

# ISOLATION AND CHARACTERIZATION OF YEAST FROM ANTHOCYANIN RICH TROPICAL FRUITS AS WINE STARTER CULTURE

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ARTICLE INFO	ABSTRACT
Received 24. 2. 2015 Revised 4. 6. 2015 Accepted 5. 7. 2015 Published 1. 10. 2015 Regular article	Tropical fruit wines are gaining importance for its health benefits. However, the potential is unexplored in India and this work of isolation of indigenous yeast strains from the tropical fruit was undertaken. 28 strains of yeasts were isolated from tropical fruits, <i>Syzygium cumini</i> (Linn.) Skeel (Jamun) and <i>Garcinia indica</i> (Choisy) (Kokum) on a selective medium. The screening parameters were glucose and ethanol tolerance. Three most glucose and ethanol tolerant cultures were selected by testing tolerance for glucose (10-25% w/v) and ethanol (6-15 % v/v). Further characterization of these 3 cultures was carried out using biochemical and molecular test by sequencing internal transcribed spacer (ITS) region. Infer molecular phylogeny established that the three isolates <i>viz</i> , FJ 10, JR 01 and KF 01 were <i>Saccharomyces sp. FJ 10, Candida tropicalis JR 01, Saccharomyces sp. KF 01</i> respectively. Till date to the best of our knowledge we are the first to report the isolation of tolerant <i>Saccharomyces</i> species from Jamun and Kokum fruits. Further studies on fruit wine production from the selected isolates showed promising results.
	Keywords: Jamun, Kokum, yeast isolation, internal transcribed spacer

# INTRODUCTION

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Yeasts are ubiquitous in nature and indispensable in manufacture of alcoholic beverages, distilleries and in baking industry (Ligras *et al.*, 2007). Current research trend emphasizes mainly upon isolation and characterization of yeast strain which are tolerant to both sugar and ethanol concentration. Ethanol tolerance has been also studied by genetic modification of yeast. Kyung Man You *et al.*, (2002) have altered *OLE1 desaturase* gene responsible for unsaturated

fatty acid composition of yeast cell membranewith*acyl-CoA desaturase* from other sources. Isolation of wild yeast strains belonging to genera *Saccharomyces*, *Debaryamyces*, *Kodamaea*, *Sporobolomyces*, *Candida*, *Pichia*, *Rhodotorula*, *Crptococcusetc* from rotten fruit or fruit rind have been attempted by various researchers and is depicted in the Table 1 given below. Other than fruits, yeast isolation is also reported from flowers, insects (feed on flower and fruits), grains, leaves, tree sap, dung and soil (Spencer & Spencer, 1997).

able 1 Different native v	veast species from fruits an	d their sugar and ethanol tolerance

Source	Sugar tolerance	Ethanol tolerance	Yeast species identified	References
	(% w/v)	(% v/v)		
Tamarind	20	14	Saccharomyces cerevisiae	
Yoghurt	20	14	Saccharomyces cerevisiae	
Kanji	15	12	Saccharomyces cerevisiae	
Soil Vineyard	10	8	Saccharomyces rosinii	Ali et al.,(2014)
Soil Sugarcane	10	8	Saccharomyces rosinii	
Kanji	10	10	Saccharomyces exiguous	
Soil Fruit market	10	9	Rhodotorulaminuta	
Kiwi	30	10	Saccharomyces cerevisiae	Lee et al.,(2011)
Grape	-	12	Saccharomyces cerevisiae	Chiranjeevi et al., (2013)
Рарауа	45	12	Saccharomyces cerevisiae	
Рарауа	40	8	Saccharomyces bayanus	
Рарауа	40	8	Saccharomyces uvarum	
Рарауа	45	10	Saccharomyces italicus	C. Maragatham et al., (2011
Рарауа	45	10	Saccharomyces pasteurianus	
Рарауа	40	8	Saccharomyces pombe	
Рарауа	45	10	Zygosaccharomyces sp	
Cashew apple	15	12	Saccharomyces cerevisiae	
Cashew apple	20	11	Saccharomyces cerevisiae	$Osho \Lambda$ (2005)
Cashew apple	15	10	Saccharomyces cerevisiae	Osho A.,(2003)
Cashew apple	10	9	Saccharomyces uvarum	
Grape	NR	NR	Hanseniaspora uvarum	
Grape	NR	NR	Candida stellate	IM Clamanta limanaz at al. (2004)
Grape	NR	NR	Issatchenkia orientalis	J.1v1. Cremence Jintenez <i>et ut.</i> ,(2004)
Grape	NR	NR	Issatchenkia terricola	

