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Protein signatures across multiple neurodegenerative diseases

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State of the art

The identification of disease-associated protein signatures could contribute to an increased understanding of neurodegenerative disorders. Some key features have been identified, but much remains unknown about disease pathogenesis. We hypothesize that there are complex patterns and associations to be discovered throughout the various degree of heterogeneity within and similarities across different diseases. To reveal such patterns, it is crucial to investigate many proteins in several independent cohorts.

Methodology

Our in-house developed antibody-based suspension bead array enables the measurement of hundreds of proteins in hundreds of samples in the same assay. This is enabled by direct labeling of samples with biotin, and a single binder setup with antibodies immobilized onto magnetic color-coded beads. We primarily use antibodies produced within the Human Protein Atlas (www.proteinatlas.org) and read out is facilitated using a streptavidin-conjugated fluorophore. The selection of proteins to be analyzed is tailored for each project, allowing for high flexibility and adaptability.

Results

Over the years, we have analyzed more than 3000 CSF samples and almost 5000 plasma samples from cohorts including patients with Alzheimer's disease, Parkinson's disease, frontotemporal dementia, and amyotrophic lateral sclerosis. Additionally, we have analyzed samples from neurologically healthy and cognitively impaired controls. In total, we have analyzed almost 1000 proteins, targeted by over 1500 antibodies.

Conclusion

To identify disease-relevant protein signatures, it is crucial to analyze large and independent cohorts including different neurodegenerative diseases. These complex signatures could potentially aid in the understanding of the diseases, including the identification of relevant patient subgroups.

Conflicts of interest

N/A