



Research Article

Predicting the weight of bread pastry fermented with yeast strains and their hybrid genotypes

Mervat Ibrahim Kamal* 

Department of Genetics, Faculty of Agriculture, Mansoura University, 60 El Gomhoureya St., EL Mansoura, EL Dakahleya Governorate, Egypt.

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Prof. Dr. Gian Carlo Tenore

Corresponding Author

Prof. Dr. Mervat Ibrahim
Kamal
E-mail:
dr_mervat@mans.edu.eg
Tel: +002-01008665560

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Abstract

The leavening ability of yeast genotypes is critical for the final bread quality, as their cells produce carbon dioxide and other metabolites that affect the weight, volume, and taste of the loaf pastry. This investigation aimed to detect the correlation and regression between the weight of the fermented loaf pastry influenced by carbon dioxide production during the leavening period, to determine the weight of the loaf pastry at any leavening time. The testing was performed using three parental wild-type strains of *Saccharomyces cerevisiae*, in addition to two hybrid genotypes resulting from two hybridizations between parental strains. To achieve this correlation, this study presents the leavening ability dynamics of different yeast genotypes affecting the weight of the loaf pastry during leavening time under sucrose stress. This weight was strongly influenced by the CO₂ released by the yeast cells. To do so, the weight of the fermented pastry was measured during leavening time and the interrelationship between both factors was analyzed using regression and correlation analyses. The weight of the fermented loaf pastry was depended on variations in leavening ability time. Correlation coefficient and regression value between both factors were negative because they are varied in opposite directions. If leavening time increases, the weight of the fermented loaf pastry declines due to CO₂ production by *Saccharomyces cerevisiae* cells, which leads to an increase in loaf pastry volume and a reduction in weight and density. The results indicated that regression analysis is a powerful tool in yeast genetics. It enables microbial geneticists to describe, predict, and assess the relationship between the weight of the fermented loaf pastry and leavening time.

1. Introduction

Microorganisms are constantly exposed to environmental stimuli and stresses. The environmental stress response in *Saccharomyces cerevisiae* is a complex strategy in which responses to many stresses partially overlap [1]. Leavening at lower temperatures is associated with fresh traits and reduces the risk of bacterial contamination [2]. The use of low temperatures through the leavening performance process not only improves the quality of products but also prolongs the time needed to

complete leavening ability. This, leading to an increase in the economic costs and requirements of energy. Industrial applications are interested in developing yeast genotypes with an enhanced capability of leavening at lower temperatures (10-15 °C). It is interesting to note that cold temperatures induce biochemical, biophysical, and physiological changes in yeast cells. Cold temperatures strengthen the interaction between two strands of DNA and the secondary structure of messenger RNA (mRNA),

therefore, transcription and translation are impaired [3].

The yeast used in bread manufacturing is *Saccharomyces cerevisiae*, which can convert fermentable sugars present in loaf pastry into ethanol and carbon dioxide as the main end products. Leavening efficiency depends on the genotype, the form of yeast and the availability of fermentable sugars in wheat flour, such as maltose released by starch hydrolysis. The increase in the volume of the loaf pastry is the most apparent physical change related to leavening ability [4]. Wheat flour was used for bread manufacture because it is the only flour from cereal crops capable of generating baked loaves with a highly aerated structure. This is due to the presence of gluten, a unique protein that can develop a continuous macromolecular viscoelastic network when mixed with water and subjected to sufficient mechanical mixing [5]. The normal genome of *Saccharomyces cerevisiae* has 16 ($n = 16$) distinct chromosomes ranging in length from 230 to 1.532 kilobases [6]. *Saccharomyces cerevisiae* is an unicellular fungus. It is isolated from sugary foods and alcoholic beverages. This organism can ferment sugars and produce mainly ethanol and carbon dioxide under anaerobic conditions. By enzymatic action, *Saccharomyces cerevisiae* converts fermentable sugars and some of the loaf pastry starch into carbon dioxide and alcohol, where CO₂ causes the loaf pastry volume to rise [7]. Since the early 1900s, maize has been hybridized to increase the yield and introduce biodiversity [8]. Besides, hybrid yeast cells were obtained from leavening ability processes. Hybrid vigor in yeast confers a competitive benefit by facilitating transgressive phenotypes in different environments, which drives fungal diversity and adaptation [9].

Yeast hybrids play an important role in leavening ability traits and their related phenotypes as efficient leavening ability of maltose and maltotriose. Investigation of these hybrids supports the leavening ability of *S. cerevisiae* through hybrid vigor. Hybrids contain more genomic content of *S. cerevisiae*, which is related to higher typical viabilities and higher ethanol production [10]. Hybrid yeasts can show unique traits that are not necessarily intermediate between their

parents, which provide a selective advantage in a changing environment, this phenomenon is known as hybrid vigor. In microorganisms such as yeasts, distinct species may have few or no morphological differences, and can exhibit physiological alterations. However, these may vary widely among strains of the same species. Thus, the identification of hybrids based on morphological or physiological traits is a very difficult task. The metabolic trait of leavening capabilities was used as a marker in crosses between strains, that allowed the discovery of several yeast genotypes, described as hybrids [11]. Hybrid yeasts have been commonly found in industrial environments as those from leavening of different products [12]. In addition, yeast hybrids have also been identified in natural environments [11]. These cases suggested that the new recombinants released from hybridization in yeast are a powerful driver for adaptation to novel environments. A reasonable hypothesis is that yeast hybrids are common in other changing environments, particularly those with extreme or unusual environments [13].

Many types of wheat pastry are fermented with, *Saccharomyces cerevisiae*. When yeast is used for manufacturing bread, the loaf pastry is kneaded until smooth and then left to rise until it doubles in size. The pastry shape was left to rise until it was the correct size and then baked into the final product [14]. Yeast has been used in bread manufacturing for at least 6000 years. It is a key ingredient in bread making [15]. The success of the technological process in bread-making is the formation of gas. The volume of yeast-fermented products is based on the production of CO₂ by yeast cells [16]. Two methods are used to evaluate the fermenting power of baker's yeast, one of them measures the time required for loaf pastry rise to a given volume, and the other measures the loaf pastry volume for a given proof time [17]. Gas production can be estimated by the oven rise recorder, paleography, or pressure meter methods. The amount of gas produced was measured by measuring the volume and pressure of the released gas [18]. *Saccharomyces cerevisiae* is used for the production of fermented foods, such as bread, wine, and beer. This is because of desirable characteristics, including efficient and complete leavening ability of the medium

Table 1. Diploid baker's yeast and their hybrids used in this investigation.

Strains	Sample	Source
P ₁	Pakmaya	Made in Turkey, referred as Pak Gida Uretim Ve Pazarlama A. S.
P ₂	Holw El-Sham	Food Industries of Holw El-Sham Company for and Agriculture investment (S. A. E), 6 October City, Egypt
P ₃	Dream	New Borg El-Arab City, Alexandria, Egypt referred as Dreem Mashreq Foods (S. A. E)
H ₁	Hybrid genotype	P ₃ × P ₁
H ₂	Hybrid genotype	P ₂ × P ₁

medium containing high sugar concentrations, acceptable flavors, high ethanol production, absence of toxins, and tolerance to changing environments [19]. Produced CO₂ by baker's yeast during leavening process increases the loaf pastry size and decreases the weight via the incorporation of air bubbles into the loaf pastry matrix [20].

The fermentable sugars present in the flour were converted into CO₂ and ethanol. The leavening performance depends on the availability of fermentable sugars in flour produced through starch hydrolysis [4]. Carbohydrates present in the flour as sucrose are converted to glucose and fructose due to invertase enzyme released by yeast cells [21]. If the leavening process is delayed, the acid released through the oxidation of ethyl alcohol leads to the production of sour taste products [22].

During bread making, air bubbles are incorporated into the loaf pastry, which is considered to be the nuclei of the gas bubbles. The leavening agent produces CO₂ within the liquid phase, resulting in the nuclei expanding into gas cells, thereby reducing the density of the loaf pastry. Consequently, the weight of the fermented loaf pastry decreased. The fermenting power is characterized by the quantity of CO₂ gas produced in the loaf pastry prepared from flour, which depends on α and β -amylase that transforms part of the starch into maltose, as well as the genotype of yeast cells [23]. Several methods have been used to analyze phenotypic stability [24]. These methods are divided into two main groups: univariate and multivariate stability statistics. Joint regression is the most popular univariate method because of its simplicity and applicability [25]. Joint regression provides a conceptual model of genotypic stability [25]. The genetic-environment interactions from the diversity analysis were partitioned into the

heterogeneity of the regression coefficient [26] defined a genotype with a coefficient of regression equal to zero as stable. Meanwhile, [27] described a genotype with a regression coefficient equal to 1 as stable. According to the joint regression model, a stable genotype has high leavening ability [27]. Therefore, this investigation aimed to analyze the regression and correlation between leavening ability time and the weight of the fermented loaf pastry affected by yeast strains and their hybrids.

