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Short Communication

Long-term fermentation by microalgae-yeast consortium efficiently converts volatile fatty acids from a real wastes stream into microbial oils

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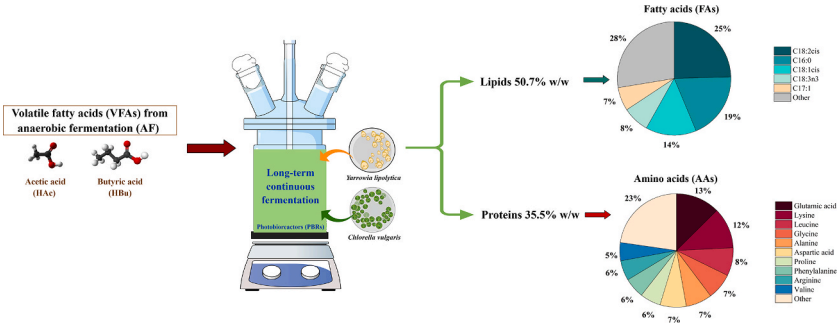
HIGHLIGHTS

- Microalgae-yeast consortium efficiently converts VFAs into lipids.
- Harvested biomass presented 50.7% lipids, 35.5% proteins, and 13.8% carbohydrates.
- Fatty acid (FAs) profile is abundant in linoleic, palmitic, oleic, and α-linolenic acids.
- The most abundant amino acid (AAs) was glutamic acid (13%).

GRAPHICAL ABSTRACT



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ABSTRACT

The present research describes the long-term fermentation of a microalgae-yeast consortium using volatile fatty acids (VFAs) supplied from a real anaerobic fermentation (AF) waste stream, enabling their efficient conversion into lipid and protein production. In addition, the macromolecular composition of the produced microbial biomass in terms of fatty acid (FAs) and amino acid (AAs) profiles highlighting its potential for diverse applications. The microbial consortium formulated by *Chlorella vulgaris* and *Yarrowia lipolytica* depicted a high lipid content of a 50.7 ± 2.5% w/w, followed by a 35.5 ± 1.1% w/w of proteins and 13.8 ± 2.0% w/w of carbohydrates. The lipids profile showed the predominance of even chain length acids (C16 and C18). In terms of AAs profile, glutamic acid was the most abundant (13.0 ± 0.1% w/w of volatile solids). This research does not only evidence long term operation feasibility but also provides an in-depth characterization of FAs and AAs profiles of this innovative microbial consortium. These data enable the rational matching of biomass-derived components with specific conversion pathways and end-use requirements, thereby maximizing their value and suitability for targeted bio-based industrial applications.

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1. Introduction

Microbial oils (MOs), also known as single-cell oils, are lipids that can be synthesized by oleaginous microorganisms including fungi, yeast, microalgae and bacteria (de Vicente et al., 2025; Nunes et al., 2024). These microorganisms can accumulate large amounts of lipids, often exceeding 20% of their dry biomass (Patel et al., 2020). Owing to their fatty acid profiles similar to vegetable oils, MOs have become valuable feedstock for the oleochemical industry (Llamas et al., 2020a; Lopes et al., 2020). Although MOs can be synthesized by pure cultures, the development of co-culture systems has emerged as a promising strategy due to the potential synergistic interactions between different microorganisms. The establishment of consortia comprising oleaginous yeasts and photosynthetic microorganisms, as microalgae, offers an efficient platform for enhancing biomass and MOs production (Li et al., 2024). The complementary metabolic activities within these microbial systems promoted efficient gas exchange (e.g., O_2/CO_2), improved carbon source utilization, pH autoregulation, and increased lipid accumulation (Lomanar et al., 2025; Suastes-Rivas et al., 2020). Despite the benefits associated with microalgae-yeast consortium, research in this area remains limited. A major constraint lies in the economic feasibility of MOs production given the high cost of carbon sources to feed oleaginous microorganisms. In fact, glucose and xylose has been estimated to account 80% of the overall production MOs cost (Patel et al., 2020; Wang et al., 2018). To overcome this major limitation, finding low-cost carbon sources for MOs production is essential. The use of volatile fatty acids (VFAs) produced in anaerobic fermentation (AF) of wastes streams arises as a new alternative to replace sugar-based technologies for MOs and biomass production (Lacroux et al., 2021, 2020; Llamas et al., 2020a, 2020b; Patel et al., 2021; Su et al., 2021). To date, the use of VFAs in the microalgae-yeast co-cultivation for MOs production is very limited, exception made for a study led by Qin et al. (2019) that evaluated the lipid production using a liquid digestate composed mainly of acetic acid as carbon source for a microbial consortium composed of *C. vulgaris* and *Y. lipolytica*. In fact, authors found that biomass concentration (1.53 ± 0.15 g L^{-1}), lipid content (12.21 ± 0.41% w/w) and lipid yield (0.183 ± 0.013 g L^{-1}) of the mixed culture was higher than those determined for pure cultures.

