OPTIMIZATION OF AFRICAN LOCUST BEANS "DADDAWA" PRODUCTION USING RESPONSE SURFACE METHODOLOGY

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ABSTRACT

In this research, optimization of 'Daddawa' production was carried out using Response Surface Methodology. Fresh samples of African locust beans seeds were obtained from Central Market, Kaduna metropolis. The Bacillus subtilis used to accomplish the fermentation was isolated from fermented products ('Ogi and Daddawa') and was identified using conventional biochemical tests and molecular method using 16SrDNA sequence homology. African locust bean seeds were processed into 'Daddawa' The laboratory methods adopted were similar to the traditional method except that glass wares were used as fermentation vessels, aluminum foil instead of the traditional sack, calabash, leaves etc. The production was done in 100 mL beaker. Three variable factors which include locust beans weight, fermentation duration and inoculum were varied to optimize the production according to the experimental runs generated by Design Expert Software based on Central composite design (CCD). Percentage protein of the Daddawa produced was used as response to analyse the optimization using Response Surface Methodology. The bioprocess was optimized for "Daddawa" production using B. Subtilis in which a percentage protein yeild of 98±0.20 was recorded. These optimum conditions were 50g locust bean weight, 5 days fermentation duration, and 0.6mL inoculum volume. The proximate composition of the optimized product shows higher values compared to the unoptimized Daddawa. Furthermore, optimization experiments showed an improvement of 18-20% over traditional methods. This has underscored the importance of response surface methodology in bioprocess optimization contributing to standardization of parameters, enhanced yields, and a scientific basis to improve this indigenous food at industrial scale.

Keywords: Daddawa, Optimazation, *Bacillus subtilis*, Response Surface Method.

INTRODUCTION

Parkia biglobosa is a savannah tree belonging to the subfamily *Mimosoidea*. It is resourceful as it provides food and shelter to human and animals (Akpi *et al.*, 2020) It is processed into a local condiment popularly called "iru" amongst the "Yoruba" people of Nigeria, other names of the condiment includes "Ogiri" among the Igbo's; "daddawa" amongst the Hausa. The condiment is obtained from seeds of *Parkia biglobosa* that have been washed, de-hulled, fermented and molded into balls (Akande *et al.*, 2010; Ezeocha *et al.*, 2022). Processing into iru is usually done traditionally with rudiment technology in the processing line which is time-consuming and labor-intenxsive (Alsalman and Ramaswamy *et al.*, 2020). Many women across the diverse ethnic groups in Nigeria feel their soup is not complete till iru is added: it is seen as a meat substitute. However, the taste, smell and appearance of iru have

stood as a deterrent in its use. Locust beans dehulling by pressing with feet, washing, wrapping with jute bags, leaves, sacks, salting and molding, air/sun drying were reported as the critical control point (CCP) during the traditional fermentation processes of locust beans (Campbell-Platt, 2017; Yadav *et al.*, 2021).

Most condiments are produced in traditional small-scale family settings with a great deal of variation in the weather. The fermentation process is typically carried out in a moist solid form, aided by ambient temperatures and requiring contact with the proper inoculum of diverse microorganisms. The techniques used to process the most of food condiments (Daddawa) have raised concerns because of the negative effects they have on both customers' health and lives.

Optimization literarily means discovering best solution, the optimum parameter in the mid of varying factors that are dependent on predefined demands known as constraints (Karamba et al., 2016). Over the years, there have been several attempts to optimize the production of this important food additive with a view to improving the quality of the finished product. In most cases, the conventional approach of one factor at a time optimization is what is being employed. However, this approach is time-consuming and was found to be inadequate in giving the details about the simultaneous interaction among the several factors that affect production and the quality of the product. Interestingly, a more robust approach based on Response Surface Methodology (RSM) is now available; in which a software such as Design Expert can be used to design a 'several factors at a time' optimization. Design of experiments (DOE) requires a systematic method of determining the relationship between factors affecting a process and the output of that process. The software predicts and designs experiments using advanced statistical tool which allows a researcher to study efficiently the effect of a large number of variables with a minimum effort in data collection.

In most of the bioprocess experiments, microorganisms are subjected to optimal nutrient and environmental condition for better growth to be attained in order to put it into its best biotechnological manipulations (Karamba *et al.*, 2017; Yadav *et al.*, 2021). In this study, an attempt was made to optimize African locust bean fermentation for 'daddawa' production using RSM and *Bacillus subtilis* as starter culture. By systematically varying fermentation parameters and modeling the results, optimal time, temperature and inoculum levels could be identified to maximize 'daddawa' protein yield.

