

# Identification of some kefir microorganisms and optimization of their production in sugarcane juice

Identificación de algunos microorganismos del kéfir y optimización de su producción en jugo de caña

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## ABSTRACT

### Key words:

Functional foods  
Lactic acid bacteria  
Probiotics  
Yeasts

Kefir grains are a consortium of bacteria and yeasts grouped in a polysaccharide called kefirano. They ferment sugar substrates to produce organic acids, CO<sub>2</sub>, vitamins and ethanol. They also have positive effects on health. This research project aimed to optimize the fermentation process of sugarcane concentrate using kefir grains. The microorganisms were first identified morphologically and biochemically, then isolated and purified in selective media. Optimization was conducted using the response surface methodology with a composite central design. The independent variables were: temperature, time and percentage of kefir grains added. As for dependent variables, we considered the following: increase in kefir grains (also measured as a percentage), acidity and microbial growth. Additionally, our study identified populations of *Lactobacillus curvatus* and the following yeasts: *Candida famata*, *Can. magnoliae*, *Can. krusei/incospicua* and *Can. sphaerica* in the kefir grains. The optimal conditions were 33.5 °C, 30 h and 6% w/w of added kefir grains. The increase in kefir grains reached was of 193 ± 12%. The lactobacilli, lactococci and yeast counts were 1.57x10<sup>8</sup>, 8.63x10<sup>7</sup> and 2.05x10<sup>7</sup> CFU mL<sup>-1</sup> respectively. Experimental optimization was an effective tool for the fermentation of kefir grains in sugarcane concentrate.

## RESUMEN

### Palabras claves:

Alimentos funcionales  
Bacterias ácido  
lácticas  
Probióticos  
Levaduras

Los gránulos de kéfir representan un consorcio de bacterias y levaduras, agrupadas en el polisacárido kefirano, que fermentan sustratos azucarados produciendo ácidos orgánicos, CO<sub>2</sub>, vitaminas y etanol, y generan efectos positivos en la salud. El objetivo de esta investigación fue optimizar el proceso de fermentación de concentrado de caña utilizando gránulos de kéfir. Los microorganismos de los gránulos, se aislaron y purificaron en medios selectivos identificándose morfológica y bioquímicamente. La optimización se realizó utilizando la metodología de superficie de respuesta con un diseño central compuesto y considerando las variables independientes: temperatura, tiempo y porcentaje de gránulo de kéfir adicionados, y las variables dependientes: porcentaje de aumento del gránulo de kéfir, acidez y crecimiento microbiano. Se identificaron *Lactobacillus curvatus* y las levaduras *Candida famata*, *Can. magnoliae*, *Can. krusei/incospicua* y *Can. sphaerica* en los gránulos de kéfir, siendo las condiciones óptimas 33,5 °C, durante 30 h y porcentaje de gránulos de kéfir adicionados 6% p/p, alcanzando un incremento de gránulos del 193 ± 12% y recuentos de lactobacilos, lactococos y levaduras de 1,57x10<sup>8</sup>, 8,63x10<sup>7</sup> y 2,05x10<sup>7</sup> UFC mL<sup>-1</sup>, respectivamente. La optimización experimental fue una herramienta efectiva para el proceso de fermentación de los gránulos de kéfir en el concentrado de caña.

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**K**efir grains (KG) consist of many individual white to bone-colored, soft, gelatinous biological masses with a cauliflower-like appearance. This mass is composed of protein, lipids and a soluble polysaccharide called kefirano in which a symbiotic association of microorganisms belonging to a diverse spectrum of lactic acid bacteria, yeasts and acetic bacteria, ferment sugar substrates. They produce lactic acid, alcohol, CO<sub>2</sub>, B vitamins and other organic acids (Lopitz *et al.*, 2006; Kabak and Dobson, 2011).