Interestingly, *Chlorella* species, such as *C. sorokiniana*, have also been identified as efficient strains for converting VFAs into single-cell proteins (SCPs), achieving protein content of 22.8 ± 0.3% w/w (Patel et al., 2022). Similarly, the yeast *Y. lipolytica* has also demonstrated the ability to produce SCPs from VFAs, reaching a protein content of 38.8 ± 0.2% w/w (Yang et al., 2022). Despite these promising results, long-term and continuous cultivation of microalgae-yeast consortia on VFAs has not been extensively investigated. Most reports are limited to short-term batch experiments, obtaining preliminary results in which detection of gradual changes such as microbial population shifts, productivity decline, or accumulation of inhibitory by-products are neglected. Because of this, long-term operation of microbial fermentation is required to confirm the stability, robustness, and adaptability of the microbial system under sustained conditions. To address this knowledge gap, the present study investigated, for the first time, the long-term fermentation of a microalgae-yeast consortium on VFAs in photobioreactors (PBRs). The study evaluated the MOs and SCP production capacity of the system and, more importantly, elucidating the fatty acid (FAs) and amino acid (AAs) profiles to provide new insights into their potential sustainable applications.

2. Materials and methods

2.1. Microorganism cultivation and microalgae-yeast consortium formulation

The strain of *C. vulgaris* was provided by the Culture Collection of Institute of Sustainable Processes (ISP) of the University of Valladolid (Valladolid, Spain). The inoculum of *C. vulgaris* was grown in Bold's Basal medium (BBM) at 25 ± 2 °C, at light intensity of 120 μmol m^{-2} s^{-1} with a dark:light cycle of 12:12 h and 150 rpm agitation. The strain of *Y. lipolytica* ACA DC 50109 was provided by IMDEA Energy (Madrid, Spain) from Agricultural Culture Collection of the University of Athens (Greece). The inoculum of *Y. lipolytica* was grown in Yeast Peptone Dextrose (YPD) medium at the same temperature and agitation conditions than microalgae. The microbial growth was monitored by measuring optical density (OD) at 680 nm for *C. vulgaris,* according described Ashtiani et al. (2021), and 600 nm for *Y. lipolytica* following the procedure described by Llamas et al. (2020c). This microalgae-yeast consortium was previously selected by Levío-Raimán et al. (2026) and was formulated using a concentrate inoculum volume of each strain at OD of 0.5.

2.2. Low-cost carbon source preparation: Real digestate rich in VFAs from AF

Real digestate rich in VFAs was obtained from pilot-scale anaerobic digesters using mixed sludge (activated and primary sludge). The digestate was centrifuged at 4,200 rpm for 30 min at 20 °C to separate and remove the larger particle size. The liquid fraction was sterilised to reduce the presence of microorganisms at 121 °C for 20 min. After sterilisation, the digestate was characterised in terms of pH, total and soluble chemical oxygen demand (CODt and CODs, respectively), ammonium concentration (NH_4^+) and VFAs profile (Table 1). As the digestate matrix was low in VFAs concentration, this effluent was spiked with acetic (HAc) and butyric (HBu) acids to ensure a consistent concentration of VFAs without altering the basal nutrient profile of the digestate. The supplemented ratios of HAc and HBu and its concentrations were selected according to typical VFA distributions reported for waste–derived fermentation effluents, ensuring physiologically relevant conditions for both yeast and microalgae systems for lipid production (Lacroux et al., 2021, 2020; Llamas et al., 2020a, 2020c; Morales-Palomo et al., 2022). Concentrations used of HAc and HBu in this study is detail in Table 1.

