

Paleoecotoxicology reveals higher tolerance of naive *Daphnia magna* genotypes to polycyclic aromatic hydrocarbons (PAH)

Florian Gigl^{1*}, Sarah Crawford², Luisa Orsini³, Henner Hollert¹

¹Department of Evolutionary Ecology and Environmental Toxicology, Goethe University Frankfurt, Max-von-Laue-Str. 13, 60438 Frankfurt am Main, Germany

²Syngenta, Guelph, Ontario, Canada

³Department of Evolutionary Systems Biology and Environmental Omics, University of Birmingham, School of Bioscience, Edgbaston, B15 2TT, Birmingham, UK

*gigl@bio.uni-frankfurt.de

Paleoecotoxicology enables the study of evolution of chemical tolerance [1]. The aim of the study is to investigate the **evolution of tolerance** to polycyclic aromatic hydrocarbons (PAH) in *Daphnia magna* in function of historical exposure to chemical stress

Resurrected populations of *D. magna* spanning a century, and including populations from semi-pristine and polluted environments were exposed to environmentally relevant concentrations (sediment) of PAH

Lake Ring: Shallow mixed lake, which was oligotrophic at the beginning of the 19th century, suffered from eutrophication from sewage inflow in the 1950-1960, suffered from increased land use from 1975 to ca. 2000 and partially recovered in modern times [2] (Fig. 2)

PAH: PAH are mainly formed by incomplete combustion or by the emergence of oil spills. Due to the low volatility, high sorption and lipophilicity of PAHs, they spread ubiquitously in the environment by binding to dust or soot in the air. Model PAH in this study was **Phenanthrene (PHE)**

