



Chronic exposure to polystyrene microparticles induces changes in the proteome of *Daphnia magna* [ID: 334247]

Trotter B.^{1,2}, Wilde M.², Brehm J.¹, Arnold G.J.², Fröhlich T.², Laforsch C.¹

¹ University of Bayreuth, Animal Ecology 1, Universitätsstraße 30, Bayreuth, Germany

² Gene Center Munich, Laboratory for Functional Genome Analysis, LMU München, Feodor-Lynen Straße 25, Munich, Germany



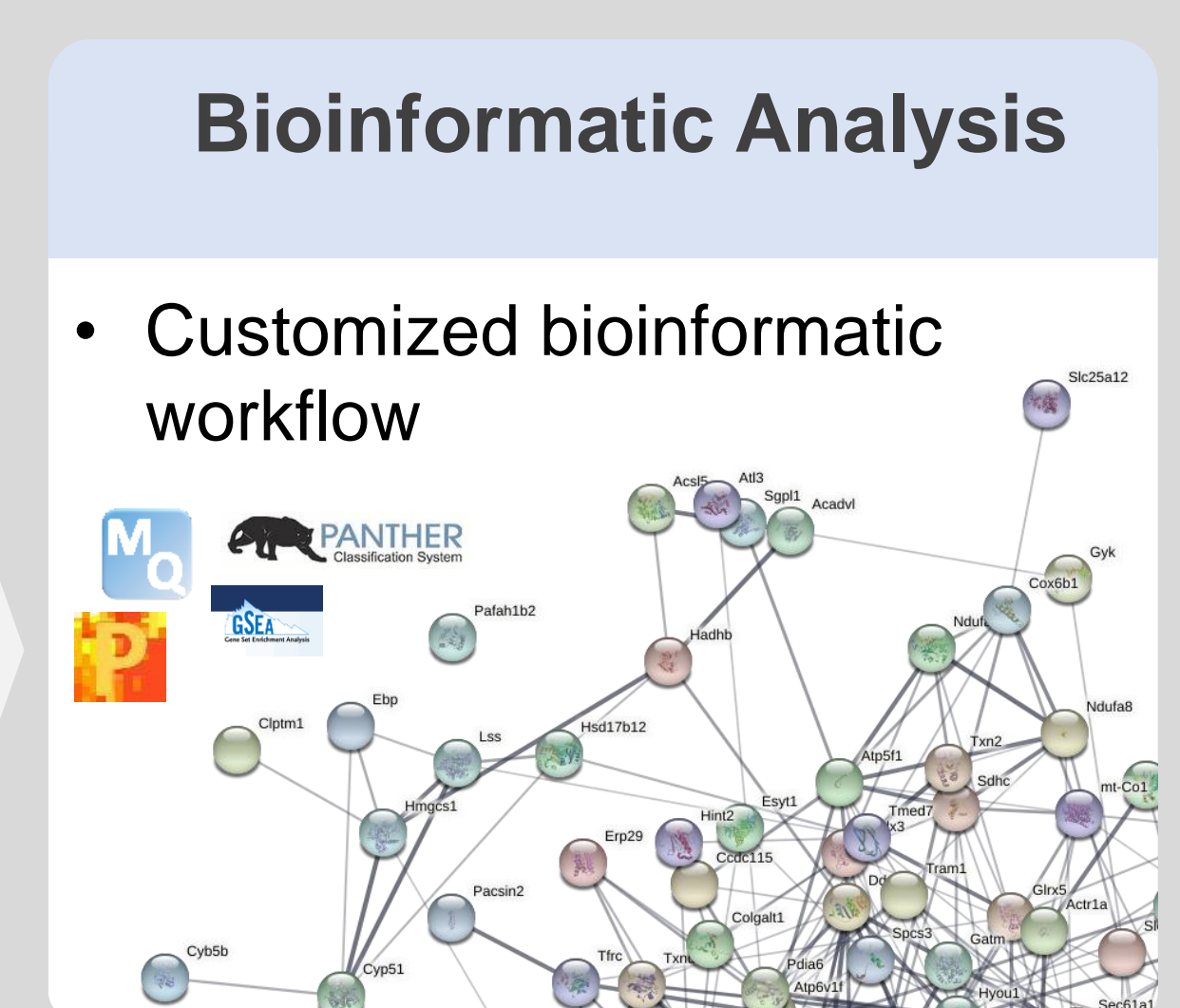