Some kefir microorganisms have been isolated by different authors, namely: *Lactobacillus kefir*, *Lb. fermentum*, *Lb. acidophilus*, *Lb. helveticus*, *Lb. brevis*, *Lb. kefiranofaciens*, *Lb. kefirgranum*, *Lb. parakefir*, *Lactococcus lactis* sub *lactis*, *Lactococcus lactis* sub *cremoris*, *Leuconostoc mesenteroides*, *Acetobacter acet*, *Acet. rasens*. Yeasts such as *Candida kefir*, *Can. krusei*, *Can. lambica*, *Saccharomyces turicensis* and *Kluyveromyces marxianus*, among others, have also been isolated (Witthuhn *et al.*, 2005; Lopitz *et al.*, 2006; Garofalo *et al.*, 2015). Furthermore, some of them have been identified by molecular techniques (Leite *et al.*, 2012; Leite *et al.*, 2013; Garofalo *et al.*, 2015). Other studies on KG, their microorganisms and kefirano explain that their consumption has positive effects on human health, these include: stimulating the immune system (Iraporda *et al.*, 2014), producing an antitumor effect (Maalouf *et al.*, 2011; Guzel-Seydim *et al.*, 2011b; Diosma *et al.*, 2014) and generating antimicrobial activity against some pathogenic microorganisms (Chifiriuc *et al.*, 2011; Ahmed *et al.*, 2013; Carasi *et al.*, 2014;). Most studies on kefir have been conducted on milk (Lasik and Jan, 2012), milk whey (Teixeira *et al.*, 2010), reconstituted skim milk (Nambou *et al.*, 2014) and other substrates like blackcurrant juice (Luckow and Delahunty, 2004), sugarcane powder (Salazar *et al.*, 2015) and walnut milk beverages (Cui *et al.*, 2013).

The microorganisms in the KG often reproduce in milk, but lactose-intolerant people cannot benefit from them. Thus, sugar rich substrates such as sugarcane juice, whose consumption is high in developing countries, are very interesting alternatives. A total of 20 million hectares of sugarcane are grown worldwide, and its production in Latin America is high because of the region's tropical weather. Brazil is the largest producer in the area: as of 2013, its production amounts to 11,758,663

t, and is followed by Peru and Colombia with 3,050,934 and 2,434,853 t, respectively. Furthermore, the highest increases in production rates during the last ten years have been observed in Colombia and Brazil (Faostat, 2013). Given the importance of this agribusiness for the Latin American population, these countries might be interested in exploring new alternatives for improving competitiveness and diversifying products by including new functional foods with the probiotic microorganisms from the KG.

In the field of fermentation processes, some research has pointed to many factors that have an important effect on the growth of the kefir microorganisms. Some of those factors are: temperature, biomass or inoculum concentrate, pH, time and aeration (Guzel *et al.*, 2011a; Bensmira and Jiang, 2012; Cui *et al.*, 2013).

The aim of this study was to determine the optimal conditions for the fermentation of sugarcane concentrate using KG. Such conditions should lead to a greater increase in the concentration of the grains and larger counts of lactobacilli, lactococci and yeasts.

## MATERIALS AND METHODS

The KG were obtained from the Water and Food Microbiology Laboratory of Universidad Nacional de Colombia, Medellín. The sugarcane concentrate (69.9 ± 3.0 °Brix) was provided by a traditional company that produces jaggery in the Jamundí rural settlement in the Girardota municipality, department of Antioquia, Colombia.

The raw material and the fermented juices of each experiment were characterized three times in terms of moisture loss (X<sub>w</sub>) when dried in an oven at 103 °C until reaching a constant weight. Other measurements were performed as follows: pH was measured with a Hanna pH-meter, and solids were measured with a refractometer. The values for the latter were expressed as °Brix at 25 °C. Acidity was measured by titration and expressed as milliequivalents of acid per milliliter (meq acid mL<sup>-1</sup>) (Horwitz, 2005), water activity (a<sub>w</sub>) with a dew point hygrometer at T = 25 °C (Decagon Aqua LAB 3TE series), density with a pycnometer.

