A Large-Scale Phosphoproteomic Comparison of the Developing Mouse Brain

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Developmental processes are governed by diverse cellular and sub-cellular mechanisms including a suite of pathways employing reversible phosphorylation. With recent advances in large-scale proteomic methodologies it is now possible to identify thousands of phosphorylation sites from tissues at distinct developmental stages. This advance is particularly significant to neurodevelopment, where phosphorylation is absolutely essential for proper development. Towards a global characterization of phosphoproteomic changes across development, here we highlight the results of a large-scale quantitative mass spectrometry study identifying 2444 proteins and 993 phosphorylation sites from a comparison of embryonic, newborn and adult murine brain. Using strong-cation exchange coupled to immobilized metal affinity chromatography and an immuno-affinity enrichment for phosphotyrosine we illustrate diverse developmental profiles of several identified phosphoproteins. We further utilize gene ontology enrichment to assess changes in biological processes as a function of protein expression and relative level of phosphorylation. Orthogonally-supported by western blot data, this study provides evidence for considerable dynamic change across development in the mouse brain phosphoproteome and will be an asset for further study.