

## CHARACTERIZATION AND TECHNOLOGICAL PROPERTIES OF YEASTS ISOLATED FROM RETTING CASSAVA

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### Abstract

Yeasts are predominant microorganisms that play important roles during cassava fermentation. Most efforts to develop starter culture for cassava-based fermented products have been unsuccessful because of the little attention given to evaluating the technological potentials of yeasts as co-culture involved in the fermentation process. pH and total titratable acidity (TTA) of retting cassava samples were determined over a 72-hour fermentation period. Yeasts isolated from the retting cassava samples were characterized using phenotypic methods and assessed for technological properties, including extracellular enzymes (amylase, protease, lipase and pectinase) production and susceptibility pattern to antifungal agents by *in vitro* methods. Simultaneous decrease and increase in pH and total total titratable acidity respectively was observed over the 72 hours fermentation period. Four yeast species, namely *Saccharomyces cerevisiae* (44%), *Candida krusei* (22%), *C. parapsilosis* (17%) and *C. tropicalis* (17%) were isolated from retting cassava. High amylase production was observed for all the yeast isolates. About 94.55% of the yeast strains produced protease at varying concentrations. The yeast strains were susceptible to voriconazole and nystatin with the exception of 5 strains which were resistant to nystatin. In conclusion, selected yeast strains possess properties that will aid their selection and application in a controlled process to valorize cassava roots for food use.

**Keywords:** Yeasts, Enzymes, Antifungal compounds, Fermentation, Cassava

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### 1. INTRODUCTION

A wide physiological diversity of yeasts and lactic acid bacteria (LAB) play important roles in the traditional fermentation of several plant derived substrates. During fermentation, yeasts enhance safety and improve the stability, nutritional value and organoleptic properties of foods (Jespersen, 2003). Traditional fermented foods enjoy wide acceptability among African population and play a predominant role in their diet (Holzapfel, 2002; Jespersen, 2003). However, the spontaneous nature of the fermentation processes, whereby the metabolic activities of the best adapted strains from a contaminating mix of LAB and yeasts determines the quality of the product has been implicated in the inconsistencies of product quality and the high risk of product failure (Holzapfel, 2002). The optimization of food fermentation processes to derive products with predictable and desirable qualities requires the careful selection and use of multifunctional

strains of microorganisms as starter culture (Jespersen, 2003).

Cassava (*Manihot esculenta*) is the most important root crop in tropical countries (Tamang, 2010), especially Nigeria as a source of calorie. However, it is low in energy density and protein content, high in cyanide and anti-nutrient levels and prone to rapid deterioration (FAO, 1984; Kimaryo *et al.*, 2000; Kostinek *et al.*, 2007; Hellstrom *et al.*, 2010). In Sub-Saharan Africa, the tuber is traditionally fermented to mitigate these limitations and valorized into respective products such as *gari*, *fufu*, *agbelima*, *chikawgue*, *kivunde*, *kocho* and *togwa* (Oyewole, 2001; Kimaryo *et al.*, 2000; Olasupo, 2006; Hellstrom *et al.*, 2010; Tamang, 2010). The levels of cyanogenic glucosides and enteric pathogens in some of these spontaneously fermented products remain unacceptable (Kimaryo *et al.*, 2000).

Most efforts to develop starter culture to optimize the fermentation of cassava have been directed towards the selection and use of multifunctional strains of LAB. Kimaryo *et al.*

(2000) and Kostinek *et al.* (2007) have successfully selected superior LAB strains from the microflora involved in the spontaneous fermentation of cassava. However, the use of single-species starter culture for the production of traditional fermented foods has not been successful because traditional fermented foods are generated from the activities of a complex microflora (Tamang, 2010). In Kimaryo *et al.* (2000), the *Lb. plantarum* starter culture fermentation process was longer and the product was without the characteristic attributes compared to the spontaneous fermentation. The protein content of *Lb. plantarum*-fermented cassava was lower than a spontaneously fermented cassava sample (Sobowale *et al.*, 2007). Navarrete-Bolanos (2012) recommended that the use of a mixed microflora of the species that desirably impart the fermentation processes will be suitable as starter culture to produce wholesome and acceptable products.

