A high-throughput quantitative proteomics approach to identify altered synaptic protein content in an animal model of depression

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Research question and background

In our recent investigations on major depression disorder (MDD), we demonstrated in mouse and rat models that gene βCaMKII's over-expression in a brain structure called habenula significantly elevates its neuronal activity, which in turn represses downstream reward centers such as ventral tagmental area and dorsal raphe nuclei and leads depression-like behaviors such as despair and anhedonia. These results strongly indicate that βCaMKII is among the candidate pathogenic genes of MDD in human, and its overexpression may be the main molecular mechanism. As such, it is vital to interrogate the level of βCaMKII expression in human brain tissues as to test such hypothesis.

Methods and tissues used

Therefore during 2014 we ordered **12** brain samples from Netherlands Brain Bank. Among these samples **3** were from diagnosed depression patients, and **9** from individuals who weren't, which wereas negative control.It should also be noted that these samples include samples from both male and female donors, although female donors significantly outnumbered male.
From these brain samples,total protein have been extracted and the level of βCaMKII are to be determined by western blot. We expect to have a more comprehensive report on the experiments and analyses on this project in the coming year.

Results and conclusions

Based on the results we have so far, in 2015 we will request more brain samples to continue our current investigation. And in addition to analyzing the level of βCaMKII in habenula, we wish to collect additional tissues such as hippocampus and cortex. Through comparingβCaMKII expression levels between habebula and other brain structures/regions, we will gain deeper insight about the role of βCaMKIIin normal neuronal activity and its role in human depression.

In addition we wish to have access to more brain samples from depression patients. The 3 brain samples from depression patients that we used in our investigation proven to be extremely valuable. But we need more brains from depression patients to gain more statistical significance and rigorousness in our data analyses.