MATERIALS AND METHODS

Collection and Identification of African Locust Bean Seed Samples

Fresh samples of African locust beans seed were obtained from Central market in Kaduna metropolis. Kaduna State, Nigeria. The samples were taken to the Botany Unit, Department of Biological Sciences, Kaduna State University for taxonomic identification.

Isolation and Identification of Bacillus subtilis

Two fermented products (Ogi and "Daddawa") were used as a source of the organism (*Bacillus subtilis*). One (1) g of each fermented food sample was weighed and suspended in 9 mL of sterile peptone water (1:9); the mixture was homogenized and diluted serially to 10-folds. Five hundred (500) μ L inoculum was taken from 10⁻⁸ dilutions and cultured using pour plate technique onto Tryptone Soy Agar (TSA). The culture was incubated at 37 °C for 24 h. Separate and distinct colonies were sub-cultured on a nutrient agar to obtain the pure culture. The pure isolates were preserved in 20% glycerol. The sub-cultured colonies were used for the gram reactions and other biochemical tests (Cheesbrough, 2006).

Identification of the Isolates

Culture characterization and Grams' staining

The colony appearances of the isolates were examined physically with naked eyes to determine the colony characteristics. Pure culture of the isolate was Gram stained and observed using under microscope using X100 oil immersion objective lens as described by Cheesbrough (2006).

Biochemical characterization of the isolates

Biochemical test which include catalase, coagulase, oxidase, citrate, urease, Voges Proskauer, Triple Sugar Iron (TSI) and motility test were carried out to identify the isolate (Farinde *et al.*, 2014).

Catalase test

About 2mL of hydrogen peroxide solution was poured into a test tube. Using a sterile glass rod, colonies of the test organisms were picked aseptically and placed into hydrogen peroxide solution and observed for bubbles. Catalase positive organisms produced bubbles while catalase negative organisms did not (Idise, 2010).

Oxidase test

A piece of oxidase test strip was held with forceps and the strip was placed onto an area of heavy growth of the test organism. Change of colour to purple within 10 seconds was taken as positive result while no change in colour for more than 60 seconds was taken as negative change (Idise, 2010).

Voges Proskauer test

Sterile glucose phosphate broth (10mL) in a test tube was inoculated with the test isolates and incubated for 48 h at 37°C. After incubation, 0.5mL of 0.5% alpha-Naphthol solution and 0.5mL of 16% potassium hydroxide solution were introduced into the mixture. The mixture was then shaken vigorously and left for about 10 min. A red colour indicated a positive result, signifying acetoin production, while the absence of colouration indicated a negative result. (Cheesebrough, 2006).

Methyl red test

Ten milliliters of glucose phosphate peptone broth were dispensed into test tubes, which were then capped with cotton wool wrapped in foil and sterilized. The test organisms were inoculated and incubated at 37°C for 48 h. After the incubation period, a few drops of methyl red indicator were added to the cultures. The production or development of a red colour was considered a positive reaction, while the absence of the colour indicated a negative reaction (Cheesebrough, 2006).

Citrate utilization

The isolates were stab-inoculated onto Simon citrate medium. The tubes were subsequently incubated at 37°C for 24 h. A positive result was observed as the indicator changed from green to an intense Prussian blue colour (Farinde *et al.*, 2014). The colour change from green to Prussian blue indicates the utilization of citrate.

Indole test

The peptone broth was inoculated with the test organism and incubated at 30°C for 48 hours, with a control kept for comparison. Kovac's reagent was added gradually, drop by drop. The tubes were gently shaken and left to stand for 10 minutes to allow the formation of a distinct layer. The presence of a red-coloured layer on top of the tube indicated a positive result (Farinde *et al.*, 2014).

Sugar Fermentation Test

A 1% (w/v) peptone water and sugar broth were prepared by combining peptone water and the respective sugars. Bromocresol was added as an indicator. The sugars include glucose, maltose, fructose and lactose. Each test tubes were dispensed with 10 mL of the broth, with durham tubes inverted inside them, and sterilized by autoclaving at 115 °C for ten minutes. The test organisms were then inoculated into the broths in the test tubes and incubated at 37°C for 48 h. Uninoculated tubes served as controls. A positive reaction was indicated by a colour change of the broth medium from red to yellow, and sometimes gas production in the Durham tube (Cheesebrough, 2006).