To activate the KG, they were inoculated into sugarcane concentrate at 30 °Brix, 25 °C for 24 h. They were then separated with a clothperla® 500312 filter and washed with

distilled water. This procedure was repeated for three days. The KG were homogenized in 0.1% (w/v) peptone water, and aliquots of 0.1 mL were placed into the following selective culture media through surface depletion: MRS, M17 and YGC agar (Aquilanti *et al.*, 2012; Chen *et al.*, 2008). Additionally, each colony was isolated and purified on the basis of its morphological features and the microscopic characteristics of its microorganisms. In order to identify the microbial genus, the colonies were characterized biochemically through bioMérieux's API<sup>®</sup> galleries: 50CHL for lactobacilli and 20CAUX for yeasts, as stated in the manufacturer's instructions. In addition, they were identified using the API WEB software.

Fermentation processes took place in Erlenmeyer flasks made of glass with a total volume of 200 mL of sugarcane juice in accordance with the proposed experiment design (Table 2). Counts of viable microorganisms (CFU mL<sup>-1</sup>) in each fermentation were conducted with the serial dilution method in the previously mentioned selective media. Microorganisms were incubated at 37 °C / 5 d anaerobically for lactobacilli and cocci, and at 37 °C / 24 to 48 h for yeasts. The percentage of increase in KG was calculated as follows:

$$IKG = \frac{W_{KG}^f - W_{KG}^i}{W_{KG}^i} \times 100 W_{KG}^f = \text{final weight KG}$$

$W_{KG}^i$  = initial weight KG

The optimization of the fermentation process was performed using the response surface methodology based on a central composite experiment design (15 experiments). In addition,

three factors or independent variables were considered: added KG (2.4-9.6%) (Factor A), fermentation temperature (29-38 °C) (Factor B) and fermentation time (12-48 h) (Factor C). The response or dependent variables were: Increase in Kefir grains (IKG) (%) (to be maximized), acidity (meq acid mL<sup>-1</sup>) (to be minimized) and lactobacilli, lactococci and yeast counts (to be maximized). The statistical analysis of the results was conducted with the Design Expert 8.0, software, State-Ease, Inc., additionally, an analysis of variance (ANOVA) with a level of significance of 5% was conducted. The regression analysis and the relationship between the independent and dependent variables were calculated using a second order polynomial model.

## RESULTS AND DISCUSSION

Table 1 shows the mean values and standard deviations of the sugarcane concentrate used in the fermentation process. The sugarcane concentrate was obtained as an intermediate product of the jaggery manufacturing process during the final stage of juice concentration and prior to the mixing and molding of the product (Osorio, 2007). This concentrate has an important content of soluble solids provided mainly by sucrose, glucose and fructose (Wisuthiphaet and Napathorn, 2016). Moreover, its Xw and aw identified this substrate as susceptible to microbial activity, which is favored by its acidity and pH conditions. Information on sugarcane concentrate is scarce in the reviewed literature, but some studies stand out: Largo *et al.* (2015), reported findings on sugarcane concentrate at 48.6 °Brix, an Xw: 41.0; a<sub>w</sub>: 0.962; pH: 5.7; acidity: 0.026%; Naranjo (2008) obtained similar values for density (1.35 g cm<sup>-3</sup>) and Xw (30%) with sugarcane concentrate at 70 °Brix.

**Table 1.** Physicochemical characteristics of sugarcane concentrate.

Parameter	Sugarcane concentrate
Xw (%)	29.4 ± 0.4
a <sub>w</sub>	0.846 ± 0.001
Soluble solids (°Brix)	69.9 ± 3.0
Acidity (meq acid/g)	0.062 ± 0.004
pH	5.3 ± 0.1
Density (g cm <sup>-3</sup> ) (T= 25 °C)	1.36 ± 0.02

The microorganism isolation process identified six bacterial colonies in the KG: two colonies of *Lactobacillus curvatus* with a degree of confidence of 99.9% that were white,

bright, umbonate and round with even borders, and four colonies of gram-positive, catalase and oxidase negative cocci that grew properly in the selective culture medium for

cocci (M17) and showed a tendency to cluster in strings. Microscopic observations confirmed that these colonies were transparent, bright, punctuate and flat, but their genus and species need to be confirmed via molecular techniques. Other studies reported that the composition of microorganisms in the KG is variable and depends on their source, culture conditions and substrate. However, the *Lactobacillus* genus is predominant (Leite *et al.*, 2013; Garofalo *et al.*, 2015).