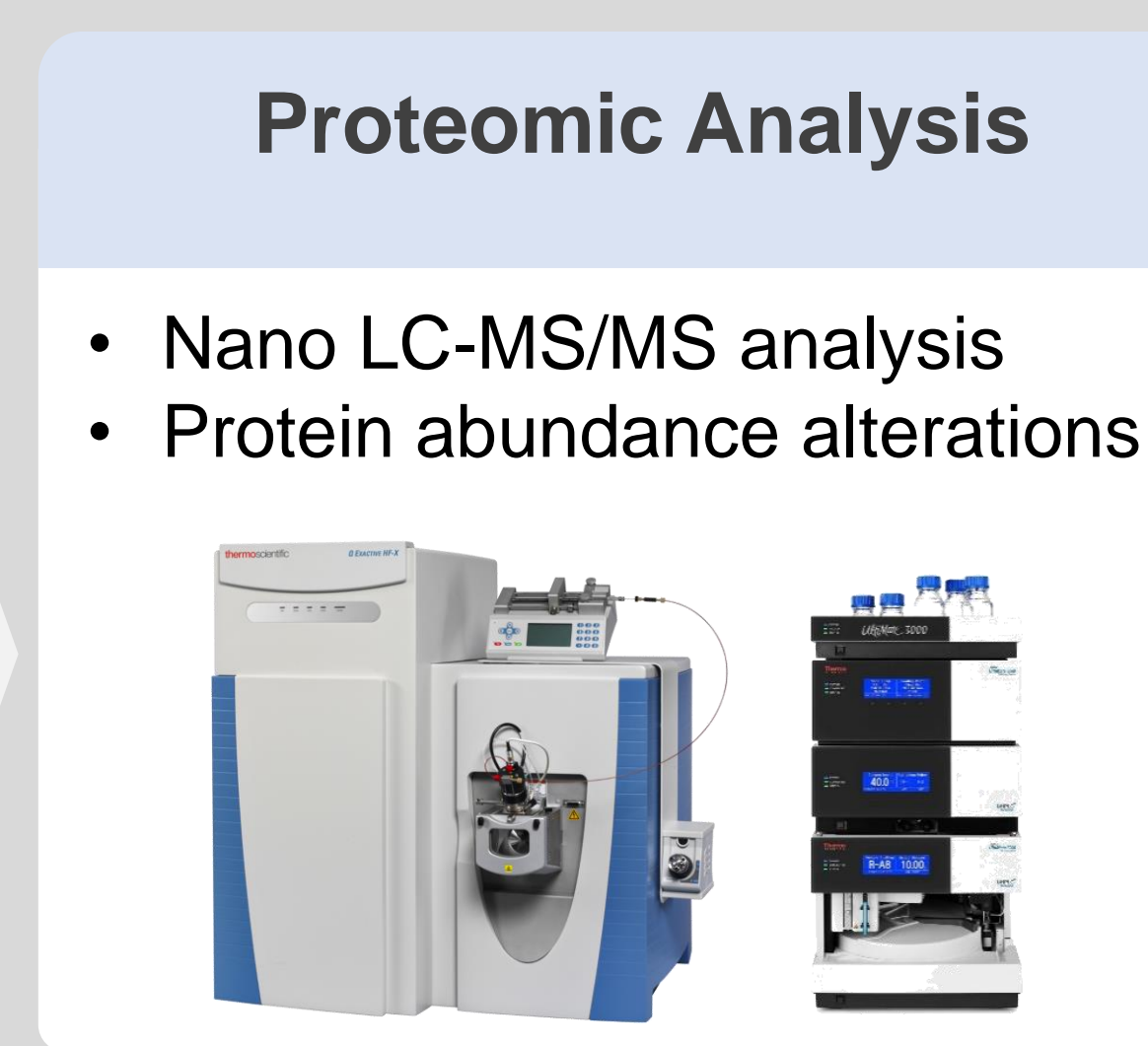
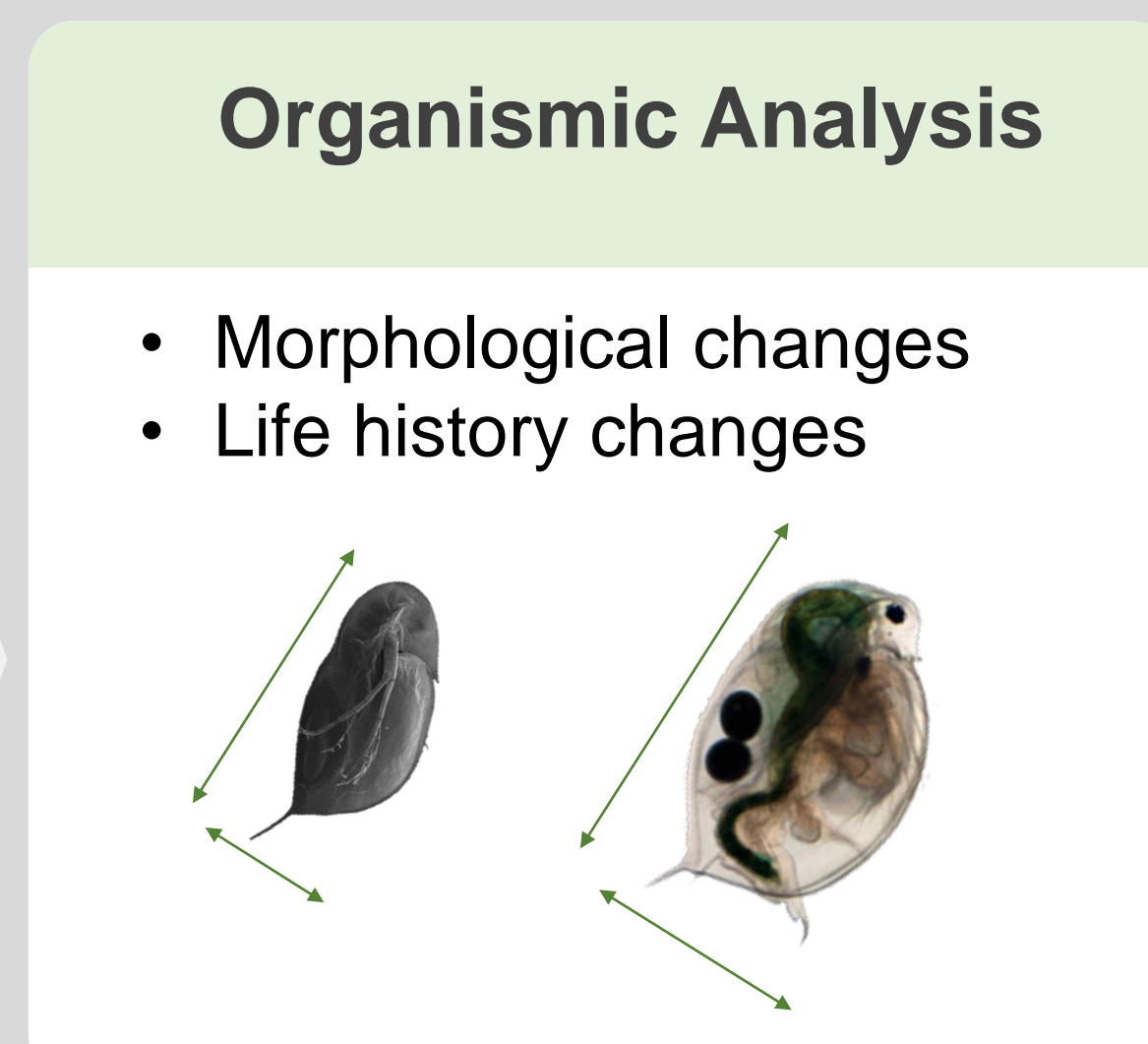
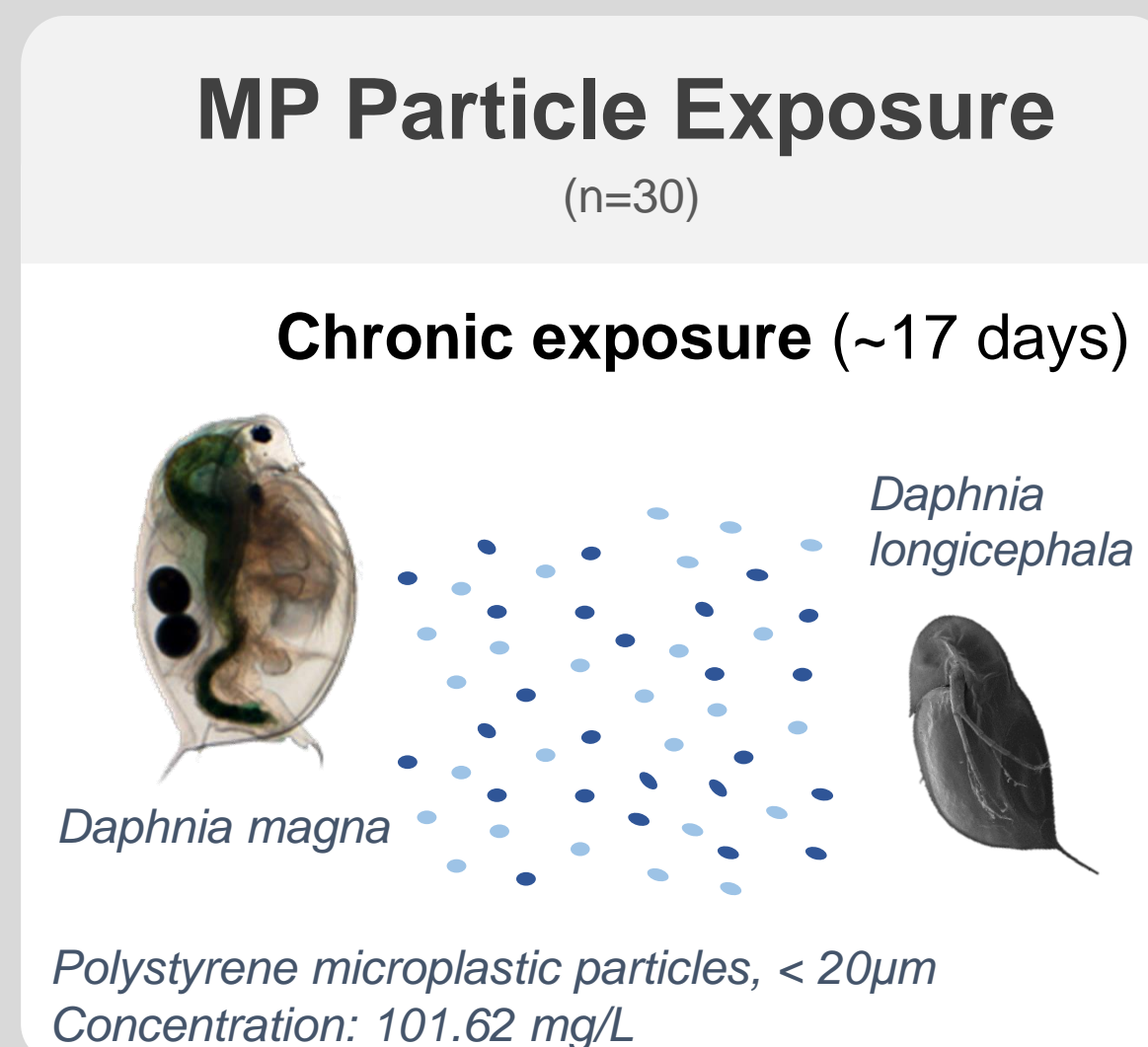
INTRODUCTION

