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Original article

# PRODUCTION OF YEAST-BASED PRODUCTS: MULTI-PURPOSE USE OF TRADITIONAL FERMENTATION

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**Background.** Traditional industrial production of *Saccharomyces cerevisiae* primarily yields pressed baker's yeast through multi-stage fed-batch fermentation. However, there is increasing demand for diverse yeast-based products with tailored functional properties, requiring a more flexible production approach than the conventional single-product focus.

**Objective.** This study aimed to develop and propose a flexible fermentation scheme for an industrial *S. cerevisiae* strain to enable the production of a variety of yeast products from a single line by optimizing fermentation parameters to achieve desired biomass characteristics.

**Methods.** Using the industrial strain *S. cerevisiae* in fed-batch bioreactors, key fermentation parameters – including temperature, pH, and carbon/nitrogen dosing profiles – were systematically varied. The resulting yeast biomass was analyzed for composition (protein, trehalose, glycogen, RNA) and functional properties (rising power, ethanol tolerance) to assess the impact of the parameter modifications.

**Results.** Modifying fermentation parameters significantly influenced yeast biomass composition and functional traits. Specific fermentation profiles were successfully developed to produce biomass suitable for various products, including different forms of baker's yeast, yeast for alcohol/wine/beer production, protein source yeast, and yeast for extracts. Targeted control of parameters allowed for the accumulation of specific components essential for each application.

**Conclusions.** Optimizing *S. cerevisiae* fermentation parameters is product-specific and allows for the production of a diverse range of yeast-based products from a single industrial line. Controlling nutrient dosing, temperature, pH, and ethanol concentration enables tailoring biomass composition and characteristics, representing a significant advancement towards a versatile multi-product fermentation model.

**Keywords:** yeast; biomass; *Saccharomyces cerevisiae*; fed-batch fermentation; yeast-based product.

## Introduction

The industrial production of baker's yeast has a long-established technological framework, which has remained largely unchanged over decades. This classical scheme includes sequential operations such as the preparation of the nutrient medium, development of seed cultures, fed-batch fermentation in large-scale bioreactors, separation and filtration of yeast biomass, followed by forming and packaging of the final product [1, 2]. While this production line is well optimized and widely adopted across the baking industry, it remains structurally rigid and tailored almost exclusively to the production of a single output – pressed baker's yeast.

However, in recent years, a profound shift in consumer demand, industrial application, and sustainability considerations has occurred. The global interest in yeast-derived ingredients now extends far beyond traditional baking. *Saccharomyces cerevisiae*, the primary workhorse of industrial fermentation, is increasingly being considered as a multipurpose platform for the production of brewing and wine yeasts, ethanol-producing strains, dietary protein supplements, and functional yeast extracts [3–5, 6]. These developments are motivated not only by market diversification but also by the broader need for sustainable, circular biomanufacturing strategies [4, 6]. Despite this shift, conventional yeast production plants remain constrained by their single-product design, unable to adapt efficiently to the production of biomass with distinct compositional or functional characteristics [4].

This disconnects between existing infrastructure and new industrial needs defines the core problem addressed in the present study – the technological inflexibility of conventional yeast fermentation processes. Most industrial processes are optimized for high-yield biomass under growth-favorable conditions, but they do not accommodate modulation of biomass quality [1, 4]. As a result, producers are often forced to invest in separate infrastructure or downstream processes to meet varied product specifications, which increases both

operational complexity and production costs. Furthermore, while recent advances in genetic engineering offer solutions for customizing yeast strains, regulatory and economic barriers frequently limit their implementation at scale [7, 8].

Given this context, there is a clear need for a process-level solution that enables manufacturers to use a single strain and bioreactor line to generate multiple product types with differentiated characteristics. This study aims to develop and validate such a solution by designing a flexible, multi-output fermentation platform for an industrial strain of *S. cerevisiae*. The central hypothesis is that, through deliberate adjustment of upstream process parameters, rather than genetic modifications, it is possible to direct yeast metabolism toward the biosynthesis and accumulation of specific components (e.g., protein, glycogen, trehalose, RNA) that are essential for applications [9–11].

The research focuses on the systematic modification of core fermentation parameters, including nutrient feeding profiles (carbon/nitrogen ratios and dosing recipes), environmental conditions (pH and temperature control throughout fermentation), and stress triggers (e.g., temperature shock, ethanol exposure at specific phases) [9–11].

These parameter sets are configured based on the known metabolic responses of yeast and tailored to distinct product classes: pressed and dry baker's yeast, ethanol yeast, brewing/winemaking yeast, protein-enriched biomass for feed/food, and extract-rich biomass for nutritional additives. The experimental platform uses industrial-scale bioreactors to evaluate how changes in fermentation dynamics influence biomass composition and downstream product functionality.

