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Enhanced Lipid Production from *Zygosaccharomyces siamensis* AP1 by UV Mutagenesis and Cerulenin Selection

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Abstract. *Yeast-derived single-cell oils (SCOs) are promising renewable lipid sources for biodiesel and high-value bioproducts. Among oleaginous yeasts, Zygosaccharomyces siamensis AP1, isolated from Indonesian wild bee honey, demonstrates significant potential for lipid production; however, further improvement is needed for industrial-scale applications. This study aimed to enhance lipid accumulation in Z. siamensis AP1 via ultraviolet (UV) mutagenesis, followed by selective screening with cerulenin and ethanol/hydrogen peroxide (H_2O_2) stress. The yeast underwent repeated UV exposure to achieve 60% lethality. The surviving cells were then screened on media with increasing concentrations of cerulenin (5–160 µmol/L) or ethanol/H_2O_2 (2–4% v/v, 1–2 mmol/L). Lipid-producing mutants were characterized for growth kinetics, lipid content, and fatty acid profiles. Among the 43 mutants obtained, the cerulenin-resistant strain CR15 exhibited superior performance, reaching 28.6% lipid content after 96 hours, an increase from 24.6% at 72 hours. At the same, the wild type and the oxidative-stress mutant (MT19) showed reduced lipid accumulation over time. The wild-type lipid content decreased from 22.86% at 72 hours to 18.53% at 96 hours, while lipid content from strain MT19 decreased from 24.64% at 72 hours to 20.09% at 96 hours. Gas chromatography analysis revealed that CR15 produced a diverse fatty acid profile with both even- (arachidonic acid (16%), eicosadienoic acid (5.88%), gondoic acid (18.70%), linoleic acid (26.63%), palmitoleic acid (11.89%) and odd-chain (margaric acid (14.46%)) fatty acids, suggesting mutations in fatty acid synthase (FAS) enzyme function. In contrast, MT19 primarily produced linoleic acid (45.75%) as an adaptive response to oxidative stress. These results indicate that UV mutagenesis coupled with cerulenin selection can effectively enhance lipid biosynthesis and alter fatty acid composition in Z. siamensis. The CR15 mutant represents a promising candidate for advancing sustainable microbial oil production. Further transcriptomic analysis is suggested to clarify the genetic basis of these metabolic changes.*

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INTRODUCTION

Yeast-derived lipids are promising sustainable alternatives for biodiesel, food additives, cosmetics, and pharmaceuticals (Bandhu et al., 2020; Beopoulos & Nicaud, 2012; Lee et al., 2024; Szczepańska et al., 2022). Their controlled fermentation enables consistent quality independent of agricultural land and seasonal variations (Beopoulos & Nicaud, 2012). Yeast biorefineries utilizing agro-industrial wastes can produce bio-oils alongside value-added co-products, enhancing economic viability (Cosío-Cuadros et al., 2023; Llamas et al., 2020; Samavi & Rakshit, 2022). Oleaginous yeasts accumulate over 20% of their dry cell weight as lipids (Qian et al., 2023; Wusnah et al., 2023). Key species include *Yarrowia lipolytica* (Beopoulos et al., 2010; Szczepańska et al., 2022), *Rhodotorula species* (Babau, 2015; Martinez-Silveira et al., 2019), *Lipomyces starkeyi* (Saha et al., 2025), and *Rhodosporidium* sp. and *Trichosporon* sp. (Bandhu et al., 2020; Sajish et al., 2022).

Indonesia's biodiversity offers novel microorganisms with biotechnological potential (Kanti, 2022; Ikhwani et al., 2023). Wild bee honey harbors osmotolerant yeasts adapted to high sugar concentrations (Kanti, 2022). The isolation of oleaginous *Zygosaccharomyces siamensis* AP1 from wild bee honey in Ampana, Central Sulawesi (Anjani & Ilmi, 2018), exemplifies this potential. *Zygosaccharomyces* sp. exhibit remarkable stress tolerance, including osmotolerance and moderate ethanol tolerance (Csoma et al., 2023; Jagtap et al., 2022), making them suitable for industrial bioprocesses. *Zygosaccharomyces lentus* tolerates up to 8% (v/v) ethanol and high osmotic pressure (Csoma et al., 2023), traits that are advantageous for lipid production.