Several species of yeasts have been described as predominant microflora in cassava fermentation (Oyewole, 2001; Oguntoyinbo, 2008; Hellstrom *et al.*, 2010). The flavor-active volatile compounds generated by yeast metabolism impart the characteristic taste and aroma of fermented cassava products (Okafor and Ejiofor, 1990). Enzymes from cassava yeasts contribute to retting and breakdown complex compounds in cassava to simpler compounds that can constitute nutrients for other microbial species (Oyewole, 2001). Yeasts have the potentials to improve the nutritional value of cassava, due to their ability to secrete vitamins and phytase (Hjortmo *et al.*, 2005; Hellström *et al.*, 2010).

Despite the predominance and importance of yeasts during cassava fermentation, there is little or no information on the starter culture potentials of yeasts isolated from fermented cassava products. A screening of yeast species present in retting cassava may reveal novel multifunctional strains that will serve as starter/adjunct culture to produce wholesome and acceptable cassava products. In this paper, yeasts were isolated from retting cassava and evaluated for their technological properties.

## 2. MATERIALS AND METHODS

### Sample collection

Samples of fresh cassava with the fermenting water at the initial stage of retting were collected from two clusters of indigenous producers of *fufu*. Two samples each were collected from the clusters in Samonda and Ojoo both in Ibadan, South-West Nigeria. The samples were aseptically collected in sterile containers and transferred to the laboratory for physicochemical and microbial analysis over a period of 3 days.

### Determination of pH and total titratable acidity (TTA)

The pH of aliquot from the retting cassava roots samples was determined as percentage lactic acid by using the method of Oyewole and Odunfa (1990). The TTA was determined by titrating 5 ml aliquot of each sample with 0.1 M of NaOH using 2 drops of phenolphthalein as indicator. The formula below was used to calculate (A.O.A.C., 1990). Samples were taken in triplicates at 24-hourly interval over a period of 3 days for both determinations.

$$\text{Total titratable acidity (\%)} = \frac{V_x M \times 0.009}{V_s} \times 100$$

Where,  $V$  = Volume of NaOH used;  $M$  = Molarity of NaOH used; 0.009 = milliequivalent factor for lactic acid;  $V_s$  = Volume of sample

### Isolation and characterization of yeasts

#### Yeasts isolation

One ml of aliquot from the samples was serially diluted using sterile distilled water. One ml of appropriate serial dilution was plated in Malt Extract Agar (MEA) supplemented with 0.01 mg /ml of streptomycin. Incubation was done at 35°C for 48-72 h. Distinct colonies were selected from the culture plates and purified by repeated streaking on MEA plates. The pure cultures were preserved on MEA slants at 4°C.

#### Characterization and identification of yeast isolates

Key features of yeast colonies were examined on MEA and cell morphology was determined

after lactophenol cotton blue staining and examined by using X40 objective lens of a compound microscope. Biochemical characterization was carried out by standard taxonomical methods (Kurtzman *et al.*, 2011). The biochemical tests carried out include urea hydrolysis, acid production from glucose, tolerance to 1% acetic acid and fermentation of different sugars. The yeast isolates was identified by comparing with already described yeasts in Kurtzman *et al.* (2011).

### **Determination of technological properties of yeast isolates**

#### **Screening of by yeast isolates for extracellular enzyme production**

##### **Preparation of yeast inoculum**

A suspension of 24 h old broth culture of each yeast isolates was prepared. The suspension was standardized to  $10^6$  CFU/ml and inoculated on the surface of appropriate agar using multipoint inoculator.

##### **Production of amylase**

Amylase production was determined by using starch agar (per litre; 3g Beef extract, 10g soluble starch, 12g Agar). The yeast isolates were inoculated on the surface of the solidified starch agar medium and incubated at 30°C for 48 hours. Plates were then flooded with Gram's iodine. Clear zones around regions of growth indicate hydrolysis of starch, while the unhydrolyzed starch appears as blue-black coloration (Harrigan and MaCance, 1966). Diameters of clear zones were measured (Ong *et al.*, 2011).