By shifting the paradigm from fixed to flexible fermentation, this study contributes to the development of a more adaptable and economically efficient model of yeast-based biomanufacturing [4, 5].

## Materials and Methods

### *Strain*

Industrial strain of *S. cerevisiae* YR-1 was provided by LLC Enzym Company (Lviv, Ukraine).

### *Medium and cultivation*

Yeast growth was investigated during a fed-batch industrial fermentation in a commercial 120 $m^3$ bubble column bioreactors at LLC Enzym Company. Beet molasses previously dissolved to a content of 300 g/l of total fermentable sugars was used as a carbon source. Ammonia solution (25% by weight) was used as a nitrogen source. Sulfuric acid (96% by weight) was used to adjust the pH of the medium. All components of the nutrient medium were kindly provided by LLC Enzym Company (Lviv, Ukraine). After sterilization, the bioreactor was immediately filled with water, initial carbon and nitrogen sources, trace elements and vitamins were added, and the pH was adjusted to 5.4. After that, the inoculum was set, and the fed-batch fermentation was started. Dosing of molasses, ammonia, aeration, control of pH, temperature, and alcohol in the medium occurred automatically according to predetermined dosing profiles. After the end of fermentation, the bioreactor was discharged, and the yeast biomass was separated from the wort by means of industrial separation unit (GEA Westfalia Separator).

### *Growth rate*

The growth rate of yeast biomass in the fermenter was determined as the ratio of biomass growth per unit time to the initial biomass concentration in the medium. The average growth rate was determined as the average value of the growth rate at each hour of fermentation.

### *Biomass concentration (YDM)*

10 mL of sample was pipetted, weighed (Mettler Toledo AT200; Columbus) and heated for 24 h at the temperature of 105 °C (drying oven, PF60, Carbolite Gero). Dried sample was once again weighted, and the dry matter content (DM) was calculated according to the following formula:

$$YDM = \frac{(mdS - m)}{VS} \text{ [g/L]},$$

where mdS is mass of the crucible with the dried sample (g); $m$ is mass of the crucible (g); and VS is volume of the sample (L).

### *Yield of biomass by substrate*

The yield of biomass by substrate was determined as the ratio of dry biomass grown in the bioreactor to the mass of raw molasses used for its cultivation recalculated to 46% total fermentable sugar (TFS), according to the formula

$$Y_{x/s} = \frac{m(\text{biomass}\,100\%\ \text{d.m.})}{M(\text{molasses}\,46\%\ \text{TFS})} \times 100\%.$$

*Determination of total nitrogen and raw protein in yeast biomass*

Quantitative determination of total nitrogen was performed according to the method of Kjeldahl [12]. The raw protein content in yeast is calculated by multiplying of total nitrogen with factor 6.25.

*Determination of free amino nitrogen*

Free Amino Nitrogen were determined with commercial kit (Free Amino Nitrogen Assay Kit, Merck KGaA, Darmstadt, Germany).

*Trehalose determination*

Trehalose contents of yeast were determined by the Anthrone reagent method [13].

*Glycogen determination*

Glycogen were determined with commercial kit (EnzyChrom™ Glycogen Assay Kit, BioAssay Systems, Hayward, USA).

*Determination of RNA*

The amount 0.4–0.8 gm. of yeast cream was weighed out into a centrifuge tube. Then, 8 ml of cold 0.25N $HClO_4$ was added to the tube, and the tube was placed into a 4 °C water bath and held for 15 min. at 4 °C. Afterward, the tube was centrifuged for 10 min at 4000 rpm, and the supernatant was decanted. To the yeast pellet, 5 ml of 0.5N $HClO_4$ was added and shaken thoroughly. The tube was then placed in a 70 °C water bath for 15 min, with shaking every 3-4 minutes. Afterward, the tube was centrifuged for 10 min at 4000 rpm. Without disturbing the yeast pellet, 1 ml of supernatant was removed and added to 100 ml DI $H_2O$ in a volumetric flask. The mixture was thoroughly mixed, and measurements were carried out by spectrophotometer at 260 nm using DI $H_2O$ as a blank. The RNA content was calculated by averaging three consecutive measurements using the formula

$$\%\,\text{RNA in cream yeast} = \frac{(\text{Absorbance value} \times \text{Dilution} \times 0.03365 \times 5\ \text{ml} \times 100)}{(\text{Wt. of sample in mg} \times \%\ \text{solids in sample}/100)}.$$

*Determination of viable yeast cells*

YM agar medium (MALT WICKERHAM) was used to determine the number of viable cells. After preparation, the medium was autoclaved at 120 °C for 20 min. Following inoculation with the appropriate dilutions of the sample to achieve 30–300 colonies, the dishes were incubated at 25–30 °C under aerobic conditions for 48 to 72 hours. The number of colonies forming units (CFU) in the dishes containing 30–300 colonies was counted, and the weight of the dry matter was referenced [14].

