Across 1.5T and 3.0T MR Field-Strengths: Comparison of Regional Brain Volumes Derived from Atlas-based Parcellation Data

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Introduction

Longitudinal MRI studies designed to be conducted at a single field strength can be seriously limited by system enhancements and replacements from lower to higher field strength. Merging data across field strengths, however, has not been endorsed for a variety of reasons, including differences in field strength effects from B1-field homogeneity on various brain tissue types and their locations in the magnetic field (1). Yet, the ability to combine 1.5T and 3.0T data, typically used in clinical research, could expand sample sizes and holds other possibilities for broadening longitudinal investigations of changes in regional brain morphology and tissue integrity associated with normal development, normal aging, disease progression, and spontaneous or therapeutic resolution of disease. Accordingly, we examined the correspondence between SPGR data collected at 1.5T and 3.0T and whether a correction function could be determined and applied to improve measurement agreement.

Materials and Methods

To determine whether structural T1-weighted data acquired across MR field strengths could be merged, archival SPGR parcellation data acquired at 1.5T and at 3.0T within 3 weeks in 84 men and 30 women (mean age=47.5±10.2 years) were compared. Comparability of regional volume determination at 1.5T and 3.0T was assessed with intraclass correlation (ICC) computed on 24 cortical, subcortical, and CSF-filled volumes (2) derived from the automated and unsupervised SRI24 atlas registration and parcellation method (3) (http://nitrc.org/projects/sri24). To ensure that differences between datasets were not a function of the lack of reliability of the registration/parcellation approach, a second set of analyses measured the reliability of the registration and quantification using the same approach on longitudinal data acquired in 69 healthy adults (mean age 50.2±15.5 years) at a single field strength, 1.5T, at an interval of less than 2 years.

1.5T data were collected on a GE 1.5T Signa Twin whole-body system with a quadrature head coil (General Electric Healthcare, Waukesha, WI). Two coronal structural sequences were used for the analysis: SPGR sequence (TR=25 ms, TE=5 ms, flip angle=30˚, matrix=256x192, thick=2 mm, skip=0 mm, 94 slices) and a dual-echo fast spin echo (FSE) sequence (TR=7500 ms, TE1/2=13.5/108.3 ms, matrix = 256x192, thick=4 mm, skip=0 mm, 47 slices).

3.0T data were collected on a GE 3T Signa whole-body system with an 8-channel phased-array head coil. Data were derived from T1-weighted Inversion-Recovery Prepared SPGR images (TR=7 ms, TE=2.2 ms, TI=300 ms, thick=1.25 mm, skip=0 mm, 124 slices) and dual-echo FSE images (TR=8583 ms, TE1/2=13.5/108.3 ms, thick=2.5 mm, skip=0 mm, 62 slices).

Results

A regression-based correction function (CF) significantly improved correspondence measured by ICC. The scatter of the regional volumes from the identity line of a perfect correlation indicated that 13 regions were larger at 3.0T than 1.5T by .3 to 15.0% and 11 were smaller at 3.0T than 1.5T by .2 to 19.1%. The inter-scan ICCs ranged from .216 for the globus pallidus to .995 for the lateral ventricles (mean ICC=.801; median ICC=.834). Improvement in ICC was not forthcoming with a simple scaling correction approach. Rather, application of a regression correction function for each regional volume yielded significant increase in ICCs (t(23)=3.770, p=.001), representing an average ICC improvement of .087. The post-correction ICCs ranged from .599 to .998 (mean=.888; median=.881). ICCs improved for 17 regions, declined insubstantially for 4 regions, and remained unchanged for 3 regions (Fig. 1).

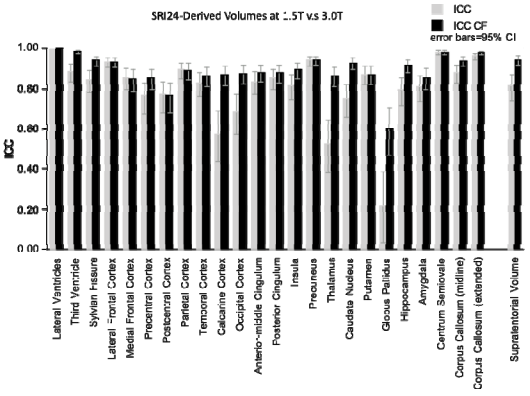

Fig. 1. Uncorrected and CF adjusted ICCs for each SRI24-derived regional volume pair of 1.5T and 3.0T data from 114 adults scanned at each field strength within 3 weeks.

The potential utility of the regression procedure was confirmed by applying the procedure to split-half independent samples, where regional correction functions were calculated for each sample, and then applied to the other sample. For the *a-b* comparison, the ICC of 19 regions improved and 5 declined, which was an average increase of .079 (t(23)=3.784, p=.001). 21 were in the "substantial" range (greater than .80 (4)), 2 (putamen and postcentral cortex) were in the "moderate" range, and globus pallidus ICC was "fair" (.585). The *b-a* comparisons were similar, whereby 20 improved and 4 got worse (t(23)=3.180, p=.0042), mean ICC difference=.072; only the globus pallidus (ICC=.454) failed to reach the "substantial" ICC range. Correspondence was high between most selected cortical, subcortical, and CSF-filled spaces; correspondence was lowest in the globus pallidus, a region rich in iron, which in turn has a considerable field-dependent effect on signal intensity.

Discussion and Conclusion

The application of a regression-based correction function that improved the correspondence in regional volume estimations argues well for the proposition that selected T1-weighted regional anatomical brain data can be reliably combined across 1.5T and 3.0T field strengths with the application of an appropriate correction procedure.

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References

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