Motility test

A luxuriant growth of the organisms was picked up and stabbed onto the Nutrient agar slant at right angle to the bottom of the tube. This was then incubated at 37°C for 28h and observed for pattern of growth of the organism (Idise, 2010). Motile organisms grew away from the line of stabbing while non motile organisms grew along the line of stabbing.

Molecular Identification of the Isolates

Genomic DNA Extraction

The genomic DNA of isolate was extracted and purified using the DNA isolation kit Quick-DNATM (Zymo Research, USA) according to the manufacturer's directions and confirmed using 0.5% agarose gel electrophoresis.

Amplification of 16S RNA Gene

The Polymerase chain reaction (PCR) was conducted using the universal primers 341F and 962R (Mafra *et al.*, 2008). The PCR reaction mixtures consist of master mix and the conditions was profiled for 30 minutes consisting of about 30-40 cycles, with denaturation at about 94 °C for the period of 30 seconds, annealing

at 51 °C for the period of 45 seconds and extension at 72 °C for the period of 1-5 minutes.

Agarose gel electrophoresis

About 1.5g of agarose was heated in a boiling water until it was completely dissolved. Appropriate number of combs was placed in gel tray. Five micro- liters of ethidium bromide was added to the cooled gel and poured into gel tray. The gel casting was made after cooling to about 55°C, it was then allowed to cool for 30 minutes at 30°C. The gel was placed in the electrophoresis chamber and covered with buffer (TBE). DNA amplicon and standard (Ladder) were loaded into gel wells. The electrophoresis system was connected to power supply and run for 1 hour. Deoxyribonucleic Acid (DNA) bands were visualized using gel imaging system.

Sequencing

The PCR product was purified and analyzed by Sanger (dideoxy) sequencing Technique to determine the nucleotide sequence of the amplified gene of the isolates using automated PCR cycle-Sanger Sequencer™ 3730/3730XL DNA Analyzers from Applied Biosystems. The sequencing analysis was done at Inqaba Biotechnology Pty South Africa.

Sequence Analysis and BLAST

The sequences in the forward and reverse files were analyzed using the Sequence Scanner Software v1.0 (Applied Biosystems Thermo Fischer Scientific). The gene sequence of each isolate was used as query sequence in the Genbank to identify the organism using BLAST (Basic local alignment search tool) at the website of the National Center for Biotechnology Information (NCBI); http://www.ncbi.nlm.nih.gov/blast) (Souza *et al.*, 2016).

Optimization of Fermentation Conditions using Response Surface Method

Three factors were varied to optimize the production, these include locust beans concentration, fermentation duration and inoculum volume. The Design Expert software 6.0.8 (Stat-EaseInc. Minneapolis, USA) was used to generate the experimental runs based on the central composite design (CCD) of the Response Surface Methodology. Table 1 gives information about the variable factors used and the respective lower and upper limits used in the design. Upon completion, the % protein was considered as the response, (Y-axis). Verification of the experiment was carried out using the same method comparing the experimental predicted value and the actual value obtained from the experiment

Table 1: Design of the Experimer	ital Factors
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Factors	Notation	Units	Levels	
			-	+
Locust Bean weight.	А	Gram	10	50
Fermentation Duration	В	Days	1	5
Inoculum Volume.	С	mĹ	0.1	0.5

Table 2 shows the experimental runs generated by the software based the minimum and maximum levels of the variable factors used. The design produced 15 experimental runs.

 Table 2: Design of the Experimental Results of Percentage Protein

 Yield of "Daddawa"

	Α	В	С
Run	Locust Bean weight	Fermentation Duration	Inoculum Volume.
	(g)	(Days)	(mL)
1	30	2	0.3
2	30	3	0.6
3	10	5	0.5
4	58	3	0.3
5	30	3	0.3
6	50	1	0.5
7	30	3	0.3
8	10	1	0.1
9	30	3	0.3
10	50	5	0.1
11	30	6	0.3
12	30	3	0.3
13	30	3	0.3
14	10	3	0.3
15	30	3	0.2

Key: g = grams, mL =Millilitre

Preparation of African Locust Bean Seed Sample

The locust beans seeds were washed with tap water and boiled for 3 h using a pressure cooker to facilitate extraction of the cotyledons from seed coat. The boiled beans were then dehulled by pressing in between palms and then washed to remove the seed coats. The extracted cotyledons were boiled for 1 h to aid softening prior to fermentation setup (Odunfa, 2010). The processed sample was weighed using electric weighing balance.

