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PROMiSE

Protist metabolome screening

”Unlocking the biotechnological potential of marine eukaryotic protists by comprehensive Omics”

Tilmann Harder (Alfred Wegener Institute, Germany)

Partners:
Helmholtz Zentrum München
University of British Columbia
Institut de Ciences del MaR
University of Oslo

ERA-MBT 3rd Transnational Joint Call: Metagenomics

21st November 2017

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THE CONSORTIUM

PRINCIPAL INVESTIGATOR	INSTITUTION	COUNTRY
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Phillipe Schmitt-Kopplin	Helmholtz Centre Munich	DE
Ramon Massana	Inst. de Ciences del Mar	ES
Patrick Keeling	University of British Columbia	CA
Bente Edvardsen	University of Oslo	NO

Project period: 02/2018 to 01/2021

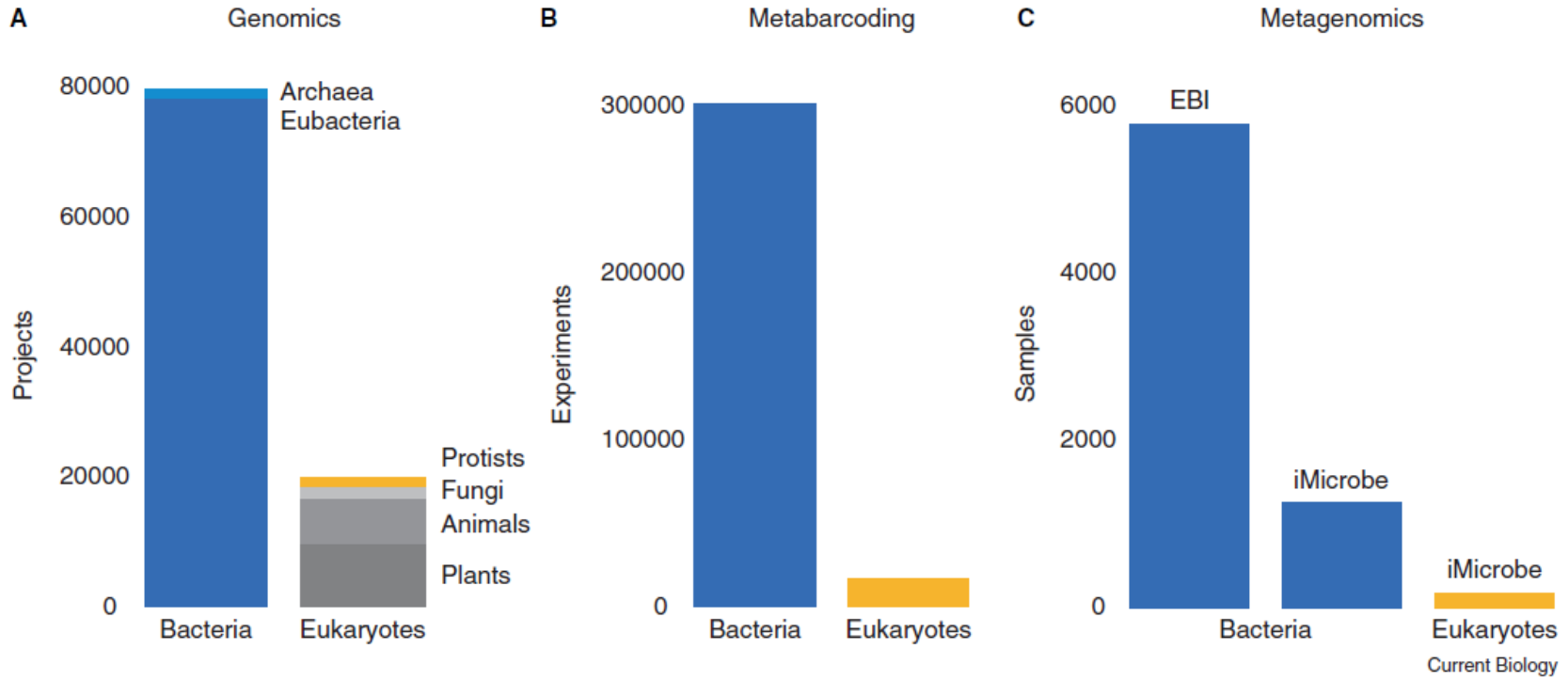
Rationale for PROMiSE

Marine protists are not just big bacteria

Given the unique adaptations of protists through symbiosis, endosymbiosis and organelle acquisition, their ecological functionalities present a largely untapped source to discover novel metabolic pathways and bioactivities.

Bacteria vs Eukaryotes

Keeling, P. J. and del Campo, J. 2017. Curr. Biol., 27, R541-R549.



Protists represent an **enormous reservoir of untapped metabolic and biotechnological potential**, just as bacteria did two decades ago.