##### **Production of protease**

Protease production was determined on modified MEA (per litre; 50g MEA, 100g skimmed milk). The modified MEA plates were inoculated with yeast isolates and incubated at 30°C for 3 days. Uninoculated plates served as control. Clear zone around the growth area indicate protease production. Positive result was confirmed by flooding plates with mercury chloride solution (Harrigan

and MaCance, 1966). Diameters of clear zones were measured (Ong *et al.*, 2011).

##### **Production of lipase**

Lipase production was assessed on a chemically defined medium (per litre; 20g olive oil, 2.5g  $K_2HPO_4$ , 1.3g  $(NH_4)_2SO_4$ , 0.5g  $MgSO_4$ , 0.5g yeast extract, 6.5ml urea, 20g agar, aniline blue indicator). The medium plates were inoculated with yeast isolates and incubated at 30°C for 24 h. Zone of clearance around isolate indicated that they possessed lipolytic characteristics (Kambiz *et al.*, 2008). Diameters of clear zones were measured (Ong *et al.*, 2011).

##### **Production of pectinase**

Each of the isolated yeast was screened for pectinase production using pectin agar (per litre of phosphate buffer; 0.5g  $CuSO_4 \cdot 5H_2O$ , 0.5g KCl, 0.01g  $MnSO_4 \cdot 7H_2O$ , 3g  $FeSO_4 \cdot 7H_2O$ , 1g  $NaNO_3$ , 0.5g  $ZnSO_4$ , 10g pectin, 15g agar; pH 6.2). The agar was inoculated with the yeast isolates followed by incubation at 30°C for 5 days. After incubation the plate were then flooded with Gram's iodine. Clear zones around a region of growth indicate hydrolysis of pectin, while the unhydrolyzed pectin appears as blue-black coloration (Naga and Divakar, 2013). Diameters of clear zones were measured in millimeter (Ong *et al.*, 2011).

### **Determination of the susceptibility pattern of yeast isolates to antimicrobials**

##### **Preparation of inoculum**

Yeast isolates were inoculated into sterile Malt Extract Broth and incubated for 24 h. The broth culture was standardized with 0.5 McFarland standard. Sterile cotton swab was dipped into standardized broth culture and used to inoculate antimicrobial sensitivity plates.

##### **Antifungal and antibacterial susceptibility pattern**

Antifungal and antibacterial susceptibility patterns were respectively determined by agar overlay diffusion method. The antifungal discs include; 25µg Fluconazole, 1µg Voriconazole,

50µg Nystatin. The following antibacterial discs were used; 10µg Erythromycin, 30µg Augmentin, 10µg Gentamicin, 10µg Ofloxacin, 10µg Cloxacillin, 30µg Cefuroxime, 30µg Ceftazidime and 30µg Ceftriazone. The soaked cotton swab was used to spread the yeast over the entire surface of a solidified MEA plate and discs were aseptically and gently placed on the agar surface. The plates were incubated in inverted position at 30 °C for 24 h. The zones of clearance around the discs were examined and measured (John *et al.*, 1999). Values obtained were interpreted as either susceptible (S), intermediate (I) or resistant (R) by using a zone diameter interpretative chart for respective antifungal agent (NCCLS 2004; CLSI 2012).

### 3. RESULTS AND DISCUSSION

During the 72 h of retting, decrease in pH and increase in total titratable acidity of the four cassava samples was observed (Table 1). The pH of the samples ranged from 3.9 to 4.1 at the beginning of the retting process (0 h) while at the end of 72 h retting the pH had significantly changed to between 3.2 and 3.4. There was a general increase in total titratable acidity over the 72 h retting period with sample JE4 showing the most significant change from 0.24 to 0.88%. A similar observation was made by Oyewole (2001) and Ogunnaiké *et al.* (2013). During cassava fermentation, LAB are mainly responsible for the release and accumulation of organic acid, resulting in lowered pH. Reduced pH improves the stability and safety of foods (Caplice and Fitzgerald, 1999) and the organic acids are carbon sources for yeast growth (Walker, 2009).