Inoculum Preparation of Bacillus subtilis

Inoculum used for the experiment was freshly prepared. Using where a loopful of single bacterial isolate from pure culture plate was aseptically transferred into a conical flask containing 10 mL of sterilized Nutrient Broth. The flask was incubated in orbital shaker set at a speed of 150 rpm at 37°C for the period of 24 h. Optical density of the culture was determined to assess the need of adjusting the cells concentration of the inoculum.

Laboratory Production of "Daddawa" from Locust Bean Seeds Raw African locust bean seeds were processed into "daddawa" using the modified method by Achi (2005). The laboratory methods adopted were similar to the traditional method except that glass wares were used as fermentation vessels, aluminum foil instead of the traditional sack, calabash, leaves etc. so also the cooking methods of the seeds, pressure cooker was used instead of the traditional firewood. Processing of the seeds was carried out by boiling the locust bean seed for 2h during which water was removed twice. The testa was then removed by pounding lightly in a laboratory mortar and pestle. The seeds were then washed to remove the testa from the cotyledon. The cotyledons were then reboiled for 2 h and the water discarded. The processed seeds were measured in accordance with the research design suggested by RSM and placed in 100 mL beaker (Table 2). All the experiments were conducted in duplicates and the inoculum was added in accordance with the RSM design (Table 3.2). The beakers were then covered with aluminum foil and incubated at $25\pm5^{\circ}C$ (Odunfa, 2010). The fermentation was carried out for 1-5 days.

Preparation of Extract for Protein Estimation

After the fermentation, the fermented products were extracted as reported by Odunfa (2010) where 5 g of the sample was weighed into a 100 mL conical flask and ethanol water (50:50vol./vol) was added and grounded using mortar and pestle. The suspension was then washed with 5 mL petroleum ether to extract the oil, centrifuged at 5000rpm and refrigerated at 5 °C for 30 min. The supernatants were collected and used for further analysis.

Determination of Amino Acids

One (1) mL each of the extract solutions was pipetted into clean test tubes. Distilled water was added to each tube to make a total volume of 4 mL. One (1) mL of the ninhydrin solution reagent was added to each tube and mixed properly. The tubes were placed in boiling water bath for 15 minutes. They were allowed to cool and 1 mL of 50% ethanol was added to each tube. The change in color developed was measured in spectrophotometer at 450 nm wavelength (Smith and Agiza, 2010). Standard calibration curve was prepared according to Karamba and Ahmad, (2019).

Preparation of Protein Standard Curve

Initially, 0.0-1.0mg/mL concentrations of protein solutions from a stock of 200 mg/mL were prepared at different ranges of 0.0, 0.2, 0.4, 0.6, 0.8 and 1.0. Five (5) mL of protein solution from were transferred in the test tubes labelled of respective concentration along with 1 extra test tube in which 1 mL of distilled water and 0.5 mL of unknown solution was transferred to serve as control. One (1) mL of clean cupper reagent was added in all the test tubes incubated for 10 minutes at room temperature the colour turned to blue followed by adding 0.5 mL of Follin Clocalteu's phenol reagent and further incubated for 10 minutes at room temperature. Afterwards the test tubes were allowed to cool to room temperature. The absorbance of each of the samples was then measured at 650 nm in a spectrophotometer. A standard curve was prepared plotting the standard protein concentration (mg/mL) (xaxis) against the respective absorbance (y-axis) in order to achieve a best fit straight line.

Calculation of the Amount of % Protein Yield

Amount of Protein in 1mL of the Unknown Sample (%) = OD X Dilution Factor

Volume of Unknown used

Where, OD= optical density of unknown sample. Determination of Proximate Composition of "Daddawa"

The proximate composition: percentage moisture content, ash content, protein, fats and oil, crude fibre content, and carbohydrate content of the "daddawa" were determined in triplicates using the method described by AOAC (2011). The procedure is described below.

Determination of Percentage Moisture Content

Aluminum dishes were washed and dried to a constant weight in an oven at 100°C. They were later removed and cooled in a

desiccator and weighed (W1). Two (2) grams of the grounded (powder) of each sample was placed in the weighed moisture dish (W2). The dish containing each sample was kept in an oven for about 3 hours, the samples were removed and cooled in the desiccator and weighed W3.