Unlocking the reservoir (poster)

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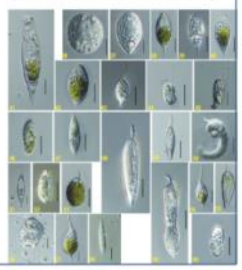
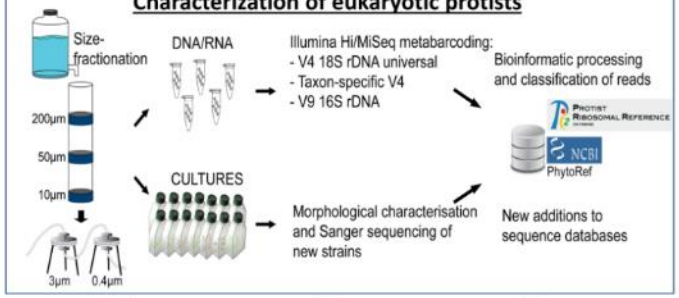
Experimental workflow

Sampling of eukaryotic plankton

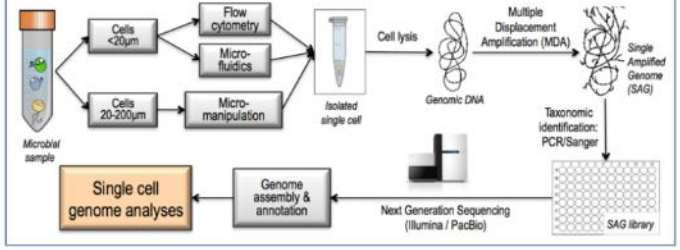
Eukaryotic plankton



Characterization of eukaryotic protists



Single cell -omics



Metabolomics platform & structural elucidation

12 Tesla ICR-FT/MS

Key features:
- **Mass resolution** > 500.000 at m/z 400
- **Mass accuracy** < 0.2 ppm
- Unambiguous identification of empirical molecular formula
- high order of magnitude (dynamic range)
- Low sample consumption (µL)
- high-throughput metabolomics analyses (10 minutes of acquisition)

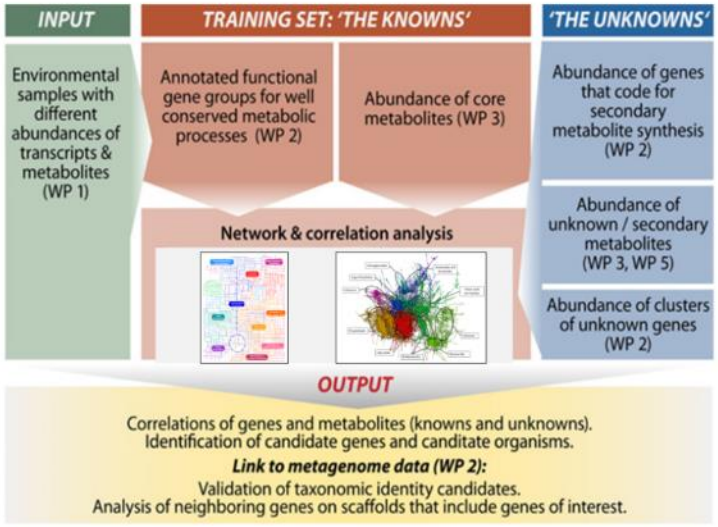
First UPLC-qTOF/MS

Key features:
- **Mass resolution** > 40.000 at m/z 400
- **Mass accuracy** < 5 ppm
- **Chromatographic separation** by using different **column chemistries**
- Separation of isomeric and isobaric metabolites
- **MS/MS** for identification (fast and automatic)

800 MHz Cryo-NMR

Key features:
- **Qualitative & quantitative data** in one analysis
- **Non-destructive**
- **Structural** information
- Reproducible
- Abundant metabolites
- Low sensitivity

Meta-Omic data integration



Why this partnership?

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ALFRED-WEGENER-INSTITUT
HELMHOLTZ-ZENTRUM FÜR POLAR- UND MEERESFORSCHUNG

Marine Chemical Ecology
Structure Elucidation (MS & NMR)
Plankton molecular ecology
Ecophysiology
Bioinformatics

UNIVERSITY OF OSLO

Aquatic biology
Plankton cultivation
Metabarcoding
Medicinal Chemistry
Drug Discovery

HelmholtzZentrum münchen
German Research Center for Environmental Health

Meta-metabolomics
ICR-MS
High Content Screening

ICM
Institut de Ciències del Mar

Plankton Ecology
Single cell genomics
Bioinformatics

THE UNIVERSITY OF BRITISH COLUMBIA

Plankton Ecology
Single cell genomics & transcriptomics

Outlook

With its focus on some of the least-investigated corners of biology, PROMiSE bears high innovative potential to correlate unique chemically-mediated behaviors and capacities of protists, e.g.

- Catabolic and anabolic enzymes
- Allomones (predation, bacterial colonization, competition)
- Quorum sensing & quenching signals
- Kairomones (symbiosis)
- Host recognition and infection
- Toxins
- Pheromones…

with novel pathways and bioactive compounds and explore and exploit their effect in medically and biotechnologically inspired test settings.