Introduction

Postnatal bilateral whisker trimming was used as a model system to test how synaptic proteomes are altered in barrel cortex by sensory deprivation during synaptogenesis. Using quantitative mass spectrometry, we quantified more than 7,000 synaptic proteins and identified 89 significantly reduced and 161 significantly elevated proteins in sensory-deprived synapses, 22 of which were validated by immunoblotting.

Results

1. We quantified more than 7,000 synaptic proteins and identified 89 significantly reduced and 161 significantly elevated proteins in sensory-deprived synapses, 22 of which were validated by immunoblotting.

2. Proteins that promote mature spine morphology and synaptic strength, such as excitatory glutamate receptors and known accessory factors, were reduced significantly in deprived synapses. Immunohistochemistry revealed that the reduction in SynGAP1, a postsynaptic scaffolding protein, was restricted largely to layer I of barrel cortex in sensory-deprived rats.

3. In addition, protein-degradation machinery such as proteasome subunits, E2 ligases, and E3 ligases, accumulated significantly in deprived synapses, suggesting targeted synaptic protein degradation under sensory deprivation. These data demonstrate the feasibility of defining synaptic proteomes under different sensory rearing conditions and could be applied to elucidate further molecular mechanisms of sensory development.

Conclusions

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References