)	0.341 (0.084)
MD	7.657 (0.328)	7.744 (0.536)	7.942 (0.927)	8.429 (1.300)
R2*	25.995 (4.358)	25.745 (6.198)	24.023 (4.750)	27.732 (6.096)
CB				
FA	0.248 (0.032)	0.252 (0.023)	0.224 (0.039)	0.220 (0.027)
MD	8.013 (0.673)	8.029 (0.611)	9.516 (2.468)	9.415 (2.083)
R2*	19.633 (2.503)	19.791 (3.348)	18.412 (2.317)	19.220 (2.140)
SCP				
FA	0.671 (0.123)	0.682 (0.124)	0.640 (0.153)	0.483 (0.201)
MD	10.635 (1.931)	10.752 (2.283)	12.274 (2.845)	14.408 (4.945)
R2*	18.466 (3.389)	19.713 (4.507)	16.899 (4.996)	17.898 (4.376)
MCP				
FA	0.542 (0.032)	0.534 (0.062)	0.506 (0.056)	0.524 (0.084)
MD	7.322 (0.340)	7.151 (0.346)	8.009 (1.367)	7.881 (1.708)
R2*	20.481 (3.941)	21.934 (4.017)	19.580 (4.325)	19.617 (3.840)

Note:—antSN indicates anterior substantia nigra; postSN, posterior substantia nigra; Hipp, hippocampus; AM, amygdala; CB, cerebellum; DN, dentate nucleus; GP, globus pallidus; MCP, middle cerebellar peduncle; SCP, superior cerebellar peduncle.

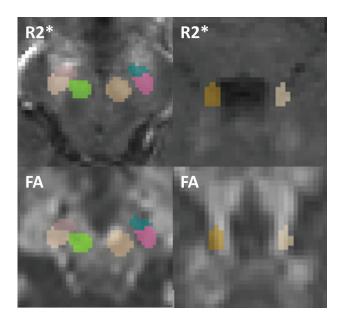[a] Data represent the mean (SD) of the imaging measures in each region for each group of subjects.

ON-LINE FIG 1. Illustration of ROIs in templates for segmentation. ROIs are illustrated in T1-weighted or T2-weighted template images. Hipp indicates hippocampus; AM, amygdala; GP, globus pallidus; SCP, superior cerebellar peduncle; MCP, middle cerebellar peduncle; antSN, anterior SN; postSN, posterior SN; CB, cerebellum; DN, dentate nucleus.

ON-LINE FIG 2. ROC curves for differentiating controls and patients with parkinsonian syndromes by using MR imaging measurements. The *green line* represents the model with DTI measurements alone, the *red line* represents the model by using the R2* measurement alone, and the *blue line* represents the model by using both R2* and DTI measurements. The ROC curves were generated by using a nested 10-fold cross-validation.

ON-LINE FIG 3. An example of the final segmentation quality for small structures (SN, RN, and superior cerebellar peduncle).