*Determination of dead cells*

The percentage of dead cells was determined through microscopy using methylene blue. To do this, 1 ml of yeast suspension was mixed with 1 ml of methylene blue buffer solution. The cell counting chamber was carefully filled using a pipette. After filling, the chamber was allowed to stand for 3 minutes to allow the yeast cells to settle and evenly distribute in the field of view. Following this, the number of cells was counted. The percentage of dead cells was determined by dividing the number of blue-stained cells, shrunken, and deplasmolyzed cells by the total number of cells counted in the chamber, using the formula:

$$X = \frac{a}{S} \times 100\%,$$

where $a$ is the number of dead, shrunken, deplasmolyzed cells, and $s$ is the total number of cells counted in the chamber [14].

*Determination of ethanol in wort*

Ethanol in liquid sample was extracted by Tri-n-butyl phosphate (TBP, Sigma Aldrich, USA). One mL of TBP and 1 mL of aqueous sample was mixed in a microtube and then vortex vigorously for 1 min. The mixture was centrifuged at 3,420 × g for 5 min to separate into two phases. Upper phase, TBP layer, was clear and transparent, while lower phase, water later, was turbid. Then, 500 μL of upper phase was transferred to a new microtube and mixed with 500 μL of dichromate reagent (containing 10% w/v of $K_2Cr_2O_7$ in 5M of $H_2SO_4$), and vortex vigorously for 1 min. The mixture was set still for 10 min at room temperature to allow oxidation product in lower phase developed its color to blue green. One hundred microliters of the oxidation products were diluted with 900 μL of deionized water. The optical density at 595 nm (A595) of tested sample was measured in spectrophotometer (T80+ UV/Vis Spectrometer, PG Instrument Ltd., USA). The ethanol concentration in sample was estimated from the ethanol standard curve representing the relationship between A595 and the concentrations of ethanol [15].

*Ethanol tolerance determination*

The yeast isolates were screened for its efficiency in ethanol; the tolerance of each isolate was studied by allowing the yeast to grow in liquid

YEPG medium. The prepared medium was dispensed into (150 ml) Erlenmeyer flasks and sterilized by autoclaving at 121 °C for 15 min. The medium in the flasks were allowed to cool to a temperature of about 45 °C and absolute ethanol was added in varying percentage concentrations from 6% to 15% with a step of 0.5 [16].

*Yeast rising power determination*

The rising power was determined according to the method of the VH Berlin Yeast Industry Institute. 7.5 g of fresh compressed yeast; or 2.25 g of Instant Active Dry Yeast (IADY); or liquid yeast equivalent to 7.5 g of Fresh yeast at 30% YDS were used. A beaker or measuring vessel with 200 ml of tempered potable water (30 °C) was prepared. The tempered flour was placed into the kneading chamber, and the kneader was switched on. The salt solution was added to the flour, followed by the yeast suspension. Water was added until a total of 180 ml was used. All ingredients were thoroughly mixed for 1 minute, and then water was added until a dough strength of 500 FE ± 50 FE was achieved on the Farinograph-scale. The dough was left to rest for 5 min with the lid on the kneading chamber. The dough consistency was adjusted with small additions of water until it reached 500 FE ± 50 FE again. The dough was removed from the kneader chamber, and 350 g of dough was placed on a PE-foil-sheet, then transferred and pressed into the baking form of the SJA Fermentograph. The filled baking form was transferred into the tempered SJA Fermentograph chamber (30 °C). The raising power, defined as the amount in ml of $CO_2$ gas produced over 2 hours from 1 g dry yeast biomass, was calculated from the $CO_2$ gas amount measured after the break at 60 minutes and the amount developed until the 120th minute (ml $CO_2$/2 hr/g d.m.) [17].

## Results

The study investigated the impact of varying fermentation parameters on the biochemical composition and functional properties of *S. cerevisiae* strain YR-1 biomass. Key parameters analyzed included protein, trehalose, glycogen, and RNA content, as well as functional indicators like rising power and ethanol tolerance [18].

Dependence of protein accumulation on temperature and pH was determined (Fig. 1). Maximum protein accumulation was observed at a medium pH in the range of 5.0–6.5, with the highest accumulation at pH 5.5. Lowering the temperature from 36 °C contributed to protein accumulation, reaching a maximum at 30 °C. Thus, the optimal parameters for maximum protein accumulation by the strain were found to be a fermentation temperature of 30 °C and pH of 5.5.