2.3. Long-term fermentation of microalgae-yeast consortium on VFAs-rich digestate

The experimental set-up was carried out in cylindrical borosilicate glass PBRs filled with 1 L of prepared digestate (Section 2.2) and inoculated with the microalgae-yeast consortium. Three independent PBRs were used as biological replicates and operated under identical conditions. The PBRs were fed and the effluent withdrawn daily to maintain a hydraulic retention time (HRT) of 7 d. The PBRs were operated for 42 days until stable performance was achieved. Stability was defined based on quantitative operational criteria: stable concentrations of VFAs, CODs, ammonium, biomass, and pH with less than 5–10% deviation in mean values over three consecutive HRTs. The PBRs were maintained at 25 ± 2 °C using water jacketed reactors and agitation at 150 rpm. The PBRs were illuminated with LED light panels assembled around the PBRs, providing 200 μmol m^{-2} s^{-1} of light intensity at dark:light cycle of

Table 1
Chemical characterization of real digestate rich in VFAs used in this study.

Parameter	Value
pH	7.0 ± 0.0
CODt (g L^{-1})	10.6 ± 0.1
CODs (g L^{-1})	9.4 ± 0.0
NH_4^+ (g L^{-1})	0.2 ± 0.1
C/N	15.2 ± 0.1
VFAs profile (g L^{-1})	
HAc (C2)	3.0 ± 0.1
HBu (C4)	3.4 ± 0.1

12:12 h. The pH was monitored every day but not controlled during PBRs operation. Samples were regularly collected to measure microbial growth (volatile suspended solids, VSS), VFAs consumption, pH, total chlorophyll (Chl), NH_4^+, CODt and CODs. The biomass macromolecular distribution profile (lipid, protein and carbohydrates) was analyzed weekly, and FAs and AAs profiles were determined when the cultures reached stability. The experiment was carried out in triplicate.

2.4. Analytical methods

Microbial growth was estimated by measuring OD in a spectrophotometer and corroborated by cell dry weight. For that, a fixed sample volume (5 mL) was filtered through 0.45 μm glass fiber membrane and collected cells were dried at 105 °C until constant weight (Llamas et al., 2020c). A calibration curve was established to correlate OD with cell dry weight. For that, samples were collected at different growth stages for each culture, and OD was measured at 600 nm for yeast and 680 nm for microalgae. Cell dry weight was determined and plotted against OD to generate the calibration curve used to estimate biomass concentration. NH_4^+ and COD concentrations were monitored and determined using colorimetric commercial test kits (ISO 000,683 and Merck, ISO 7150–1, respectively). The pH was monitored daily using a pH meter (SensION™ + PH3; HACH, Spain). Chl was determined spectrophotometrically using methanol as the extraction solvent, following the method described by Ritchie (2006). Biomass yield (g g^{-1}) was determined as the ratio between the maximum biomass produced (g) with respect to VFAs consumed (g). VFAs concentration was measured by liquid high-performance chromatography (HPLC) equipped with refractive index and UV–Vis detectors (Shimadzu LC-2050) and a carbohydrate column H + HyperREZ XP.

2.5. Determination of the biomass macromolecular profile and FAs and AAs profiles

The content of carbohydrates, proteins and lipids were determined in the harvested biomass. The biomass was collected and centrifuged at 10,000 rpm for 10 min, and the resulting pellet was washed three times with distilled water. Total carbohydrate content was determined by phenol–sulphuric acid method through a colorimetric assay based on sugar dehydration and chromophore formation according described by DuBois et al. (1956). Total protein content was estimated based on the Total Kjeldahl Nitrogen (TKN) method and converted from nitrogen-to-protein applying a conversion factor according to Standard Methods (APHA, 2017). The total lipid content was calculated as the difference between the volatile solids (VS) and the protein and carbohydrate contents and then, further corroborated and validated by a mass balance using measured FAs and AAs, which confirmed the consistency of the VS-based calculation. The FAs composition was determined by gas chromatography (GC) after fatty acid transmethylation, according to the AFNOR method (Llamas et al., 2020a). The AAs composition of the cellular proteins was determined by ion exchange chromatography and post-column derivatization with ninhydrin in a Biochrom 30 analyzer.

2.6. Statistical analysis

Statistical analyses of variance (ANOVA) and mean separations were determined using Tukey's test ($p < 0.05$) using SPSS Version 17.0 (SPSS, Chicago, IL, USA). All figures were generated using OriginPro software (OriginLab Corporation, Northampton, MA, USA).