*Lactobacillus curvatus* is a sucrose-fermenting and facultative heterofermentative microorganism that lowers the pH of the substrate as it produces lactic acid (De Vos *et al.*, 2009). It has been isolated from KG, fermented vegetables, meat and dairy products. Witthuhn *et al.* (2004) isolated it from South African KG; Ahmadova *et al.* (2013) isolated it from homemade cheese in Azerbaijan and observed antimicrobial effects against *Listeria monocytogenes* and *Bacillus cereus* as well as antifungal activity against *Cladosporium* and *Fusarium* ssp caused by a bacteriocin called curvacin. In addition, it also showed resistance to physiological concentrations of bile salts and no multiresistance to antibiotics. Similarly, Cocolin *et al.* (2009) reported that *Lactobacillus curvatus* and *Lb. sakei* were the most frequent bacteria in three types of salami. These results are consistent with those obtained by a study with spontaneously matured European style sausages (Amor and Mayo, 2007, cited by Rivera and Gallardo, 2010). Likewise, Hebert *et al.* (2012) sequenced the genome of this lactobacillus after isolating it from artisanal sausages from Argentina that produced this bacteriocin.

Strains of *Lactobacillus curvatus* have been isolated from vegetables such as kimchi with good results in terms of acidification properties and excellent results when used as starter culture for fermentation in sausages. Equal results have been obtained with *Lb. casei*, *Lb. pentosus*, *Lb. plantarum*, *Lb. sakei*, *Pediococcus acidilactici* and *Ped. Pentosaceus* (Lee *et al.*, 2006). Rühmkorf *et al.* (2013) found that the exopolysaccharide produced by this lactobacillus together with that of *Lb. reuteri* and *Lb. animalis*, improved the quality of gluten in bread making. This shows the potential uses of *Lb. curvatus* in the food industry as well as its behavior as a probiotic.

Figure 1 shows gram staining micrographs for *Lactobacillus curvatus*, gram positive cocci and the *Candida famata*, *Can.*