2. Materials and methods

2.1. Strains and growth conditions

Diploid *Saccharomyces cerevisiae* strains isolated from dry yeast, as well as their hybrids as described by Kamal [28], were used in this study (Table 1). The strains and their hybrids were grown in a complete yeast extract peptone glucose (YEPG) medium according to Tomova et al. [29].

2.2. Loaf pastry manufacturing

The following ingredients were mixed well to develop the loaf pastry: 325 g wheat flour, 3.5 g salt, 210 mL cell suspension of *S. cerevisiae*, as well as, sucrose (0, 2, 4, 6, and 8 g). Each concentration of sucrose was added to each pastry ingredient to develop loaf bread.

2.3. Prepare yeast cell suspension

Yeast strains and their hybrids were grown in 250 mL medium in 500 mL Erlenmeyer flasks at 30°C. The pH was then adjusted to 6.0. Different yeast genotypes were grown under shaking (160 rpm) for three days. The cells were harvested by centrifugation, washed twice, and then suspended in 210 mL of water to be used as a leavening agent during the preparation of the loaf pastry.

2.4. Leavening ability

The leavening ability of *S. cerevisiae* strains and their hybrid genotypes was assessed by weighing the

fermented loaf pastry every five minutes without placing the wheat pastry in water containing the baker's yeast as a leavening medium [30]. After manufacturing the loaf pastry, it was divided into three symmetrical cores. The cores were weighed at zero time and directly transferred into a 300 mL baker without water. The loaf pastry cores were weighed every 5 min during the leavening time of 15 min according to [31].

2.5. Regression and correlation analyses

The association between two quantitative variables was analyzed using correlation and regression analyses. Correlation analysis quantifies the value of the relationship between two factors. The regression equation expresses this relationship. To quantify the strength of the association between the weight of fermented loaf pastry and the leavening time, the calculation of correlation coefficient and linear regression equation was discussed and illustrated according to Bewick et al. [32]. Briefly, simple linear regression has only one independent variable named x variable and one dependent variable named y variable. If the data points on the scatter plot fit a regression line. This allows estimates of y values from the x values [33]. Correlation does not allow such estimations but describes the strength of relationships. In Pearson's correlation analysis, both factors were normally distributed. In contrast, in linear regression, the independent variable values (x) are considered constants because they are chosen by the investigators in the experimental protocol. Therefore, Pearson's correlation measures a linear relationship between two normally distributed random variables [33].

3. Results and discussion

3.1. Regression analysis of leavening dynamics by P_1 genotype

As shown from the results diagrammatic in Fig. 1, the regression coefficient at zero sucrose concentration between leavening ability time and the weight of the fermented loaf pastry influenced by the parental strain P_1 genotype is -0.0082 . It is indicated that, in this technique, the weight of the fermented loaf pastry decreased by -0.0082 g with each additional minute of leavening time. Therefore, linear regression can be used to estimate the weight of fermented loaf pastry

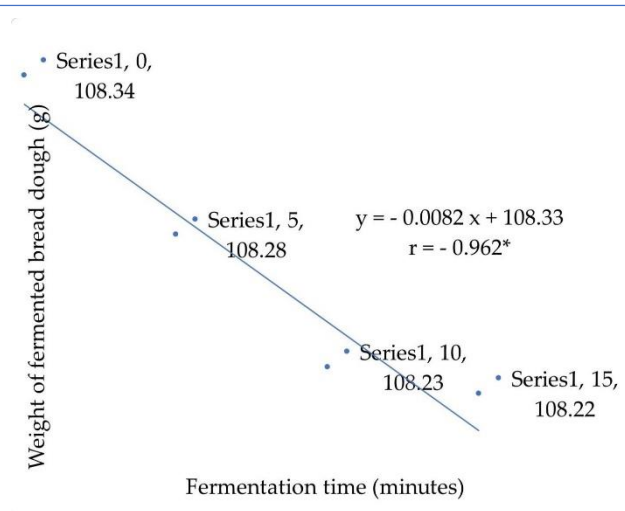


Figure 1. Regression line for the association between response variable weight of fermented bread dough affected by P_1 genotype and the independent variable fermentation time at zero concentration of sucrose (*significance at 0.05).

at any time during the leavening period inside this figure. Mathematically, it is possible to estimate the weight of the loaf pastry whose time of leavening ability was located outside the leavening time used herein. However, such extrapolation is common, and not useful. Thus, the regression line can be used to predict the weight of the fermented loaf pastry for a given leavening time. This line shows the direction in which the weight of fermented loaf pastry responded to each minute of the explanatory variable. The correlation coefficient (r) assess how well the regression line describes the obtained data. However, the correlation coefficient (r) was equal to -0.962 , therefore, $r^2 = 0.9254$. This indicated that 92.54% of the diversity in the weight of fermented loaf pastry is attributed to the leavening time. The negative correlation obtained between both factors reflected that the variations in both factors were not in the same pathway. This indicated that the lower weight of the loaf pastry was associated with the increase in leavening time. The remaining 7.46% of the diversity in the weight of the loaf pastry might be explained by other factors that were not included in the analysis.

According to Fig. 2, the regression coefficient between both factors at 2 g sucrose concentration was equal to -0.0086 . In this model, the weight of the fermented loaf pastry was decreased by -0.0086 g with each additional minute of leavening time. Furthermore, the

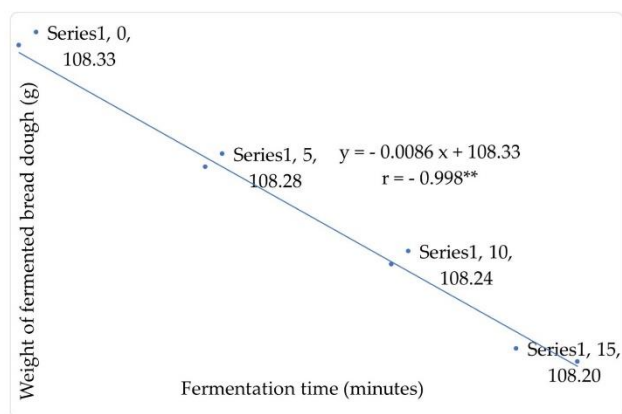


Figure 2. Regression line for the association between response variable weight of fermented bread dough affected by P₁ genotype and the independent variable fermentation time at 2 g concentration of sucrose (**0.01 probability levels).

correlation coefficient (r) between both factors was equal to - 0.998, therefore $r^2 = 0.9960$. This indicates that 99.60% of the diversity in the weight of the fermented pastry was attributed to leavening time. The remaining 0.4% is due to other factors that are not included in this analysis. These results were in harmony with Moore et al. [34], who decided that the correlation coefficient above 0.7 was higher because if $r = 0.7$, then $r^2 = 0.49$, which means that approximately 50% of the diversity in the dependent variable can be attributed to the independent variable or explanatory variable.

Regarding Fig. 3, the regression coefficient at 4 g sucrose concentration of - 0.0084 means that, in this model, the weight of the fermented loaf pastry decreases by - 0.0084 g with each additional minute of leavening time. This indicates that the regression line shows the extent and direction of the change in the weight of the fermented loaf pastry when the leavening ability time increases. Therefore, the regression line can be used to predict the weight of the fermented loaf pastry for a given value of leavening time. Therefore, the purpose of the regression line is to predict the response variable. The correlation coefficient (r) between both factors was -0.984, then $r^2 = 0.9682$. This reflected that 96.82% of the diversity in the weight of the fermented pastry is attributed to the leavening time. Meanwhile, the remaining 3.18% is due to other variables that are not included in the regression analysis. The negative relationship

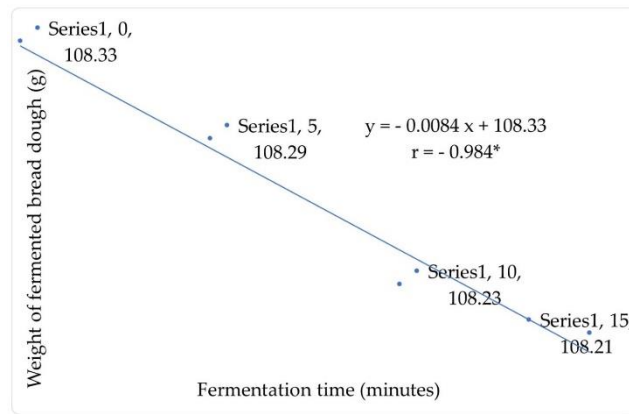


Figure 3. Regression line for the association between response variable weight of fermented bread dough affected by P₁ genotype and the independent variable fermentation time at 4 g concentration of sucrose (*significance at 0.05).

between both factors reflected that the changes in both factors were not in the same criteria.