3. Results and discussion

3.1. Performance of the microalgae-yeast consortium using VFAs as carbon source

The performance of the long-term fermentation in terms of VFAs concentrations, pH, biomass growth, NH_4^+concentration, and Chl/VSS correlation is presented in Fig. 1. The results indicated that the microalgae-yeast consortium was able to grow in real AF effluent, reaching a biomass concentration of 1.86 ± 0.05 g L^{-1}. The microbial consortium exhibited a preferential consumption of HAc over that of HBu (Fig. 1a). HAc was completely consumed at 10 d, while HBu consumption reached 76.6 ± 1.1% and remained stable after day 35 of fermentation. This trend aligns with previous studies on yeast cultivation, in which higher consumption rates for HAc compared to HBu were reported (Pereira et al., 2021). The higher HAc consumption may be attributed to the preffered metabolic pathways, in which acetate is directly converted into acetyl-CoA, facilitating its assimilation (Llamas et al., 2020c). Contrarily, HBu is predominantly dissociated at pH 9, as butyrate, limiting cellular uptake due to low membrane permeability (Lacroux et al., 2020).

VFAs consumption was correlated with the alkalinization of the medium, with pH values increasing to 9.2 (Fig. 1.b). The VFAs consumption reduced medium acidity and contributed to increase the pH (Ashtiani et al., 2021). In addition, yeast respiration produces CO_2, which is taken up by microalgae during photosynthesis to produce O_2, also contributing to an increase in the pH of the medium. Remarkably, in this study, the pH increase from 7 to 9 did not negatively affect microbial growth or VFA consumption, indicating that HAc and HBu were efficiently converted into biomass, with system stabilization occurring around pH 9. Similar observations were reported by Lacroux et al. (2020), who found that at high pH values (> 9), VFAs predominantly remain in their anionic forms, which can reduce proton availability and stabilize both VFAs consumption and biomass growth. In addition, NH_4^+ consumption has also been linked to pH dynamics in microbial systems. Initial NH_4^+ uptake can cause a decrease in pH due to the release of H^+ ions, whereas subsequent acetate (CH_3COO^-) consumption and the associated production of OH^- can increase the pH (Gao et al., 2020; Zheng et al., 2013). This pattern agrees with the obtained results, in which NH_4^+ in the medium was gradually consumed from 220 to 50 mg L^{-1} (Fig. 1b), concomitantly with the pH increase.

Chl, a key photosynthetic pigment, is an important indicator of microalgal nutrient conversion capacity and light utilization efficiency (Tong et al., 2024). To better understand its role in the fermentation process, Fig. 1c presents the relationship between VSS (representing microbial growth) and total Chl (representing microalgae presence). VSS increased proportionally with Chl content, and linear regression analysis revealed a strong correlation between the two variables ($R^2 = 0.977$; $p = 0.037$), indicating a close coupling between biomass growth and microalgal activity.

Overall, these results demonstrated that the microalgae-yeast consortium can efficiently grow in a VFA-rich real AF effluent while maintaining sustained biomass production despite the stable alkaline conditions. The strong Chl-VSS correlation and preferential HAc consumption highlighted cooperative microbial behavior not previously reported for mixed cultures in real effluents from AF.

3.2. Microalgae-yeast consortium transforms efficiently VFAs into lipids

The biomass of the microalgae-yeast consortium was characterized in terms of lipids, proteins and carbohydrates. The results showed a predominant lipid fraction (50.7 ± 2.5% w/w), followed by proteins (35.5 ± 1.1% w/w) and carbohydrates (13.8 ± 2.0% w/w). This MOs percentage was higher than those typically reported for microalgae and yeast cultivated as pure cultures on similar VFA-rich effluents. For microalgae pure cultures, Su et al. (2021) demonstrated that VFAs are a suitable carbon source for *Scenedesmus quadricauda* which reached a lipid content of 29.5% w/w using an HAc:HPro:HBu ratio of 6:1:3. In the same line, Patel et al. (2022) evaluated two microalgae species for growth and lipid accumulation using VFAs finding that both species effectively metabolized VFAs, particularly acetate, with maximum lipid contents of 33.9% w/w for *Auxenochlorella protothecoides* and 39.8% w/