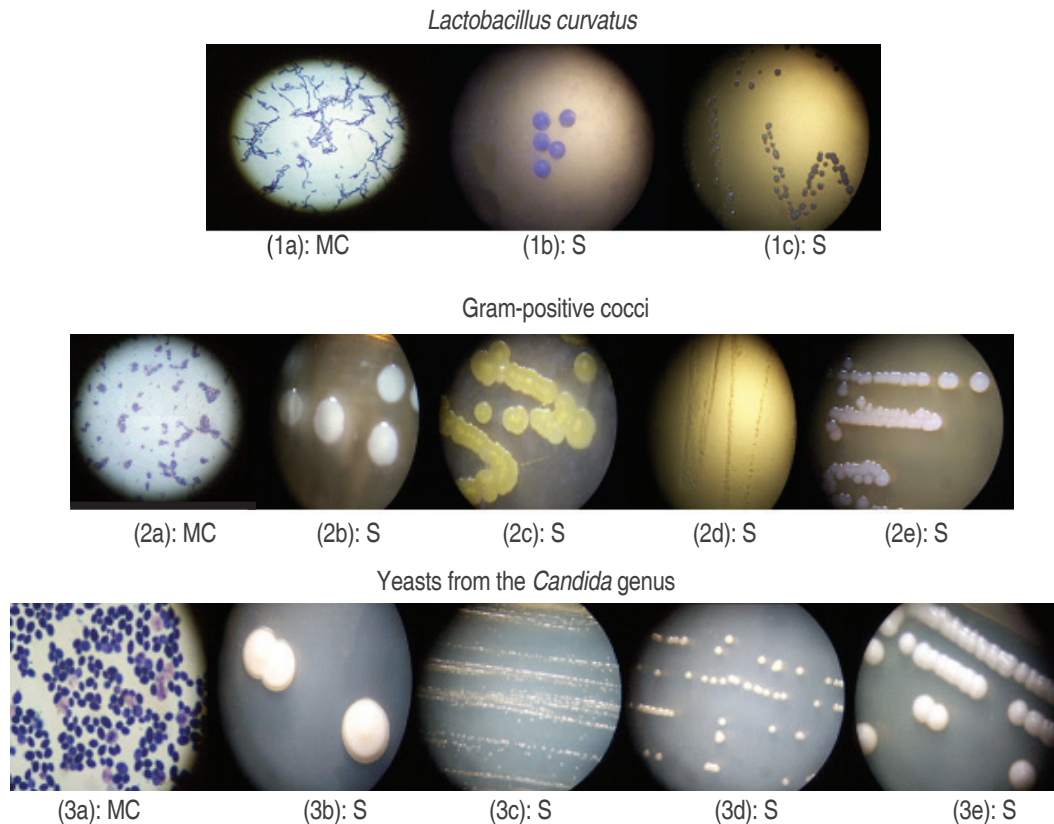
*magnoliae*, *Can. krusei/incospicua* and *Can. sphaerica* yeasts. These micrographs were taken with an optical microscope and a stereoscope.

The gram positive cocci and *Lactococci* have also been isolated from KG (Hsieh, *et al* 2012; Witthuhn *et al.*, 2005; Leite *et al.*, 2015) and dairy beverages prepared with them (Altay *et al.*, 2013). Monteagudo *et al.* (2012) found that samples of *Lactococcus lactis*, isolated from cow and sheep milk had high adherence to Caco-2 cells, low pH tolerance, and tolerance to pancreatin and bile salts. In addition, they also showed antimicrobial activity against *Bacillus cereus*, *Listeria innocua*, *L. monocytogenes*, *Staphylococcus aureus* and *Pseudomonas fluorescens*. These results show the potential uses of *Lactococcus lactis* as a probiotic microorganism.

As for the yeasts found in the KG in our study, they were more diverse for species from the *Candida* genus: *Can. magnoliae*, *Can. sphaerica*, *Can. famata*, *Can. krusei/incospicua*, with confidence values of 81.0%, 67.2%, 93.9% and 99.9% respectively. The latter two having been identified on the basis of the cycle in which they were found: *Candida krusei* (anamorphic) or *Issatchenkia orientalis* (telomorphic); *Candida famata* (anamorphic) or *Debaromyces hansenii* (telomorphic) (Lopitz *et al.*, 2006). The following morphological characteristics were observed in the colonies: they were bright, white, creamy, umbonate and round with even borders. *Candida krusei*, *Debaromyces hansenii* (*Candida famata*) and *Candida inconspicua* have been isolated directly from the KG (Witthuhn *et al.*, 2005; Loretan, *et al.*, 2003); moreover, *Candida inconspicua* has been also isolated from dairy beverages (Altay *et al.*, 2013). In studies conducted with eight strains of yeasts isolated from cheese and kefir, *Debaromyces hansenii* (*Candida famata*) showed good adherence to cultures of human Caco-2 cells as well as resistance to acidic conditions. However, the strain of *Kluyveromyces lactis* exhibited the best probiotic characteristics (Kumura *et al.*, 2004).

In general, we can say that the study using South African KG shares similarities with ours regarding the microorganisms contained in the kefir. This is due mainly to the presence of *Lactobacillus curvatus*, *Candida krusei* and *Debaromyces hansenii* (*Candida famata*) (Witthuhn *et al.* 2004).