A total of eighteen yeasts were isolated from MEA plates at 24, 48 and 72 h, during the retting of pieces of cassava roots. The isolates were cream or white colonies, with spherical or ovoid cells. All of the isolates did not hydrolyse urea, fermented glucose, fructose and maltose but failed to ferment lactose, mannitol and sorbitol.

**Table 1: Changes in pH and total titratable acidity of retting cassava samples**

Time (h)	pH				Total titratable acidity (%)			
	SA1	SA2	JE3	JE4	SA1	SA2	JE3	JE4
0	4.1	4.0	4.1	3.9	0.28	0.28	0.28	0.24
24	3.9	3.8	3.9	3.7	0.31	0.30	0.32	0.31
48	3.7	3.6	3.6	3.5	0.69	0.62	0.65	0.60
72	3.3	3.2	3.4	3.3	0.87	0.87	0.86	0.88

Key- SA: Samonda, JE: Jerusalem

The most frequently occurring (44%) yeast isolate were presumptively characterized as *Saccharomyces cerevisiae*. Other probably identified species include *Candida krusei* (22%), *C. parapsilosis* (17%) and *C. tropicalis* (17%) (Table 2). The wide taxonomical and physiological diversity of microorganisms in traditional fermented food substrates makes them flourishing sources of technologically important microbial strains (Franz *et al.*, 2014). Yeasts are microorganisms that are significantly involved in the fermentation of most African traditional fermented foods but their roles are barely investigated (Jespersen, 2003).

These species have been widely reported in varieties of traditional fermented foods, including cassava-based products such as *agbelima*, *fufu*, *gari*, *kivunde*, *lafun*, *togwa* and cassava starch (Oyewole, 2001; Lacerda *et al.*, 2005; Oguntoyinbo, 2008; Hellstrom *et al.*, 2010). The predominance of *S. cerevisiae* among the yeast species in this study confirms the view of Jespersen (2003) that *S. cerevisiae* is a predominant yeast species in African fermented non-alcoholic starchy foods. The relative diversity of the species of *Candida* also agrees with the studies of Oguntoyinbo (2008) that revealed the presence of *C. tropicalis*, *C. rugopelliculosa*, *C. inconspicua* and *C. krusei* during cassava fermentation for *gari* production. *C. tropicalis* was reported in cassava fermentation for *lafun*, *fufu* and *attiéké* production (Nwachukwu and Edwards, 1987; Oyewole, 2001; Coulin *et al.*, 2006). The yeast species isolated in this study have been safely consumed in several indigenous fermented foods over decades and some are listed to have beneficial uses in foods (Hansen 2011;

Bourdichon *et al.*, 2012). *S. cerevisiae* has a Qualified Presumption of Safety status as confirmed by European Food Safety Authority (EFSA, 2007).

As shown in Table 3, all the yeast strains examined exhibited strong amylase activity

with diameter of clear zones ranging between 5 and 10 mm. Eight and seven strains produced protease and lipase respectively while none produced pectinase.

**Table 2: Characterization and percentage occurrence of yeasts isolated from retting cassava samples**

<b>Colony and cell morphology</b>				
Colour	Cream	White	Cream	Cream
Elevation	Raised	Flat	Raised	Raised
Edge	Entire	Undulating	Lobed	Lobed
Cell shape	Spherical	Ovoid	Spherical	Spherical
<b>Biochemical characteristics</b>				
Urea hydrolysis	-	-	-	-
Acid production from glucose	+/-	-	-	+
Tolerance of 1% acetic acid	-	-	-	-
<b>Sugar fermentation</b>				
Glucose	+	+	+	+
Galactose	+	-	-	+
Sucrose	+	-	-	-
Lactose	-	-	-	-
Fructose	+	+	+	+
Maltose	+	+/-	+	+
Mannitol	-	-	-	-
Sorbitol	-	-	-	-
<b>Probable identity</b>	<i>Saccharomyces cerevisiae</i>	<i>Candida krusei</i>	<i>Candida parapsilosis</i>	<i>Candida tropicalis</i>
<b>Percentage occurrence (%)</b>	44	22	17	17