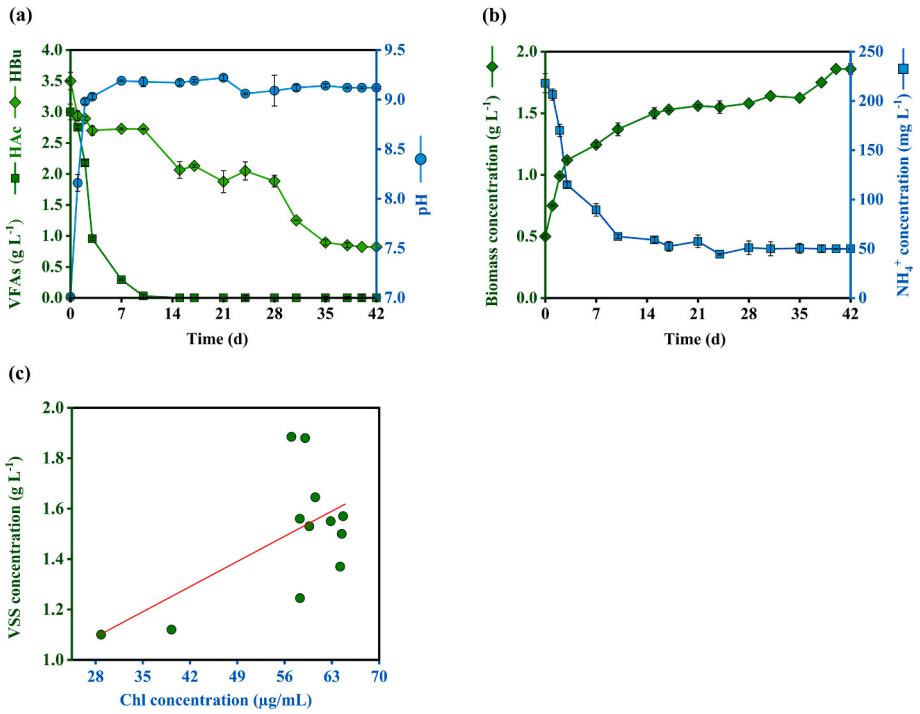

Fig. 1. PBR performance in terms of VFAs concentration (HAc and HBu) and pH dynamics (a), biomass and NH_4^+ concentrations (b), and correlation between VSS and Chl concentrations (c), by the microbial consortium cultivated on a VFAs-rich effluent.

w for *Chlorella sorokiniana*. In terms of yeast pure cultures, Llamas et al. (2020a) reported lipid content values between 7.4 and 36.9% w/w across five yeast strains (*Y. lipolytica*, *Cyberlindnera saturnus*, *Rhodotorula toruloides*, *Cutaneotrichosporon curvatum* and *Lipomyces lipofer*) grown on VFA-rich digestate at concentrations of 5–15 g L^{-1}. In addition, lipid accumulation by the pure strain *Y. lipolytica* has been reported to require high C/N ratios (150:1–200:1) to reach lipid contents of 37.3 and 43.4% w/w, respectively (Morales-Palomo et al., 2022). In this context, it is important to highlight the high lipid content (50.7 ± 2.5% w/w) achieve by the microalgae-yeast consortium under low C/N conditions (15.2), indicating its potential to efficiently produce MOs without the need for severe nitrogen limitation, since the MO content previously reported for *C. vulgaris* and *Y. lipolytica* co-cultivated on VFA-rich effluents have been limited to 10.0–12.2% w/w (Qin et al., 2019).

In the present study, lipid accumulation in the microalgae-yeast consortium cultivated on VFAs, mainly HAc and HBu, could be explained by complementary metabolic interactions. In oleaginous yeasts, short length VFAs are assimilated through the *de novo* pathway: acetate is directly converted to acetyl-CoA, while butyrate is activated and metabolized to acetyl-CoA units, increasing the cytosolic precursor pool for fatty acid synthesis (Žganjar et al., 2025, 2024). These precursors are processed by the fatty acid synthase complex and subsequently esterified via the Kennedy pathway into triacylglycerols (TAGs), which accumulate under carbon excess and nitrogen limitation during long-term fermentation. Within the microbial consortium, microalgae can also assimilate acetate into plastidial acetyl-CoA, supporting their own FAs biosynthesis, while photosynthetic activity provides ATP and NADPH, enhancing reducing power availability. Simultaneously, the O_2 released by microalgae sustains yeast respiration, and CO_2 produced by yeast can be reassimilated by microalgae, improving carbon recycling. This metabolic coupling likely optimizes acetyl-CoA flux, redox balance, and energy supply, thereby synergistically enhancing TAG accumulation in the VFA-based system.