UV mutagenesis remains a cost-effective approach for strain improvement (Choi et al., 2015; Saravanan et al., 2017; Soedarmodjo et al., 2019). It induces random mutations, creating genetic diversity without requiring detailed genetic knowledge (Choi et al., 2015). UV mutagenesis improves lipid production through: (1) redirecting carbon flux by downregulating competing pathways; (2) enhancing NADPH supply; (3) suppressing competing carbon sinks; (4) increasing lipogenic enzyme activity; and (5) inducing stress-responsive signaling cascades (Ji et al., 2024; Lim et al., 2015; Liu et al., 2015; Muthuraj et al., 2019; Sivaramakrishnan & Incharoensakdi, 2023; Teco-Bravo et al., 2019; Tensingh & Shankar, 2022; Vardar-Yel et al., 2024; Wen et al., 2025; Yamada et al., 2017). Examples include *Schizochytrium* sp. mutants with 40.3% increased DHA production (Wen et al., 2025), *Saccharomyces cerevisiae* mutants achieving 44% cellular lipid content (Ji et al., 2024), and *Chlorella* sp. mutants with lipid content increases from 34% to 48% (Muthuraj et al., 2019; Liu et al., 2015).

Effective screening methods are critical for identifying desired mutants (Bao et al., 2021; Cao et al., 2022). Selective screening imposes constraints that couple metabolic activity to cell fitness (Akhgari et al., 2022; Chen et al., 2024; Raman et al., 2014). Cerulenin inhibits fatty acid synthesis by targeting fatty acid synthase (Bao et al., 2021; Kataya et al., 2025), while oxidative stress agents like ethanol and hydrogen peroxide affect membrane lipid composition (Bonatto, 2020; Santos et al., 2012; Sekova et al., 2020). Combining mutagenesis with multi-step selective screening increases the likelihood of isolating high-lipid-producing mutants (Chen et al., 2024; Raman et al., 2014).

Despite the industrial potential of *Zygosaccharomyces* sp. and the documented success of UV mutagenesis in improving lipid production, the application of UV mutagenesis to *Z. siamensis* remains unexplored. Previous work demonstrated that *Z. siamensis* AP1 possesses

inherent lipid-producing capability (Ilmi & Siswontoro, 2021; Ilmi et al., 2023; Salsabila & Ilmi, 2021), but productivity may be insufficient for industrial applications. This study aimed to enhance the lipid production capacity of *Z. siamensis* AP1 through UV mutagenesis combined with selective screening using cerulenin and ethanol/hydrogen peroxide mixture.

MATERIALS AND METHODS

Yeast Strain

The wild-type yeast strain *Zygosaccharomyces siamensis* AP1 was isolated from wild bee honey collected in Ampana, Sulawesi, Indonesia (Anjani & Ilmi, 2018). The mutant strains (MTxx and CRxx; Table 1) were generated by mutagenesis in this study. All strains are maintained in the Laboratory of Microbiology at the Faculty of Biology, Universitas Gadjah Mada.

Random Mutation of Strain AP1 Using Ultraviolet Radiation

Mutagenesis of strain AP1 was performed according to Yamada et al. (Yamada et al., 2017). Briefly, the yeast was grown in an Erlenmeyer flask containing 50 mL Yeast Peptone Dextrose (YPD [HiMedia]) for 24h at 28°C and 200 rpm agitation. The cells were then transferred into a sterile Petri dish and irradiated with an ultraviolet (UV) lamp 15 W [Sankyo Denki G15T8] using a wavelength of 253.7 nm until achieving 60% cell death. Surviving cells were incubated until the cells' density (OD_{600}) reached 1. The cells were transferred into YPD containing increasing concentrations of cerulenin [Sigma-Aldrich] (5 – 160 µmol/L) as a selective agent, then incubated until OD_{600}= 2. UV mutagenesis was then repeated as described above. UV mutagenesis was also conducted using a mixture of ethanol [Merck] and hydrogen peroxide (H_2O_2) [Merck] as a selective agent at two concentrations: 2% (v/v) with 1 mmol/L and 4% (v/v) with 2 mmol/L. The surviving mutants from the last cycles were kept in YPD with agar [Oxoid] (15 g/L) containing the highest corresponding selective agent concentration. Mutant strains from cerulenin selection were given CR as strain code, while mutant strains from ethanol/H_2O_2 selection were coded MT (Table 1).

Lipid Production Characterization

All mutant strains were assayed for lipid content by growing them in 50 mL of Nitrogen-Limited Medium (NLM) containing glucose [Millipore] (100 g/L), peptone [Millipore] (3 g/L), and yeast extract [Oxoid] (8 g/L). The flasks were incubated for 48h in a rotary shaker [B-One] at 28°C and 200 rpm agitation. Strains with the highest lipid content from each UV mutagenesis with different selective agents were further characterized by measuring cell density every 24h for 96h at λ=600 nm, along with their biomass and lipid content at 72 and 96h.

