No differences in uptake were observed in other organs. **Conclusions:** This preliminary work further supports the capacity of this CatD targeted CA to help differentiate between AD mice and controls.

IC-P-025 WITHDRAWN

IC-P-026 AMYLOIDOSIS INDUCES REORGANIZATION OF THE HIPPOCAMPAL METABOLIC NETWORK

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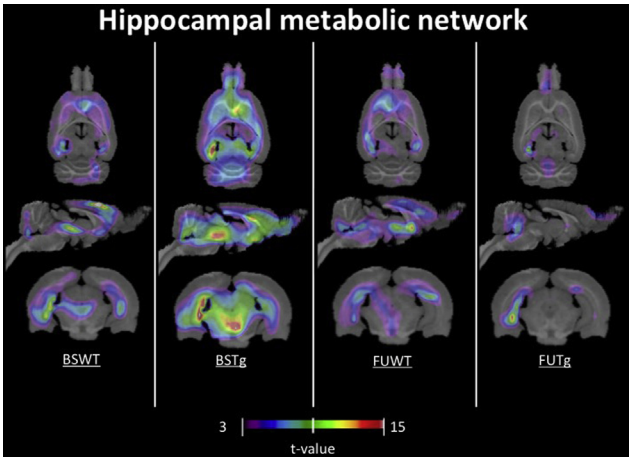
Background: Rat transgenic models of human brain amyloidosis constitute a unique opportunity to explore the impact of amyloid pathology on imaging biomarkers without the bias of tau pathology invariably present in the human brain. The cerebral metabolic rate of glucose measured by Positron Emission Tomography using [^{18}F] FDG is often used as a biomarker of neurodegeneration in Alzheimer's disease (AD). Metabolic network refers to population-based maps depicting large-scale organization of brain glucose utilization. There has been growing evidence, suggesting that brain amyloidosis modulates metabolic changes observe in the progression of AD pathophysiology. Here, we investigate the effect of amyloidosis on hippocampal metabolic network in wild type (wt) and transgenic (Tg) Mcgill-R-Thy1-APP rats, which express amyloidosis in the absence of tangles or cell depletion. We hypothesized adaptations of brain metabolism in early stages of amyloidosis followed by declines in the metabolism in aged animals. **Methods:** A total of 17 rats (10 WT, 7 Tg) were used for this study. The FDG-PET acquisition was done longitudinally with 11.5 mo (baseline) and 16.8 mo (follow-up). Individual FDG SUVRs were generated using pons as a reference region. Population based correlation analysis were generated using the dorsal and ventral hippocampi. Tg and wt hippocampal metabolic networks maps were compared at voxel- levels using Fisher's Z transformation. **Results:** WT hippocampal metabolic network [Baseline vs follow-up] contrast did not reveal significant differences. As compared to McGill-R-Thy1-APP rat showed increased strength of correlation and recruitment of additional cortical areas at baseline, while in the follow up it a drastic decline in the hippocampal metabolic network was noted. When performed Fisher's Z transformations, baseline Tg showed significant correlation in subcortical structures such as thalamus and small regions in medial temporal lobe compared to baseline and follow-up WT. Baseline Tg showed significant correlation in medial temporal lobe, bilateral hippocampi, amygdala, and cingulate cortex compared to follow-up Tg (figure 1). **Conclusions:** These results demonstrate that amyloidosis per se alter brain metabolism and large-scale brain metabolic networks. Similar to what has been reported in humans, while early brain amyloidosis evokes enhances and declines of glucose metabolism, late stages of amyloidosis leads to significant hypometabolism.



IC-P-027 DYNAMICS OF LONGITUDINAL BIOMARKER CHANGES IN THE MCGILL-R-THY1-APP RAT

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Background: Rat transgenic models of human brain amyloidosis constitute a unique opportunity to explore the impact of amyloid pathology on imaging biomarkers without the bias of tau pathology invariably present in the human brain. Due to its size, the McGill-R-Thy1-APP rat is ideal for multi-modal neuroimaging observations as compared to transgenic mouse. Here, we studied the associations between the rates of structural brain remodeling as a function of the rate of progression of hypometabolism in transgenic rats. We hypothesize regional specific interactions between biomarkers. **Methods:** McGill-R-Thy1-APP rat (n=9) and wild type (wt; n=12) had [^{18}F]FDG and structural MRIs scans at 11-month (baseline) and 16-month (follow-up). Structural images were acquired using a Bruker 70/30USR Biospect MRI (FISP; TE/TR: 2.5/5.0ms; FOV: 3.6cm^3; isotropic 250um voxels; 8 angles). Voxel-based morphometry was performed to obtain longitudinal deformation maps. [^{18}F]FDG PET images were acquired and analyzed as described previously (3). For both scans, longitudinal difference maps were generated. Global uptake values obtained from these maps were then correlated with structural deformation maps using a voxel-level linear model. **Results:** The olfactory bulb, anterior pituitary lobe, multiple cortical areas, lateral ventricle, and a portion