In the case of SCPs, Patel et al. (2022) reported to the microalgae *C. sorokiniana* as an efficient strain to transform VFAs into SCPs, achieving protein content of 22.8 ± 0.3% w/w. Similarly, Yang et al. (2022) reported that *Y. lipolytica* can produce SCPs from VFAs, reaching a protein content of 38.8 ± 0.2% w/w. In the case of the microalgae-yeast consortium, no recent studies have reported its use as a SCP producer. However, a study conducted by Wang et al. (2019) hypothesized that, in the symbiotic co-culture of *C. pyrenoidosa* and *Y. lipolytica*, the presence of yeast promotes the formation of proteins with higher molecular weight and an specific AAs profile. This effect was attributed to metabolic complementarity within the consortium, where yeast metabolism may supply growth-promoting factors, CO_2, vitamins, or readily assimilable nitrogen sources, thereby stimulating microalgal protein biosynthesis. Such interactions suggest that, beyond lipid enhancement, microalgae-yeast consortium can modulate nitrogen assimilation pathways and protein metabolism, improving overall biomass quality and biochemical composition.

Thus, previous studies have demonstrated that pure cultures of microalgae and yeasts can grow and efficiently accumulate lipids and proteins using VFAs as a carbon source (Lacroux et al., 2021, 2020; Llamas et al., 2020c, 2020a; Patel et al., 2022, 2021; Yang et al., 2022). However, these investigations were conducted exclusively in batch mode, limiting their relevance for long-term and stable biomass production, whereas the present study employed a continuously fed PBR and a co-culture system. This shift in operational strategy and the microbial consortium evaluated provides novel insights evidencing efficient transformation of VFAs under steady-state co-cultivation conditions, a scenario that has been scarcely explored so far and showcasing promising results.

The biomass, lipid and protein productivities, along with their corresponding yields per VFAs consumed ($Y_{X/S}$, $Y_{L/S}$ and $Y_{P/S}$) are presented in Table 2. These parameters quantitatively supported the high conversion efficiency, demonstrating that the microalgae-yeast consortium did not only produce a lipid-rich biomass but also transformed VFAs into biomass and macromolecules with notable efficiency under continuous cultivation. Due to the limited information available for bioreactors operating under similar conditions, yields values were interpreted by comparing them with batch experiments. In batch experiments, reported yields ($Y_{L/S}$) ranged from approximately 0.13–0.33 g g^{-1} for yeast and

Table 2
Biomass, lipid and protein productivities and yields by the microalgae-yeast consortium cultivated with a VFA-rich effluent in PBRs. Biomass, lipid and protein yields per VFAs consumed (g g^{-1}), expressed as $Y_{X/S}$, $Y_{L/S}$ and $Y_{P/S}$ respectively.

Biomass productivity (g L^{-1} d^{-1})	Lipid productivity (mg L^{-1} d^{-1})	Protein productivity (mg L^{-1} d^{-1})	$Y_{X/S}$ (g g^{-1})	$Y_{L/S}$ (g g^{-1})	$Y_{P/S}$ (g g^{-1})
0.22 ± 0.01	127.46 ± 0.31	78.51 ± 1.92	0.36 ± 0.01	0.64 ± 0.05	0.38 ± 0.02

around 0.02 g g^{-1} for microalgae (Llamas et al., 2020a; Morales-Palomo et al., 2022; Su et al., 2021), which are substantially lower than the values calculated in this study.

3.3. FAs and AAs profiles produced by the microbial consortium

An in-depth characterization of FAs and AAs profiles produced by the microbial consortium was conducted when steady-state in the PBRs cultivation was reached (Fig. 2). The FAs composition of the microbial consortium depicted the presence of 18 different fatty acids, being predominant the even chain length-acids (C16 and C18). The mono-unsaturated fatty acid (MUFA) content in the microbial consortium was 29.3 ± 0.2% w/w VS (being predominant the FAs C18:1cis, C17:1, C16:1, C14:1, C15:1 and C20:1n9), whereas polyunsaturated fatty acid (PUFA) content was 32.2 ± 0.2% w/w VS (mainly the FAs, C18:2cis and C18:3n3). Such a FAs profile is particularly advantageous for oleochemical applications (Llamas et al., 2020a). A similar FAs composition was reported by Llamas et al. (2020a), with C18 and C16 FAs predominating in different pure yeast cultures on VFAs, revealing the high similarity of these MOs with vegetable oils traditionally used. In terms of PUFA content, Patel et al. (2022) reported similar values for *A. protothecoides* and *C. sorokiniana* on acetate with values of 24.93 an 24.73%. Interestingly, long-chain saturated and monounsaturated FAs (such as palmitic (C16) and oleic (C18) acids) are foundational raw materials for detergents, fatty alcohols and lubricant, while unsaturated FAs (linoleic acids), expand their potential use towards emulsifiers, plasticizers and bio-resins (Rahmawati et al., 2024).