Biomass was measured gravimetrically by harvesting cells via centrifugation, washing with distilled water, drying at 70°C to constant weight, and weighing to determine the dry cell weight per mL of fermentation medium. Lipid amount was determined using the Bligh and Dyer method (Bligh & Dyer, 1959), in which cells were homogenized with chloroform: methanol (1:2, v/v), followed by the addition of chloroform and water to achieve a final ratio of 2:2:1.8 (v/v/v) for phase separation. The lower chloroform phase containing extracted lipids was recovered, evaporated, and weighed to determine total lipid mass per mL of fermentation medium. Lipid content was expressed as a percentage of lipid amount per biomass dry cell weight (Eq. 1).

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$$\text{Lipid content } (\%) = \frac{\text{Lipid amount } (g/mL)}{\text{Dry cell biomass } (g/mL)} \times 100 \quad \text{Eq.1}$$

Lipid Profile Analysis

Lipids produced from the selected mutants after 96h in NLM were analyzed using a gas chromatography method. Samples were methylated before injection, as described by Ichihara and Fukubayashi (2010). Afterward, 1 µL of methylated sample was injected into GC [Agilent 7890B] using HP-88 column (100 m length) and He as carrier gas. Column temperature was set initially at 100 °C and held for 5 minutes, then increased to 240°C (4°C per minute) and held for 15 minutes. Detector temperature was set to 260 °C. External standards were used as references.

Data Analysis

Data were analyzed and visualized using Microsoft Excel 2019 [Microsoft]. GC chromatograms were analyzed using ChemStation Software [Agilent]. Data comparisons between groups were performed statistically using paired-samples t-tests ($\alpha = 0.05$) in JASP (ver. 0.95.3).

RESULTS AND DISCUSSION

Random Mutation of *Zygosaccharomyces siamensis* AP1 Using Ultraviolet Irradiation

Mutagenesis of *Z. siamensis* AP1 was performed using a 15 W UV lamp with a wavelength of 253.7 nm. The surviving mutants were then screened using either cerulenin or a mixture of ethanol and hydrogen peroxide (H_2O_2). A total of 43 mutants were obtained, comprising 18 from the cerulenin screening and 25 from the ethanol and H_2O_2 screening (Table 1). Four mutants produced high lipid content (CR15, 52.8%; CR25, 20%; MT17, 13.1%; and MT19, 16.6%), while two other mutants (MT29 and MT34) did not accumulate any detectable lipid (Figure 1). The best mutants selected from the cerulenin screen had higher lipid content than the 19% reported for the wild-type strain in a previous study (Anjani & Ilmi, 2018). In contrast, the best mutants selected from the ethanol and H_2O_2 screen produced lower lipid content than the wild-type.

Table 1. Mutant strains obtained from UV-mutagenesis of *Z. siamensis*

Strains from cerulenin screening	Strains from ethanol/H_2O_2 screening
CR11, CR12, CR13, CR14, CR15, CR16, CR17, CR18, CR19, CR20, CR21, CR22, CR23, CR24, CR25, CR26, CR27, CR28	MT11, MT12, MT13, MT14, MT15, MT16, MT17, MT18, MT19, MT20, MT21, MT22, MT23, MT24, MT25, MT26, MT27, MT28, MT29, MT30, MT31, MT32, MT33, MT34, MT35

Lipid synthesis in fungi involves several key enzymes, including ATP: citrate lyase, malate dehydrogenase, acetyl-CoA carboxylase, and fatty acid synthase (Ratledge, 2014). Due to the complexity of these pathways, random mutagenesis is a suitable approach for strain engineering, given its simplicity and rapidity. However, an efficient screening method is required to isolate the desired mutants. In this study, we used cerulenin and a mixture of ethanol and H_2O_2 as screening agents.

The cerulenin screening in our study identified mutants with higher lipid content, consistent

with previous studies on *Lipomyces starkeyii* (Tapia et al., 2012) and *Rhodosporidium toruloides* (Yamada et al., 2017). Cerulenin is a known antibiotic that inhibits lipid synthesis in fungi (Ono et al., 1974) and bacteria (Heath et al., 2001). It specifically inhibits the β-ketoacyl synthase component of FAS, restricting de novo synthesis of saturated fatty acids and directing cellular metabolism toward desaturation and storage pathways; hence, mutants surviving cerulenin selection can produce high amounts of lipid (Ratledge, 2014; Tanaka et al., 1976; Wang et al., 2009).

