

# Valorization of microalgae by-products in biorefinery

Guillaume Delfau--Bonnet (PhD student)  
Florent Allais (Pr), Anne-Lise Hantson (Pr)

Unité de Recherche et Développement Agro Biotechnologies Industrielles, AgroParisTech, France  
Génie des Procédés Chimiques et Biochimiques, Université de Mons, Belgium  
[guillaume.delfau-bonnet@agroparistech.fr](mailto:guillaume.delfau-bonnet@agroparistech.fr) / [guillaume.delfau-bonnet@umons.ac.be](mailto:guillaume.delfau-bonnet@umons.ac.be)



# I. Biorefinery:

## A. What is it?

- **OECD (2018)** : “The biorefinery also fits the **circular economy** concept, particularly ‘bio-waste’ biorefineries that **use wastes or residues as the feedstocks**. The nature of this fit may be subtle however. Using such materials is clearly not classical recycling, reuse or remanufacturing as biorefining is **making value-added ‘virgin’ materials from waste sources**. This value creation distinguishes waste biorefining from standard waste management practices, and thus placing it within the waste management hierarchy is difficult. It highlights a need for re-defining such materials as, perhaps, ‘secondary raw materials’ to avoid a clash with waste management regulation.”
- **The International Energy Agency (2014)** (International Energy Agency Bioenergy Task 42 Biorefinery, 2012) described a biorefinery as “the **sustainable processing of biomass** into a spectrum of **marketable products** (food, feed, materials, chemicals) and **energy** (fuels, power, heat)”.