In terms of AAs profile, glutamic acid was the prevailing one (13.0 ± 0.1% w/w VS), followed by lysine and leucine, each exceeding 8% of the total AAs content. Comparable trends have been reported in pure cultures. For instance, *Chlorella* biomass rich in proteins (51.7%) has also been reported to exhibit high glutamic acid content (28.9%) (Sriket et al., 2025). In contrast, *Y. lipolytica* cultivated on VFAs from anaerobic food-waste fermentation yielded balanced levels of glutamic acid, leucine, and lysine (Yang et al., 2022). At this point, it should be highlighted that while glutamic acid is not a core oleochemical, it can provide indirect functional benefits acting as a precursor for value-added biochemicals products (surfactants, biomaterials, among others) (Sabbah et al., 2020). Given the multiple functional groups of AAs, easy chemical modification (amidation, esterification) with fatty chains might contribute to expand the portfolio of oleochemical derivatives. Indeed, FAs and AAs are well aligned as green alternatives to petrochemical surfactants (Nagtode et al., 2023).

4. Conclusions

This investigation demonstrated the successful production of microbial oils by a microalgae-yeast consortium operated under long-term continuous fermentation using a real AF waste stream. The work provides new insights into the resulting biomass composition, revealing interesting FAs and AAs profiles. The combination of high-value FAs and AAs highlights the production of a highly potent, multifunctional biomass, expanding its potential for diverse applications, particularly in oleochemical and bio-based material sectors.

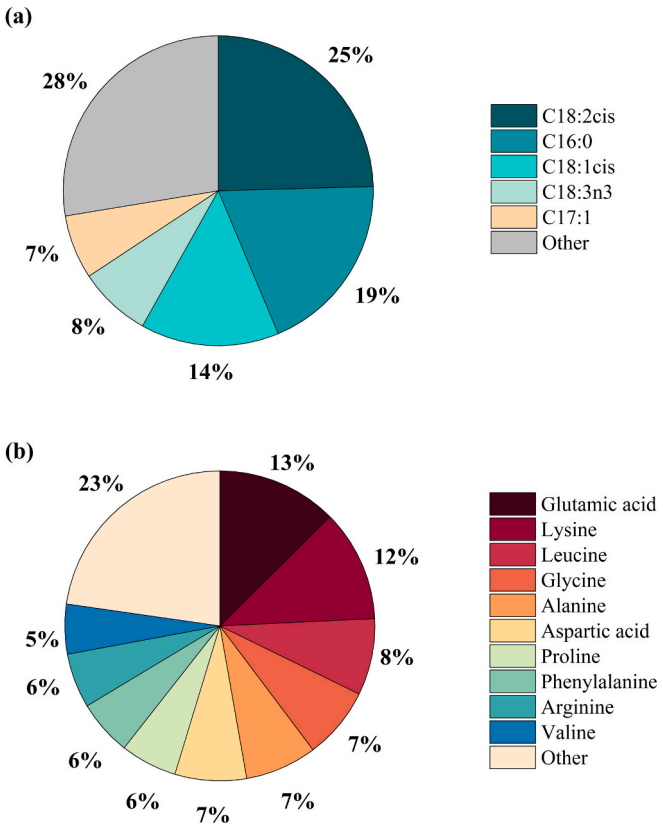

Fig. 2. Fatty acids (FAs) (a) and amino acids (AAs) (b) profiles (% w/w VS) produced by the microbial consortium microalgae-yeast cultivated with VFA-rich effluent in a PBR. Representative values ≥ 5% are presented.

CRediT authorship contribution statement

Marcela Levío-Raimán: Writing – review & editing, Writing – original draft, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Elia Tomás-Pejó:** Writing – review & editing, Visualization, Validation, Methodology, Investigation, Formal analysis, Conceptualization. **Cristina González-Fernández:** Writing – review & editing, Visualization, Validation, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

Data will be made available on request.

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