Grape	NR	NR	Metschnikowia pulcherrima	
Grape	NR	NR	Pichiafermentans	
Grape	NR	NR	Saccharomyces cerevisiae	
Kola nuts	NR	NR	Candida tropicalis	
Cassava	NR	NR	Kluyveromyces marxianus	Ehabbi at $al (2012)$
Maize	NR	NR	Pichiacaribbica	= Ebabili et al.,(2015)
Sorghum	NR	NR	Saccharomyces cerevisiae	
Grape	NR	NR	Aureobasidium pullulans	
Grape	NR	NR	Candida zemplinina	
Grape	NR	NR	Hanseniaspora uvarum	
Grape	NR	NR	Hanseniaspora occidentalis	$\mathbf{Y}_{un} = \sup_{\boldsymbol{\alpha}}   \boldsymbol{\alpha}   (2014)$
Grape	NR	NR	Issatchenkia terricola	1 uli suli <i>el ul.</i> ,(2014)
Grape	NR	NR	Metschnikowia pulcherrima	
Grape	NR	NR	Pichiakluyveri	
Grape	NR	NR	Saccharomyces cerevisiae	
Grape	NR	NR	Candida azyma	
Grape	NR	NR	Candida quercitrusa	
Grape	NR	NR	Debaryomyce shansenii	$\mathbf{P}$ Chaven at al. (2000)
Grape	NR	NR	Hanseniaspora guilliermondii	P. Chavall <i>et al.</i> ,(2009)
Grape	NR	NR	Hanseniaspora viniae	
Grape	NR	NR	Sacharomyces cerevisiae	
Grape	NR	NR	Sacharomyces cerevisiae	E. Nikolaou et al., (2006)
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NR: not reported

Although tropical fruits are abundant in several essential bioactive compounds and are mainstay in Indian traditional medicinal system, Ayurveda but still

remain underutilized. Some of the tropical fruits with their bioactive compounds have been mentioned in Table 2.