Worldwide production of synthetic polymers and the influx of inappropriately disposed plastic litter into ecosystems has grown exponentially since the 1980ies. Especially the abundance and effects of microplastics (MP, < 5 mm) on marine and freshwater ecosystems gained attention and is discussed controversially. Many recent studies show significant effects of MP on different fresh-water taxa, while others record no such effects.

The cladoceran *Daphnia* has been studied intensively as model organism, because it inhibits a central role in ecosystems and is shown to ingest MP of different morphology and polymer type. Some studies already showed substantial negative effects on daphnids. To unravel the underlying molecular mechanisms this work combines phenotypic analysis with sophisticated proteome analysis.

STUDY DESIGN

- Effects of chronic MP exposure on two different daphnid species were studied
- Morphological and reproduction rate changes were monitored
- Shock frozen individuals were used for proteomic analysis
- Generated MS data was analyzed bioinformatically

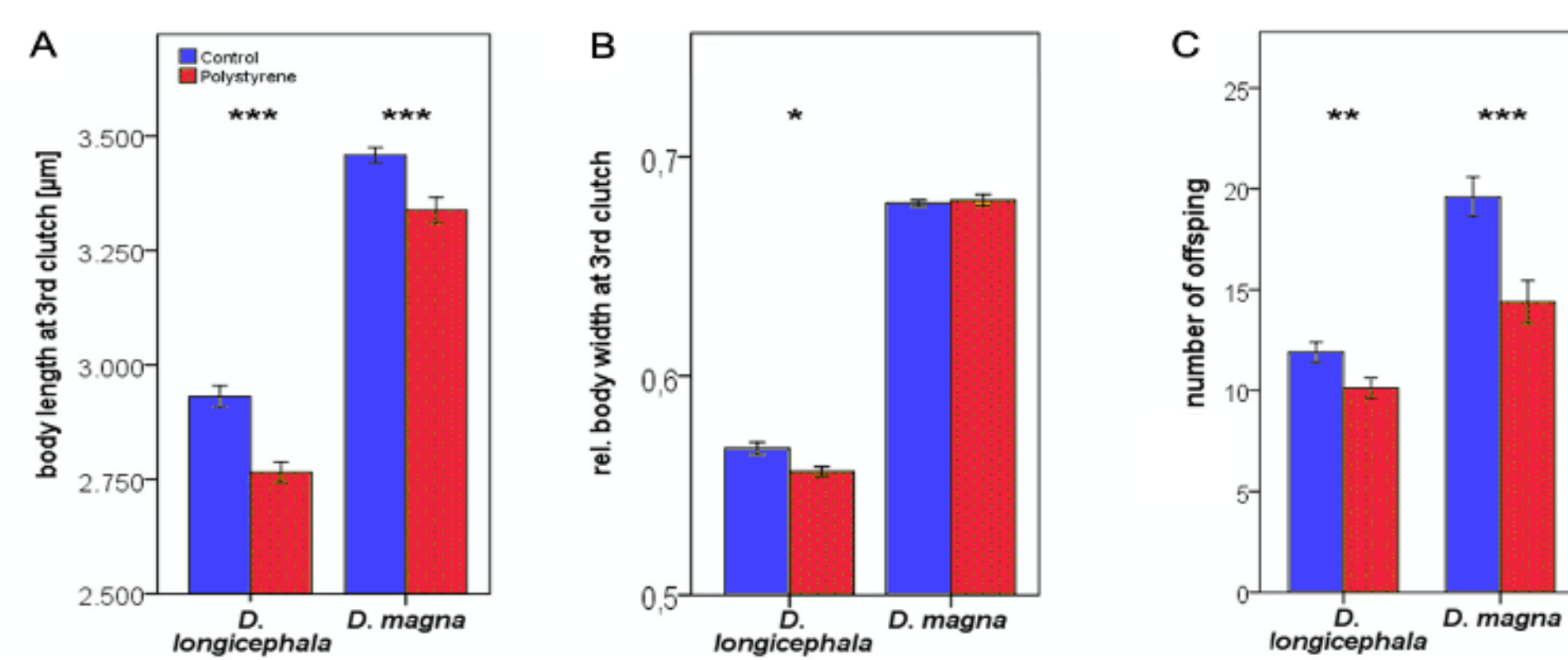


RESULTS

ORGANISMIC

Morphological/Life history Analysis (after chronic exposure)