The accumulation of storage carbohydrates, glycogen and trehalose, was also found to be dependent on temperature (Fig. 2). Glycogen accumulated in optimal conditions for growth with an excess of carbon source, with the optimal temperature for glycogen accumulation being 30 °C. Trehalose began to accumulate in the stationary phase of growth under nitrogen limitation, with an optimal temperature of 36 °C. Maximum trehalose content as a reaction to temperature shock was achieved with a sharp change in temperature from optimal for growth to a temperature close to critical for cell viability.

Different fermentation schemes were investigated for obtaining yeast biomass suitable for various products: yeast concentrate, pressed yeast for bakery, pressed yeast for alcohol production, dry instant baker's yeast, dry yeast for wine and beer production, yeast as an alternative protein source, and yeast for yeast extracts. Table 1 summarizes

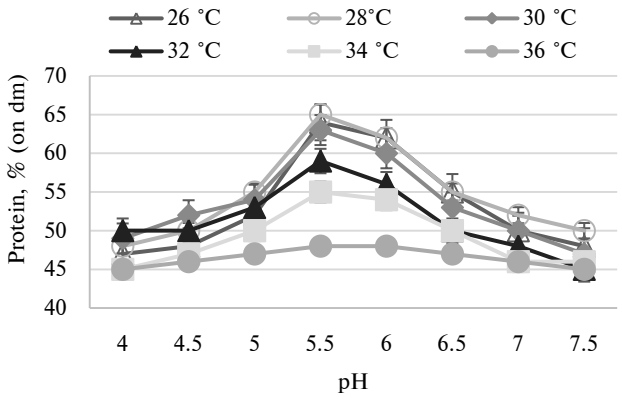


**Figure 1:** Dependence of protein accumulation on temperature and pH

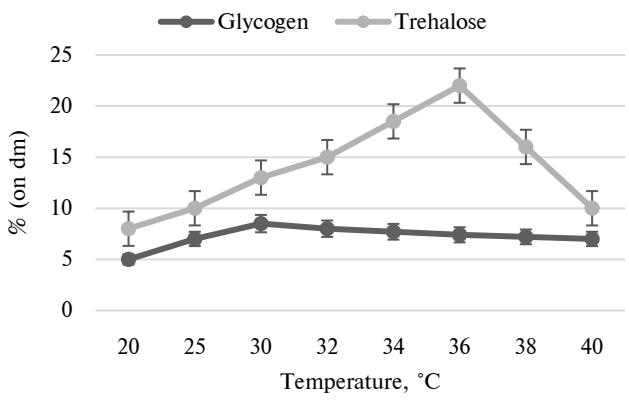


**Figure 2:** Dependence of accumulation of glycogen and trehalose on temperature

the main fermentation parameters (fermentation time, specific growth rate, seed percentage, initial and final YDM concentration, protein, trehalose, glycogen, and RNA content, and yield) for each product type. Table 2 presents the characteristics of the final yeast products, including rising power, shelf life, ethanol tolerance, total nitrogen, free amino nitrogen, viable cells, and dead cells.

For yeast concentrate (liquid yeast for bakery), fermentation parameters were set to achieve maximum biomass accumulation, presence of glycogen, and absence of trehalose, without temperature shock (Fig. 3a). Ethanol concentration was maintained at 0.15% (w/w). Nitrogen dosing stopped one hour before carbon dosing.

**Table 1:** Characteristics of the fermentation process under different yeast growing conditions

| Product type | Fermentation time, h | μ (average), h (–1) | Seed, % | Initial concentration YDM, g/l | Final concentration YDM, g/l | Protein, % (on dm) | Trehalose, % (on dm) | Glycogen, % (on dm) | RNA, % (on dm) | Yield, gYDM/gTFS |
|---|---|---|---|---|---|---|---|---|---|---|
| Liquid yeast for bakery | 17.0 | 0.15 | 7.8 | 5.5 | 69.9 ± 1.2 | 48.1 ± 0.8 | 9.0 ± 0.2 | 7.0 ± 0.3 | 4.0 ± 0.3 | 51.1 ± 0.5 |
| Pressed yeast for bakery | 16.5 | 0.13 | 11.7 | 7.6 | 65.0 ± 0.9 | 44.0 ± 0.5 | 12.0 ± 0.3 | 8.0 ± 0.2 | 4.5 ± 0.3 | 54.2 ± 0.7 |
| Pressed yeast for alcohol fermentation | 17.0 | 0.14 | 9.3 | 6.0 | 65.3 ± 0.8 | 47.3 ± 0.8 | 10.0 ± 0.2 | 8.0 ± 0.3 | 4.0 ± 0.3 | 52.0 ± 0.4 |
| Dry yeast for bakery | 19.0 | 0.12 | 10.2 | 7.1 | 69.8 ± 0.8 | 42.2 ± 0.7 | 18.0 ± 0.4 | 5.0 ± 0.2 | 3.0 ± 0.2 | 54.5 ± 0.5 |
| Dry yeast for wine & beer production | 16.5 | 0.13 | 11.7 | 7.0 | 60.0 ± 0.6 | 38.0 ± 0.5 | 22.0 ± 0.3 | 5.0 ± 0.2 | 4.5 ± 0.3 | 50.7 ± 0.7 |
| Protein source yeast | 15.0 | 0.18 | 6.7 | 3.7 | 54.8 ± 0.7 | 65.1 ± 0.9 | 1.8 ± 0.1 | 1.3 ± 0.3 | 6.0 ± 0.3 | 46.0 ± 0.8 |
| Yeast for yeast extracts | 12.0 | 0.21 | 8.0 | 4.0 | 49.7 ± 0.9 | 60.5 ± 0.8 | 2.1 ± 0.1 | 1.9 ± 0.2 | 8.0 ± 0.4 | 48.5 ± 0.5 |