# I. Biorefinery:

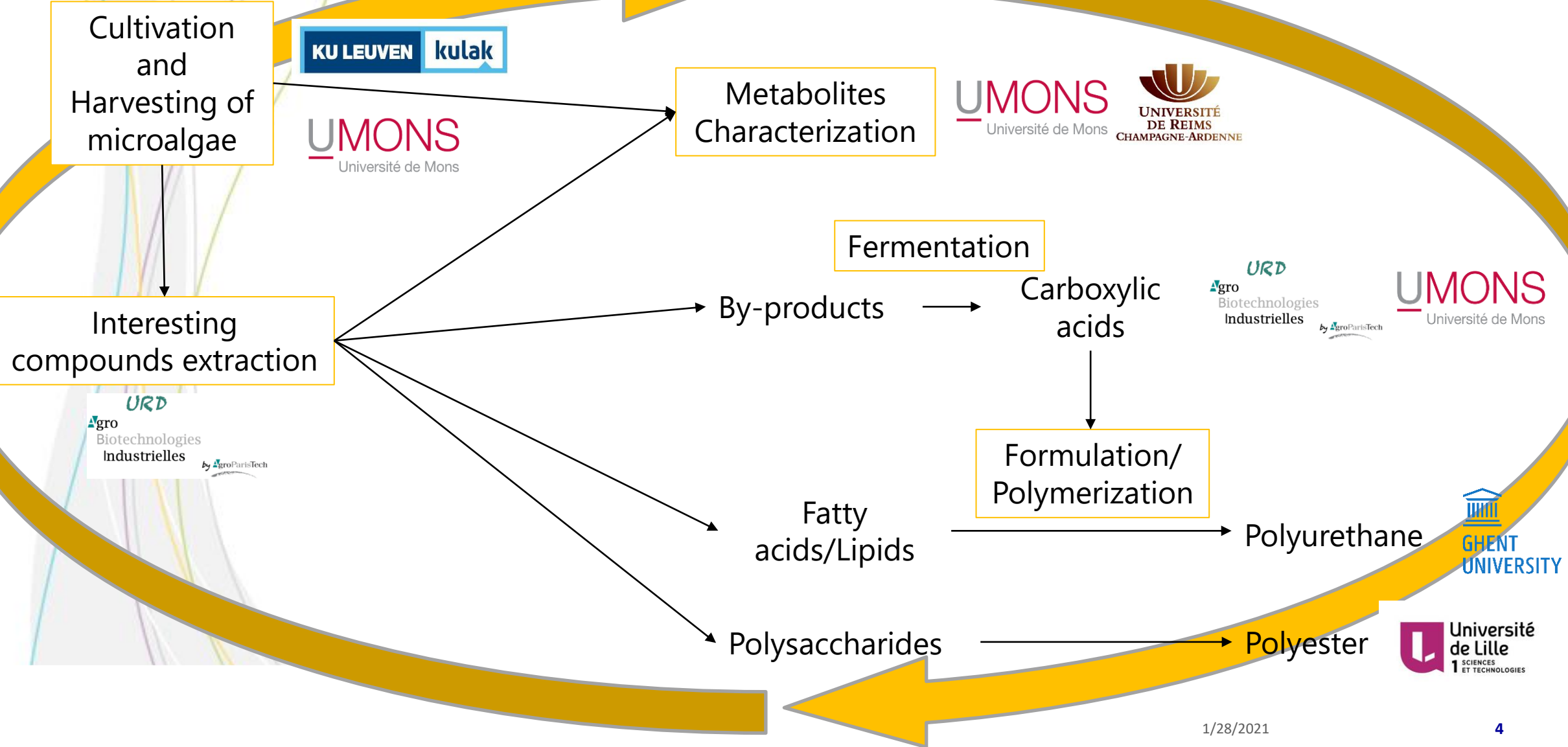
## B. Classification

- 1<sup>st</sup> Generation: Use of edible parts of crops
- 2<sup>nd</sup> Generation: Use of residues, non-edible crops and agroindustrial by-products
- 3<sup>rd</sup> Generation: Use of Algae



# I. Biorefinery:

## C. Backgrounds



# I. Biorefinery:

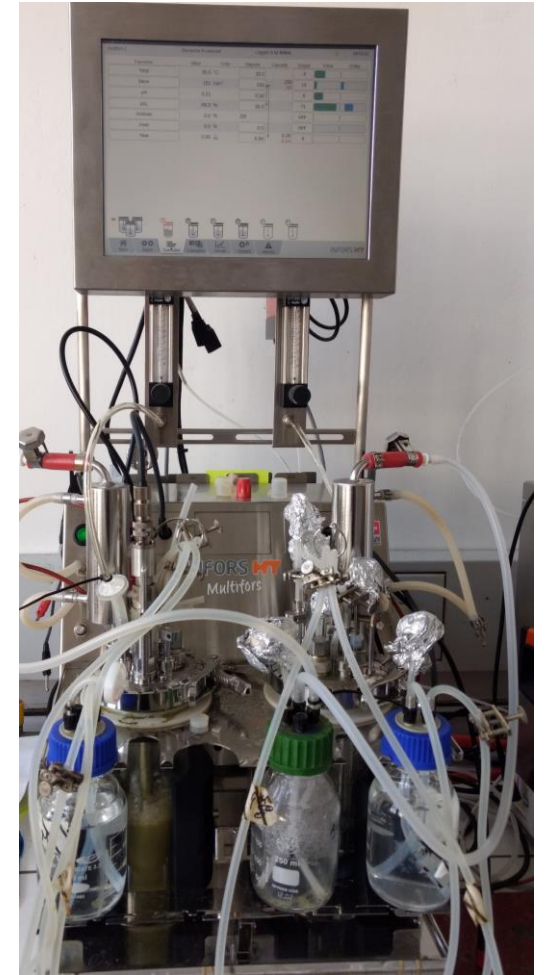
## D. Valorization of microalgae by-products

- Feed or food: source of proteins (Spiegel et al, 2013)
- Anaerobic digestion: biomethane (Uggetti et al, 2014)
- Fermentation:
  - Bioethanol production (Velazquez-Lucio et al, 2018; Lee et al, 2011; Phwan et al, 2018; Mirsiaghi et al, 2015)
  - 2-pyrone 4,6-dicarboxylic acid (Htet et al, 2018)
  - Lipids by oleaginous yeasts (Younes et al, 2020)