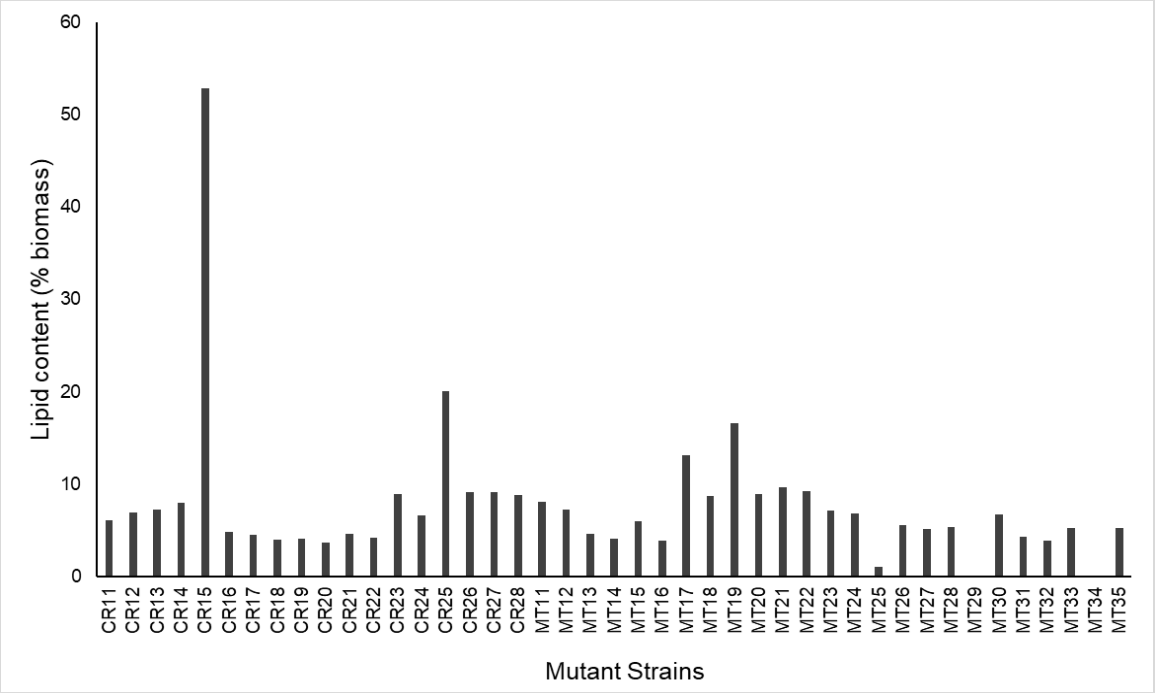

Figure 1. Mutant strains and their lipid contents after grown in Nitrogen Limited Medium (NLM) for 24h. with incu bation temperature 28°C and 200 rpm agitation. CRs are mutant strains from mutation using cerulenin as a selective agent, MTs are mutant strains from mutation using ethanol/H_2O_2 as a selective agent.

Ethanol and H_2O_2, on the other hand, are environmental stressors that reduce membrane integrity and induce ROS-mediated oxidative stress, altering membrane lipid composition (Ma et al., 2013; Yang et al., 2012). Similar to cerulenin, mutants with enhanced lipid production can withstand the effects of ethanol and H_2O_2 (Wu et al., 2020); however, the increase is moderate compared to cerulenin-screened mutants, as shown by our result (Figure 1) and confirmed by Guo et al. (2019) and Yamada et al. (2017). Hence, cerulenin proved to be a more effective selection agent than the ethanol/H_2O_2 mixture.

Growth Profiles of Chosen Mutants

Growth profiles were performed on the mutants with the highest lipid content from each screening method, namely CR15 from the cerulenin screening and MT19 from the ethanol/H_2O_2 screening. Mutants and wild-type (AP1) strains were grown in NLM medium for 96 h. Cell density was measured every 24 hours using a spectrophotometer at an A600. The plot of cell absorbance values against time is shown in Figure 2.