*Notes.* μ – specific growth rate, YDM – yeast dry matter, TFS – total fermentable sugar ($p < 0.05$).

**Table 2:** Characteristics of yeast-based finished products

| Product type | Raising power, ml$CO_2$/2hr/g d.m. | Shelf life, days | Ethanol tolerance, %(v/v) ethanol | Total nitrogen, % | Free amino nitrogen, % | Viable cells, CFU/g | Dead cells, % |
|---|---|---|---|---|---|---|---|
| Liquid yeast for bakery | 990 ± 27 | 5 | 8.0 | 7.7 ± 0.2 | N/A | >1.0·10E + 09 | <5 |
| Pressed yeast for bakery | 930 ± 23 | 40 | 9.5 | 7.0 ± 0.2 | N/A | >1.0·10E + 09 | <10 |
| Pressed yeast for alcohol fermentation | N/A | 24 | 13.5 | 7.5 ± 0.2 | N/A | >1.0·10E + 09 | <10 |
| Dry yeast for bakery | 890 ± 25 | 730 | 10.0 | 6.7 ± 0.2 | N/A | >5.0·10E + 09 | <30 |
| Dry yeast for wine & beer production | N/A | 1095 | 12.0 | 6.1 ± 0.2 | N/A | >1.0·10E + 10 | <10 |
| Protein yeast (dry) | N/A | 730 | N/A | 10.5 ± 0.3 | 1.2 ± 0.1 | <1.0·10E + 02 | N/A |
| Yeast extracts (dry) | N/A | 730 | N/A | 12.2 ± 0.4 | 6.7 ± 0.2 | <1.0·10E + 02 | N/A |

*Notes.* N/A – not applicable ($p < 0,05$).