Key: + = positive, - = negative, +/- = variable

**Table 3: Extracellular enzyme production by yeasts isolated from retting cassava**

Isolates	Diameter of zone of clearance (mm)			
	Amylase	Protease	Lipase	Pectinase
<i>S. cerevisiae</i> RC1	++	+	-	-
<i>C. krusei</i> RC2	++	-	-	-
<i>S. cerevisiae</i> RC3	++	+	-	-
<i>S. cerevisiae</i> RC4	++	-	-	-
<i>C. parapsilosis</i> RC5	++	-	+	-
<i>S. cerevisiae</i> RC6	++	+	-	-
<i>C. tropicalis</i> RC7	++	++	-	-
<i>C. krusei</i> RC8	++	-	-	-
<i>S. cerevisiae</i> RC9	++	+	-	-
<i>C. tropicalis</i> RC10	++	+	+	-
<i>C. krusei</i> RC11	++	-	-	-
<i>C. tropicalis</i> RC12	++	+	-	-
<i>S. cerevisiae</i> RC13	++	+	-	-
<i>C. parapsilosis</i> RC14	++	-	+	-
<i>C. krusei</i> RC15	++	-	-	-
<i>S. cerevisiae</i> RC16	++	-	-	-
<i>C. parapsilosis</i> RC17	++	-	-	-
<i>S. cerevisiae</i> RC18	++	-	++	-

Key: '-' = no clear zone (enzyme not produced), '+' = clear zone < 5 mm (enzyme produced) and '++' = clear zone > 5 mm (enzyme highly produced)

*C. tropicalis* RC10 produced amylase, protease and lipase. Protease activity was not observed in strains of *C. krusei* and *C. parapsilosis*. This study revealed the potentials of the yeast isolates to produce enzymes that are of importance during food fermentation. The production of extracellular amylase by all the yeast strains could be a reflection of the abundance of starch in cassava and the adaptation of associated yeasts (FAO, 1984). A wide distribution of amylase production among yeast species isolated from retting cassava was earlier reported by Oyewole (2001). Yeasts associated with maize fermentation produced extracellular amylase (Omemu *et al.*, 2007). Yeast amylase in cassava may contribute to the breakdown of cassava starch to simple sugar, thereby increasing the energy density of cassava and providing carbon source for LAB in view of the fact that amylase production is a rare trait among LAB isolated from starchy foods (Sanni *et al.*, 2002; Kostinek *et al.*, 2007; Ogunremi and Sanni, 2011). Protease and lipase activities were relatively weak and not well distributed among the yeast isolates. Yeasts from starchy sources were previously reported to be weak in the activities of protease (Omemu *et al.*, 2007; Ogunremi *et al.*, 2015). Lipase hydrolyzes lipids in foods to produce flavor compounds and precursors of flavor compounds (Steinkraus, 1997; Arroyo-Lopez *et al.*, 2012). The few yeasts strains that showed lipase activity in this study have the potentials to impart the aromatic profile of retted cassava products. Pectinases are a group of tissue (pectin) degrading enzymes that contribute to the softening of cassava during retting (Ampe *et al.*, 1995). Our study showed that no yeast strain produced pectinase. It was earlier suggested that the softening of cassava is mediated by bacterial activity (Ampe *et al.*, 1995). However, yeast species isolated during cassava retting showed polygalacturonase activity (Oyewole, 2001).