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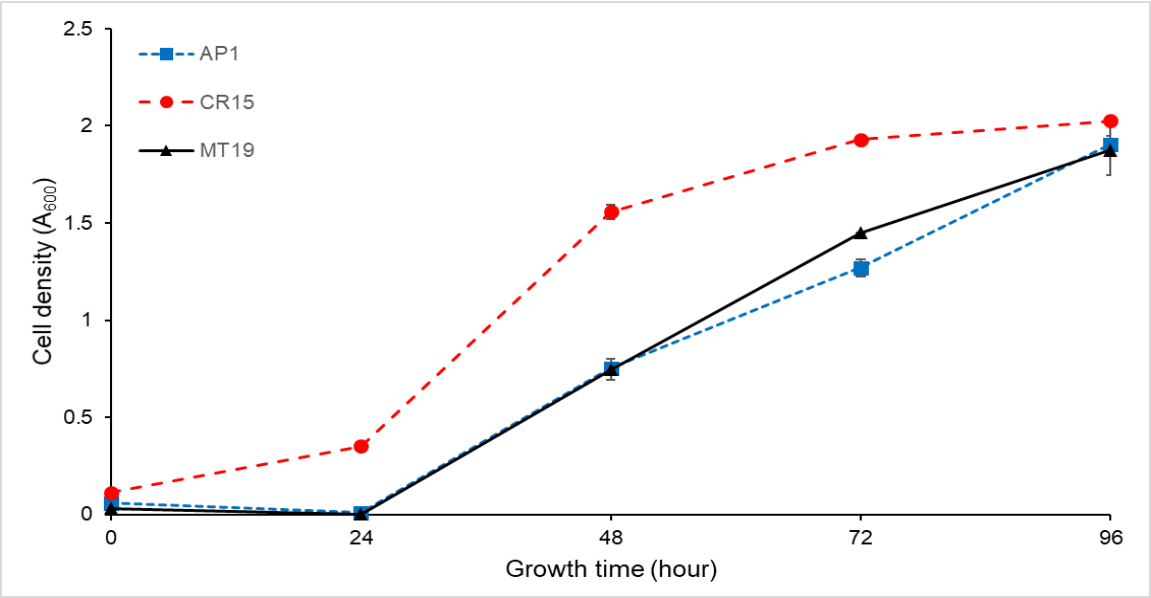

Figure 2. Growth curve of wildtype strain *Zygosaccharomyces siamensis* AP1 and the selected mutants (CR15 and MT19) in Nitrogen Limited Medium (NLM) for 96h. The incubation temperature was 28 °C with 200 rpm agitation

The CR15 strain exhibited an accelerated growth profile, achieving a cell density (OD_{600}) of 0.35 at 24 hours, compared to 0.05 for both the AP1 and MT19 strains. This early growth advantage was maintained throughout the cultivation period, with CR15 reaching a maximum cell density (OD_{600}) of 2.05 at 96 hours, representing an 8% increase over the wildtype strain. Higher growth performance of CR15 following cerulenin selection suggests that UV mutagenesis altered its lipid biosynthesis pathways. Cerulenin specifically inhibits acetyl-CoA carboxylase (ACC1) and fatty acid synthase (FAS1/FAS2), which are rate-limiting enzymes in fatty acid synthesis (Omura, 1976; Wakil et al., 1983). Surviving mutants from cerulenin may possess an enhanced fatty acid synthesis capacity through the overexpression or modified kinetics of ACC1 and FAS enzymes, alternative lipid synthesis pathways that bypass cerulenin-sensitive steps, or improved lipid salvage mechanisms to maintain membrane integrity with reduced de novo synthesis (Henry et al., 2012; Tehlivets et al., 2007). These lipid-synthesis adaptations likely conferred a metabolic advantage to CR15 under the nitrogen-limited fermentation conditions used in this study. Nitrogen limitation is a well-established trigger of lipid accumulation in oleaginous yeasts: when nitrogen is depleted in the presence of excess carbon, the reduced demand for amino acid and protein synthesis reroutes carbon flux into triacylglycerol (TAG) storage (Calvey et al., 2016; Kerkhoven et al., 2016). Mechanistically, nitrogen exhaustion elevates AMP deaminase activity, lowering cellular AMP levels and reducing NADH-dependent isocitrate dehydrogenase (ICDH) activity in mitochondria, leading to citrate accumulation and export to the cytosol (Gluth et al., 2025; Kerkhoven et al., 2016). Cytosolic citrate is then cleaved by ATP: citrate lyase (ACL) to generate acetyl-CoA, the primary precursor for fatty acid biosynthesis, with NADPH supplied via the pentose phosphate pathway (Zhang et al., 2016). Consequently, nitrogen limitation simultaneously suppresses biomass and protein synthesis while actively driving carbon into lipid storage through the adenylate–citrate–ACL axis (Calvey et al., 2016; Zhang et al., 2016). CR15, with its cerulenin-

selected lipid synthesis adaptations, was likely better positioned to exploit this nitrogen-limited carbon overflow, thereby achieving higher lipid accumulation and, consequently, greater growth performance than the wild-type under these conditions. On the other hand, the similar growth performance of MT19 and the wild-type AP1 suggests that MT19's oxidative stress adaptations do not provide significant advantages under nitrogen limitation, confirming the specificity of the cerulenin selection effect.