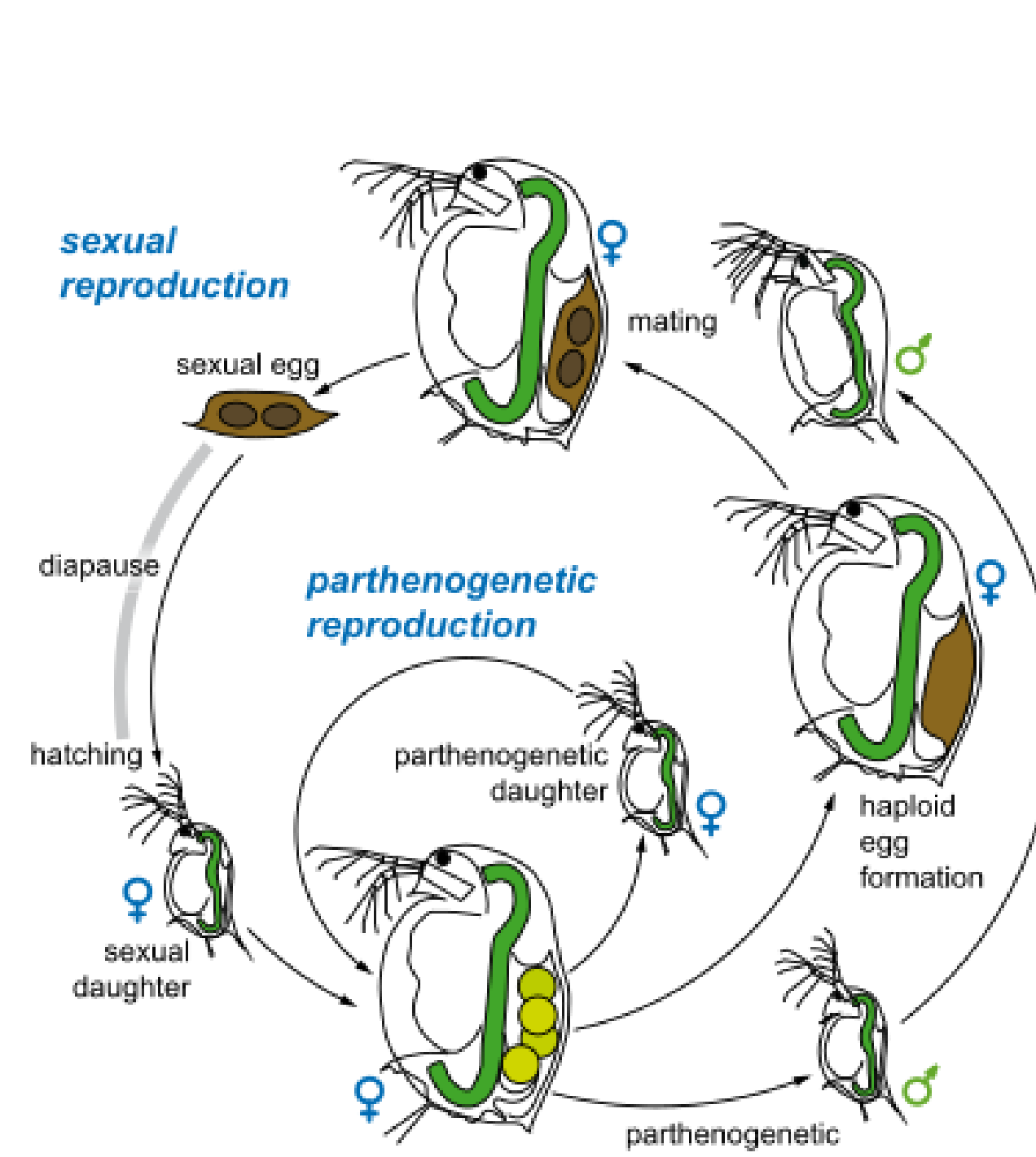
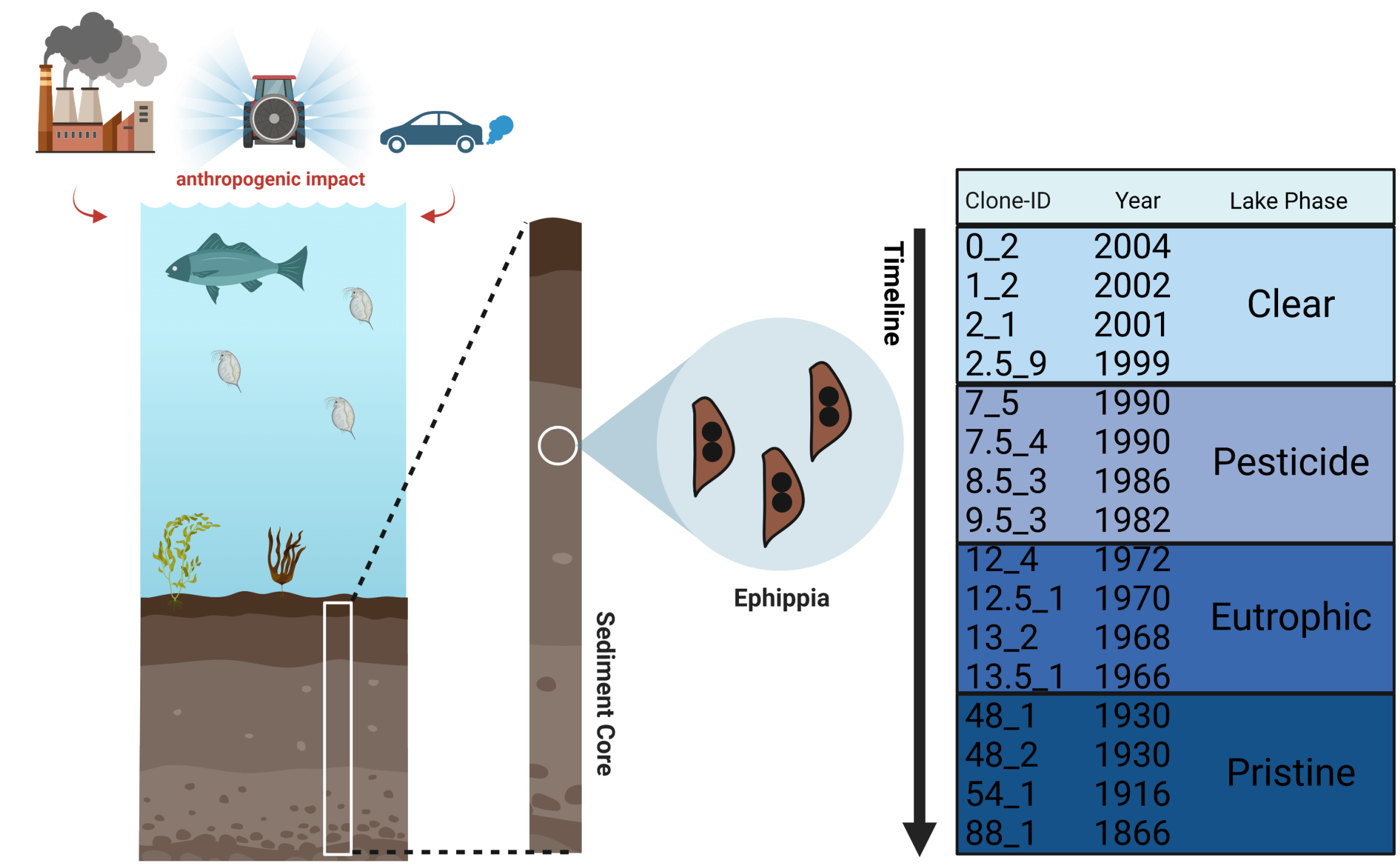
