Kamalian et al. conducted an in-depth proteomic study of cerebrospinal fluid (CSF) in 28 shunt-responsive idiopathic normal pressure hydrocephalus patients, 38 Mild Cognitive Impairment (MCI) due to Alzheimer's disease, and 49 healthy controls. Utilizing the Olink Explore 3072 panel, they identified distinct proteomic profiles in iNPH that highlight significant downregulation of synaptic markers and cell-cell adhesion proteins. Alongside vimentin and inflammatory markers upregulation, these results suggest ependymal layer and transependymal flow dysfunction. Moreover, downregulation of multiple proteins associated with congenital hydrocephalus (e.g., L1CAM, PCDH9, ISLR2, ADAMTSL2, and B4GAT1) points to a possible shared molecular foundation between congenital hydrocephalus and iNPH. Through orthogonal partial least squares discriminant analysis (OPLS-DA), a panel comprising 13 proteins has been identified as potential diagnostic biomarkers of iNPH, pending external validation. These findings offer novel insights into the pathophysiology of iNPH, with implications for improved diagnosis [1)].

1)
Kamalian A, Shirzadeh Barough S, Ho SG, Albert M, Luciano MG, Yasar S, Moghekar A. Molecular signatures of normal pressure hydrocephalus: a large-scale proteomic analysis of cerebrospinal fluid. Fluids Barriers CNS. 2024 Aug 8;21(1):64. doi: 10.1186/s12987-024-00561-5. PMID: 39118132.

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