## II. Fermentation of lipid-extracted *C. vulgaris* residue

### A. Culture conditions

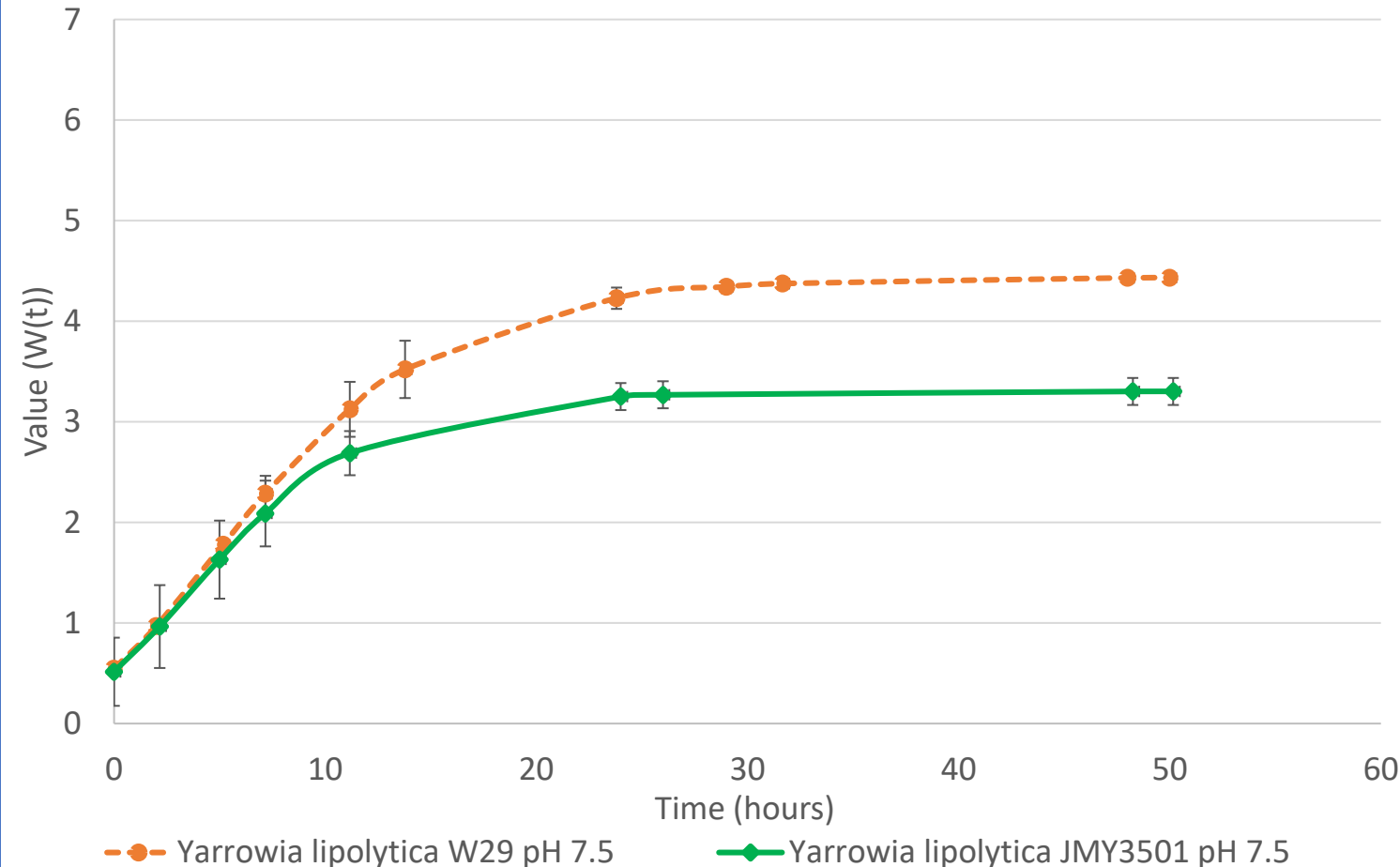
- Substrate: 30 g.L<sup>-1</sup> *C. vulgaris* residue
- Bioreactor: 300 mL operating volume
- Strains: *Y. lipolytica* W29 (Wild-type) and JMY3501 (GMO)
- pH: 7.5 (H<sub>2</sub>SO<sub>4</sub> 2M and KOH 4M)
- Dissolved oxygen: 30% saturation level



## II. Fermentation of lipid-extracted *C. vulgaris* residue

### B. Growth of *Y. lipolytica*

Growth curves of *Y. lipolytica* W29 and JMY3501 at pH 7.5 in *C. vulgaris* residue (30 g.L<sup>-1</sup>) obtained with Gompertz model



Strains	Specific growth rate (h <sup>-1</sup> )	Generation time (h <sup>-1</sup> )	Stationary phase (h)
<i>Y. lipolytica</i> W29	0.26 ± 0.01	2.64 ± 0.09	25
<i>Y. lipolytica</i> JMY3501	0.26 ± 0.03	2.69 ± 0.30	15