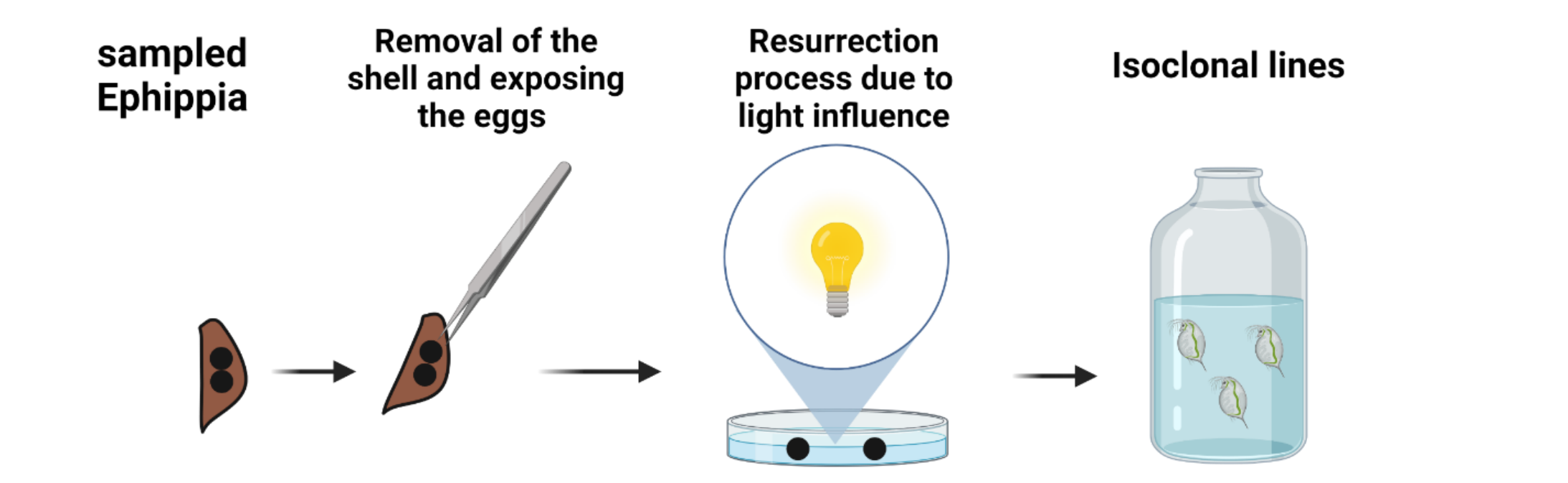