The effects of fluconazole and nystatin on the yeasts isolates were strain-specific. Out of the eight *S. cerevisiae* and three *C. parapsilosis* strains, four and two strains were susceptible to fluconazole respectively. None of the *C. tropicalis* strains was susceptible and at least one strain of *S. cerevisiae*, *C. parapsilosis* and *C. tropicalis* showed intermediate susceptibility to fluconazole. All the four *C. krusei* were observed to be resistant to fluconazole. Seven *S. cerevisiae* isolates were susceptible to nystatin and all the yeasts were susceptible to voriconazole (Table 4). All the yeast isolates showed resistance to the following antibiotics; erythromycin, augmentin, gentamicin, ofloxacin, cloxacillin, cefuroxime, ceftazidime and ceftriazone (results no shown). The resistance shown by all the yeast strains to antibiotics further confirms the natural resistance of yeasts to antibacterial and these is particularly desirable because this attribute in yeasts is not mediated by mobile genetic elements (Czerucka *et al.*, 2007; Kourelis *et al.*, 2010). Hence, they do not constitute public health concerns. The emergence of new fungal infections and rising incidence of resistance of fungi to antifungal agents has made the evaluation of foodborne yeasts for resistance to antifungal compounds to be of utmost importance (Chakrabarti, 2011). In this study, the effect of antifungal agents varied from resistant, intermediate to susceptible based on the yeast strains. Broad spectrum of antifungal activity was exhibited by voriconazole and nystatin. Voriconazole is a second generation broad spectrum triazole (Donnelly *et al.*, 2004; Vandeputte *et al.*, 2012). Food borne yeasts are generally not of clinical or veterinary importance (Jacques and Casaregola, 2008), however, in rare cases opportunistic infections due to antifungal resistant strains may lead to treatment failure (Ghannoum and Rice, 1999).

**Table 4: *In vitro* antifungal susceptibility pattern of yeasts isolated from retting cassava**

Yeast isolates	Zone of clearance (mm)		
	Fluconazole (25 µg)	Voriconazole (1 µg)	Nystatin (50 µg)
<i>S. cerevisiae</i> RC1	15.0 (I)	22.0 (S)	20.0 (S)
<i>C. krusei</i> RC2	5.0 (R)	19.0 (S)	13.0 (R)
<i>S. cerevisiae</i> RC3	16.0 (I)	21.0 (S)	19.0 (S)
<i>S. cerevisiae</i> RC4	19.0 (S)	20.0 (S)	18.0 (S)
<i>C. parapsilosis</i> RC5	22.0 (S)	28.0 (S)	12.0 (R)
<i>S. cerevisiae</i> RC6	20.0 (S)	21.0 (S)	17.0 (S)
<i>C. tropicalis</i> RC7	14.0 (R)	20.0 (S)	14.0 (I)
<i>C. krusei</i> RC8	7.0 (R)	18.0 (S)	13.0 (R)
<i>S. cerevisiae</i> RC9	18.0 (I)	19.0 (S)	16.0 (I)
<i>C. tropicalis</i> RC10	13.0 (R)	20.0 (S)	14.0 (I)
<i>C. krusei</i> RC11	9.0 (R)	19.0 (S)	17.0 (S)
<i>C. tropicalis</i> RC12	15.0 (I)	20.0 (S)	17.0 (S)
<i>S. cerevisiae</i> RC13	20.0 (S)	23.0 (S)	19.0 (S)
<i>C. parapsilosis</i> RC14	21.0 (S)	25.0 (S)	12.0 (R)
<i>C. krusei</i> RC15	9.0 (R)	20.0 (S)	12.0 (R)
<i>S. cerevisiae</i> RC16	14.0 (R)	22.0 (S)	21.0 (S)
<i>C. parapsilosis</i> RC17	17.0 (I)	24.0 (S)	17.0 (S)
<i>S. cerevisiae</i> RC18	19.0 (S)	21.0 (S)	20.0 (S)

Key: S = susceptibility, I = intermediate and R = resistance

#### 4. CONCLUSION

In conclusion, this study revealed the predominance of *Saccharomyces cerevisiae* and species of *Candida* during cassava retting. Few of the yeast strains possess properties that will aid their selection and application in a controlled process to valorize cassava roots for production of foods with consistent and predictable quality.

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