Omics tools for assessing effects of environmental stressors on the northern Atlantic key species *Calanus finmarchicus*

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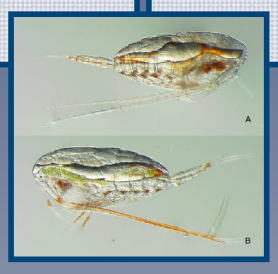
Calanus finmarchicus

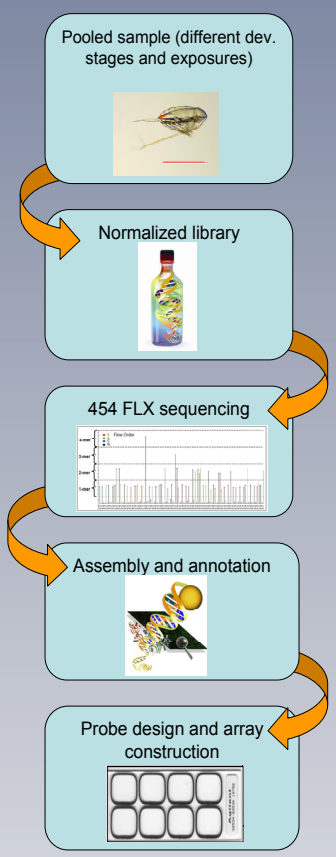
- Marine ecological key species
- 2-3 mm pelagic copepod (zooplankton, microcrustacean)
- 300 mill tons annual production in the North Atlantic and Barents Seas
- Short generation time (~80 days in culture)
- Up to 50% of dry weight is lipids → Very important food resource for commercial fish
- Important transfer route of environmental contaminants in the marine food web

Main objectives of the project:

- Launch a large-scale EST sequencing program
- Develop a custom-made oligonucleotide microarray → transcriptomics
- Develop methods for metabolic profiling and fingerprinting → metabonomics
- Use bioinformatics tools in order to analyze and correlate omics output for controlled exposure experiments



TRANSCRIPTOMICS



Pooled sample

Copepods exposed to heavy metals (mercury and copper), oil, heat, CO_2, H_2O_2 and sampled at different developmental stages.

Library construction and sequencing

We already have established three SSH libraries from copepods exposed to a mixture of stressors. Here a normalized library will be constructed by EcoArray Inc..

454 FLX sequencing

The normalized library will be sequenced by 454 FLX sequencing by EcoArray Inc./University of Florida.

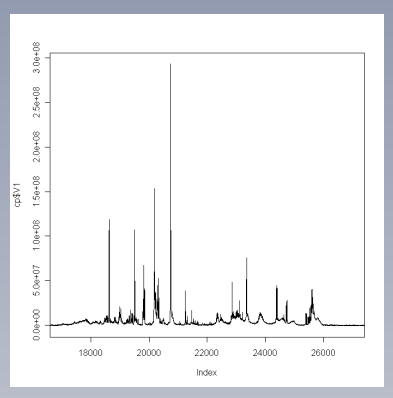
Sequence annotation and array construction

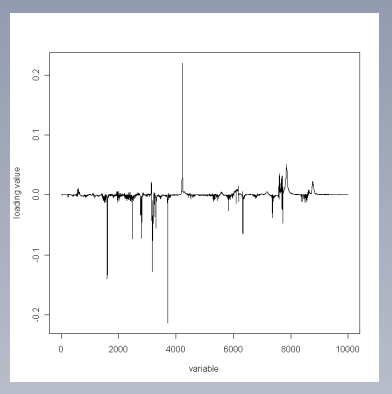
Sequences will be assembled and annotated (Blast2GO) before probes are designed and oligoarray produced (Agilent).

METABOLOMICS

High Resolution Magic Angle Spinning NMR

Whole copepods were analyzed (n=5) with HR MAS NMR, and of the resulting spectrum 60 metabolites were resolved and characterized.



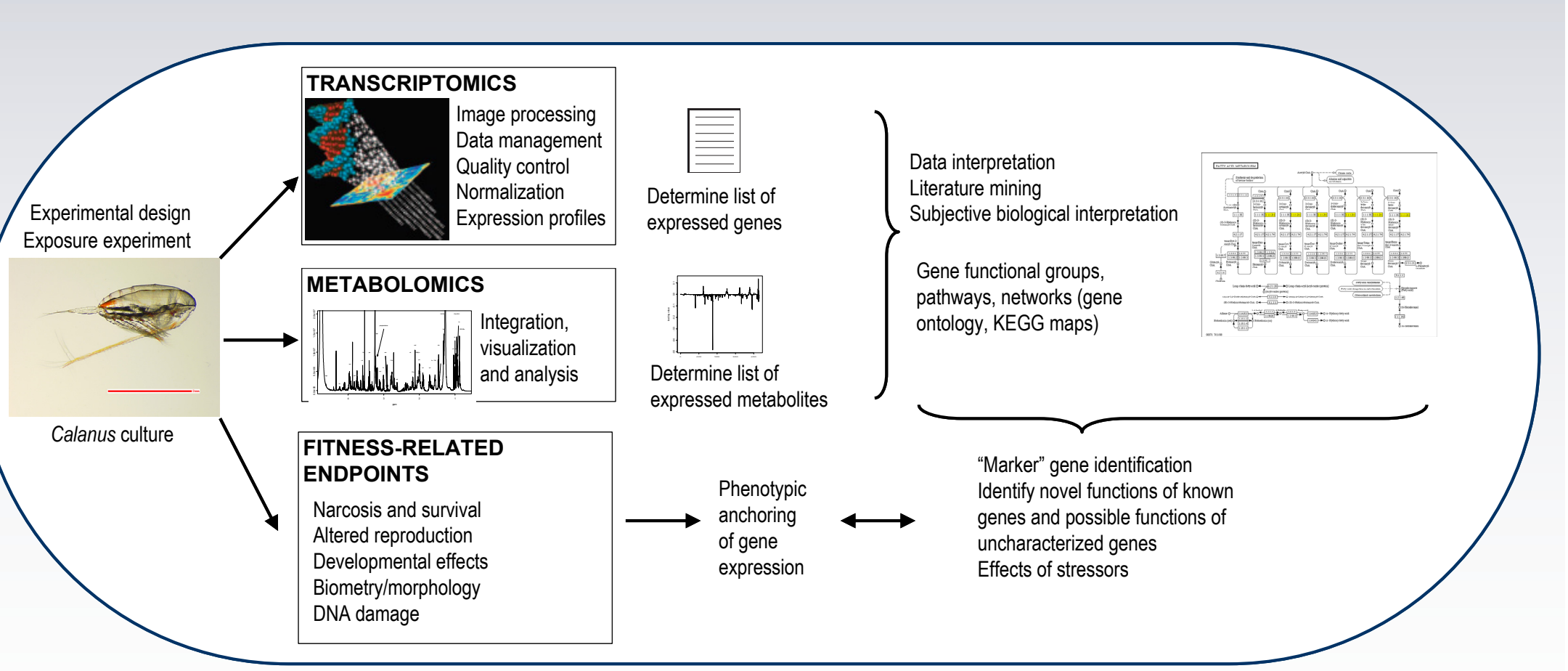


GC-MS and LC-MS

Chromatographic methods will also be used to further study lipophilic endogenous metabolites in particular.

Statistics

Using PLS/PCA we visualize differences in metabolic profiles between different experimental groups.



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