Fig. 1: Reproduction cycle of *Daphnia* [3]



Template adapted from: Dakota Holmes
Fig. 2: Sampling strategy Lake Ring (Jutland, Denmark)



Acute Daphnia Immobilisation Test:
Range finding for chronic exposure (EC₁₀)

Daphnia magna Reproduction Test:
Endpoints: Time of primiparity, time of first and second brood, total number of offspring, morphological changes, size.

Sampling for RNA sequencing and Microbiome:
10 isoclonal *Daphnia* each sampled for RNA seq and Microbiome (Sampling of exposed *Daphnia* at the same developmental point before primiparity)

RNA Seq and Microbiome:
Analysis of differential gene expression and differential splicing of mRNAs.
Study of the microbiome composition.

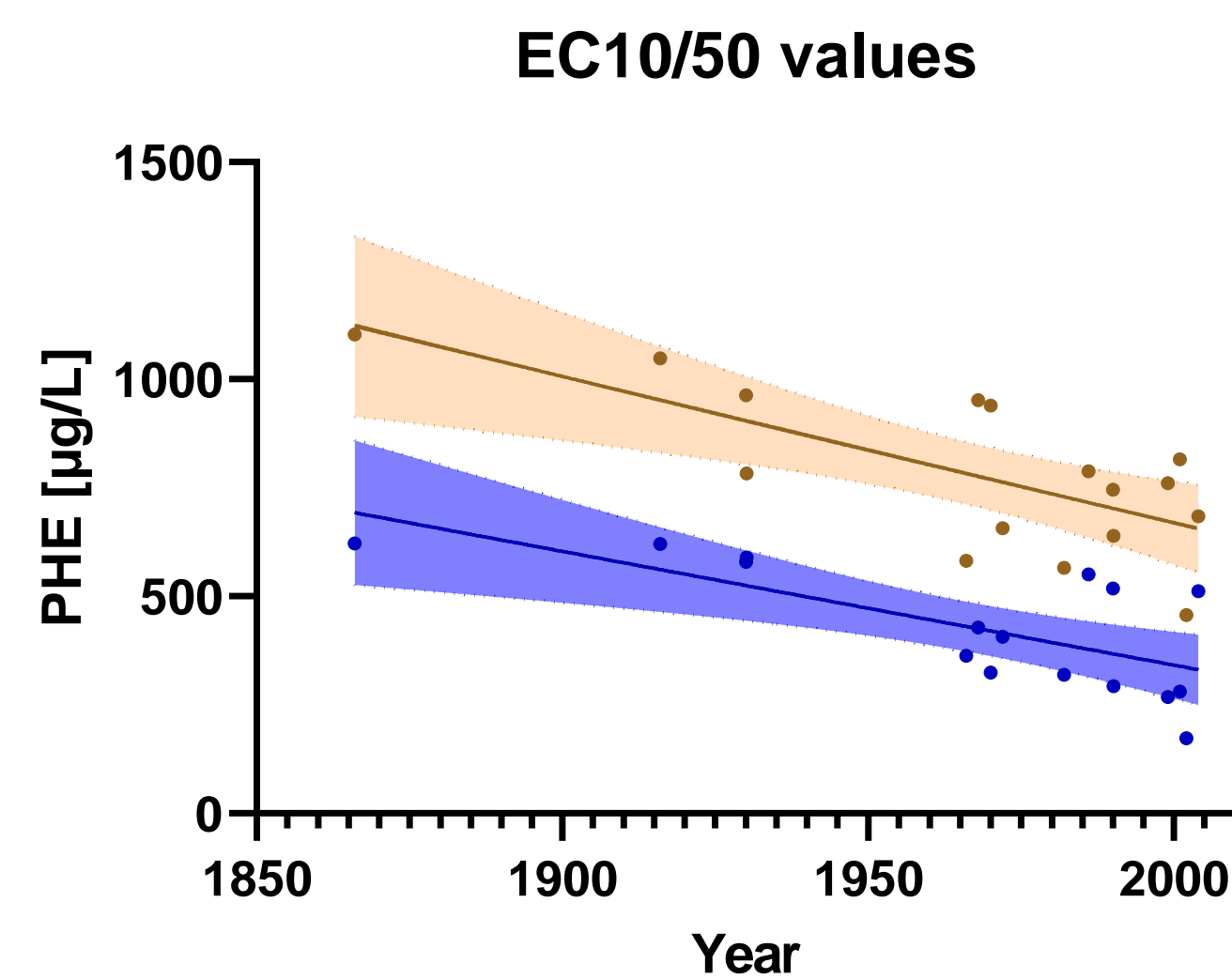


Fig. 3: EC₁₀ & EC₅₀ values of the 16 *D. magna* clones resurrected from 1866-2004 exposed for 48h to PHE (n=3)