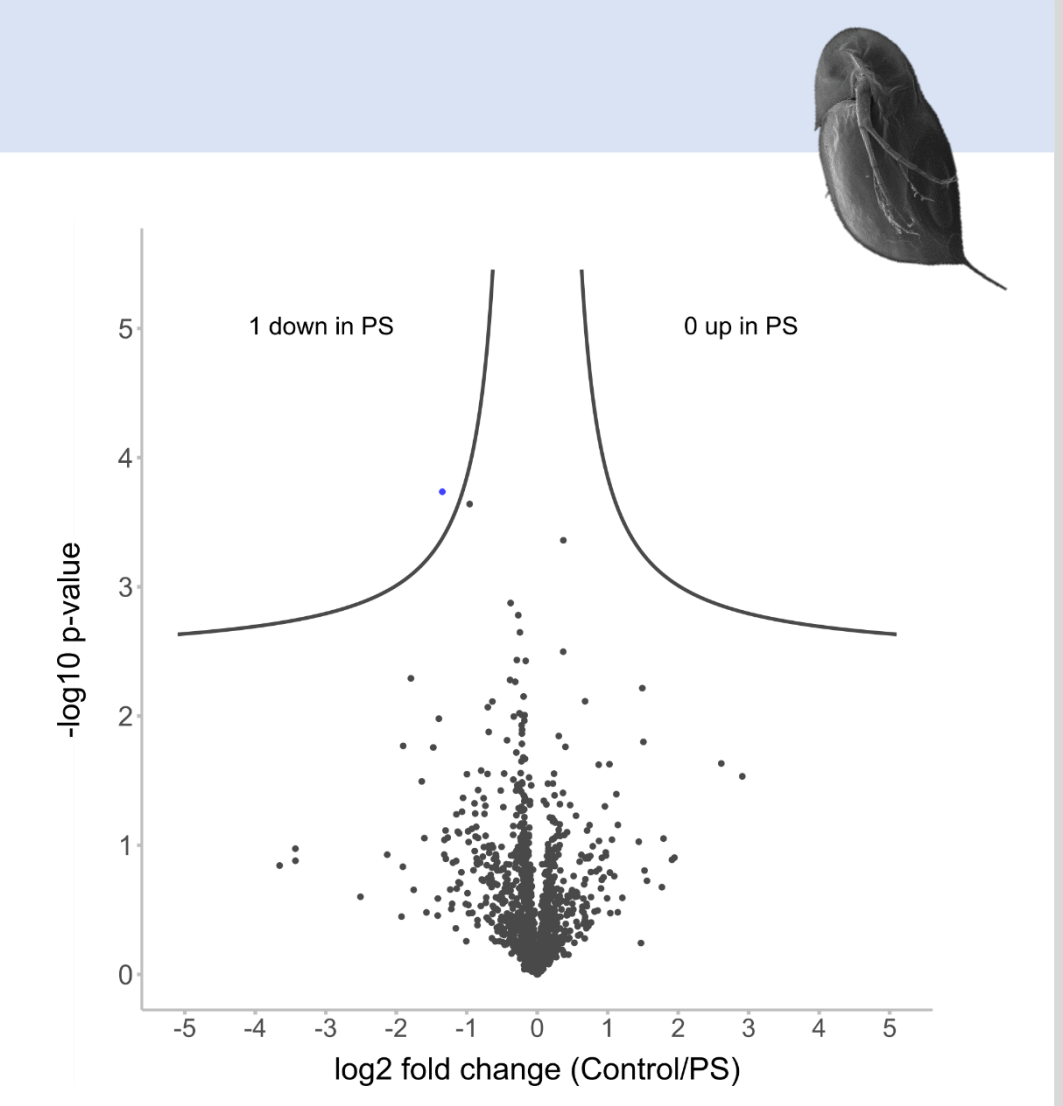
- Reduced body length of *D. magna* and *D. longicephala*
- Reduced relative body width of *D. longicephala*
- Reduction in the number of offspring



PROTEOMICS (*D. longicephala*)

Identification/Statistical Analysis

2465 protein IDs (FDR < 1%)
LC-MS/MS analysis revealed only minor differences between proteomes of PS exposed and control animals



PROTEOMICS (*D. magna*)