The % of moisture was calculated as: <u>W2-W3</u> × 100 W2-W1

Determination of Percentage Ash Content

Crucibles were cleaned and dried in the oven, cooled in the dessicator and weighed (W1). Two (2) grams of the grounded (powder) of each sample was placed in the crucibles and weighed (W2). They were transferred into the Muffle furnace for about 550° C, then removed and cooled in the dessicator and weighed (W3). The % of Ash was calculated as follows: W3-W1 \times 100

W2-W1

Determination of Percentage Crude Protein

Protein determination was achieved through three stages which include digestion, distillation and titration. Briefly, two (2) gram of each sample was weighed into a kjeldahl flask. Catalyst (copper) and 15mL concentrated sulphuric acid (H₂SO₄) were added. The solution was heated till it assumed a green colour in the fume cupboard. It was then cooled and any black particles showing at the mouth and neck of the flask was washed down with distilled water. After cooling, the digest was transferred with several washings into 100ml with distilled water.

The Markham distillation apparatus was steamed for 15minutes before use. A 100ml conical flask containing 10ml of Boric indicator was placed under the condenser. Ten (10)ml of the digest was added into the body of the apparatus via the small funnel aperture, it was washed down with distilled water followed by 10ml of 40% NaOH solution. Steam through for about 5-7 minutes to collect ammonium sulphate (30-40ml). The receiving flask was removed and the tip of the condenser was washed down into the flask.

Finally, the solution was titrated into the receiving flask using N/100 (0.01N) hydrochloric acid, the Nitrogen content was calculated and hence the protein content of the sample. The blank was measured along with the sample always. The % of protein was calculated as: Final reading –Initial reading-blank (0.2) x standard number of Nitrogen (1.4) divide by initial weight (0.5) x standard number of protein (6.25).

Determination of Percentage Lipids (Fat) Content

Oven dried 250 mL clean round bottom flask was transferred into the dessicator and allowed to cool. Empty filter paper was weighted and labeled W1. Two (2) gram of each sample was weighted into labeled thimbles (filter paper) W2. Boiling flask was filled with petroleum spirit or N-hexane. Soxhlet apparatus was assembled and allowed to reflux for 8hours. It was removed and transferred to an oven to dry. Then transferred from the oven into a dessicator and allowed to cool then weighed W3.

The % of Fat was calculated as: <u>W2-W3</u> × 100 W2-W1

Determination of Percentage Fiber Content

Exactly two (2) grams of the each sample was placed in a beaker containing 1.2 mL of H_2SO_4 per 100ml of solution and boiled for about 30min, the residue was filtered and wash with hot water, the residue was transferred to a beaker containing 1.2 gram of NaOH per 100 mL of solution and boiled for about 30 min, the residue was

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washed with hot water and dried in an oven and weighed (C2), each of the weighed sample was incinerated in a furnace for about 550°C, removed and allowed to cool, and weighed (C3). The % of Fibre was calculated as: $\frac{C2-C3}{W}$ × 100

Determination of Percentage Carbohydrate (CHO) Content

By difference, in this method carbohydrate content was obtained by calculations having estimated all other fractions by proximate analysis.

CHO =100- (% of moisture + %Ash + %Protein + %Fat)

Estimation of Total Mesophilic Bacterial Count of the Optimized Products

The total viable count was determined using methods describe by Omafuvbe *et al.* (2010) where pour plate method was employed. The bacterial load was estimated using dilution technique. For the optimized fermenting seeds, 5-fold serial dilution of the seeds was prepared using sterile distilled water for up to 10^{-5} . A 0.1 mL of 10^{-4} dilution was inoculated in duplicates by pour plate method on nutrient agar for total aerobic bacterial count. All the plates were incubated at 37 °C for 24 h. Total aerobic counts were taken using digital illuminated colony counter. The count for each plate was expressed in colony forming units per milliliter CFU/g).

Analysis of the Designed Experiment

At the end of the optimization experiment, percentage (%) protein yield was determined and used as response. Based on the combination of 3 variables, analysis of the regression of the experimental data was carried out using the same software used to design the experiment, The response (dependent) variable (% Protein yield) was represented on the Y-axis. Each independent variable was studied at two levels. The data were analyzed by fitting it to the second- order polynomial regression equation as below:

$$y = \beta 0 + \sum_{i=1}^{k} \beta_i x_i + \beta_i x^2_i + \sum_{i=1}^{k} \sum_{j=1}^{k-1} \beta_{ij} x_i x_j$$

Where y= the response (dependent) variable.