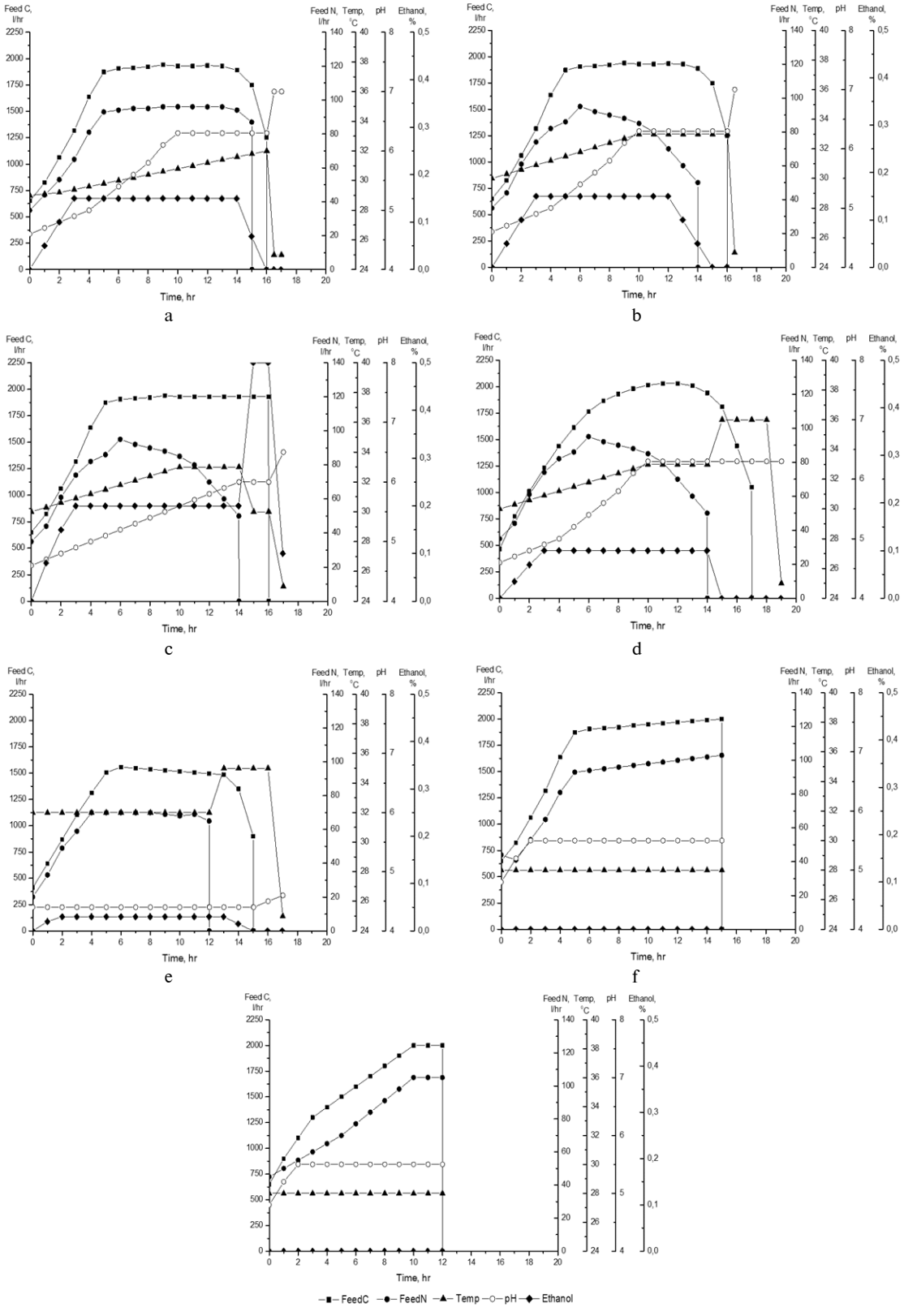


**Figure 3:** Parameters of the fermentation process of *S. cerevisiae* yeast strain YR-1 for various fields of application: (a) liquid yeast, (b) pressed baking yeast, (c) pressed baking yeast for alcohol production, (d) instant dry baker's yeast, (e) dry yeast for winemaking and brewing, (f) protein source yeast, (g) yeast for the yeast extracts

For pressed baking yeast, fermentation included a changed nitrogen dosing profile, stopping two hours before molasses completion, and an increased temperature to 33 °C in the second half (Fig. 3b). A maturation stage was included.

Pressed yeast for the alcohol industry involved maintaining a higher ethanol content (0.2% w/w, rising to 0.5% w/w after nitrogen stop), similar nitrogen dosing to pressed baking yeast, and increased temperature to 33 °C in the second half (Fig. 3c).

Instant dry baker's yeast fermentation featured increased carbon dosing duration, nitrogen dosing with initial excess followed by decrease and stop three hours before molasses completion, and a sharp temperature rise (thermal shock) after nitrogen stop (Fig. 3d).

Dry yeast for winemaking and brewing used a shorter fermentation time, reduced nitrogen dosage, and lower alcohol content compared to dry baker's yeast fermentation (Fig. 3e).

Yeast as a source of alternative protein involved carbon dosing throughout fermentation to maintain maximum growth rate, maintaining optimal temperature and pH for biomass accumulation, and nitrogen dosing before the end of molasses dosing (Fig. 3f).

Yeast for yeast extracts production featured maximum and simultaneous dosing of carbon and nitrogen sources throughout fermentation, maintaining optimal temperature (28 °C) and pH (5.5), and a significantly decreased fermentation duration (12 hours) (Fig. 3g).

Table 1 and Fig. 3 illustrate the specific parameter profiles and their resulting impact on biomass composition and yield for each product type. Table 2 shows the corresponding functional properties of the final products.

The observed dependencies of protein, glycogen, and trehalose accumulation on temperature, pH, and nutrient availability (Figs. 1 and 2) align with established knowledge regarding yeast metabolism and stress response. Specifically, the optimal conditions identified for protein synthesis (30 °C, pH 5.5) correspond to favorable conditions for general anabolic processes. Glycogen accumulation under excess carbon and optimal growth conditions reflects its role as a readily mobilizable storage compound for maintaining vitality. The accumulation of trehalose under nitrogen limitation and temperature shock confirms its crucial role in protecting cells against environmental stresses, particularly dehydration encountered during drying processes (Tables 1 and 2).