**Figure 1.** Gram staining micrographs as seen through a light microscope (MC) at 100X and a stereoscope (S). The stainings correspond to *Lactobacillus curvatus* (1a, 1b and 1c), Gram positive cocci (2a, 2b, 2c, 2d and 2e) and the following yeasts: *Candida famata*, *Can. magnoliae*, *Can. krusei/incospicua* and *Can. sphaerica* (3a, 3b, 3c, 3d and 3e).

Tables 2 and 3 show the results of the experiment design for the fermentation process, as well as the ANOVA for the dependent variables labeled IKG (%), acidity (meq mL<sup>-1</sup>) and Log yeast (CFU mL<sup>-1</sup>) in relation to factors A (KG), B (temperature) and C (time) respectively.

There were statistically significant differences ( $P < 0.05$ ) for IKG in relation to factors A, B and C; in contrast, there were no significant differences ( $P > 0.05$ ) for their interactions or for quadratic interactions. The entire fermentation temperature range showed a higher IKG with low percentages of KG. For instance, 2.4% of KG led to values of approximately 350 and 250% at 29 and 38 °C respectively, while 9.6% of KG led to an IKG ranging from 150 to 170% IKG. The interaction of factors A and B on IKG had a negative effect, as there is less competition for space and nutrients among the microorganisms as well as lower production of inhibitory metabolites. However, since this is a microbial succession, some of the generated metabolites

become the substrate for the growth of others. Furthermore, these microorganisms are considered mesophilic (optimal temperature: 30-40 °C) and their growth is favored in the lower limit of this range because of the balance in their metabolic processes. In the entire range of studied KG concentrations, the IKG showed little variation with low fermentation times, but became maximized once time was increased; this happened mainly when adding 2.4 to 6.0% of KG. The long time required for higher IKG and log yeast values could be due to the fact that the growth of lactobacilli and lactococci starts when the pH is close to neutrality (the initial stage of fermentation) and decreases when acids are produced from glucose. Moreover, high acidity stimulates yeast growth (long fermentation times) (De Vos *et al.*, 2009).

Some researchers have found that the IKG is favored when *Lactobacillus kefirifaciens* and *Saccharomyces cerevisiae* are present in the fermentation process (Cheirslip *et al.*, 2003). This confirms the symbiosis

between bacteria and yeasts occurring in the KG. Gao *et al.* (2012) showed a lower IKG in a dairy substrate at 30.05 °C with 20 hours of fermentation. These conditions caused an increase of only 39.4%. Furthermore, Guzel *et al.* (2011a) obtained an IKG of

around 392 and 223% in dairy substrates enriched with whey proteins; however, this required higher times (30 days). This study, on the other hand, reached similar IKG values with shorter times and no dairy or enriched substrates.

**Table 2.** Results of the experiment design for the fermentation of sugarcane concentrate using KG.

Test	KG (%)	Temperature (°C)	Time (h)	IKG (%)	Acidity (meq mL <sup>-1</sup> )	Log <i>Lactobacillus</i> (CFU mL <sup>-1</sup> )	Log <i>Lactococcus</i> (CFU mL <sup>-1</sup> )	Log Yeast (CFU mL <sup>-1</sup> )
1	9.6	33.5	30.0	149.7	0.121	8.03	7.95	5.70
2	6.0	33.5	30.0	205.2	0.121	8.13	7.85	6.90
3	6.0	33.5	48.0	287.4	0.299	8.34	7.11	8.09
4	2.4	33.5	30.0	300.7	0.117	7.96	8.15	7.32
5	4.0	36.0	40.0	317.2	0.189	7.27	8.31	6.76
6	4.0	31.0	20.0	181.0	0.085	7.82	8.00	7.37
7	6.0	38.0	30.0	149.2	0.144	8.01	8.00	6.00
8	6.0	33.5	30.0	185.7	0.111	8.06	7.73	7.29
9	8.0	36.0	20.0	123.8	0.098	8.00	7.66	7.65
10	6.0	33.5	12.0	54.1	0.065	7.77	7.58	7.03
11	6.0	29.0	30.0	220.0	0.164	8.26	8.36	7.19
12	6.0	33.5	30.0	179.5	0.102	8.23	7.49	7.54
13	6.0	33.5	30.0	202.3	0.124	8.32	8.28	7.29
14	6.0	33.5	30.0	208.7	0.124	6.95	7.70	7.37
15	8.0	31.0	40.0	233.5	0.164	7.78	8.04	7.15