 $\beta 0$ = the intercept; βi , $\beta i j$, $\beta i j$ = the regression coefficients variables for linear, quadratic and interaction, respectively, whereas *xi* and *xj* = independent variables.

Statistical Analysis of Data

The data collected were analyzed using Statistical Design Expert Software Version 13.0 (Stat-Ease, Minneapolis, MN, USA). The data were subjected for Analysis of Variance (ANOVA), and the Duncan Multiple Range was tested for the significant difference at p<0.05.

RESULTS

Morphological and Biochemical Characterization of the Isolates

The cultural morphology of bacterial isolates in terms of color, size, shape and margin shown in Table 3. Colonies of all the isolates appeared whitish, with size ranging from big to small, rough and circular shape, and entire to undulate margin. The biochemical characteristics indicated that all the isolates were positive to Gram reaction, Motility, catalase, citrate, and lactose, fructose and glucose, catalase, maltose, but were negative to Voges Proskauer, methyl red and indole, as presented in Table 3. The 16S rDNA sequence analysis confirmed the isolate as *Bacillus subtilis*. Figure 1 shows the electropherogram of the amplify 16SrDNA gene of the isolate.

Table 3: Cultural Morphology and Biochemical Characteristics of Suspected Bacillus specie Isolates

Isolate Code	Colour	Size	Shape	Margin	Gram Reaction	Oxidase	Motility	Catalas	Voges Proskauer	Urease	Citrate	Indole	Methyl Red	Maltose	Glucose	Lactose	Fructose	Probable Organisms
D1	Whitish	Big	Rough	Undulate	+	+	+	+	+	-	+	-	-	+	+	+	+	Bacillus sp.
D2	Whitish	Big	Citcular	Entire	+	+	+	+	+	-	+	-	-	+	+	+	+	<i>Bacillu</i> s sp.
O1	White	Small	Rough	Entire	+	+	+	÷	+	-	+	-	-	+	+	+	+	<i>Bacillu</i> s sp.
O2	Whitish	Big	Rough	Entire	+	+	+	+	+	-	+	-	-	+	+	+	+	<i>Bacillu</i> s sp.

Key: D ="daddawa", O =Ogi, + = Positive, - = Negative, sp = specie

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	Μ	1
	1	
1500bp		-

Figure 1: Gel Electropherogram of 1the 6S rRNA for Bacillus subtilis. M=Biomarker (1kbpladder), 1=Bacillus subtilis, bp=base pairs

Optimized Conditions for "Daddawa" Production

The designed experimental runs of RSM optimization for 'Daddawa' production with the respective values of both experimental (Actual) and predicted response are presented in Table 4. From the table, it can be seen that the values of

experimental response were in most cases close to the corresponding predicted values. Highest protein yield was recorded when 30 g of the locust bean, 3 days of fermentation duration and 0.6 mL inoculum volume were used.

Run	А	В	С	Response		
	Locust Bean	Fermentation Duration	Inoculum Volume.	% Protei	n Yield	
	weight (g)	(Days)	(mL)	Predicted Value	Actual Value	
1	30	2	0.3	32.78	32.00	
2	30	3	0.6	88.67	87.94	
3	10	5	0.5	46.21	47.00	
4	58	3	0.3	43.66	42.85	
5	30	3	0.3	44.21	40.00	
6	50	1	0.5	59.88	60.67	
7	30	3	0.3	44.21	50.60	
8	10	1	0.1	43.31	44.10	
9	30	3	0.3	44.21	42.00	
10	50	5	0.1	50.08	50.87	
11	30	6	0.3	52.43	51.70	
12	30	3	0.3	44.21	40.30	
13	30	3	0.3	44.21	49.60	
14	10	3	0.3	40.89	40.09	
15	30	3	0.2	33.38	32.60	

Table 4: Designed Experimental runs of RSM Optimization for 'Daddawa' Production

The absolute equation in relation to coded factors is explained below:

Y = + 44.21 + 0.9689A + 6.87B + 18.31 C + 1513 AB + 8.59 AC - 4.14BC

Analysis of Variance (ANOVA) for the response surface regression is shown in Table 5. The P-value of 0.05 were used to determine the significance of the model. A large value of lack of fit obtained implies that the models are adequate to predict the responses. Three-dimension (3D) contour plots of the interaction between locust beans weight and fermentation duration is shown in Figure 2. Likewise, the interaction between locust beans weight and lnoculum volume is depicted Figure 3.