The results recorded in Fig. 4 showed that the regression coefficient between both factors at 6 g sucrose concentration was equal to - 0.0152. This reflected that the weight of fermented loaf pastry decreased by - 0.0152 g with each additional minute of leavening time.

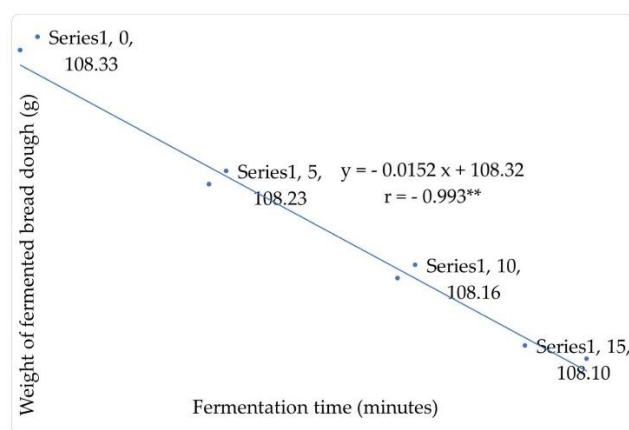


Figure 4. Regression line for the association between response variable weight of fermented bread dough affected by P₁ genotype and the independent variable fermentation time at 6 g concentration of sucrose (**0.01 probability levels).

The correlation coefficient (r) between both factors was equal to - 0.993. This correlation was above 0.7, which is considered strong because $r^2 = 0.9860$. This means that 98.6% of the diversity in the weight of fermented loaf pastry can be explained by the

leavening time. The remaining diversity in the weight of the loaf pastry (- 1.4%) was due to other factors that were not included in the regression equation.

The results shown in Fig. 5 indicated that the regression coefficient at 8 g. sucrose concentration of - 0.0218 indicated that the weight of fermented loaf pastry was decline by - 0.0218 g with each additional minute of leavening time. Furthermore, the correlation coefficient (r) between both factors was equal to - 0.999; therefore, $r^2 = 0.9980$. This means that 99.8% of the diversity in the weight of fermented loaf pastry is due to the leavening time. The remaining 0.2% was attributed to other variables that were not indicated in the regression formula. Thus, the association between both factors is not in the same pathway. Therefore, the correlation coefficient helps microbial geneticists identify the weight of fermented loaf pastry that can be attributed to leavening time. The coefficient of determination can be obtained by squaring the correlation coefficient. The resulting value, denoted by r^2 , represents the percentage of diversity attributed to the independent variable. These results are in agreement with [34], who stated that a correlation coefficient of 0.3 indicates a fair association between both factors. Squaring this number yields 0.09. Therefore, only 9% of the variation in the dependent variable can be attributed to the independent variable.

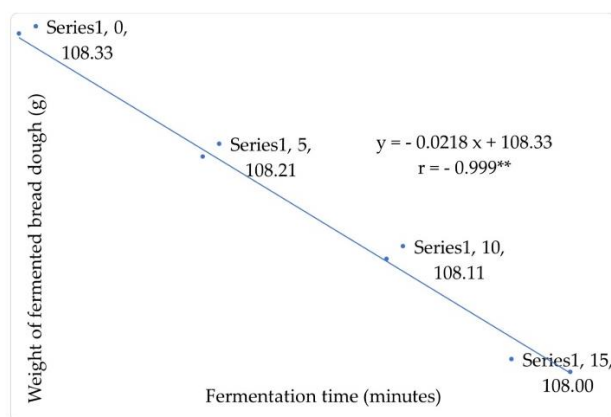


Figure 5. Regression line for the association between response variable weight of fermented bread dough affected by P₁ genotype and the independent variable fermentation time at 8 g concentration of sucrose (**0.01 probability levels).

3.2. Regression analysis of leavening ability dynamics by P₃ genotype

According to Fig. 6, the regression coefficient between both factors in the medium containing, zero sucrose concentration was equal to - 0.0354. This reflected that the weight of fermented loaf pastry decreased by - 0.0354 g with each additional minute of leavening time. Therefore, distinguishing between explanatory and response factors is essential. The correlation coefficient between both factors was equal to - 0.312. This reflected that the slope will be negative and the line will move downward. In contrast, if the correlation was positive, the slope would be positive and the line would move upward. The square of correlation (r^2) also called the coefficient of determination, which in this figure was equal to 0.0973. This reflected that 9.73% of the diversity in the weight of fermented loaf pastry is due to the leavening time. The remaining 90.27% is due to other factors that are not included in the regression equation. The square of the correlation is the fraction of the variation in the response values (y) that is explained by the least squares regression of the response variable (y) on the explanatory variable (x).

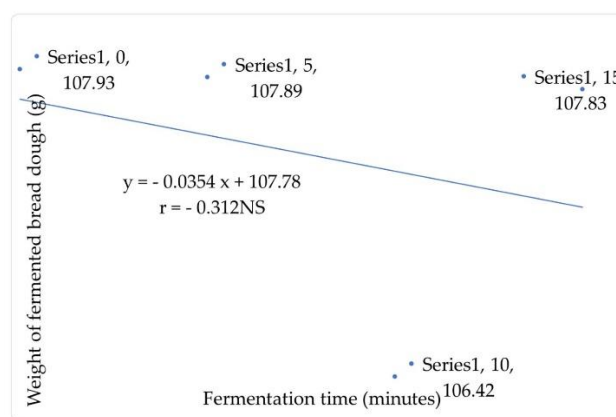


Figure 6. Regression line for the association between response variable weight of fermented bread dough affected by P₃ genotype and the independent variable fermentation time at zero sucrose concentration (Not significant).

According to Fig. 7, the regression coefficient between both variables under the effect of 2 g sucrose was equal to - 0.006. This indicated that the weight of fermented loaf pastry was decreased by - 0.006 g with each additional minute of the leavening time. The correlation coefficient between the leavening time and weight of the fermented loaf pastry was estimated to be 1.00. This reflected that the determination

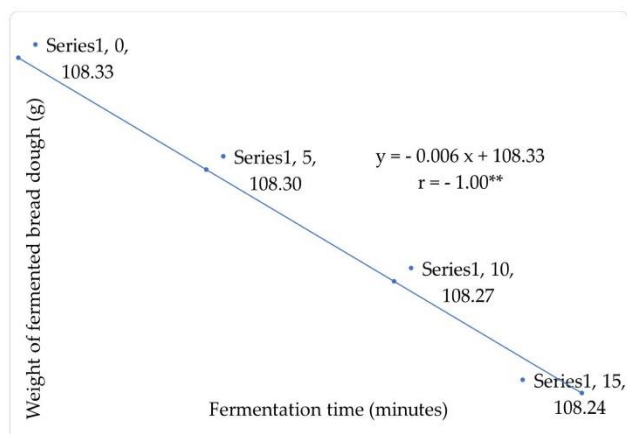


Figure 7. Regression line for the association between response variable weight of fermented bread dough affected by P₃ genotype and the independent variable fermentation time at 2 g sucrose concentration (**0.01 probability levels).

coefficient (r^2) is equal to 1.00, indicating that 100% of the diversity in the weight of the fermented loaf pastry is due to the leavening time. The negative association between both factors means that the changes in both factors are not in the same criteria; therefore, the line will move downward. These results indicated that the relationship between these two factors is strong because the correlation is above 0.7. Therefore, the remaining diversity in the weight of the fermented loaf pastry was equal to zero because the coefficient of determination was 100%, thus the data points were closer to the regression line, as seen in the figure. The remaining diversity is positive if the points are located above the line, or negative if the data points are located below the line.

