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Title:

"Quantitative assessment of ^{18}F-flutemetamol uptake in cerebral amyloid angiopathy using a reduced PET-MR acquisition time frame"

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Abstract

We performed quantitative analysis of ^{18}F-flutemetamol PET-MR data in cerebral amyloid angiopathy. We showed consistent differences of pharmacokinetic estimates in cases versus controls for reduced against full PET acquisition. This may support future protocol optimisation in the clinical setting.

Question

PET imaging using ^{18}F-flutemetamol may improve the detection of β-amyloid plaque density in cerebral amyloid angiopathy (CAA), versus the current clinical standard MRI biomarkers[1].

It is unknown whether pharmacokinetic estimates extracted by reduced (<90 min) acquisition time frames can robustly detect CAA.

We performed quantitative analysis of dynamic PET-MR data to assess pharmacokinetic estimates in CAA patients against controls, for a reduced (60 min) against our full (120 min) PET acquisition.

Methods

We analysed 18F-flutemetamol PET-MRI (Siemens Biograph) dynamic data from a pilot cohort of 6 cases with probable CAA (age: 72±10 years) and 6 age-matched controls (69±10 years) with no CAA, defined by the modified Boston criteria[1]. PET acquisition started at the time of tracer injection and lasted for 30 min, with a second period of data acquisition from 90 to 120 min. An exponential function was fitted to each regional time-activity curve, to interpolate regional brain uptake from 30 to 90 min (Matlab).

For both a reduced PET acquisition (RA-60 min) and our full PET acquisition (FA-120 min) time, four pharmacokinetic models were investigated across 12 brain atlas-derived time-activity curves restricted to the cortical areas: 1-tissue compartment (1-TC), 2-tissue-4k compartment (2-TC), simplified reference tissue (SRTM) and full reference tissue model (FRTM)[2] (PMOD). Statistical analysis was performed in R.

Results

Initially, all models were assessed in FA. 1-TC-derived volume of distribution (Vd: a tracer uptake estimate) and SRTM/FRTM-derived R1 (a relative cerebral blood flow estimate) were significantly higher and lower in patients against controls ($P<0.01$, Figure 1), respectively. No other significant differences were observed.

Subsequently, all models were assessed in RA. Significant differences for 1-TC-derived Vd and SRTM/FRTM-derived R1 were consistent between patients and controls ($P<0.01$, Figure 1).

Conclusions

We showed significant differences in pharmacokinetic estimates in patients with probable CAA versus controls, which were consistent when a reduced (60 min) PET acquisition time was used for analysis against our full (120 min) acquisition. This quantitative assessment may support careful optimisation of the minimum PET acquisition time required, for the accurate detection of CAA. Further pharmacokinetic assessments are currently performed in our full cohort (N=20) between reduced (<60 min) and full PET acquisition times.

References

1. Samarasekera N, et al. *J Neurol Neurosurg Psychiatry;*2012.
2. Gunn RN, et al. *J Cereb Blood Flow Metab*;2001.

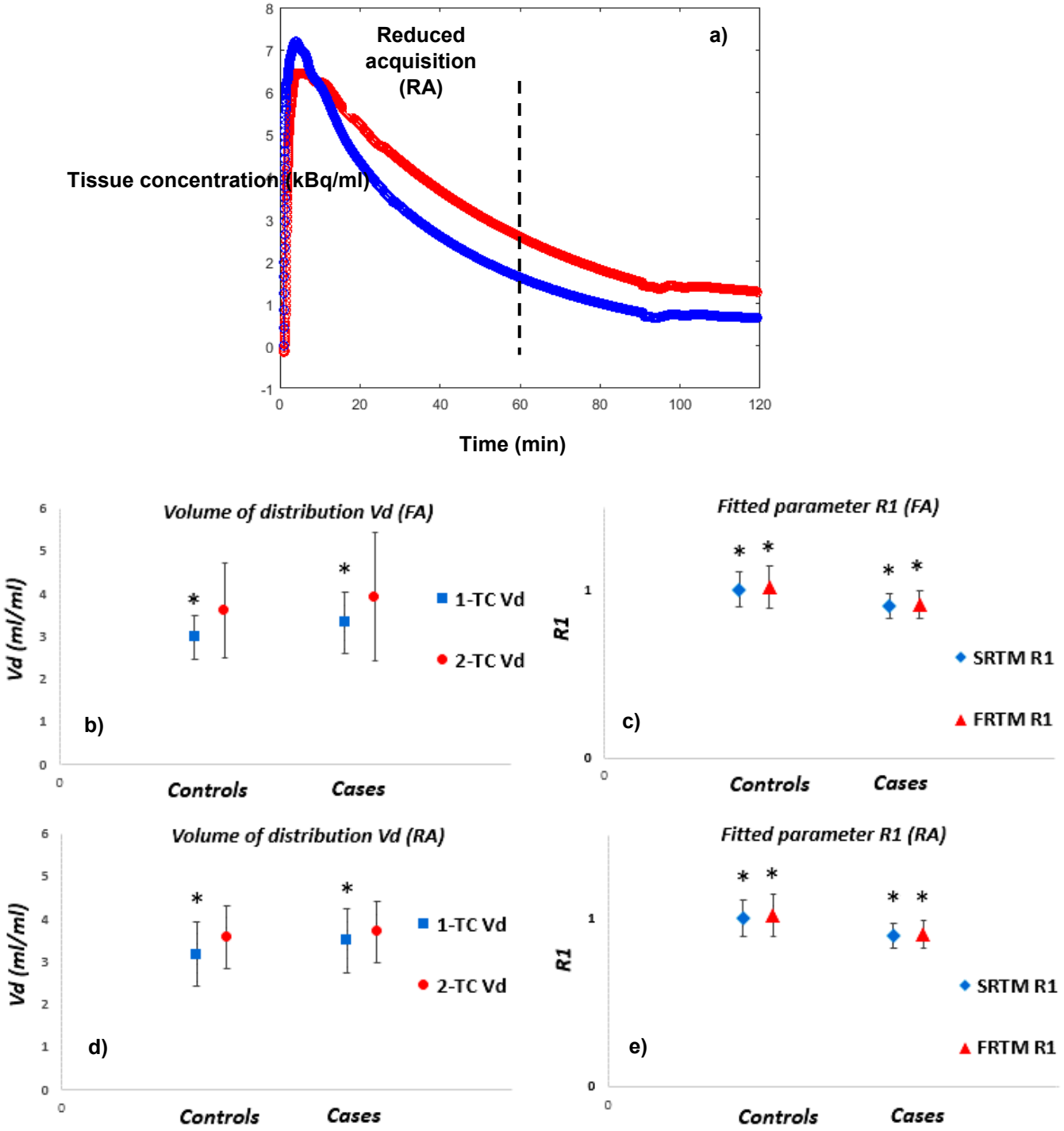

Figure footnote: Note that R1 reflects a normalised value (R1=K1/K1', where K1: rate constant of tracer delivery from blood to tissue, K1': rate constant of tracer delivery from blood to cerebellum reference region)

Figure 1) (a) Time-activity curves from a patient with CAA (red) and a control (blue, dashed line shows the RA). (b, c) Mean (SD) values for patients and controls in FA (for 1-TC, 2-TC-derived Vd and SRTM, FRTM-derived R1). (d, e) Similarly, mean (SD) values for patients and controls in RA. Significant differences are shown with *. FA: full PET acquisition time.