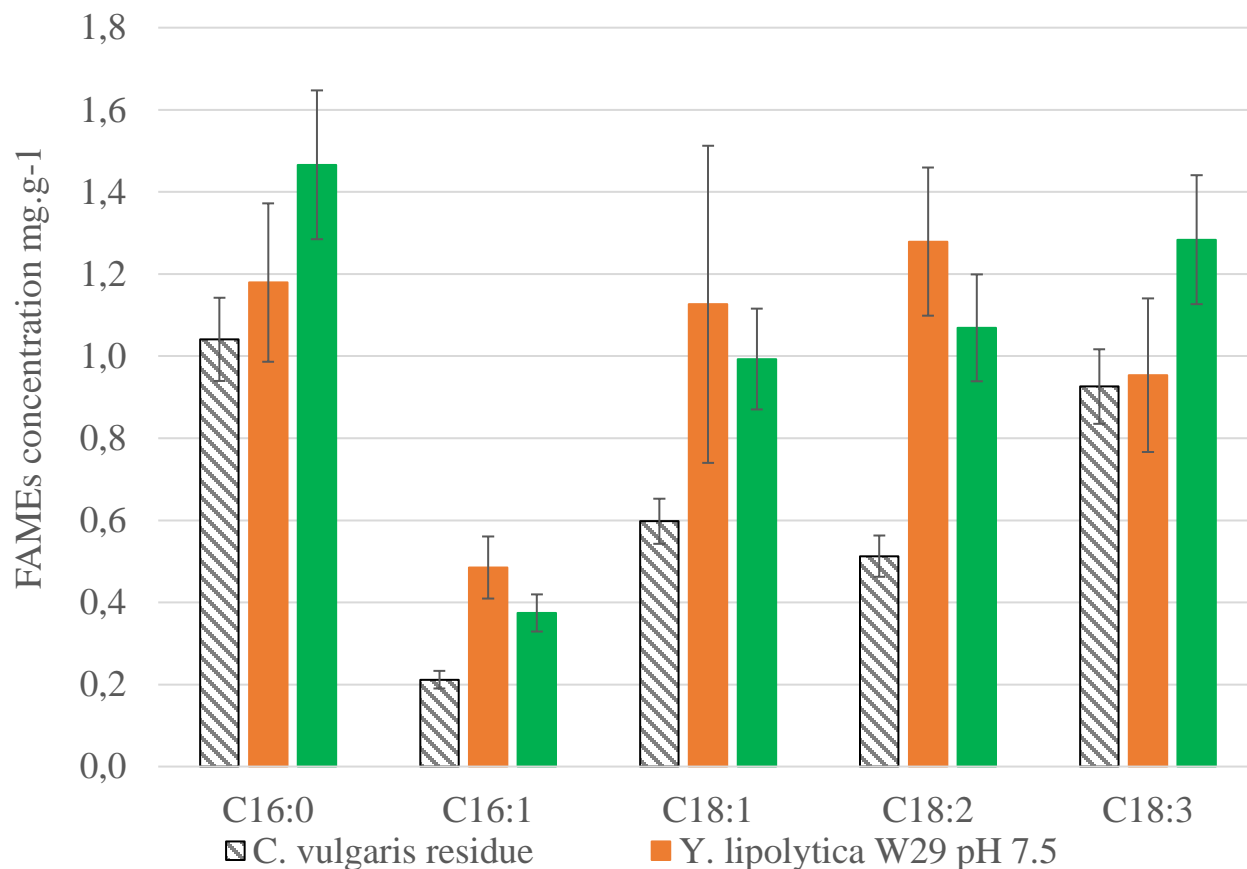
Gompertz model:  $W(t) = Ae^{-e^{\left(\frac{\mu_{max} \cdot e}{A}(\lambda - t) + 1\right)}}$

- $\mu_{max}$ : Maximal growth rate
- $\lambda$ : lag time
- t: time
- $A = \frac{\ln x_{max}}{\ln x_0}$