According to Fig. 8, the regression coefficient between both variables affected by 4 g of sucrose in the leavening medium was equal to -0.0062 . This reflected that the weight of the fermented loaf pastry decreased by -0.0062 g with each additional minute of leavening time. Therefore, the regression coefficient was used to estimate the weight of the fermented loaf pastry based on the leavening time. The correlation coefficient between both factors was equal to -0.993 . This reflected a strong association between both variables because most points are closer to the regression line. Therefore, the coefficient of determination (r^2) = 0.9860, then 98.60% of the diversity in the weight of the fermented loaf pastry can be attributed to leavening time. The remaining diversity of 1.40% was due to other factors that were

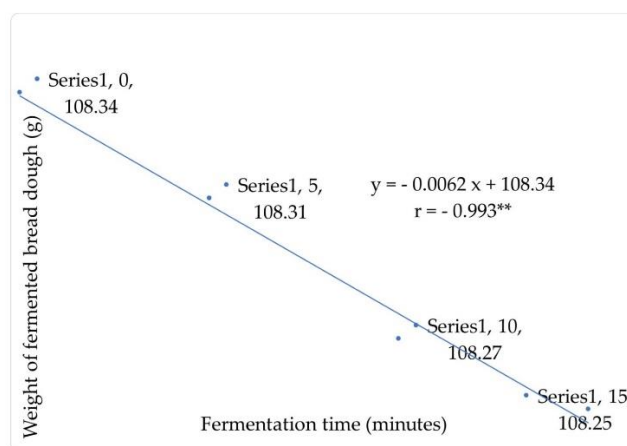


Figure 8. Regression line for the association between response variable weight of fermented bread dough affected by P₃ genotype and the independent variable fermentation time at 4 g sucrose concentration (**0.01 probability levels).

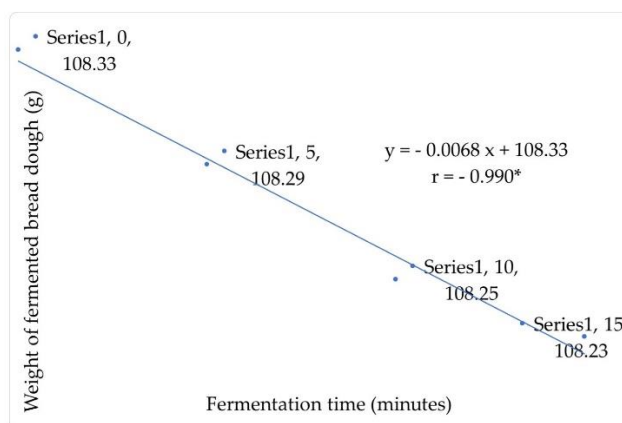


Figure 9. Regression line for the association between response variable weight of fermented bread dough affected by P₃ genotype and the independent variable fermentation time at 6 g sucrose concentration (*significance at 0.05).

not included in the regression equation.

As shown in Fig. 9, the regression coefficient obtained by the parental strain P₃ affected by 6 g of sucrose containing leavening medium was equal to -0.0068 . This indicated that the weight of the fermented loaf pastry decreased by -0.0068 g with each additional minute of leavening time. This line was used to estimate the weight of the fermented loaf pastry, based on the leavening time. The correlation coefficient between both factors was to 0.99 reflected that the changes in the two factors were not in the same criteria. On the other hand, the coefficient of determination, $r^2 = 0.9801$, reflected that 98.01% of the

diversity in the weight of the fermented loaf pastry could be explained by the leavening ability time. Whereas, the remaining diversity of 1.99% was due to other variables that were not indicated in the regression equation. The correlation coefficient between both factors was considered to indicate a strong association because it was above 0.7. This is an agreement with Moore et al. [34], who considered correlations above 0.7 as strong because approximately 50% of the diversity in the dependent factor can be attributed to the independent variable.

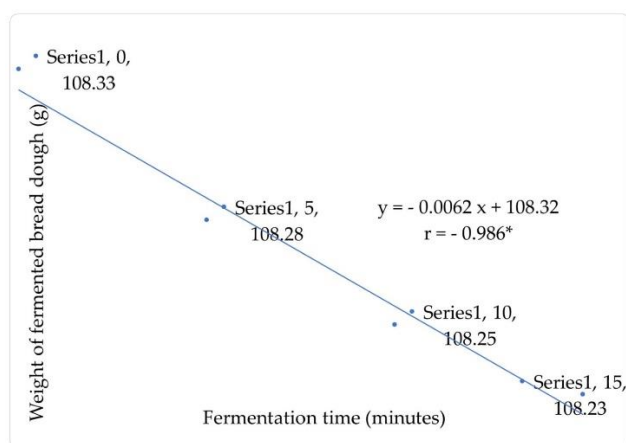


Figure 10. Regression line for the association between response variable weight of fermented bread dough affected by P₃ genotype and the independent variable fermentation time at 8 g sucrose concentration (*significance at 0.05).

The results diagrammatic in Fig. 10 showed that the regression coefficient between both variables affected by 8 g sucrose in the leavening medium was equal to - 0.0062. This reflected that the weight of the fermented loaf pastry decreased by 0.0062 g with each additional minute of leavening time. The correlation coefficient between both factors was equal to - 0.986. Then $r^2 = 0.9722$, which means that 97.22% of the diversity in the weight of the fermented loaf pastry was due to the leavening time. A negative correlation between both factors means that the changes in both factors are not in the same criteria. Therefore, the weight of fermented loaf pastry decreased as the leavening time increased. Thus, the relationship between these two factors was linear.

3.3. Regression analysis of leavening ability dynamics by hybrid H₁

The results diagrammatic in Fig. 11 reflected that the

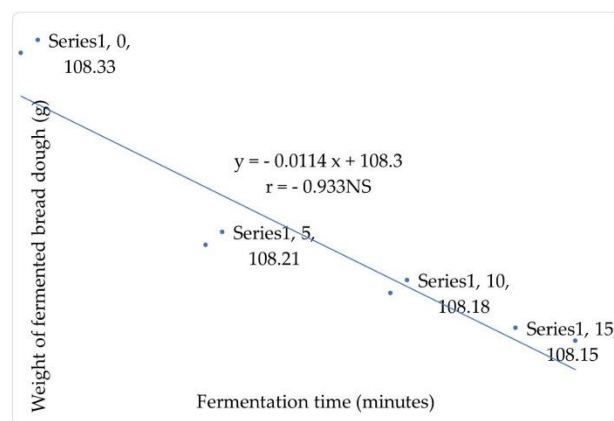


Figure 11. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₁ genotype and the independent variable fermentation time at zero sucrose concentration (Not significant).

regression line of H₁ genotype at zero sucrose concentration was equal to - 0.0114, indicating that the weight of fermented loaf pastry was declined by - 0.0114 g with each additional minute of leavening time. Therefore, the response variable, the weight of fermented loaf pastry can be predicted based on the explanatory variable, leavening time. Thus, the purpose of the regression line is to make these predictions. In addition, the regression line is a straight line that describes how the weight of the fermented pastry was varied as the leavening time changes. The correlation coefficient between both factors was equal to - 0.933. Therefore, this correlation was considered as strong, because the coefficient of determination (r^2) = 0.8705. This indicated that 87.05% of the diversity in the weight of fermented loaf pastry was due to the leavening time. Meanwhile, the remaining diversity of 12.95% in the weight of fermented loaf pastry was due to other variables that were not included in the regression equation. These factors include hybrid genotype, leavening temperature, variability of nutrients in the leavening medium, and enzyme activity related to leavening ability power.

According to Fig. 12, the regression coefficient between both variables affected by 2 g of sucrose containing leavening medium was equal to - 0.0082. This reflected that the weight of the fermented loaf pastry decreases by - 0.0082 g with each additional minute of leavening time. The correlation coefficient

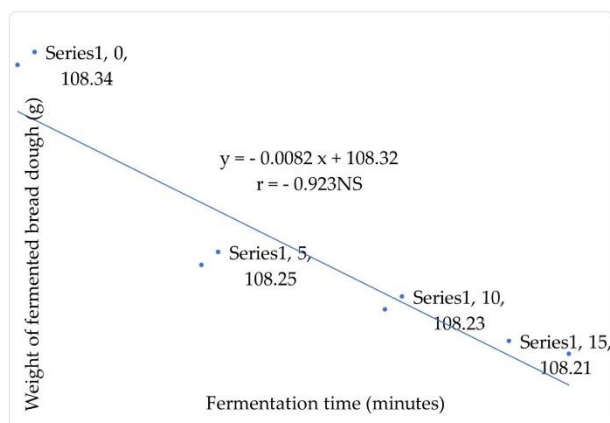


Figure 12. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₁ genotype and the independent variable fermentation time at 2 g sucrose concentration (*Not significant*).

between both factors was equal to -0.923 , and the coefficient of determination $r^2 = 0.8519$. Therefore, 85.19% of the diversity in the weight the fermented loaf pastry was due to the leavening time. Meanwhile, the rest diversity of 14.81% in the weight of fermented loaf pastry was attributed to other factors that were not included in the regression equation.

