

Variation on endothelial tight junctions in the **TgF344-AD** rat in Alzheimer's disease Marielle Rikkelman¹, Ryan Bernal Hogans¹, Nathifa Nasim¹, Anthony Valenzuela¹, Pamela J. Lein

Background and Rationale

Over half of adults over the age of 80 develop dementia, including Alzheimer's disease (AD), with the primary risk factor being age – whose cause is still largely unknown. Age-associated vascular inflammation is hypothesized to contribute to AD development, as the neurovascular inflammatory response creates a ripe environment for neurodegenerative disease.

Disruption of the blood brain barrier(BBB) leaves potential for increased neuronal and glial injury as a result of increased efflux of toxic chemicals from the vasculature, as well as reduced metabolites accessible to these now-vulnerable cells. Given that the effectiveness of the BBB decreases with age, it is worth investigating what aspects of BBB function change with time in an AD-like phenotype.

Endothelial tight junction (TJ) proteins strictly regulate influx and efflux of plasma proteins such as albumin, immunoglobulin, and fibrinogen; dysfunction of these TJs would suggest paracellular openings that allow serum proteins to leak into the brain parenchyma, potentially causing cytotoxicity.



Hypothesis

Tight junction proteins claudin-5 and occludin will be decreased in brains that display AD-like phenotypes. AD-like phenotypes present with regional heterogeneity, brain regions are not equally affected by AD; specifically, claudin-5 and occludin will be decreased in highly vascularized regions of the hippocampus (CA1, CA3, and the dentate gyrus). Claudin-5 and occludin will also decrease in these regions over time.

Methods

This study leveraged the rat model TgF344-AD which recapitulates the inflammatory responses seen in AD-like clinical features due to the overexpression of the human mutant amyloid precursor protein and presinilin 1 genes. Age- and sex-matched wildtype (Wt) and TgF344-AD (Tg) rats were reared for brain tissue collection at 10 months of age (n=10 total; n_{Wt} =4 & n_{Ta} =6) and at 15 months of age (n=9 total; n_{Wt} =4 & n_{Ta} =5). Tissues were cry sectioned at 10mm at ~bregma -4.80 mm to reveal the hippocampus in its entirety, the prefrontal cortex, and piriform and entorhinal cortices for later data collection.

Immunohistochemistry (IHC) was performed on at least one tissue from each animal. Stains included occludin (OCCLN) and claudin-5 (CLDN5) and amyloid- β (OC) deposition as a control to confirm an ADphenotype. Claudin-5 and occludin were stained on the same tissue for relevant quantitative analysis, and amyloid- β staining occurred on separate section of similar bregma. Amyloid-β antibodies were monoclonal, claudin-5 antibodies were monoclonal, and occludin antibodies were polyclonal; all tissues were treated with DAPI for nuclear staining.



Using the ImageXpress® Micro by Molecular Devices, the hippocampal regions of each tissue were imaged at 20x. IHC images were cropped by a blinded researcher to isolate hippocampal regions of interest (CA1, CA3, and the dentate gyrus). Cropped images were analyzed by generating a binary mask using an intensity threshold dictated by a negative (no primary antibody) and positive control sample. Binary masks were used to calculate immunopositive area and average intensities are calculated by custom analysis module.

Data were exported, compiled, and analyzed. Amyloid- β was analyzed for area via a two-tailed t-test and tight junction proteins were analyzed for average ratio of immunofluorescence via multiple unpaired t tests with Welch correction and multiple comparisons for false discovery rate.



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