The verification of experiment was carried out using the optimum parameters of 50 g Locust Beans weight, 5 days of fermentation

period and 0.5 mL of inoculum volume. This yielded a percentage protein of 98±0.20 which is very close to the corresponding predicted value of 95.60 as shown in Table 6.

Mesophilic Bacterial Count of the Optimized Product

The mesophilic bacterial count of the optimization experiments is shown in Table 7. Highest count (9.0 X 10^4 CFU/g) was recorded in run 12, whereas the lowest mesophilic count of 1.1 X 10^4 CFU/g

Table 5: Analysis of Variance (ANOVA) Quadratic Model for Central Composite Design

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was recorded in run 6.

Proximate Composition of Optimized and Unoptimized Produced "Daddawa"

Optimized produced 'Daddawa' had the highest yield of % protein of 38.73%, 28.18% lipid, moisture content and carbohydrate content of 29.58%. The unoptimized produced 'Daddawa' had 29.4 % of protein, 22.13% lipid, 0.6 % ash and 33.41 % carbohydrate.

Source	Sum of Squares	df	Mean Square	F-value	p-value	Remarks
Model	2426.91	9	269.66	11.84	0.0071	Significant
A-Locust Bean weight.	3.72	1	3.72	0.1633	0.7029	-
B-Fermentation Duration	196.66	1	196.66	8.63	0.0323	Significant
C- Inoculum Volume.	1397.81	1	1397.81	61.37	0.0005	Significant
AB	467.61	1	467.61	20.53	0.0062	Significant
AC	150.73	1	150.73	6.62	0.0499	Significant
BC	34.13	1	34.13	1.50	0.2754	
A²	7.20	1	7.20	0.3161	0.5982	
B ²	7.08	1	7.08	0.3108	0.6012	
C ²	472.83	1	472.83	20.76	0.0061	Significant
Residual	113.89	5	22.78			-
Lack of Fit	6.53	1	6.53	0.2433	0.6477	Not Significant
Pure Error	107.36	4	26.84			-
Cor Total	2540.80	14				

P<0.05= significance.



Figure 2: A 3D-Contour Plot Showing the Interactions between Locust Bean weight (A) and Fermentation duration (B).

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Figure 3: A 3D-Contour Plot Showing the Interactions between Locust Bean weight (A) and Inoculum Volume (C)

Variable	Optimum Range	% Protein Yield	
		Predicted Value	Actual Value
Locust Bean weight.	50 g		
Fermentation Duration	5 Days	95.60	98±0.20
Inoculum Volume	0.5 mL		

Table 6: Verification/Validation of Experiment

Key: g = grams, mL = Millilitre

Table 7: Mesophilic Bacterial Count of the Optimized Product

Run	Locust Bean weight <u>.</u> (g)	Fermentation Duration (Days)	Inoculum Volume. (mL)	Mesophilic bacterial count (X104 CFU/g)
1	30	2	0.3	2.1
2	30	3	0.6	1.80
3	10	5	0.5	1.70
4	58	3	0.3	1.50
5	30	3	0.3	1.20
6	50	1	0.5	1.10
7	30	3	0.3	1.50
8	10	1	0.1	7.0
9	30	3	0.3	1.20
10	50	5	0.1	1.50
11	30	6	0.3	2.02
12	30	3	0.3	9.0
13	30	3	0.3	1.20
14	1.7	3	0.3	8.7
15	30	3	0.02	1.60

Key: CFU =Colony forming unit, mL =Millilitre, g = grams

DISCUSSION

All the Isolates were found to have the colonial morphology and biochemical characteristics as that of Bacillus species. Isolates appeared as gram-positive rods. This clearly shows that those bacteria isolated from the fermented food have the characteristic of Bacillus sp. The result is in conformity with the report of Antai and Ibrahim (2016), who reported a progressive increase of the dominant Bacillus species throughout the use of fermented food ("Daddawa") for isolation of bacteria. Presently, Bacillus species are agreed to be the predominant species developed in fermentation processes of various legumes (Ouoba et al., 2003). Bacillus sp was reported as being responsible for the fermentation in "Daddawa" and the important flavoring compounds (Beaumont, 2002; Odunfa, 2015). The predominance growth of Bacillus sp is favored by the low oxygen tension during the fermentation. The Bacillus species isolated from the test condiments ("Daddawa") in this work were observed to be Gram positive, rod-shaped and catalase positive. This is in agreement with the findings of Allaf (2011). Many species of this genus exhibit a wide range of physiologic abilities that allow them to live in many natural environments (Ahn et al., 2011). The Bacillus species play an increasingly important role in food and beverage industries (Grass et al., 2014). Bacillus sp has been identified to be the main fermenting bacterium during indigenous production of "Ogiri"; a traditional soup flavoring rich in protein.