According to Fig. 13, the regression coefficient of the H₁ genotype affected by 4 g of sucrose containing leavening medium was equal to -0.008 . This reflected that the weight of fermented loaf pastry decreased by -0.008 g with each additional minute of leavening time. The correlation between the two variables was equal to -0.923 , and the coefficient of determination, $r^2 = 0.8519$. This indicated that approximately 85.19% of the diversity in the weight of the fermented loaf pastry was due to the leavening time. Meanwhile, the remaining diversity of 14.81% is regarded as other variables that have not been indicated in the regression formula. Therefore, regression analysis is a powerful and useful tool with many applications in microbial genetic research. It enables microbial geneticists to estimate, describe and predict the relationship between interrelated factors of any investigated phenomenon in the field of yeast genetics.

As shown in Fig. 14, the regression coefficient of the H₁ genotype affected by 6 g sucrose containing leavening medium was equal to -0.0116 . This indicated that the weight of fermented loaf pastry

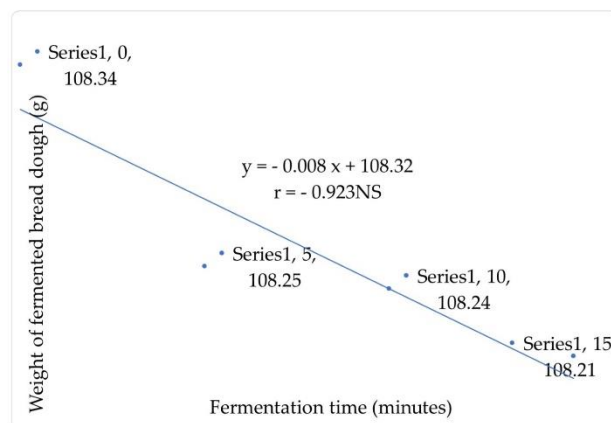


Figure 13. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₁ genotype and the independent variable fermentation time at 4 g sucrose concentration (*Not significant*).

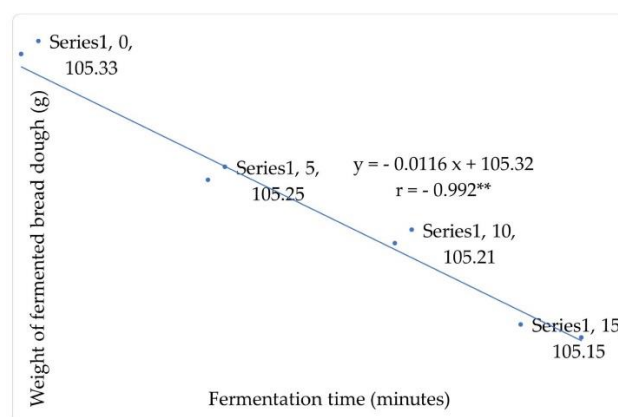


Figure 14. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₁ genotype and the independent variable fermentation time at 6 g sucrose concentration (**0.01 probability levels).

decreased by -0.0116 g with each additional minute of leavening time. This describes how the weight of the fermented loaf pastry decreased as the leavening time increased. This line of regression can be used to predict the weight of the fermented loaf pastry for a given leavening time under the influence of a 6 g sucrose containing leavening medium. The correlation coefficient between both factors was equal to -0.992 , and $r^2 = 0.9841$. This means that approximately 98.41% of the diversity in the weight of the fermented loaf is due to leavening time. Meanwhile, the other diversity of 1.59% is due to variables not included in the regression equation.

As in Fig. 15, the regression coefficient of the H₁ genotype affected by 8 g sucrose containing leavening medium was equal to -0.0108 . This indicated that the weight of fermented loaf pastry was decreased by -0.0108 g with each additional minute of leavening time. This linear regression can be used to estimate the weight of the fermented loaf pastry for any leavening time under the effect of 8 g sucrose whose leavening time lies within the times used in this model. The correlation coefficient between both factors was equal to -0.97 , and $r^2 = 0.9409$. Therefore, approximately 94.09% of the diversity was attributed to the leavening time. Whereas, the rest diversity of 5.91% is due to other variables that are not included in the regression equation. This correlation between both factors is considered as a strong association because the correlation value is above 0.7, based on the conclusion of [34]. Thus, the slope of the regression line was dependent on the correlation between the weight of the fermented loaf pastry and the leavening time. This correlation helps microbial geneticists to identify the extent of decrease in the weight of the fermented loaf pastry, due to the leavening time. The negative correlation obtained between both factors reflected that the changes in both factors were not in the same criteria.

3.4. Regression analysis of leavening ability dynamics by P₂ genotype

As shown in the data diagrammatic in Fig. 16, the regression coefficient of 0.0008 indicated that the weight of the fermented loaf pastry was increased by 0.0008 g with each additional minute of leavening time at zero sucrose concentration in the leavening medium of the P₂ genotype. The correlation coefficient (r) between the both factors were equal to 0.316, and $r^2 = 0.0998$, therefore 9.98% of the diversity in the weight of the fermented loaf pastry can be explained by the leavening time. The remaining diversity of 90.02% led to the identification of other variables that were not indicated in the regression formula. These results indicate that the changes in both factors are in the same criteria. Therefore, the correlation coefficient characterizes the direction of the relationship between the two factors. These results are in agreement with Nishimura et al. [35], who found that the correlation coefficient of 0.042 corresponds to the coefficient of

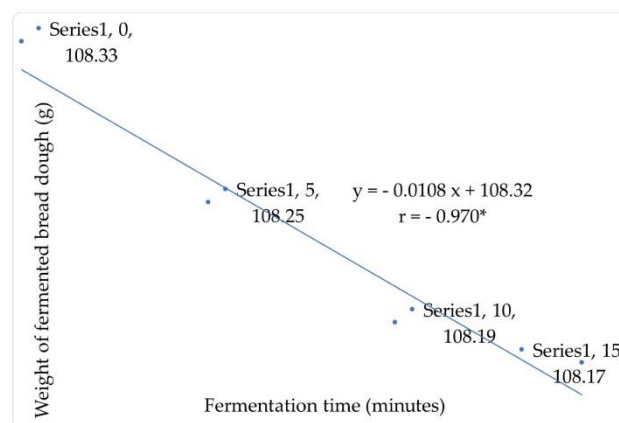


Figure 15. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₁ genotype and the independent variable fermentation time at 8 g sucrose concentration (*significance at 0.05).

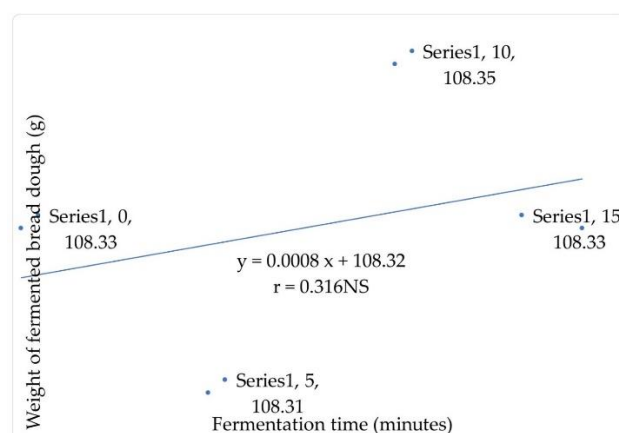


Figure 16. Regression line for the association between response variable weight of fermented bread dough affected by P₂ genotype and the independent variable fermentation time at zerosucrose concentration (Not significant).

determination (r^2) of 0.18. This means that about 18% of the variability in the response factors can be explained by the independent factor, as more than 80% of the variability is yet unexplained, which must be due to one or more other relevant factors that are related to interstitial leakage. It is interesting to note that the coefficient of determination the squared correlation coefficient is always a positive value, and the information about the direction of a relationship is lost [36]. The increase in the weight of the fermented loaf pastry with increasing leavening time may be due to the transformation of carbon dioxide into carbonic acid (H_2CO_3) and bicarbonate ions (HCO_3^-) which are

heavy, leading to an increase in the weight of the fermented loaf pastry over the leavening time [37].