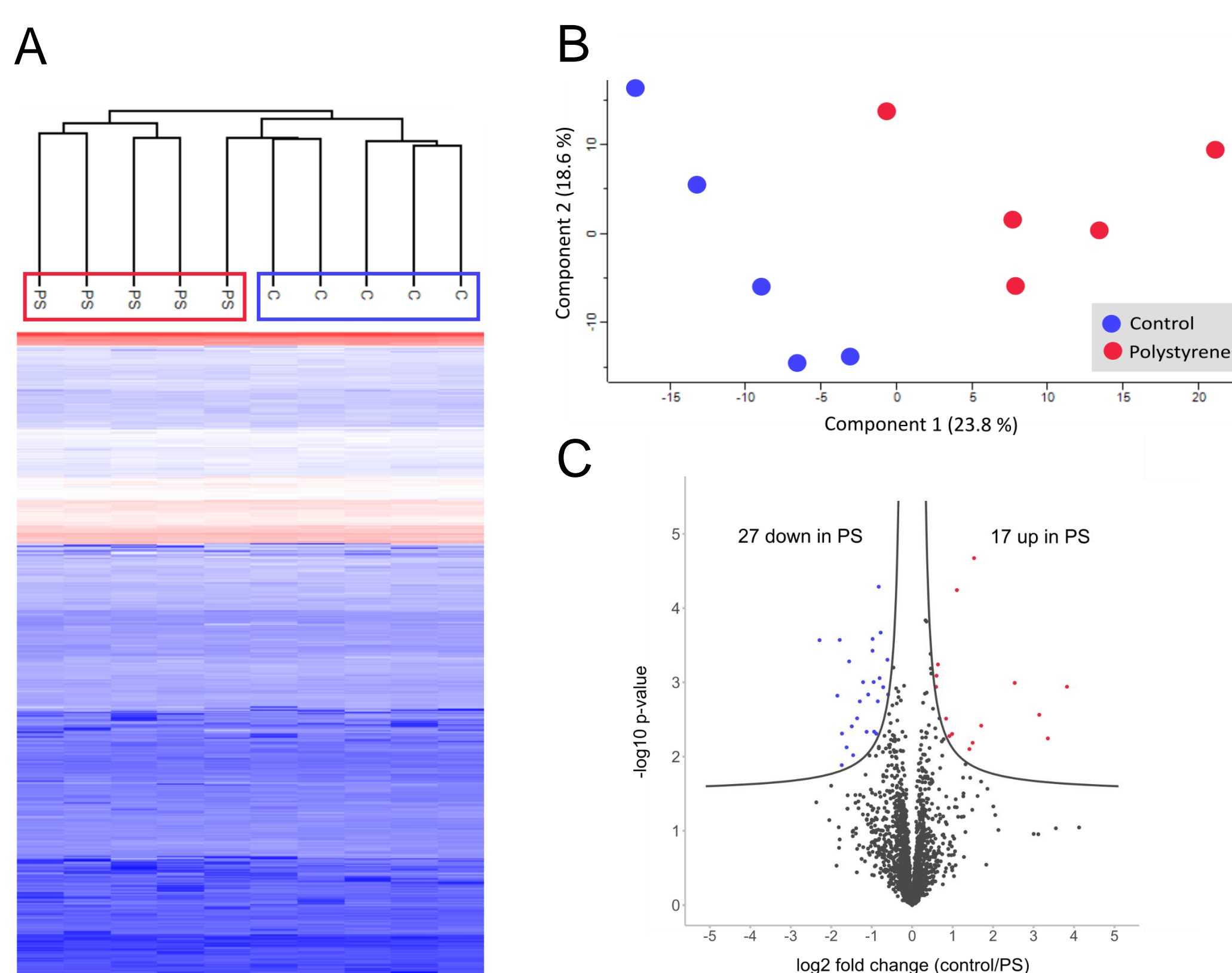
Identification/Statistical Analysis

3784 protein IDs (FDR < 1%)