The 16S rDNA nucleotide sequences analysis of the isolated *Bacillus* revealed that the strain *is B. subtilis* After Blasting.

With respect to the optimization of Production Process, RSM was used to determine the optimum condition for fermentation of locust beans. The method of analyses illustrated the response gotten after the modification of some parameters that are liable for the fermentation. The percentage protein yield was considered as the response (Karamba et al., 2017). Protein hydrolysis is the most important biochemical change during "Daddawa" fermentation which is due to proteinase activity resulting in rapid production of amino acid (Farinde et al., 2014). The foremost objective of RSM is to determine the optimal condition aimed at obtaining a maximum result. The design and response are illustrated in result sections. Central composite design response was utilized to produce response surfaces in order to disclose the effects of these parameters in locust beans fermentation. The Y-axis is the anticipated response, A is the locust beans weight, B is the fermentation period and C as Inoculum Volume. The precision of a model is judged by the determination coefficient (R²). The R² values of the model were found to be 0.0071. It assessed how inconsistent tested response is clarified by research parameters and their interface. Adjusted R² value was realized to be 0.0071 in which the value was acceptable. It exercises the signal to noise ratio. The "Pred R-Squared" of 0.6477 is in rational pact with the "Adjusted R-Squared" of 0.9558. The significance of every coefficient was proven by *p*-values. In essence, all the parameters are significant model' terms. Lack of fit test measures signal to noise ratio and Ibrahim et al. (2015) reported not significant lack of fit and described that the model was in an excellent fit.

Three-dimension contour plots of the central composite design of the response surface method disclose the interrelations between the 2 variables interacting with each other. The interaction between locust beans weight and fermentation period illustrates the relationship in which at both the extremes and the response was low. At locust beans weight and fermentation period, response was divergent illustrating high axis and very low relationship between the factors depicted by inverted contour curve as the factors; locust beans weight and fermentation period and above the interaction were high illustrating low axis and peak of the reactions (Ibrahim *et al.*, 2015). On the interaction between locust beans weight and Inoculum Volume, the research illustrates the relationship in which at both interactions the response was low. At locust beans weight and Inoculum Volume, response was low. At locust beans weight and loculum Volume, response was divergent illustrating high axis relationship between the factors depicted by contour plot. In the design of the experiment by the central composite design, locust beans weight was utilized against a progressive increase in inoculum volume that have result to % increase in protein yield as similar to the research by Ibrahim *et al.* (2015).

Verification of experiment was carried out using the optimum parameters of locust beans weight, fermentation period and lnoculum Volume in comparison with the experimental and predicted value of the designed experiment. A 50 g Locust Beans, 5 days fermentation period and 0.6 mL inoculum volume were adjudged to be the optimum conditions for the production of 'Daddawa' with higher protein yield of up to 98 ± 0.20 % in this work. This indicates the reliability of the optimum factors, reducing the wastage in the utilization of inoculum with respect to amount of locust beans weight to be fermented for the production of "Daddawa" thus reducing the cost of production.

Conclusion

Bacteria of the genus Bacillus sp. was successfully isolated from fermented foods. The organisms were characterized and found to be a Bacillus subtilis. The optimization of fermentation yield using varying condition based on Inoculum Volume interaction, Locust Beans weight interaction and fermentation period has been optimized for "daddawa" production using B. Subtilis at the optimum conditions of 98±0.20 over predicted value 95.60. This work clearly established an optimum condition for Daddawa production (50g, 5 days, 0.5mL) shows a maximum percentage protein, lipid and carbohydrate yield of optimized over unoptimized Daddawa.. Verification designed optimization experiments showed an improvement of 18-20% over traditional methods. Aseptic techniques ensured quality and safety. The project established a template to integrate starter cultures in 'Daddawa' production, contributing standardized parameters, enhanced yields, and a scientific basis to improve this indigenous food at industrial scale.

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402

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403

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