

Role of Amyloid Responsome in Amyloid Aggregation

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Proteomic and biomarker research reveals that Alzheimer's disease (AD) involves complex brain changes across all cell types, culminating in organ failure. Cross-species comparisons of brain proteomes, including AD patients and A β -depositing mice, have identified a conserved A β amyloid responsome. A key network, M42, contains proteins that accumulate in plaques, cerebrovascular amyloid (CAA), and dystrophic neurites, marking them as potential therapeutic targets. According to the "amyloid scaffold" hypothesis, A β aggregation alone may not cause neurodegeneration unless accompanied by the buildup of amyloid-associated proteins (AAPs). Prior studies showed that overexpressing M42 proteins like midkine and pleiotrophin increases amyloid deposition. Building on this, we tested the effects of additional M42 proteins—Vtn, Sdc4, and Smoc1—by overexpressing them in CRND8 mouse brains via AAV delivery. Mice receiving these constructs showed robust gene expression and a striking reduction in amyloid deposition. The overexpressed proteins also influenced APP processing and A β aggregation in distinct ways, underscoring the complex role of M42 proteins in AD pathogenesis. This work highlights the intricate molecular landscape of AD, validates five key proteins involved in disease progression, and supports the hypothesis that A β acts as a scaffold for bioactive proteins that modulate degeneration. Continued multi-omics research and broader disease modeling are needed to further elucidate amyloid-driven mechanisms and uncover new therapeutic strategies.

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