Lipid Production Characteristics of Chosen Mutants

Lipid production characteristics of the wild-type strain and chosen mutant strains were determined after 72 and 96 hours of growth in NLM medium. At each time point, cell and lipid biomass were measured gravimetrically, and the resulting weights were compared within strains. The results are presented in Figure 3. The results show that after 72 hours, all three strains produced similar biomass (Figure 3A), although AP1 produced slightly higher biomass (1.1 g/L) than CR15 and MT19 (0.99 and 0.97 g/L, respectively). However, at the 96th hour, the biomass of CR15 is significantly lower ($\alpha = 0.05$) than that of AP1 and MT19, and it has only increased slightly from its biomass at the 72nd hour. Lipid productions from all strains, on the other hand, are statistically similar either after 72 or 96 hours of production (Figure 3B). Lipid contents calculated based on total biomass and lipid amount (Figure 3C) show that CR15 lipid content increased from 24.6% at 72nd hour to 28.6% at 96th hour. In contrast, the lipid content of AP1 and MT19 decreased after 96 hours of production, from 22.9 to 18.5% and from 24.6 to 20%, respectively.

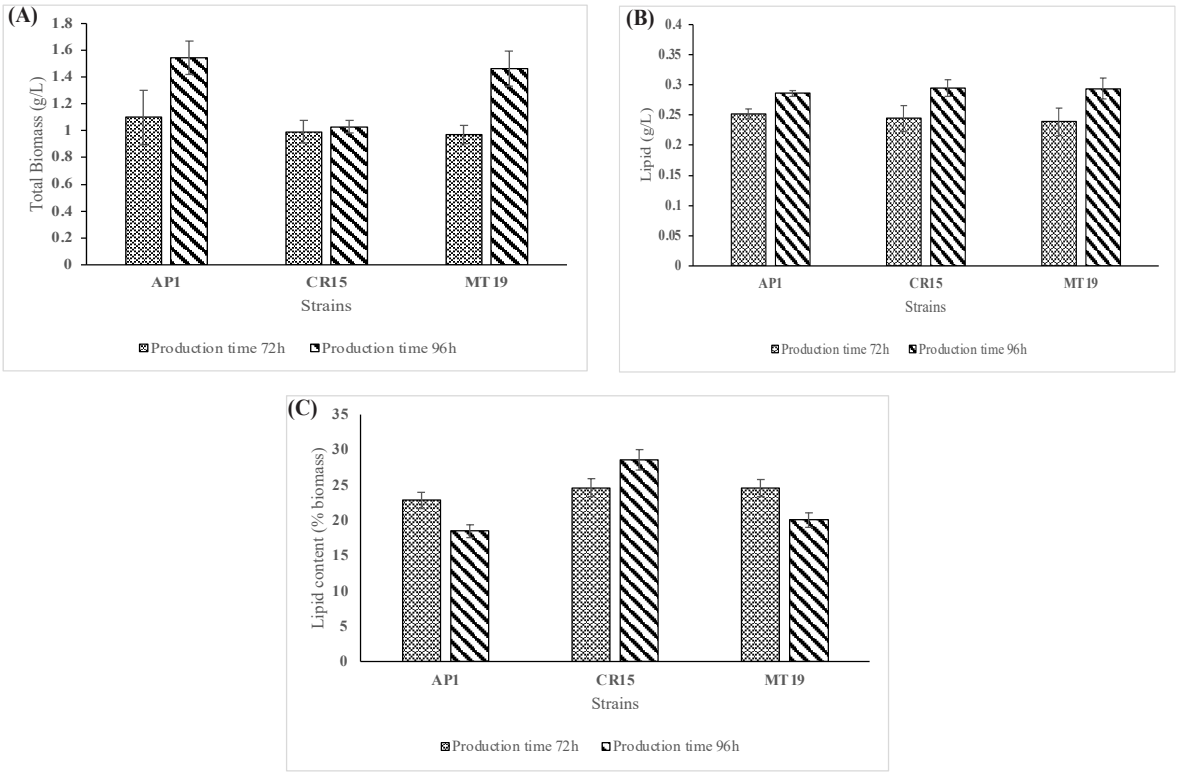

Figure 3. Biomass (A), lipid (B), and lipid content (C) of the wild-type *Zygosaccharomyces siamensis* AP1 strain and selected mutants (CR15 and MT19) grown for 72 and 96 hours in a Nitrogen-Limited Medium (NLM) at 28°C with 200 rpm agitation