According to Fig. 17, the regression coefficient of -0.0122 reflected that the weight of the fermented loaf pastry declined by -0.0122 g with each additional minute of leavening time at 2 g sucrose containing leavening medium when the leavening agent is P₂ genotype. The correlation coefficient between both factors was -0.963 , and the coefficient of determination was $r^2 = 0.9274$. Though 92.74% of the diversity in decreasing the weight of the fermented loaf pastry can be attributed to the explanatory variable. The remaining diversity of 7.26% was unexplained and was due to other variables that were not indicated in the regression coefficient formula. The correlation coefficient obtained between both factors was strong because its value was above 0.7 [34]. Correlation analysis helps microbial geneticists in deriving precisely the degree, as well as, the direction of the relationship between the decrease in the weight of the fermented loaf pastry and leavening time. The prediction of decreasing the weight of fermented loaf pastry through the leavening time based on correlation analysis will be near to reality and more reliable. Thus, measuring the correlation coefficient is a relative measure of the change between the both factors.

As shown in Fig. 18, the regression coefficient of -0.0384 indicated that the weight of the fermented loaf pastry decreases by -0.0384 with each additional minute of leavening time. The correlation coefficient (r) between both factors influenced by 4 g sucrose containing leavening medium was -0.298 . Then, the coefficient of determination (r^2) = 0.0888, therefore, 8.88% of the diversity in the decline in the weight of the fermented loaf pastry was attributed to leavening time. The remaining diversity was still unclear because it was attributed to other vectors that were not indicated in the regression equation. The negative correlation obtained between both factors indicates that the changes in the weight of the fermented loaf pastry and leavening time are not in the same pathway. Therefore, correlation analysis was used in this study to investigate the degree and direction of the association between the weight of the fermented loaf pastry and leavening time using leavening agents

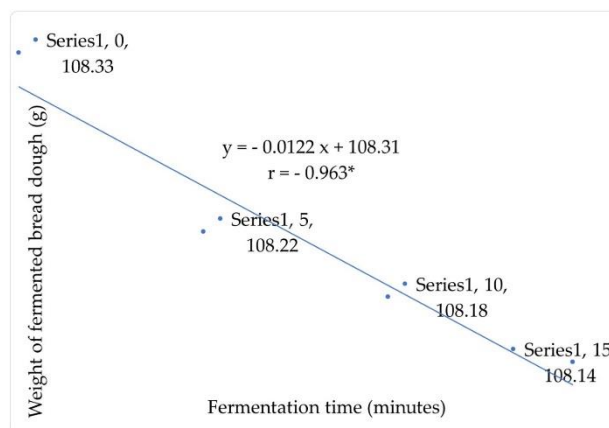


Figure 17. Regression line for the association between response variable weight of fermented bread dough affected by P₂ genotype and the independent variable fermentation time at 2 g sucrose concentration (*significance at 0.05).

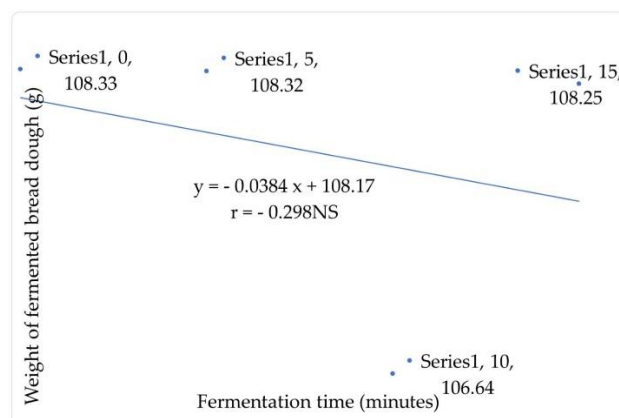


Figure 18. Regression line for the association between response variable weight of fermented bread dough affected by P₂ genotype and the independent variable fermentation time at 4 g sucrose concentration (Not significant).

of different yeast genotypes. It is reflected that which change in one variable predicts the change in another variable. Today's business world in the yeast industry came across many applications of yeast, which are dependent on each other. In the business world, a large number of problems may appear involving the use of two or more variables in the yeast industry. Identifying these variables and their dependencies can help microbial geneticists to resolve many difficulties in yeast manufacturing, based on yeast genotypes. At times, an increase in one variable is accompanied by a decline in another, as seen in the relationship between the weight of the fermented loaf

pastry and leavening time.

The results presented in Fig. 19 indicated that the regression coefficient of -0.0096 indicated that the weight of the fermented loaf pastry was decreased by -0.0096 g with each additional minute of leavening time influenced by 6 g sucrose containing leavening medium. Regression analysis of the entire genotype of the leavening agent revealed the effect of leavening time on the weight of the fermented loaf pastry. Therefore, the leavening time would be found to have a strong effect on the weight of fermented loaf pastry. The correlation coefficient (r) between both factors was -0.988 . This is a strong correlation because it was above 0.7, based on Moore et al. [34]. Besides, the coefficient of determination was equal to 0.9761. Therefore, 97.61 % of the diversity in the weight of the fermented loaf pastry influenced by 6 g sucrose in the leavening medium of the P₂ genotype can be attributed to the leavening time. The remaining diversity of 2.39% was still unclear and was due to other variables that were not indicated in the equation. The negative correlation coefficient obtained between both factors reflected that the changes in both factors were not in the same criteria. This is because the fluctuation in leavening time reliably predicts a similar fluctuation in the weight of the loaf pastry. This means that changes in one variable cause-changes in the other. Therefore, if two quantities vary in the same direction, then movements in one variable was related to the changes in the other variable, and these quantities are said to be correlated.

In Fig. 20, the regression coefficient -0.0056 indicated that the weight of the fermented loaf pastry decreased by -0.0056 g with each additional minute of leavening time. This denotes that the estimated decrease in the weight of the fermented loaf pastry was associated with every minute increase in leavening time. Therefore, regression analysis allows microbial geneticists to investigate the associations between factors. Usually, such factors are labeled as response or independent. The independent variable, leavening time is an input or driver variable that influences the response factor, the outcome variable, as the weight of the fermented loaf pastry. Thus, regression analysis can be used to predict the weight of the fermented loaf pastry based on its association with leavening time.

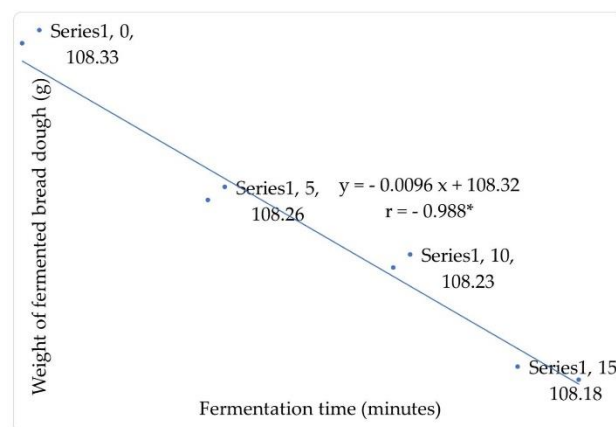


Figure 19. Regression line for the association between response variable weight of fermented bread dough affected by P₂ genotype and the independent variable fermentation time at 6 g sucrose concentration (*significance at 0.05).

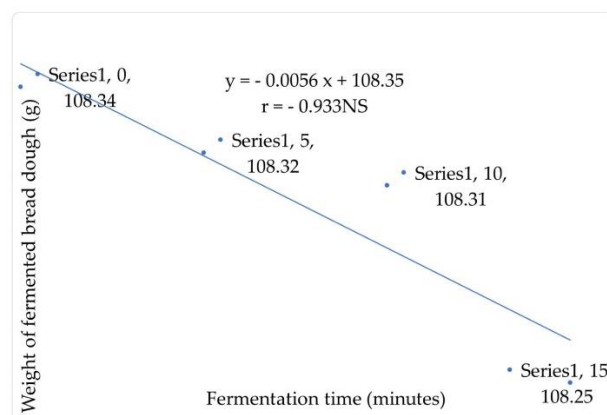


Figure 20. Regression line for the association between response variable weight of fermented bread dough affected by P₂ genotype and the independent variable fermentation time at 8 g sucrose concentration (Not significant).