KG: Kefir grains, IKG: Increase in Kefir grains

**Table 3.** ANOVA for the response surfaces model for the fermentation of sugarcane concentrate using KG.

	IKG (%)	Acidity (meq mL <sup>-1</sup> )	Log Yeast (CFU mL <sup>-1</sup> )	Log <i>Lactobacillus</i> (CFU mL <sup>-1</sup> )	Log <i>Lactococcus</i> (CFU mL <sup>-1</sup> )
Model	0.002**	0.001**	0.038*	0.986 <sup>ns</sup>	0.280 <sup>ns</sup>
A: KG (%)	0.002**	0.835 <sup>ns</sup>	0.013*	0.937 <sup>ns</sup>	0.650 <sup>ns</sup>
B: Temperature	0.042*	0.355 <sup>ns</sup>	0.041*	0.770 <sup>ns</sup>	0.399 <sup>ns</sup>
C: Time	0.001**	0.001**	0.059 <sup>ns</sup>	0.499 <sup>ns</sup>	0.294 <sup>ns</sup>
AB	0.786 <sup>ns</sup>	0.053 <sup>ns</sup>	0.033*	0.365 <sup>ns</sup>	0.152 <sup>ns</sup>
AC	0.075 <sup>ns</sup>	0.149 <sup>ns</sup>	0.180 <sup>ns</sup>	0.966 <sup>ns</sup>	0.665 <sup>ns</sup>
BC	0.590 <sup>ns</sup>	0.655 <sup>ns</sup>	0.025*	0.686 <sup>ns</sup>	0.606 <sup>ns</sup>
A <sup>2</sup>	0.060 <sup>ns</sup>	0.798 <sup>ns</sup>	0.045*	0.897 <sup>ns</sup>	0.253 <sup>ns</sup>
B <sup>2</sup>	0.772 <sup>ns</sup>	0.035*	0.069 <sup>ns</sup>	0.871 <sup>ns</sup>	0.122 <sup>ns</sup>
C <sup>2</sup>	0.270 <sup>ns</sup>	0.003**	0.171 <sup>ns</sup>	0.998 <sup>ns</sup>	0.130 <sup>ns</sup>
R <sup>2</sup>	0.974	0.977	0.907	0.247	0.758

p values (excluding R<sup>2</sup>), \*Statistically significant effect ( $P < 0.05$ ). \*\*Statistically significant effect ( $P < 0.01$ ) ns: non-significant effect.

Acidity showed statistically significant differences ( $P < 0.05$ ) when compared to factor C. This was also true for the  $B^2$  and  $C^2$  quadratic interactions. In contrast, no significant differences ( $P > 0.05$ ) were found with factors A and B, interactions between factors or in the  $A^2$  quadratic interaction. Low acidity was observed throughout the entire fermentation temperature range at short fermentation times (values ranged from 0.06 to 0.1 meq acid  $\text{mL}^{-1}$ ). Additionally, increasing the fermentation time resulted in higher acidity, with values approaching 0.3 meq acid  $\text{mL}^{-1}$ . Cui *et al.* (2013) found similar acidity values (meq acid 0.16  $\text{mL}^{-1}$ ) using a similar fermentation temperature, a shorter time and fewer KG in a different substrate.