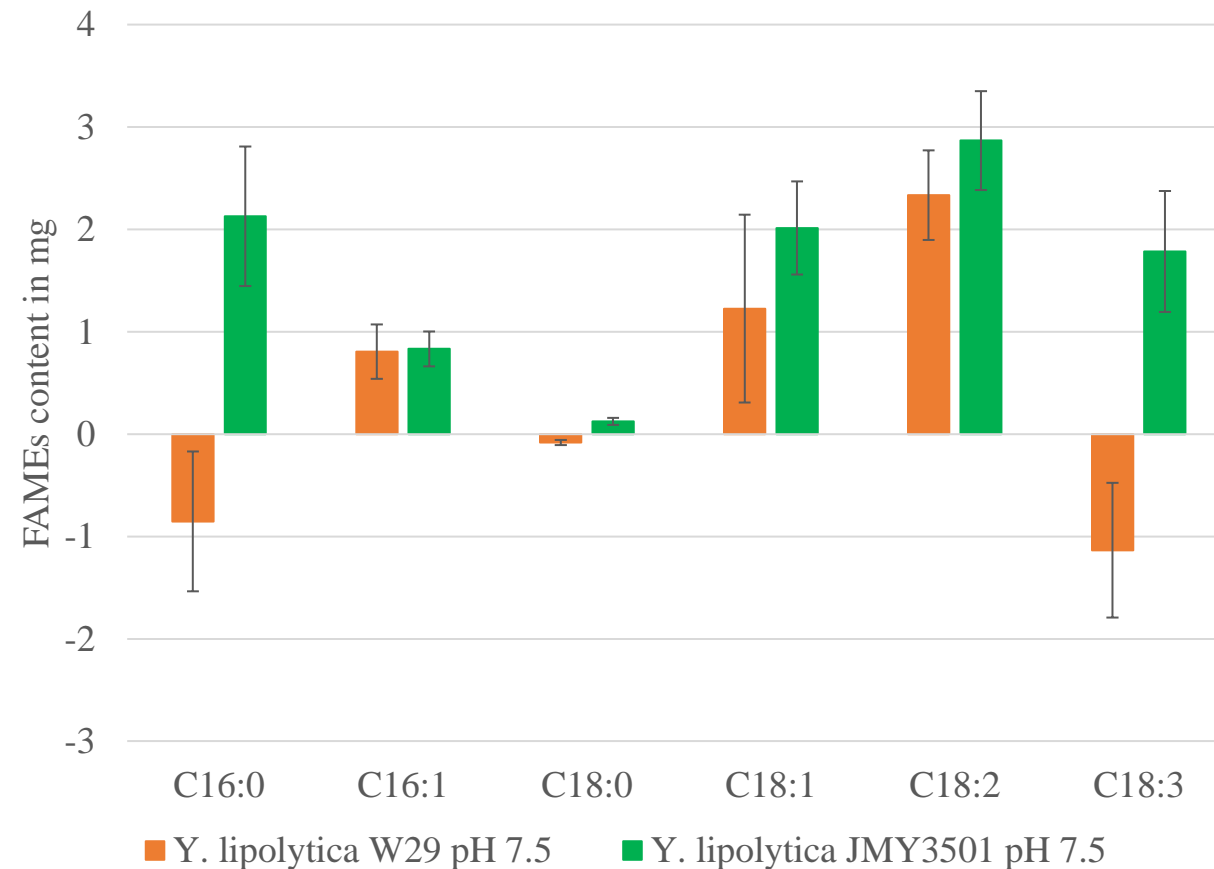
## II. Fermentation of lipid-extracted *C. vulgaris* residue

### C. FAMES profiles of *Y. lipolytica*

Fatty acids content of *C. vulgaris* residue, *Y. lipolytica* W29 and JMY3501 strains cultivated on *C. vulgaris* residue for 50 h at pH 7.5



Evolution of fatty acid quantities in the fermenter after 50 h cultivation of *Y. lipolytica* W29 and JMY3501 strains in *C. vulgaris* residue