The correlation coefficient between both factors – was 0.933, the coefficient of determination was = 0.8705. Therefore, 87.05% of the diversity in the weight of the fermented loaf pastry was attributed to the leavening time. The remaining diversity of 12.95% is due to other variables that are not indicated in the regression equation. The negative correlation between both factors reflects that the changes in the two variables are not in the same criteria. Thus, both variables vary in opposite directions. It means that if one variable increases, the other variable decreases.

3.5. Regression analysis of leavening ability dynamics by H₂ genotype

In Fig. 21, it is appeared that the regression coefficient

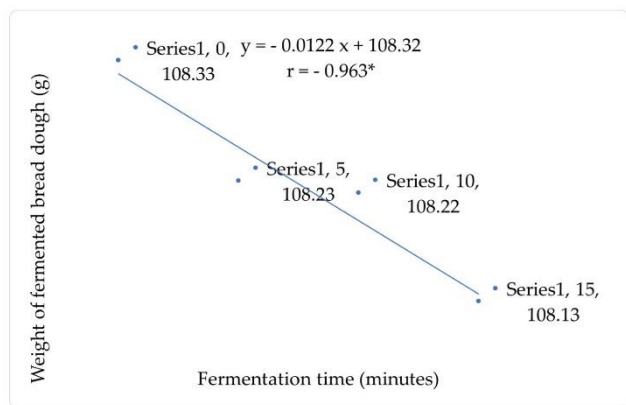


Figure 21. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₂ genotype and the independent variable fermentation time at zero sucrose concentration (*significance at 0.05).

between the weight of the fermented loaf pastry and leavening ability time without supplementation of sucrose was equal to -0.0122 . This indicated that the weight of the fermented loaf pastry decreased by -0.0122 g with each additional minute of leavening time. The correlation coefficient between both factors was -0.963 . This reflected coefficient of determination (r^2) = 0.9274 . Besides, approximately 92.74% of the diversity in the weight of the fermented loaf pastry was attributed to the leavening time. The remaining diversity of 7.26% is due to other variables that are not indicated in the regression formula.

As shown in Fig. 22, the regression coefficient between both variables at 2 g sucrose containing leavening medium was -0.0112 . This means that the weight of the fermented loaf pastry was decreased by -0.0112 g with each additional minute of leavening time. This enables microbial geneticists to predict the weight of fermented loaf pastry from the leavening time. This requires attention to the units of the leavening ability time. The correlation coefficient between both factors was -0.858 , and the coefficient of determination was 0.7362 . Thus, there is a strong correlation between both variables because 73.62% of the diversity in the weight of the fermented loaf pastry was due to the leavening time. The remaining diversity of 26.38% is attributed to other variables that are not included in the regression equation. The negative correlation observed between the two variables indicated that both variables vary in opposite pathways. The weight of the fermented loaf

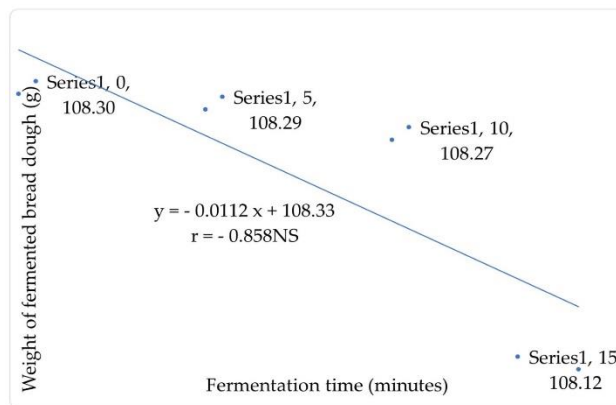


Figure 22. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₂ genotype and the independent variable fermentation time at 2 g sucrose concentration (Not significant).

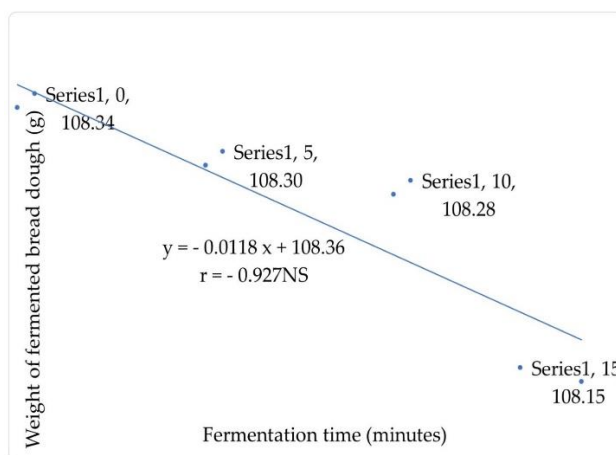


Figure 23. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₂ genotype and the independent variable fermentation time at 4 g sucrose concentration (Not significant).

pastry decreased if the leavening time increased.

According to Fig. 23, the regression coefficient between the weight of fermented loaf pastry and leavening ability time under the effect of 4 g of sucrose was -0.0118 . This indicated that the weight of the loaf pastry decreased by -0.0118 g with each additional minute of leavening time. This enables microbial geneticists to predict the outcomes of the weight of the fermented loaf pastry based on the leavening time. Therefore, regression analysis of microbial genetics data is a powerful and useful methodology with many applications in genetic research. This enables genetic researchers to assess, predict and describe the

association between the related factors of any phenomenon in microbial genetics. The correlation coefficient between the two both factors was -0.927 . There was a strong correlation between the decline in the weight of the fermented loaf pastry and the leavening ability time. The coefficient of determination was equal to 0.8593 . This indicated that 85.93% of the diversity in the weight of fermented loaf pastry is attributed to the leavening time. The remaining diversity of 14.07% was attributed to other factors such as yeast genotype, chemical composition of flour, and enzyme activity, which were not included in the regression equation.

The results shown in Fig. 24 reflected that the regression coefficient between both factors affected by 6 g sucrose is -0.0074 . This indicated that the weight of fermented loaf pastry decreases by -0.0074 g with each additional minute of leavening time. The correlation coefficient between both factors was -0.899 . This is a strong correlation, as well as, a negative correlation. This reflected that the changes in both factors were in opposite pathways. The coefficient of determination was -0.8082 . Therefore, 80.82% of the diversity in the weight of the fermented loaf pastry was attributed to the leavening time. The remaining diversity was equal to 19.18% , which is attributed to other reasons that were not indicated in the regression equation.

In Fig. 25, the results appeared that the regression coefficient between both factors was -0.5674 , which under the influence of 8 g sucrose containing leavening medium. The weight of the fermented loaf pastry decreased by -0.5674 with each additional minute of leavening time. The correlation coefficient between both factors was -0.904 . It has a strong correlation because its value was above 0.7 , based on the reported data [34]. The coefficient of determination was 0.8172 . This indicated that 81.72% of the diversity in the weight of the fermented loaf pastry is attributed to leavening time. Whereas, the remaining diversity was 18.28% , which is attributed to other variables that are not indicated in the regression equation. Therefore, the correlation coefficient identifies the percentage of the response variable as the weight of the fermented loaf pastry explained by the leavening time. Therefore, both

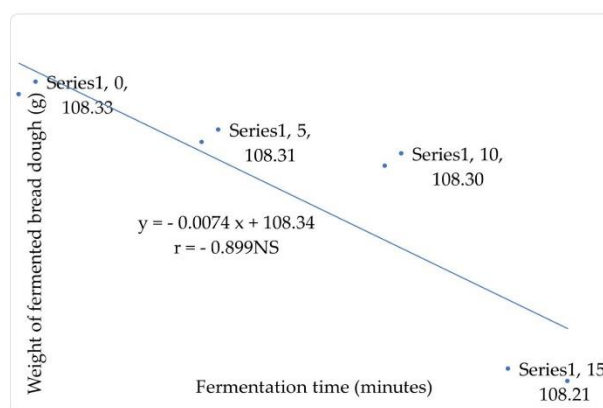


Figure 24. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₂ genotype and the independent variable fermentation time at 6 g sucrose concentration (Not significant).