The results presented in Table 1 and Fig. 3 demonstrate the feasibility of implementing distinct fermentation strategies to achieve desired biomass characteristics for seven different product types. For instance, maximizing protein content for food/feed applications requires maintaining optimal growth conditions and excess nitrogen, whereas producing dry yeast necessitates conditions promoting trehalose accumulation for drying resistance. The data in Table 2 further validates that these tailored fermentation processes result in final products with the required functional properties, such as high rising power for baker's yeast, high ethanol tolerance for alcohol yeast, and high viable cell counts for dry wine/beer yeast as per International Oenological Codex standards.

In addition to quality indicators of the fermentation process, it is also important to take into account indicators that affect the economy of the process, such as substrate yield, final biomass concentration and fermentation duration. A high yield of the process is achieved by maintaining conditions optimal for growth in the first half of fermentation and optimal for the product in the second. The necessary concentration of biomass is achieved by changing the duration of the first part of fermentation, during which intensive accumulation of biomass occurs. The findings confirm that the biochemical composition and functional properties of *S. cerevisiae* biomass are highly dependent on the specific fermentation parameters employed.

## Discussion

This study assessed the feasibility of transforming a classical single-product yeast production scheme into a flexible, multi-product fermentation platform using an industrial *S. cerevisiae* strain. The design was based on the systematic variation of key upstream parameters, including nutrient dosing strategies, temperature, pH, and ethanol concentration, with the goal of modulating yeast biomass composition and function to match application-specific requirements. While the findings demonstrate the viability of this strategy at an industrial scale, several aspects of the experimental design, limitations, and broader implications warrant critical analysis.

The study employed a quasi-factorial approach, wherein one or more variables (e.g., nitrogen depletion timing, carbon feed duration) were sequentially modified to assess their impact on biomass composition. This approach enabled the identification of causal trends between specific

fermentation conditions and biochemical or functional outcomes (e.g., protein, trehalose, and glycogen accumulation). However, the experimental design lacks full factorial structure, which restricts the ability to evaluate higher-order interaction effects, such as temperature × pH or nitrogen × ethanol, that are known to exhibit synergistic or antagonistic behavior in yeast metabolism [4, 9].

Another limitation is the scale of implementation: although the experiments were conducted in industrial-scale bioreactors (120 $m^3$), the study did not include the use of fermenters of a different volume and, accordingly, did not investigate the impact of scaling up the process. This limits the statistical power and reproducibility of the conclusions. Moreover, while biomass composition was comprehensively characterized, genomic or transcriptomic analyses were not performed, which constrains mechanistic insight into metabolic shifts observed under different conditions. While the study focused on phenotypic and biochemical endpoints (e.g., dry matter yield, trehalose content, rising power), this limits the mechanistic understanding of the observed shifts in metabolism. Integrating transcriptomic or metabolomic analyses, as proposed by Yook and Alper [8], would provide valuable insight into the regulatory circuits driving biomass differentiation.

At the same time, the results presented in the article confirm and expand existing knowledge about yeast physiology. For example, the increased protein accumulation under optimal pH (5.5) and temperature (30 °C) aligns with established models of anabolic growth [4, 9]. Similarly, glycogen accumulation during active growth and trehalose accumulation during nitrogen limitation or thermal stress are consistent with their known roles as energy storage and cytoprotective molecules, respectively [3, 11]. These observations support the conclusions of Halász & Lásztity, who describe trehalose as a stress marker critical for desiccation tolerance in dried yeast [18]. Importantly, the study advances the field by demonstrating that these metabolic shifts can be intentionally steered through process control, rather than relying on post-fermentation modification or genetic engineering. While Sirisena *et al.* [10] explored how proteolysis alters amino acid composition post-process, our findings show that biochemical profiles can be preconditioned at the fermentation stage, offering advantages in cost and functionality.

This work supports the growing consensus that *S. cerevisiae* can serve as a modular bioproduction platform, capable of yielding diverse biomass profiles under tailored process conditions [5–7]. The proposed model allows for the production of baking, brewing, ethanol, protein, and extract-grade yeast using a single strain and equipment line. This contrasts with the traditional paradigm of specialized strains and facilities [1, 2], representing a significant advancement in resource efficiency, production flexibility, and process sustainability [6].

Nevertheless, the assumption of universal strain suitability must be approached cautiously. The use of a single industrial strain *S. cerevisiae* YR-1 may limit generalizability, as strain-specific responses to stress or nutrient shifts are well-documented [5, 8]. The downstream processing protocols were also held constant, which may not be optimal for all product types, particularly dried or extract-based yeasts that require specific stabilization or cell lysis strategies [11].