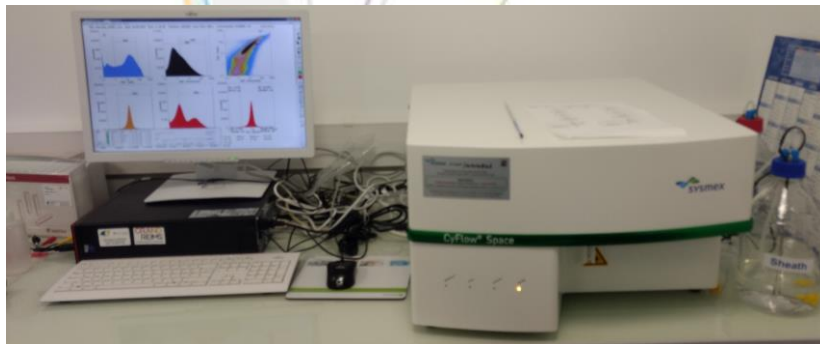




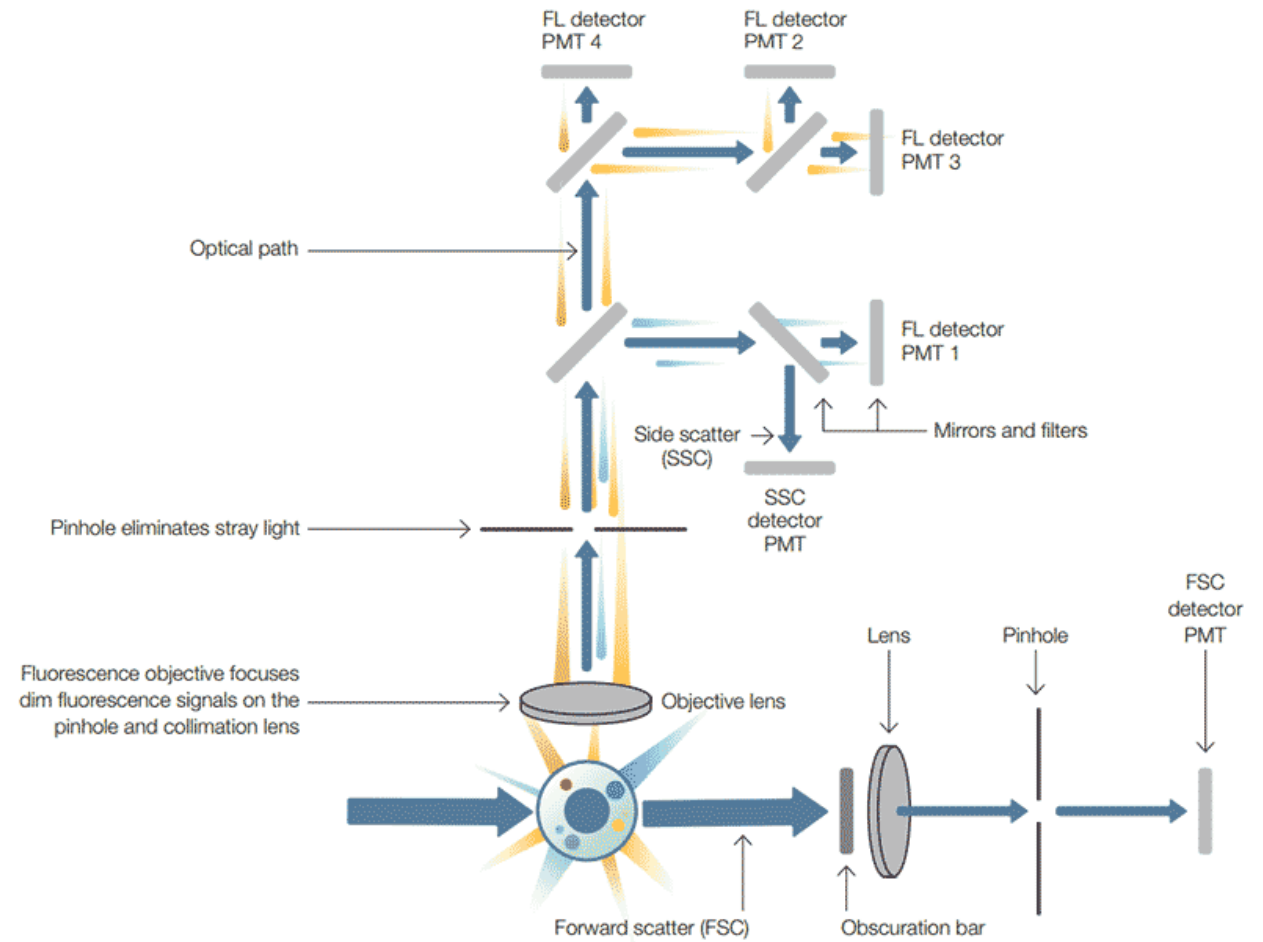
## II. Fermentation of lipid-extracted *C. vulgaris* residue

- *C. vulgaris* by-product is a convenient substrate for *Y. lipolytica* growth
- Interesting production of C18:3 at pH 7.5
- Difficulties to discriminate microalgae and yeasts
- How improve monitoring of yeasts growth ?
- How monitor lipids accumulation in yeasts ?

# III. Lipids tracking by flow cytometry



- ▶ Only one reading for:
  - ▶ Number of cells
  - ▶ Size → discriminate population
  - ▶ With staining:
    - ▶ Viability
    - ▶ Lipids content



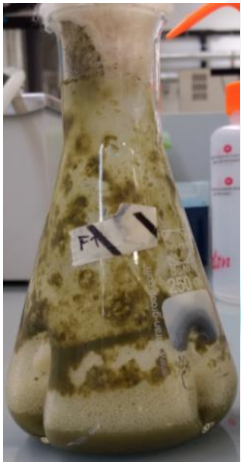
# III. Lipid tracking by flow cytometer

▶ Culture conditions:

- ▶ 50 mL in Flask (500 mL)
- ▶ 30 g.L<sup>-1</sup> *C. vulgaris* residue
- ▶ *Y. lipolytica* JMY3501
- ▶ 28°C, 220 rpm