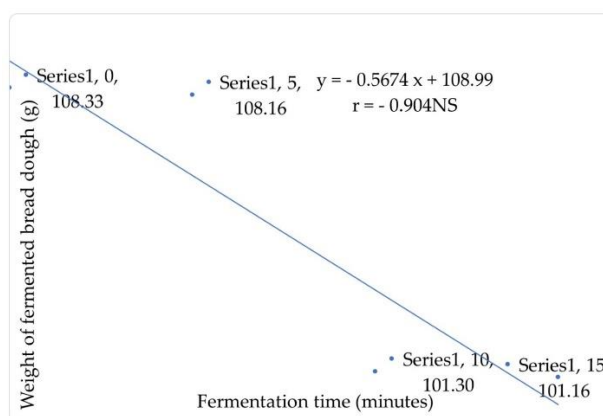


Figure 25. Regression line for the association between response variable weight of fermented bread dough affected by hybrid H₂ genotype and the independent variable fermentation time at 8 g sucrose concentration (Not significant).

factors are very important for microbial geneticists to study the direction of the relationship between two or more factors in yeast genetics. Therefore, the prediction based on the correlation between these two variables is more reliable and closer to reality. The decrease in the weight of the fermented loaf pastry with increasing leavening time was due to the carbon dioxide released by the fermenting yeast. Therefore, baker's yeast is used in manufacturing loaf pastries as a leavening agent because it converts fermentable sugars in the loaf pastry into CO₂. This causes the loaf pastry volume to rise, as well as, the weight decreases as CO₂ forms bubbles in the loaf pastry. When the loaf pastry is baked, the pockets remain, giving the baked product a soft and spongy texture.

During leavening time, the loaf pastry volume increased with decreasing weight as agitation time increased but, only to a limited time because the longer leavening period (40 min) caused a drastic drop in volume. Therefore, the period of mixing loaf pastry ingredients, as well as, leavening ability time is important because it influences the size and quality of bread. Agitation increases the ability of the loaf pastry to trap more air [14]. Hybrid genomes used in this study were more tolerant to sucrose concentrations than the parental strains. They produce more CO₂ leading to the rise and decline in the weight of the fermented loaf pastry over the parental strains. Therefore, the ability of highly diverged species from *Saccharomyces cerevisiae* makes yeast cells hybridize to study the offspring of hybrids, as well as, consequently heterosis; therefore, the hybrid genotypes might have been selected because of their beneficial characteristics or fitness benefits of the F₁ hybrid as compared with one or both parental strains [38]. Most studies on heterosis in yeast have focused on intra-specific F₁ hybrids using crosses in the populations of *S. cerevisiae* [38]. The results obtained in this study concerning heterosis in leavening ability by the hybrid genotypes agreed with the report [38], that dominance mechanism of heterosis resulted from the complementation of recessive deleterious alleles from one parent, complemented with the high-performance alleles of the other parent. This complementation leads to higher fitness obtained in sucrose tolerance of F₁ hybrid over its parents. Therefore, heterosis was mainly due to dominance effects. In addition, heterosis was correlated with the genetic divergence in the parental population [39]. Shapira et al. [40] identified the genetic mechanisms of heterosis as over-dominance and epistasis, where dominance could not solely identify heterosis. Thus, intra-specific F₁ hybrids of baker's yeast showed a balance between positive and negative heterosis.

Sucrose was used in this study at varied concentrations for improving the composition of flour and as an energy source for the cells of baker's yeast. If the sucrose concentration in the loaf pastry is high, the yeast cells experience severe osmotic stress. This damages the cellular components and decreases their leavening ability [41]. Consequently, the leavening

activity and final size of the pastry product are reduced. Therefore, the yeast cells must adapt to hyper-osmotic stress in the loaf pastry, as seen in hybrid genotypes, which showed higher tolerance to sucrose concentrations than their parental strains. This reflected that high sucrose concentration in the loaf pastry prolongs the leavening time required for the yeast cells to reach their maximal leavening power. This agrees with Aslankoochi et al. [42], who illustrated that the total amount of carbon dioxide released by baker's yeast in loaf pastry at 18% sugar was much lower than that in the loaf pastry supplemented with 6% sugar due to the long phase of metabolism required with 18% sugar. Indeed, highly tolerant hybrids to sucrose concentrations may be due to the high expression of proteins required for glycerol and trehalose production. In addition to trehalose and glycerol, proline accumulation induces tolerance to high sucrose stress [43]. Therefore, most strategies in yeast genetics concerning the osmotolerance of baker's yeast are based on the improved accumulation of intracellular glycerol, proline, and trehalose.

Interestingly, the ability of yeast cells to tolerate sucrose concentrations is essential for yeast cells used as a leavening agent in the bread industry. This is because bread making is a very important sector in food manufacturing of the technological process. Therefore, hybrid genotypes of baker's yeast are known to be a better choice for bread making [44]. The results obtained in this study are in line with Gabriela et al. [45], who reported that the maximum volume of loaf pastry was interrelated with the quantity of CO₂ produced by *Saccharomyces cerevisiae*. The bread-making industry is dependent on the yeast cells genotype and leavening time. The results obtained herein showed that hybrid genotypes are considered to have superior leavening power. It can rapidly ferment sucrose, glucose, and fructose. After an adaptation phase, maltose is the main disaccharide that develops in loaf pastry due to the action of amylase present in flour. The leavening ability process is strongly influenced by the yeast genotypes, as well as, the physiological state of yeast cells. Therefore, the cell viability of hybrid genotypes was superior in leavening power because they recorded a high percentage in lowering the weight of the fermented

loaf pastry throughout the entire leavening period, because of a larger quantity of CO₂ produced, which led to an increase in the volume of bubbles existing in the loaf pastry. The results also agreed with Munteanu et al. [46], who found a correlation coefficient of about 0.823 for loaf pastry, fermented with the yeast of Dr. Oetker, 0.80 for loaf pastry fermented with yeast Pakmaya and 0.954 for loaf pastry fermented with yeast Rapunzel. The results are also in agreement with Wongkhalaung et al. [47], who found that baker's yeast hybrids exhibited better maltose leavening ability, improved leavening ability and produced higher carbon dioxide than their parental strains, especially in non-sugar and high-sugar loaf pastry.

4. Conclusions

This study indicated that hybrid genotypes had the best performance in loaf pastry proofing and sucrose stress tolerance, compared with the parental strains from commercial baker's yeast. The parental strains and their hybrids appeared negative correlation between the weight of the fermented loaf pastry and leavening time under all concentrations of sucrose stress. Yeast hybridization produces chimeric genomes that support the assumptions about the potential effects of epistatic interactions between alleles. Loaf pastry prepared with hybrid genotypes required a shorter leavening time than that prepared using parental strains. Losses in the weight of fermented loaf pastry were higher in those prepared with hybrid genotypes than those prepared with parental strains. This is because of the higher quantities of carbon dioxide released by the hybrid genotypes. Hybrid genotypes adapted more easily to the leavening ability of sucrose than their parents. Therefore, hybrids exhibited the highest leavening activity under sucrose stress. The weight of the fermented loaf pastry decreased with the increasing in leavening time. Hybrid genotypes had a stronger capacity to produce CO₂ under all sucrose stress conditions than their parents. This capacity, in turn, might be responsible for the decrease in the weight of the fermented loaf pastry and increase in its volume. These properties make hybrid genotypes as candidates of potential value to be better leavening agents in the bread-making industry. In many countries such as Egypt, bread is a staple food. This

has increased the attention toward the bread-making industry, which is mainly influenced by yeast genotypes. This will shed light on the production of hybrid genotypes that can trigger the bread-making industry. The increase of CO₂ released by hybrid cells, it decreases the weight of fermented loaf pastry, as well as, increase the expansion of its volume. Therefore, hybrid genotypes have well-defined industrial property. This is because hybrid yeast cells have high survival, leavening ability, CO₂ production capacity, and osmotic tolerance. Regression analysis enables microbial geneticists to predict, describe, and assess the weight of fermented loaf pastry for each genotype of yeast strains used in bread making at different leavening times. The negative correlation obtained herein between both factors reflected that changes in both factors are in opposite directions.

Ethical approval

This investigation does not include any animal or human feeding or testing on fermented loaf pastry products used in this study.

Disclaimer (artificial intelligence)

Author(s) hereby state that no generative AI tools such as Large Language Models (ChatGPT, Copilot, etc.) and text-to-image generators were utilized in the preparation or editing of this manuscript.

Authors' contributions

All research steps containing, collection and analysis of data, laboratory work, writing and revising the manuscript in its final form were contribute solely, M.I.K.

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Availability of data and materials

All data will be made available on request according to the journal policy.

Conflicts of interest

The author declares that this manuscript was conducted without any financial support that could be done as no conflict of interest.

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