Furthermore, process economics, including yield, energy input, and cycle time, were only briefly discussed. As noted by Vieira *et al.* [19] and Zakhartsev *et al.* [20], optimal conditions for biomass quality may not coincide with those for maximum productivity, requiring a more detailed analysis of economic trade-offs in future work.

To progress toward a fully adaptive and industrially viable fermentation model, future research should focus on several key directions. First, implementing full factorial designs and response surface modeling would allow for a deeper understanding of interaction effects between process variables and their influence on biomass quality. Additionally, integrating omics-level data, such as transcriptomics and metabolomics, would enable the elucidation of underlying regulatory mechanisms that govern observed phenotypic changes in yeast under varying fermentation regimes. Long-term studies evaluating the genetic and physiological stability of *S. cerevisiae* strains under alternating fermentation conditions are essential to ensure process robustness and reproducibility. Equally important is the refinement of downstream processing steps, which must be tailored to the specific requirements of each product type to maintain quality and yield. Finally, a comprehensive techno-economic assessment comparing this flexible fermentation approach with conventional single-product lines would be instrumental in demonstrating its industrial viability and cost-effectiveness.

## Conclusions

This study demonstrates that precise manipulation of fermentation parameters, such as nutrient

feeding, pH, temperature, and ethanol concentration, enables targeted modulation of *S. cerevisiae* biomass composition in a fed-batch process. By adjusting these variables, it is possible to steer the accumulation of specific intracellular components such as protein, trehalose, glycogen, and RNA, thereby tailoring the biomass to meet the requirements of various industrial applications. The proposed flexible fermentation strategy allows for the production of multiple yeast-based products using a single industrial strain and platform, representing a significant advancement over traditional single-product processes. This approach enhances resource efficiency and operational adaptability without the need for genetic modification or separate infrastructure. At the same time, certain limitations were identified. The absence of molecular analyses restricts mechanistic understanding, and downstream processing was not optimized for individual product types. Moreover, strain stability under varying conditions requires further validation. Future research should focus on integrating omics approaches, refining downstream protocols, and assessing long-term process robustness. Overall, the study establishes a scalable, sustainable model for adaptive biomanufacturing, contributing to the development of versatile yeast-based production systems aligned with modern bioprocess engineering principles.

## Interests disclosure

The authors declare that there is no conflict among the contributing authors related to the financial or non-financial interests that are directly or indirectly related to the work submitted for publication.

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**ВИРОБНИЦТВО ПРОДУКТІВ НА ОСНОВІ ДРІЖДЖІВ: БАГАТОЦІЛЬОВЕ ВИКОРИСТАННЯ ТРАДИЦІЙНОЇ ФЕРМЕНТАЦІЇ**

**Проблематика.** Традиційне промислове виробництво дріжджів *Saccharomyces cerevisiae* зосереджене переважно на виробництві пресованих пекарських дріжджів. Однак попит на різноманітні дріжджові продукти зі спеціально підібраними функціональними властивостями зростає, і це вимагає більш гнучкого підходу до виробництва, ніж традиційна орієнтація на один продукт.
**Мета.** Розробити та запропонувати гнучку схему ферментації для промислового штаму *S. cerevisiae*, щоб забезпечити виробництво різноманітних дріжджових продуктів з однієї лінії завдяки оптимізації параметрів ферментації для досягнення бажаних характеристик біомаси.
**Методика реалізації.** З використанням штаму дріжджів *S. cerevisiae* у приточних біореакторах проведено систематичну зміну ключових параметрів ферментації, включаючи температуру, pH і профілі дозування вуглецю/азоту. Отриману дріжджову біомасу аналізували на склад (білок, трегалоза, глікоген, РНК) та функціональні властивості (підйомна сила, толерантність до етанолу) для оцінки впливу модифікацій параметрів.
**Результати.** Модифікація параметрів ферментації суттєво вплинула на склад і функціональні властивості дріжджової біомаси. Були успішно розроблені специфічні профілі ферментації для отримання біомаси, придатної для різних продуктів, включаючи різні форми пекарських дріжджів, дріжджі для виробництва спирту/вина/пива, дріжджі як джерело білка та дріжджі для екстрактів. Цільовий контроль параметрів дав можливість накопичувати специфічні компоненти, необхідні для кожного застосування.
**Висновки.** Оптимізація параметрів ферментації *S. cerevisiae* залежить від продукту і дає змогу виробляти різноманітний асортимент дріжджових продуктів з однієї промислової лінії. Контроль дозування поживних речовин, температури, pH та концентрації етанолу дає можливість адаптувати склад і характеристики біомаси, що є значним кроком до універсальної багатопродуктової моделі ферментації.

**Ключові слова:** дріжджі; біомаса; *Saccharomyces cerevisiae*; приточна ферментація; продукти на основі дріжджів.