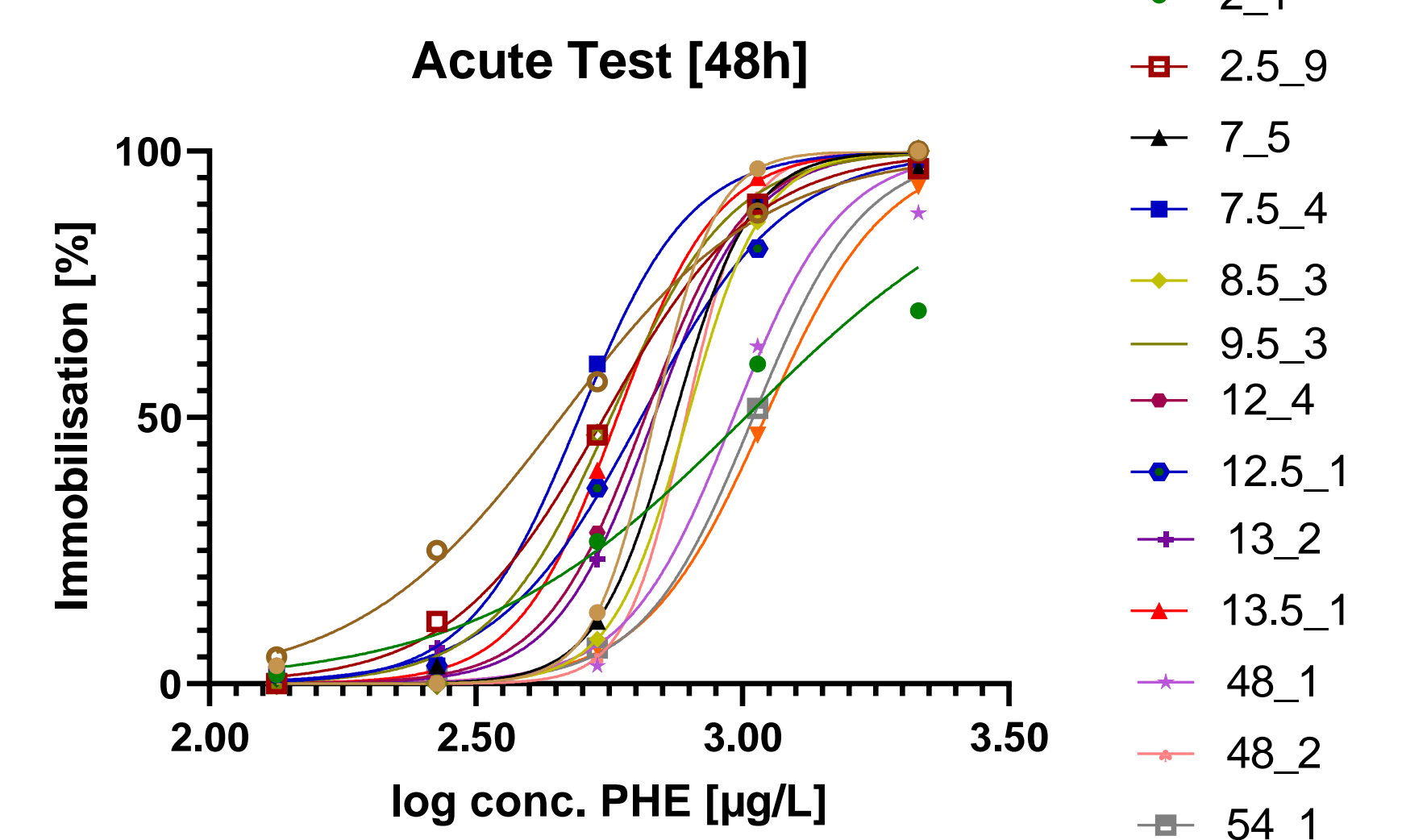


Fig. 4: Percent immobility of 16 *D. magna* clones resurrected from 1866-2004 exposed for 48 h to PHE (n=3)