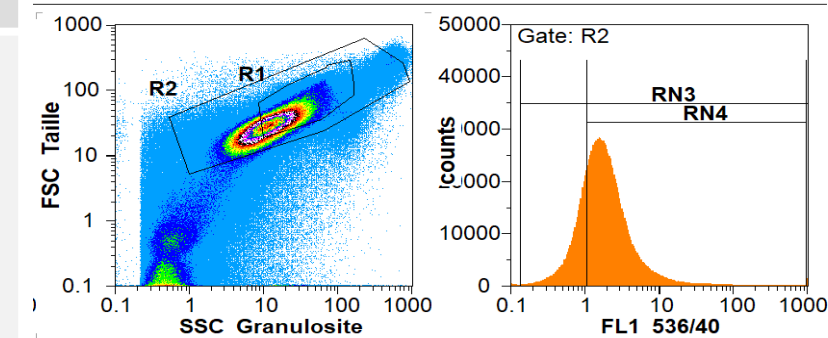
▶ Increasing with time of culture:

- ▶ Fluorescence Intensity
- ▶ Background noise

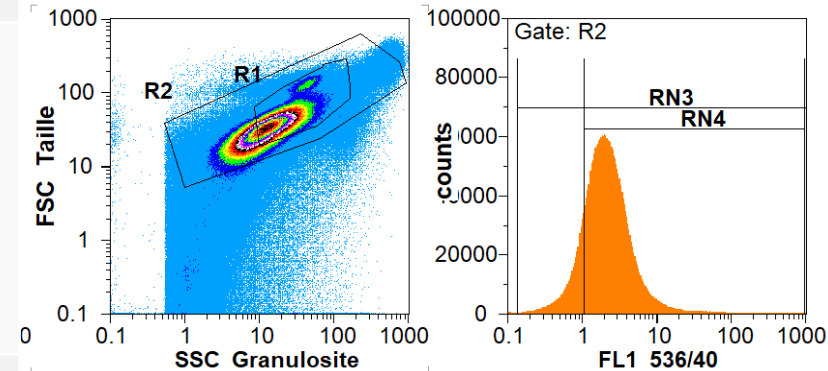


Culture Time (hours)

