

ASSESSMENT OF AMYLOID PRECURSOR PROTEIN (APP) AND TUBULIN NETWORK USING STOCHASTIC OPTICAL RECONSTRUCTION MICROSCOPY (STORM) IN AN *IN VITRO* MODEL OF ALZHEIMER'S DISEASE

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KEY WORDS: Alzheimer's disease, APP, tubulin network, STORM

Microtubule impairment and protein aggregation are implicated in the pathogenesis of Alzheimer's disease (AD)[1]. Although much is known about the molecular defects in AD, data derived from visualising the structural changes of microtubules and APP clusters under normal physiological and disease conditions using super-resolution techniques is limited. Here, we utilized STORM to assess (1) tubulin acetylation and structure in a paraquat induced injury model and (2) APP clusters in an APP over-expression model of AD following 24 h and 48 h overexpression. Our results reveal an increase in the number and size of APP clusters upon 24hrs and 48hrs of APP over-expression compared to the control (Fig.1). In addition, we observed major disruptions in tubulin network upon paraquat treatment (Fig.2).

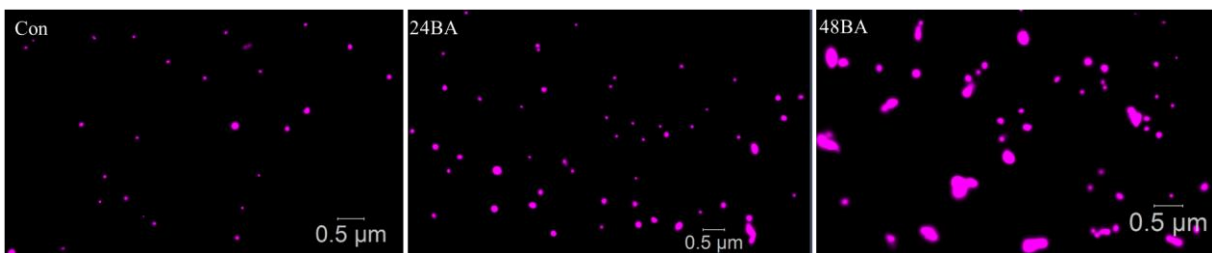


Figure 1. STORM micrograph showing APP clusters. Butyric acid exposure induced APP expression and enhanced the density of clusters compared to Control (Con). (Magenta) APP:Alexa 568. Scale bar: 1 μm .

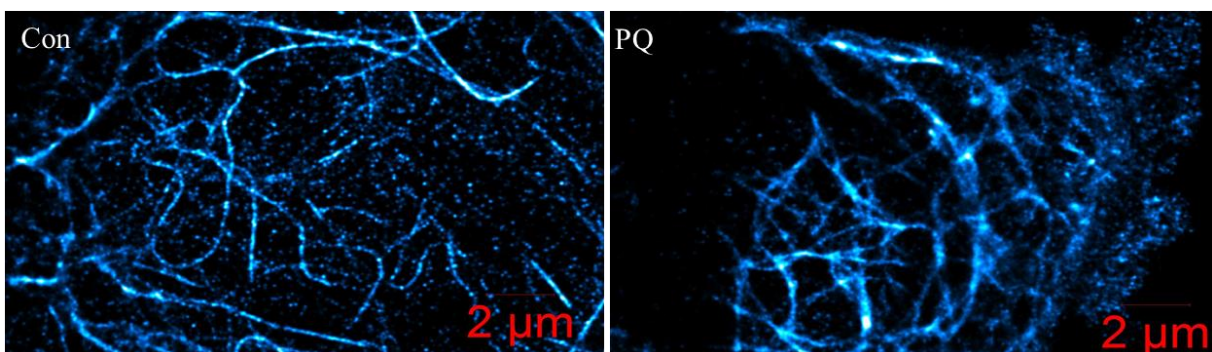


Figure 2. dSTORM micrograph showing acetylated α -tubulin. Paraquat (PQ) exposure induced tubulin dysfunction and enhanced acetylation signal and density compared to Control (Con). (Cyan) Acetylated α -tubulin: Alexa 488. Scale bar: 2 μm .

[1] Brandt, Roland, and Lidia Bakota. "Microtubule dynamics and the neurodegenerative triad of Alzheimer's disease: The hidden connection." *Journal of neurochemistry*, 4, 409-417 (2017).