The increased lipid content in CR15 suggests that the strain blocks lipid remobilization. The blockage can be caused by limited N in the growth medium, as also shown by previous studies in *Candida* sp. 107 (Gill et al., 1977) and *Yarrowia lipolytica* (Lazar et al., 2018). Proteomic analysis by Shi et al. (2013) revealed that oleaginous yeast downregulates β-oxidation and lipase proteins during nitrogen-limited accumulation phases. Another factor suspected of causing remobilization blockage is genetic modification resulting from UV mutagenesis followed by cerulenin selection. Cerulenin resistance involves not only FAS modification but also broader metabolic adaptations affecting lipid homeostasis (Yamada et al., 2017). High lipid production, which was shown by CR15 during the screening (Figure 1) and production (Figure 3) phases, can only occur when β-oxidation is disrupted. Otherwise, newly synthesized lipids were rapidly catabolized, as observed in the AP1 and MT19 strains (Leber et al., 2016). Total biomass from both strains increased along with lipid amounts (Figure 3), indicating that accumulated lipid was utilized as a carbon source for cell growth. However, further transcriptomic analyses are needed to prove those suspicions.

Based on the results, CR15 was selected as the optimal strain due to superior lipid accumulation during the 96-hour cultivation period. While all three candidate strains demonstrated oleaginous characteristics, CR15 exhibited a progressive increase in lipid content from 24.6% at 72 hours to 28.6% at 96 hours, representing a 16.3% improvement in lipid accumulation capacity during extended cultivation. In contrast, AP1 and MT19 showed declining lipid content trajectories, decreasing to 18.5% and 20.0%, respectively, by 96 hours. Lipid content and lipid productivity are established as the primary selection criteria for identifying superior oleaginous strains for biofuel production, as demonstrated by previous studies in microalgae (Griffiths and Harrison, 2009; Nascimento et al., 2013; Rodolfi et al., 2009) and oleaginous microorganisms (Vello et al., 2014). Griffiths and Harrison (2009) demonstrated that lipid productivity is the key characteristic for selecting algal species for biodiesel production, emphasizing that strains with higher lipid accumulation rates offer superior economic viability. Similarly, Nascimento et al. (2013) validated lipid productivity and lipid content as the principal selection criteria for screening microalgae strains, noting that these parameters directly determine the commercial feasibility of developing biodiesel feedstock. Rodolfi et al. (2009) further confirmed that lipid-content-guided strain selection, combined with productivity assessments, enables the identification of optimal biocatalysts for large-scale oil production. The superior and sustained lipid accumulation profile of CR15, particularly its capacity to continue increasing lipid content beyond 72 hours while competitor strains declined, positions it as the most promising candidate for scaled biodiesel production processes (Vello et al., 2014).

Fatty Acid Profiles of Chosen Mutants

Fatty acid profiles of lipids produced by the wild-type strain (AP1) and mutant strains (CR15 and MT19) were analyzed using Gas Chromatography (Agilent 7890B) with an HP-88 column (100 m length) and He as the carrier gas. The resulting chromatograms were analyzed using ChemStation Software. The fatty acid composition of the lipid samples is shown in Figure 4. The results show that the fatty acid composition of the lipids from CR15 and MT19 shifted from that of AP1. Notable fatty acid changes from CR15 are linoleic acid (26.63%), arachidonic acid (16%), margaric acid (14.46%), gondoic acid (12.71%), and palmitoleic acid (11.89%). On the other hand, MT19 fatty acid composition is less diverse. Three major fatty acids produced by the strain are linoleic acid (45.75%), margaric acid (22.78%), and gondoic acid (10%). Other fatty

acids are very low, less than 10%.

A mixture of even-chain (C16, C18, C20) and odd-chain (C17) fatty acids from CR15 lipid indicates cerulenin selection favors strains with mutated FAS enzymes, which accept alternative substrates (propionyl-CoA alongside acetyl-CoA) (Arai et al., 1982; Qiao et al., 2023) and altered chain-length determination (Heil et al., 2019; Qin et al., 2023). Cerulenin is known to block FAS enzyme activity and reduce lipid synthesis in cells (Henry et al., 2012; Tehlivets et al., 2007). Hence, modifications to fatty acid synthesis pathways create multiple independent mechanisms that enable the cell to produce enough lipids to overcome the cerulenin block.