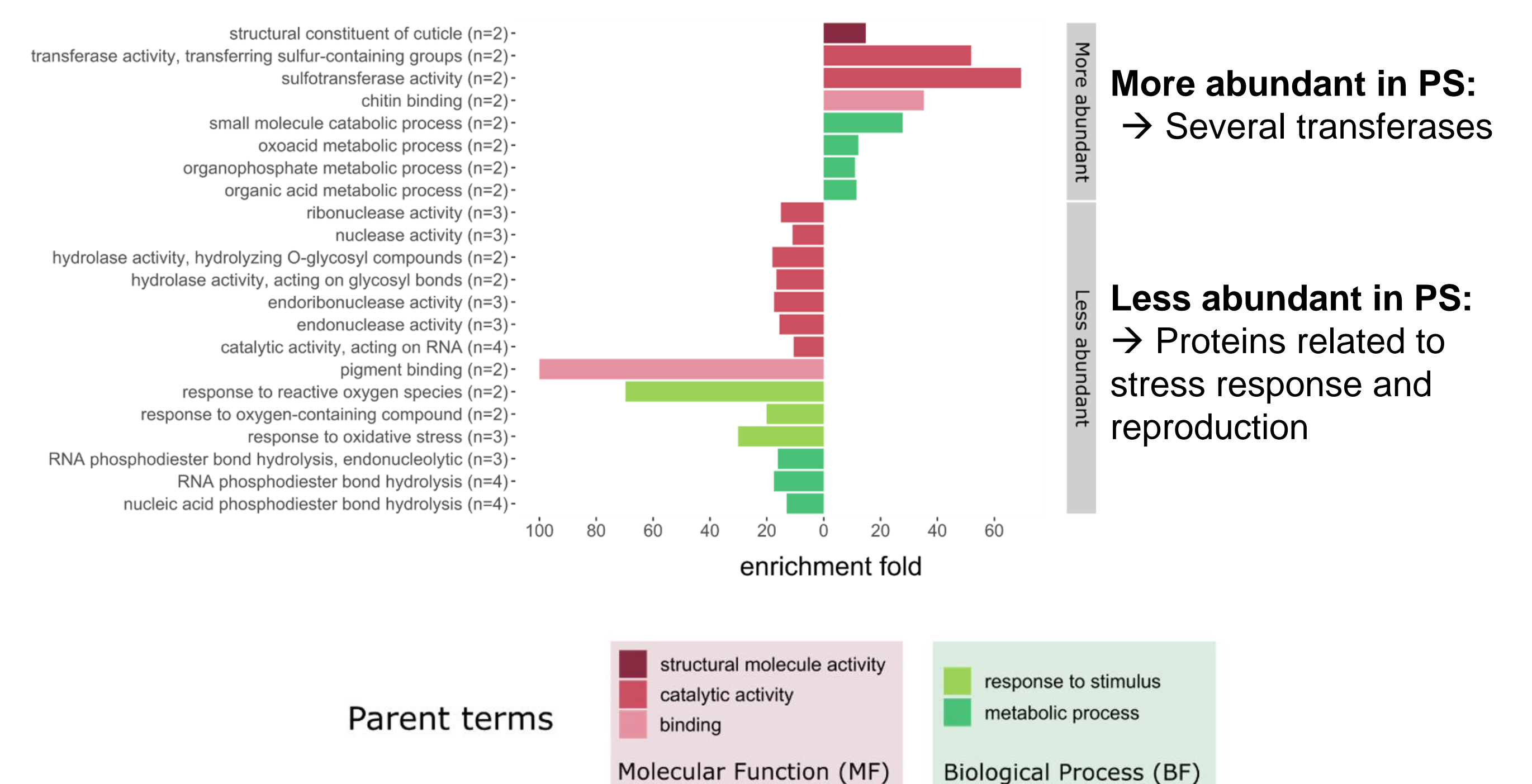
- (A) Unsupervised hierarchical clustering and
- (B) Principal Component Analysis

→ indicate separation between PS and control

(C) Volcano plot analysis revealed 44 proteins to be significantly altered in abundance (FDR < 0.05) between the PS exposed and control animals.



Overrepresentation Test (PantherDB)



The test revealed several enriched GO terms (p-value < 0.05, enrichment fold (EF) > 10)

SUMMARY & DISCUSSION

- Chronic PS exposition of *D. magna* and *D. longicephala* resulted in morphological alterations and reduced numbers of offspring
- Whereas proteome alteration in *D. longicephala* were less pronounced, MP exposure induced significant alterations in the proteomes of *D. magna*
- Several sulfotransferases crucial for cell survival were found among the upregulated proteins

- The enzyme with the strongest increase was (S)-3-amino-2-methylpropionate transaminase, which is also known to react with GABA, a prominent inhibitory neurotransmitter
- Strikingly, several downregulated proteins are related to cellular stress and reproduction
- Four digestive enzymes were decreased, indicating a reduced nutrient uptake which may explain smaller body size