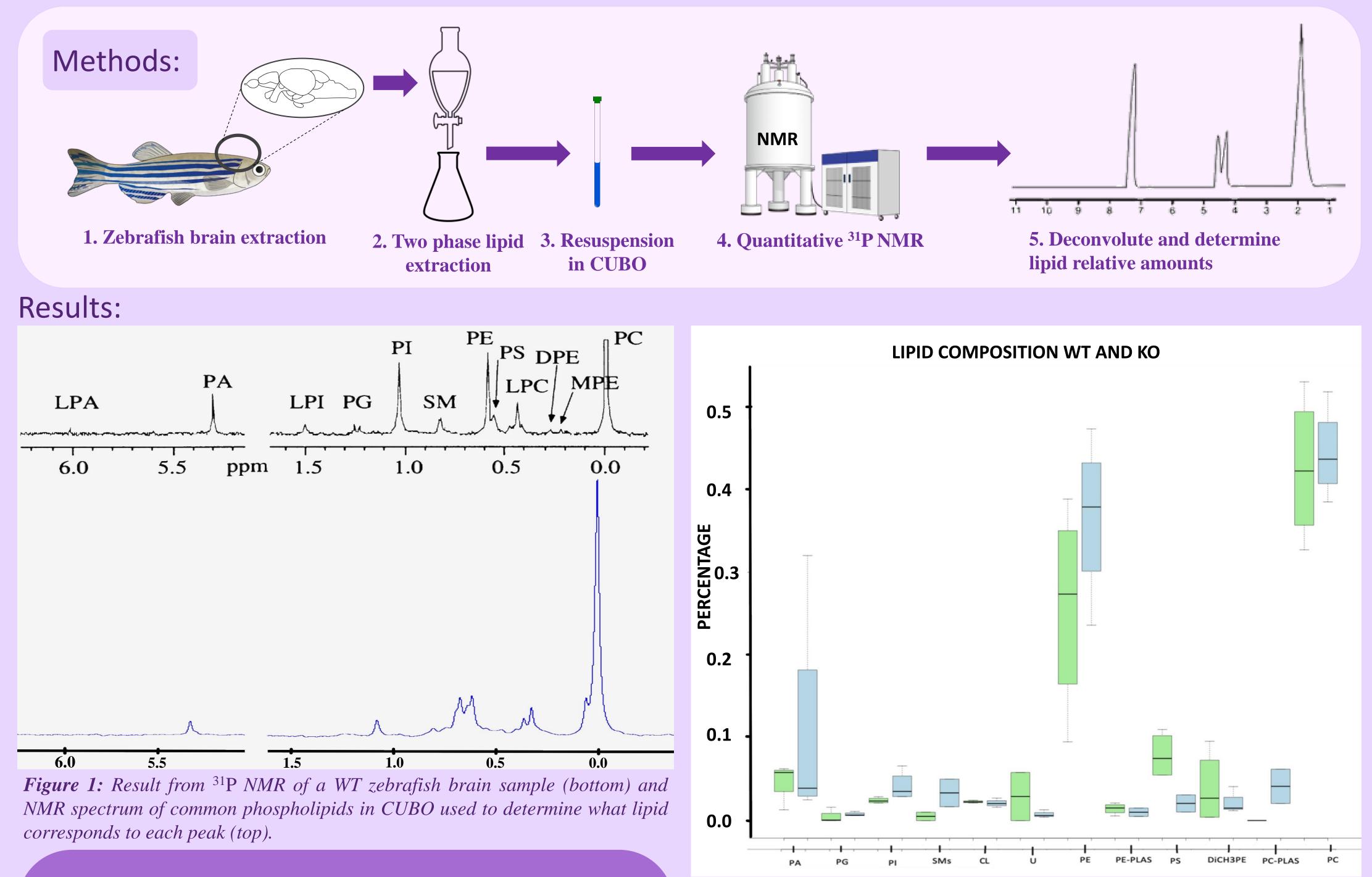
Quantitative phospholipid analysis of zebrafish brains from DJ-1 knockouts, a Parkinson's Disease model Linnea V. Løkeland*, Gina K. Barry*, Diana C. Turcu and Sarah T. Frøystad, Kari E. Fladmark, Øyvind Halskau Department of Biological Sciences, University of Bergen, Bergen, Norway

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Parkinson's disease is an age-related neurodegenerative disorder associated with both motor and non-motor symptoms. The brain consists of approximately 50% lipids by dry weight. These lipids interact with proteins and other lipids, and are active in many aspects of brain function. Dysfunctional lipid metabolism is linked to inflammation, mitochondrial dysfunction, lipid peroxidation, and oxidative stress, which are also characteristics of Parkinson's disease. **The aim of this project** is to investigate changes in phospholipids related to PD in the brain of wild-type (WT) zebrafish and zebrafish in which the DJ-1/PARK7 gene is deactivated (KO). Lipids will be extracted using a modified Bligh & Dyer method, and their compositions of phospholipids will be analyzed using quantitative ³¹P NMR.



Discussion:

Figure 2: Lipid composition of WT and KO zebrafish brain samples. Boxplot for

The results from the experiment show the composition divided by phospholipid classes. The relative amounts of each lipid classes could differ between the KO and WT. No significant differences (p > 0.05, student's t-test) between WT and KO was observed for any of the detected phospholipids.

The study is limited by ³¹P NMR not picking up signals from nonphosphorus lipids such as cholesterol. Moreover, the fatty acid chains and the oxidative state of the lipids is not detected either. WT and KO are paired for the same lipid to compare the different level of the lipid. Blue illustrates WT samples and green illustrates KO. Thick line indicates median values, box limits indicates 25^{th} and 75^{th} percentile, and whiskers shows min and max percentile. No statistical difference was found between groups (P > 0.05, pairwise student's t-test)

Future prospects:

Lipid samples from all extractions were set aside for LC-MS and GC-MS, analyses which could provide more details on more lipid molecules.



References:

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