"Two-stage biodegradation of contaminating wastes linked to bioenergy generation using genomic approaches"



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NORWEGIAN INSTITUTE OF BIOECONOMY RESEARCH

## SCIENTIFIC-SOCIETAL CONTEXT

- Major issues to be addressed:
  - > protecting the fresh-water resources;
  - organic wastes management;
  - rising energy demands;
  - energy independence.



• Biohydrogen production:

- versatile;
- environmentally friendly, renewable energy carrier;
- highest energy potential (142 kJ/g);
- ➢ biohydrogen production methods → carbon neutral or even negative.



# General objectives, strategy

## Hybrid system using fermentative and photosynthetic microorganisms

• Stage I. Dark fermentation (strictly or facultative anaerobes):

 $C_6H_{12}O_6 + 2H_2O \rightarrow 2CH_3COOH + 2CO_2 + 4H_2$ 

• Stage II. Photo-fermentation (photosynthetic bacteria and algae):

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2CH_3COOH + 4H_2O \rightarrow 8H_2 + 4CO_2
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lightenergy

Goal: to engineer the Anaerobic Degradation (AD) of wastes for selective biohydrogen generation





## APPROACH

- 1. Design of synthetic wastewater types (sterile)
- 2. Enrichment of the active inoculum (active sludge)
  - Heat treatment
  - Acid treatment
  - Ultrasonication
- 3. Anaerobic degradation experiments (in controlled small scale batch bioreactors)
  - Identification of influencing factors, interactions among them
- 4. Gas and Sludge analytics and metagenomics
- 5. Correlations, conclusions, process optimization with real wastewater



Development of a design of experiments (DOE) approach

rank the different influencing factors (IF) according to their relative importance;
 identify the directions of influence;

analysis of the effect of the interactions occurring among the investigated variables;
 process optimization.

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#### Experiment example: 3 IF tested with 3 values each

| <b>Table:</b> Coded values of the variables used in the Full and Central-Composite Factorial Experimental Design. |                                  |                        |     |      |  |  |
|---|----------------------------------|------------------------|-----|------|--|--|
| Coded symbol  | Variables —                      | Values of coded levels |     |      |  |  |
|   |                                  | (-1)                   | (0) | (+1) |  |  |
| X <sub>1</sub>  | Operating temperature (°C)       | 25                     | 31  | 37   |  |  |
| X <sub>2</sub>  | Initial value of fermentation pH | 4.8                    | 5.6 | 6.5  |  |  |
| X <sub>3</sub>  | Glucose addition (g/L)           | 5                      | 10  | 15   |  |  |

#### Experiment matrices for 2 statistical models (with hydrogen yield results)

**Table:** Full Factorial (run no. 1-8) and Central-Composite (run no. 9-16) multifactorial experimental design matrix of the three investigated variables, with the total measured  $H_2$  production for each of the experimental runs.

| Run No. |                | Variables      | ;              | Response                                     |  |
|---------|----------------|----------------|----------------|--|--|
|         | X <sub>1</sub> | X <sub>2</sub> | X <sub>3</sub> | Total hydrogen production mean<br>(ml/L/day) |  |
| 1       | -1             | -1             | -1             | 8,66   |  |
| 2       | -1             | -1             | 1              | 9,62   |  |
| 3       | -1             | 1              | -1             | 22,34  |  |
| 4       | -1             | 1              | 1              | 25,23  |  |
| 5       | 1              | -1             | -1             | 8,28   |  |
| 6       | 1              | -1             | 1              | 8,35   |  |
| 7       | 1              | 1              | -1             | 14,67  |  |
| 8       | 1              | 1              | 1              | 11,92  |  |
| 9       | -1.28          | 0              | 0              | 17,67  |  |
| 10      | 1.28           | 0              | 0              | 10,43  |  |
| 11      | 0              | -1.28          | 0              | 2,97   |  |
| 12      | 0              | 1.28           | 0              | 27,18  |  |
| 13      | 0              | 0              | -1.28          | 14,95  |  |
| 14      | 0              | 0              | 1.28           | 25,92 NOrWau                                 |  |
| 15      | 0              | 0              | 0              | 21,08 grants 🍌 🗌                             |  |



Biohydrogen yield is strongly correlated with the relative abundance of *Clostridia* 

### Identification of the optimum area for each pair of influencing factor





#### Process optimization for real wastewater

Beer Factory



Wastewater Treatment Plant



Methane producing pilot scale bioreactor



Polluted river

Substrate-dependent pretreatment approach for the possible highest AD biohydrogen yield

## WAYS for ALGAL H<sub>2</sub> GENERATION



- Direct biophotolysis of water (green algae, cyanobacteria)
- **Photodecomposition of organic compounds** (indirect biophotolysis, green algae, photosynthetic bacteria)
- Dark fermentative hydrogen production (algae, bacteria, complex microbial comm.)



#### **BOTTLENECKS OF PRESENT ALGAE TECHNIQUES**

Sulfur deprivation in light and dark fermentation

Two-phase systems (biomass and hydrogen production are separated)
Sulfur deprivation is difficult (media exchange) and lethal for algae cells
Low hydrogen yield



### ALTERNATIVE SOLUTION ALGAL-BACTERIAL ASSOCIATIONS under illumination

- Efficient bacterial respiration consumes the hydrogenase-inhibiting oxygen
- Bacterial partners enhance algal growth
- Active photosynthesis and biomass generation maintained throughout hydrogen production

| Applied Strains                 | Relevant genotype or phenotype |  |  |
|---------------------------------|--------------------------------|--|--|
| Green Algae                     |                                |  |  |
| Chlamydomonas reinhardtii cc124 | Wild type                      |  |  |
| Chlorella sp. MACC 360          | Wild type                      |  |  |
| Chlorella sp. MACC 411          | Wild type                      |  |  |
| Chlamydomonas sp. MACC 530      | Wild type                      |  |  |
| Chlamydomonas sp. MACC 549      | Wild type                      |  |  |
| Chlamydomonas sp. MACC 772      | Wild type                      |  |  |
| Chlamydomonas sp. MACC 775      | Wild type                      |  |  |
| Chlorella sorokiniana           | Own isolate                    |  |  |
| Micractinium sp.                | Own isolate                    |  |  |
| Monoraphidium neglectum         | Own isolate                    |  |  |
|                                 |                                |  |  |
| Applied bacterial partners      |                                |  |  |
| Escherichia coli JW5433         | BW25113, $\Delta hypF$ ::kan   |  |  |
| Enterobacter sp.                | Own isolate                    |  |  |





#### Molecular investigations of the algal-bacterial interaction in wastewater:

- miRNA Seq of Ch. reinhardtii under different conditions
- De novo genome sequencing of 10 selected strains, draft genomes assembled
- RNA-Seq of the 10 investigated algae strains under 4 conditions each
- key genes identified in algal hydrogen production in wastewater (PFR and 4 genes encoding hyptothetical proteins)





#### Overview of the technology



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