The log yeast variable showed statistically significant differences ( $P < 0.05$ ) with factors A and B, the AB and BC interactions and the  $A^2$  quadratic interaction. No difference was observed regarding the C factor, the AC interaction or the  $B^2$  and  $C^2$  quadratic interactions. Little variation was observed in the yeast growth at high fermentation temperatures. However, there was a

tendency to become maximized once the temperature and KG decreased. The AB and BC interactions on acidity had a positive effect.

The optimization of the fermentation process using the Design Expert 8.0 software was performed by maximizing both the IKG and the microbial counts while keeping the acidity levels within the experimental range, thus generating the following optimal conditions for fermentation: KG = 6.0% (w/w), temperature = 33.5 °C and time = 30 hours. Table 4 shows the values obtained experimentally using the optimal process conditions and the theoretical values from the models for each variable. The ANOVA (Table 3) showed that the factorial regression model was statistically significant ( $P < 0.05$ ) for the IKG, acidity (meq  $\text{mL}^{-1}$ ) and log yeast (CFU  $\text{mL}^{-1}$ ) response variables. The regression coefficients for the quadratic model were 97.4%; 97.7% and 90.4% respectively. In contrast, no statistically significant differences ( $P > 0.05$ ) were observed for the other dependent variables, factors or interactions within the studied range.

**Table 4.** Experimental and theoretical values of the response variables for the sugarcane fermentation process using KG.

Dependent variable	Experimental value	Theoretical value of the model
IKG (%)	196.3 ± 12.9	197.0 ± 18.4
Acidity (meq acid $\text{mL}^{-1}$ )	0.12 ± 0.01	0.12 ± 0.01
Log Lactobacillus (CFU $\text{mL}^{-1}$ )	8.2 ± 0.1	7.9 ± 0.5
Log Yeast (CFU $\text{mL}^{-1}$ )	7.8 ± 0.3	7.3 ± 0.3
Log Lactococcus (CFU $\text{mL}^{-1}$ )	7.3 ± 0.3	7.8 ± 0.3

Additional research conducted on fermentation processes using 3% of KG in nut milk supplemented with 8% of sucrose for 12 h at 30 °C showed yeast counts of approximately 6 logs (1 log unit less than in our study), probably due to the lower fermentation times; on the other hand, the lactobacilli and lactococci counts were similar (Cui *et al.*, 2013). Furthermore, the counts found by Leite *et al.* (2012) upon fermenting UHT skim milk with 3% of KG at 25 °C for 24 h were similar in terms of lactobacilli and yeasts, but higher for lactococci.

A number of studies have shown that the use of KG produces foods with better quality and greater acceptance than those

obtained from starter cultures that have been directly isolated from the granule (Assadi *et al.*, 2000). Therefore, it is more effective to use grains given the symbiosis existing between the organisms that compose them because they produce a wider variety of metabolites that provide the food with better sensory and nutritional characteristics.

## CONCLUSIONS

Sugarcane concentrate is an effective alternative for the development of non-dairy foods with probiotics using KG as the starter culture for the fermentation process. Consumption of this food might prevent gastrointestinal diseases and strengthen the immune system.

Six bacterial and four yeast strains were isolated from KG activated in sugarcane concentrate; their microorganism composition showed greater similarity with that of KG from South Africa. The yeasts found showed greater variety (*Candida famata*, *Can. magnoliae*, *Can. krusei/incospicua* and *Can. sphaerica*) than those from the lactobacilli genus (*Lactobacillus curvatus*).

Results made it possible to establish a technological, effective, simple and practical fermentation process that is likely to be replicable at a large scale under the following conditions: a temperature of 33.5 °C, a time of 30 hours and with 6% w/w of added KG. The increase in KG reached was of 193 ± 12% and the lactobacilli, lactococci and yeast counts were 1.57x10<sup>8</sup>, 8.63x10<sup>7</sup> and 2.05x10<sup>7</sup> CFU mL<sup>-1</sup> respectively. In addition, they showed many advantages over those found by other studies using milk-based substrates with additional nutrients.

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