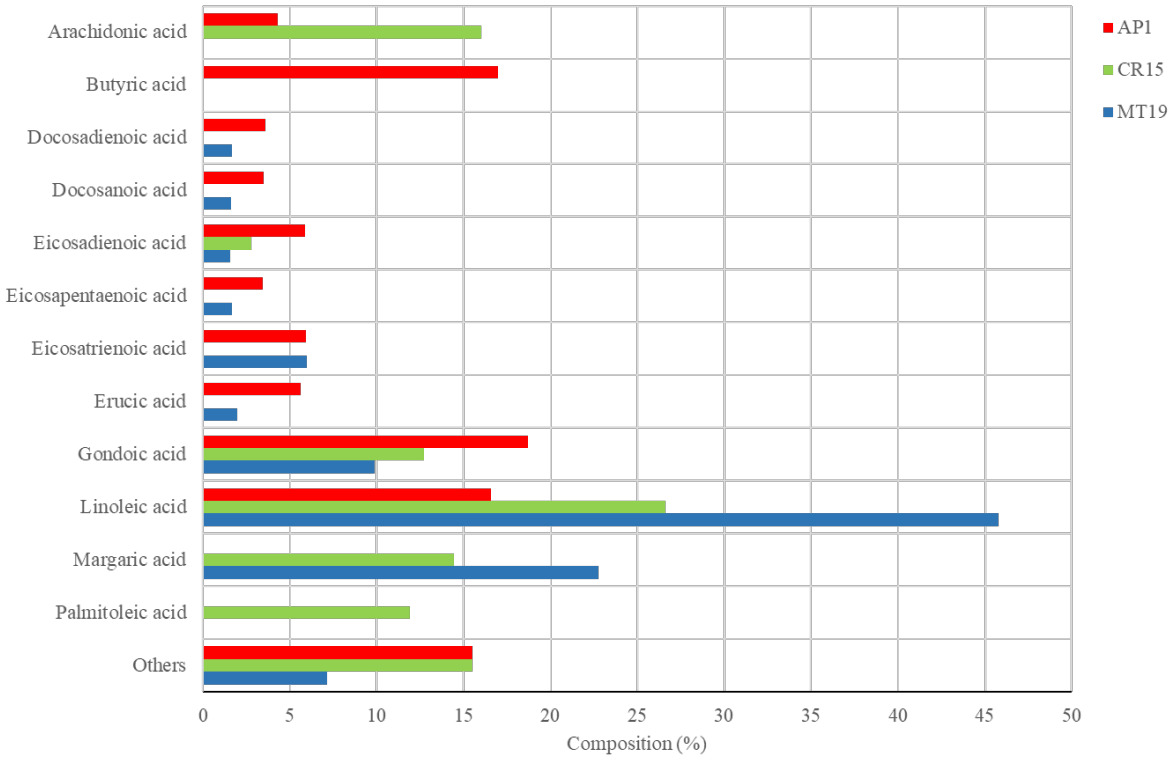

Figure 4. Fatty acid compositions of the wild-type *Zygosaccharomyces siamensis* AP1 strain and selected mutants (CR15 and MT19) after being grown for 96 hours in a Nitrogen-Limited Medium (NLM) at 28 °C with 200 rpm agitation. Analyses were done using Gas Chromatography (GC) with HP-88 column

A different fatty acid profile is observed from MT19; the lipid contains mainly unsaturated C18:2 linoleic acid. This sharp increase suggests oxidative stress created by ethanol and peroxide causes membrane lipid peroxidation and protein damage, creating a specific biophysical problem that requires a specific lipid solution. We suspected that oxidative stress favored mutants with increased expression of acetyl-CoA carboxylase (ACC1) and acyl-CoA desaturase (OLE1), which, in turn, increase linoleic acid synthesis. This causes remodeling of cell membrane components as described by Wang et al. (2015). Although a previous study reported that PUFA-producing yeasts are more sensitive to oxidative stress (Cipak et al., 2008), a recent study showed that high PUFA concentrations can increase membrane fluidity and enhance yeast adaptation to oxidative stress (Vázquez et al., 2019).

CONCLUSION

Based on the study, UV mutagenesis was successfully used to modify *Z. siamensis* AP1, with cerulenin proving more effective than an ethanol/H_2O_2 mixture as a selective agent. The best cerulenin-screened mutant, CR15, not only showed an accelerated growth profile but also demonstrated superior lipid accumulation, increasing lipid content between 72 and 96 hours (from 24.6% to 28.6%), unlike the wild-type and MT19 strains. This suggests the mutation blocked lipid remobilization. Furthermore, the selection method altered the fatty acid composition of CR15, producing a diverse mix of even- and odd-chain fatty acids, indicating mutated FAS enzymes. On the other hand, the ethanol/H_2O_2 mutant (MT19) adapted to oxidative stress by producing a high concentration of linoleic acid (45.75%). Further study is suggested to determine the effect of UV mutagenesis on the transcription of genes in the lipid synthesis pathway.

AUTHOR CONTRIBUTION

M.I. designed the study, analyzed the data, and wrote the manuscript. **C.E.B.S.** did the experiments and analyzed the data.

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CONFLICT OF INTEREST

The authors state there is no conflict of interest regarding the research or its funding.

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