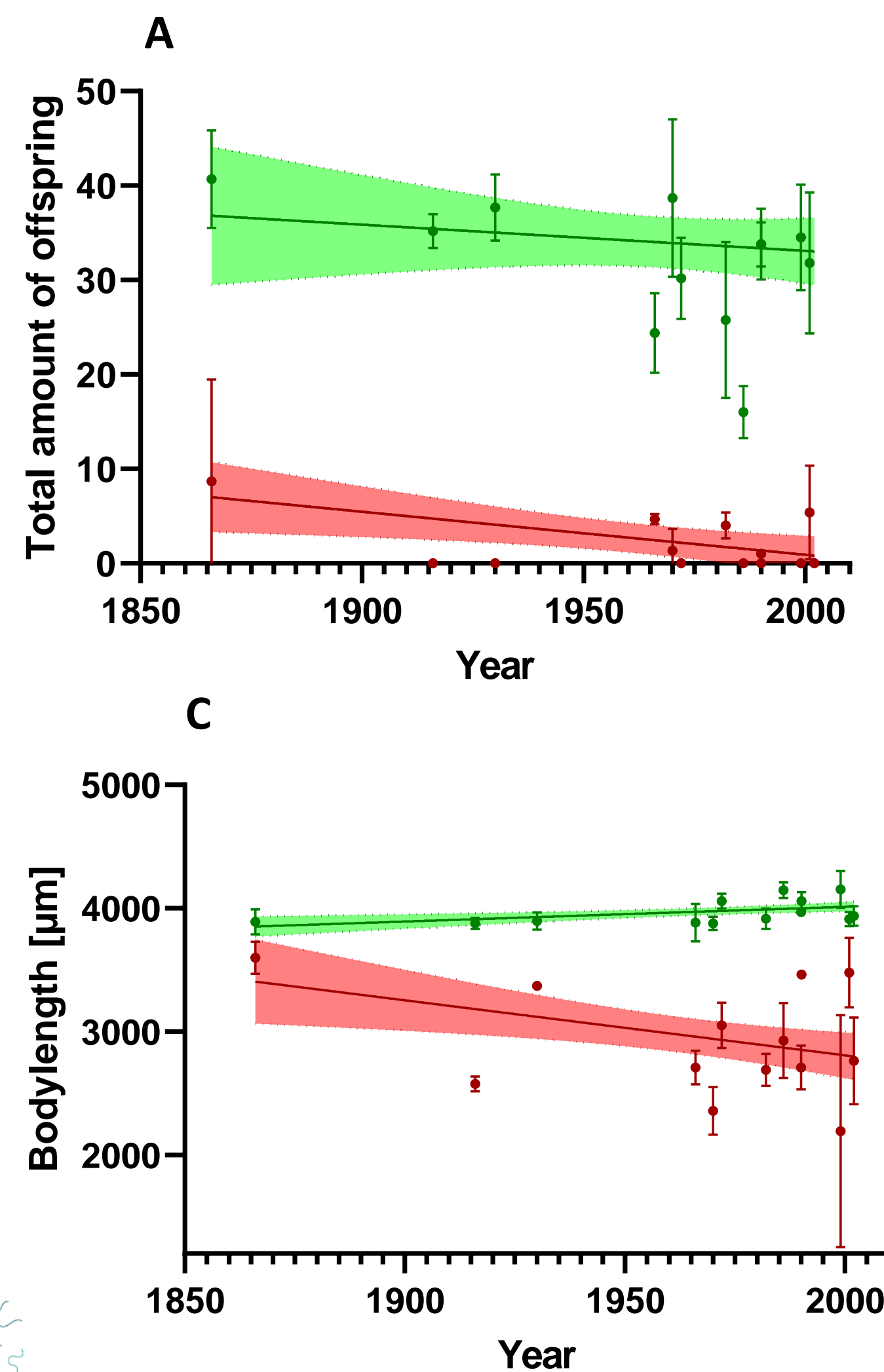


Fig. 5: Chronic effects on population level on Control and PHE exposed *Daphnia*: PHE caused reduce size at maturity, delayed maturation and lower fecundity [A] total number of offspring for 1st and 2nd brood; [B] Day of maturity; [C] length measurement of adult *Daphnia* after release of 2nd brood.

Conclusion & Next steps

Prior exposure to chemical stress reduces tolerance to novel chemical stress (e.g. PAH).

Effect-based gene expression patterns will be investigated by performing RNA-sequencing. It will also be investigated whether phenanthrene alters the functionality of the gut microbiota. A change in algae uptake by the exposed daphnia was already seen when the reproduction test was performed.

Further studies will be investigated with resurrected *Daphnia* from the Stadtsee (Bad Waldsee, Germany) (DFG funded Bad Waldsee project).



Fig. 6: Control *Daphnia* (left) and PHE exposed *Daphnia* (right) of clone 2_1 (top) and 7.5_4 (bottom)

Exposed daphnia from clear and pesticide phases show reproductive differences (delay in development of offspring in pesticide phase) in addition to size differences.