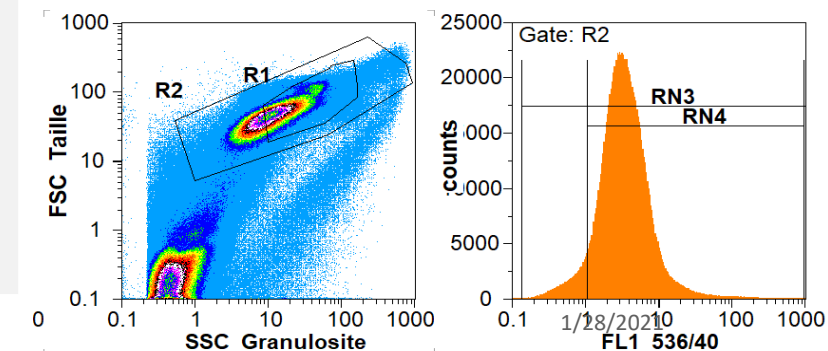
0h

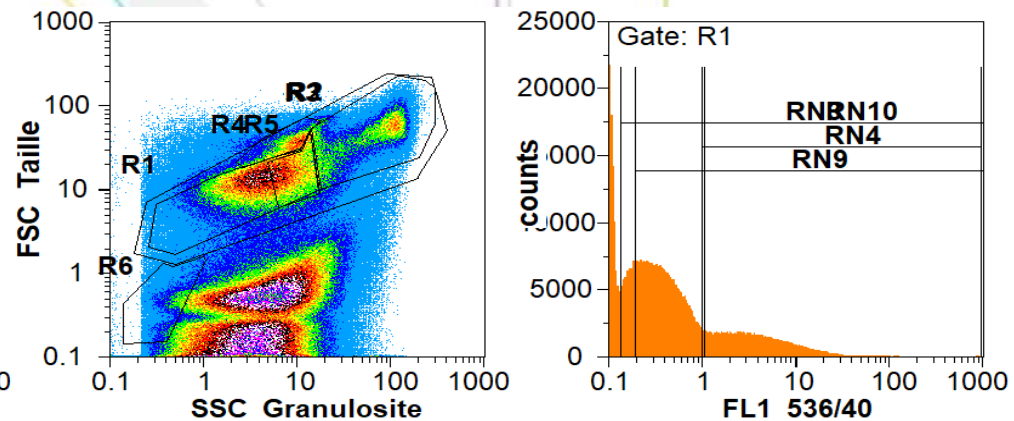


4h



24h

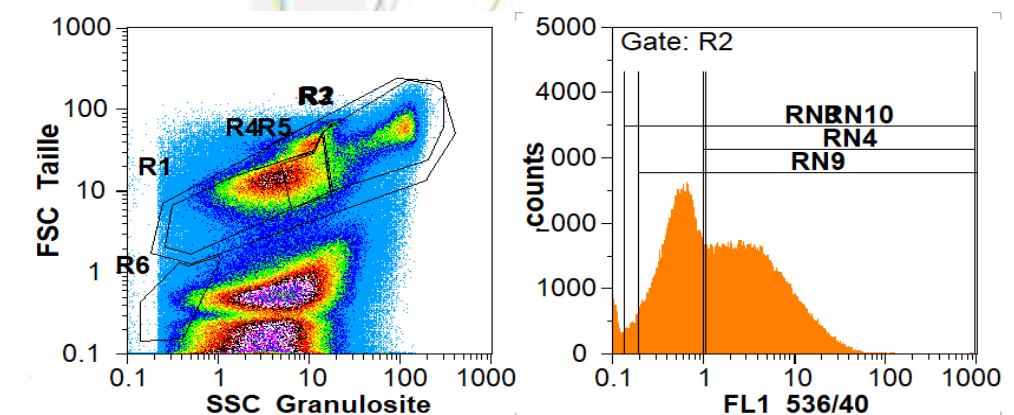




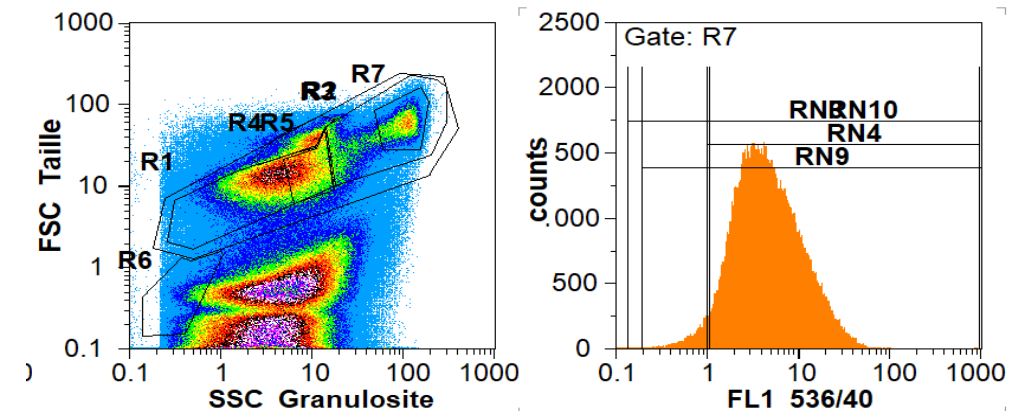
▶ After 50 h of culture of *Y. lipolytica* JMY3501 in *C. vulgaris* residue in 5L-bioreactor

▶ Culture conditions:

- ▶ 30 g.L<sup>-1</sup> *C. vulgaris* residue
- ▶ *Y. lipolytica* JMY3501
- ▶ 28°C, pO<sub>2</sub> 30% and pH 7.5
- ▶ 2 L in 5L-Bioreactor



▶ Discrimination between microalgae and yeasts is possible



▶ Specific Fluorescence of population could be used to determine lipids content in yeasts



## Conclusions and Perspectives

- Growth of *Y. lipolytica* in *C. vulgaris* residue
- pH 7.5 is the best condition for growth and lipids accumulation
- Flow cytometry to follow yeasts growth and lipids accumulation
  - Need some improvements for labelling and correlation between lipids and dye

Thank you for your attention

## Typical composition of *Chlorella vulgaris*

Reference	Lipids	Proteins	Carbohydrates	Ashes
(Mahdy <i>et al.</i> , 2016)	4.8 ± 1.1	63.4 ± 0.5	25.7 ± 2.9	6.2 ± 0.1
(Bernaerts <i>et al.</i> , 2018)	6.6 ± 1.5	39.4 ± 0.3	1.8 ± 0.1 storage polysaccharides 9.3 ± 0.7 cell wall polysaccharides 0.5 ± 0.1 extracellular polysaccharides	6.7 ± 0.1

## *C. vulgaris* residue

- Simulate substrate of project
- Extraction of lipids : Soxhlet method



<b>Proteins (% of dry biomass)</b>	<b>Reducing Carbohydrates (% of dry biomass)</b>	<b>Ashes (% of dry biomass)</b>	<b>Residual Fatty acids (% of dry biomass)</b>
40.1 ± 5.3	15.6 ± 2.1	11.2 ± 0.1	0.34 ± 0,02



