

Publication

Amyloid-beta and tau synergistically impair the oxidative phosphorylation system in triple transgenic Alzheimer's disease mice

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

ID 107138

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Year 2009

Title Amyloid-beta and tau synergistically impair the oxidative phosphorylation system in triple transgenic Alzheimer's disease mice

Journal Proceedings of the National Academy of Sciences of the United States of America

Volume 106

Number 47

Pages / Article-Number 20057-62

Keywords amyloid-beta peptide, electron transport chain, energy metabolism, mitochondrial complexes, tau protein

Alzheimer's disease (AD) is characterized by amyloid-beta (Abeta)-containing plaques, neurofibrillary tangles, and neuron and synapse loss. Tangle formation has been reproduced in P301L tau transgenic pR5 mice, whereas APP(sw)PS2(N141I) double-transgenic APP152 mice develop Abeta plaques. Cross-breeding generates triple transgenic ((triple)AD) mice that combine both pathologies in one model. To determine functional consequences of the combined Abeta and tau pathologies, we performed a proteomic analysis followed by functional validation. Specifically, we obtained vesicular preparations from (triple)AD mice, the parental strains, and nontransgenic mice, followed by the quantitative mass-tag labeling proteomic technique iTRAQ and mass spectrometry. Within 1,275 quantified proteins, we found a massive deregulation of 24 proteins, of which one-third were mitochondrial proteins mainly related to complexes I and IV of the oxidative phosphorylation system (OXPHOS). Notably, deregulation of complex I was tau dependent, whereas deregulation of complex IV was Abeta dependent, both at the protein and activity levels. Synergistic effects of Abeta and tau were evident in 8-month-old (triple)AD mice as only they showed a reduction of the mitochondrial membrane potential at this early age. At the age of 12 months, the strongest defects on OXPHOS, synthesis of ATP, and reactive oxygen species were exhibited in the (triple)AD mice, again emphasizing synergistic, age-associated effects of Abeta and tau in perishing mitochondria. Our study establishes a molecular link between Abeta and tau protein in AD pathology in vivo, illustrating the potential of quantitative proteomics.

Publisher National Academy of Sciences

ISSN/ISBN 0027-8424

edoc-URL <http://edoc.unibas.ch/dok/A5253433>

Full Text on edoc No;

Digital Object Identifier DOI 10.1073/pnas.0905529106

PubMed ID <http://www.ncbi.nlm.nih.gov/pubmed/19897719>

ISI-Number WOS:000272180900058

Document type (ISI) Journal Article