Table 2 Tropical fruits, their bioactive compounds and medicinal property.
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Scintific name	ne Common Bioactive compounds		Medicinal property	Reference	
Syzygium cumini	Jamun	Jamboline, mycaminose,3,6-hexa hydroxyl diphenoyl glucose, 4,6- hexahydroxy diphenoyl glucose, ellagic acid, gallic acid, tannins, Quercetin, Oleanolic acid, Kaempferol, Myricetin, Betulinic acid, Delphinidin, Petunidin, Malvidin, etc	Anti-inflammatory, Antioxidant, anti- diabetic, antibacterial, anti-diarrheal, antineoplastic, radioprotective	Shrikant <i>et al.</i> , (2012) Muruganandan S. <i>et al.</i> , (2001), Brito <i>et al.</i> , (2007), Ruan <i>et al.</i> , (2008), Sridhar <i>et al.</i> , (2005), Y. Zhao <i>et al.</i> , (2009), V. Benkovic <i>et al.</i> , (2008), A. Kumar <i>et al.</i> , (2008)	
Garcinia indica	a <i>indica</i> Kokum Garcinol, Hydroxy citric acid, cyanidine- 3-glucoside, cyanidine-3-sambubioside, xanthochymol, etc		Antibacterial, free radical scavenging activity, anti- obesity, gastroprotective, antidiabetic, cardioprotective, antineoplastic, antioxidant	Varalakshmi <i>et al</i> (2010), Alia <i>et al.</i> , (2008), Jena <i>et al.</i> , (2002), Chatterjee <i>et al.</i> , (2003), Kirana and Srinivasan (2010), Xu <i>et al</i> (2004), Selvi <i>et al</i> , (2003)	
Carica papaya	<i>Carica papaya</i> Papaya		Antioxidant, anti- diarrheal, digestive, sedative, diuretic, anti- obesity, abortifacient, anti-microbial, anti- malerial	Rivera-Pastrana <i>et al.</i> , (2010), Krishna <i>et al.</i> , (2008)	
Ananas comosusPineappleBromelain, $\alpha$ -carotene, $\beta$ -carotene, $\beta$ -cryptoxanthin, lutein, lycopene, neoxanthin, violaxanthin, zeaxanthin etc.		antiscorbutic, cholagogic, diaphoretic,anti- inflammatory, antioxidant	M.Kalaiselvi <i>et al.</i> , (2012), Monzon R. B. <i>et al</i> , (1995), Kongsuwan A <i>et al.</i> , (20098), Freitas A <i>et al.</i> , (2014)		
Musa acuminataBananaProdelphinidins, flavonol glycosides, procyanidin, flavan-3-ols, Norepinephrin dopamine, serotoninetc		Prodelphinidins, flavonol glycosides, procyanidin, flavan-3-ols, Norepinephrine, dopamine, serotoninetc	Antioxidant, antimicrobial, anti- diarrheal, digestive, anti- diabetic, anti cancer, cardioprotective	Rebello <i>et al.</i> , (2014), Fagbemi <i>et al.</i> , (2009), K. P. Sampath Kumar <i>et al.</i> , (2012)	
Artocarpus heterophyllus	Jackfruit	Catechin, ascorbic acid, chlorogenic acids, morin, dihydromorin, cynomacurin, artocarpin, isoartocarpin, cyloartocarpin, artocarpesin, oxydihydroartocarpesin, artocarpetin, norartocarpetin, cycloartinone, betulinic acid, artocarpanone, heterophylol etc.	Antioxidant, anti- diabetic, anti- inflammatory, immunomodulatory, antibacterial	Sharma A <i>et al.</i> , (2013), Prakash <i>et al.</i> , (2009)	
Mangifera indica	Mango	Mangiferin, Ascorbic acid, Quercetin, Kaempferol, Gallotannins, Ellagic acid, Rhamnetin 3-0 galactoside, Isomangiferin, Gallic acid, Tannin, Coumarin, Caffeic acid, Vanillin, Ferulic acid, Cinamic acid, cyanidin 3-O-galactoside, peonidin 3-O- galactoside, rhamnetin 3-O-â- galactopyranoside, rhamnetin 3-O-â- glucopyranoside etc.	Antioxidant, cardioprotective, antidiabetic, anti-viral, hypotensive, anti- inflammatory, anti parasitic, anti tumor, anti HIV, gastroprotective, hypolipidemic	Berardini <i>et al</i> (2005), Li <i>et al</i> (2014). Nicolai Berardin <i>et al</i> (2005), K. A. Shah <i>et al</i> , (2010)	

The selected tropical fruits *Syzygium cumini* (Linn.) Skeel Syn *Syzygium jambolanum, Eugenia cumini* and *Garcinia indica* (Choisy) Syn *Brindonia indica* belonging to Myrtaceae and Guttiferae family respectively. Both these fruits contain several bioactive compounds (Table 2). Percentage of Anthocyanin's in these two fruits is significantly high and hence has a huge potential in manufacture of coloured fermented beverages.

These fruits are processed at small and medium scale in unorganized sector to make beverages, preserves and concentrates. The bioactives could be made available if the preservation is by fermentation since there will be minimum thermal degradation. Tropical fruit wines are becoming popular and could be a good value addition to these fruits which are not cultivated but wildly grown. Micropropagation of these tropical fruit plants is not developed as these plants are grown naturally in forest. We observed that there is slow fermentation in Jamun and kokum fruit juices. These fruit juices have very low pH and have antibacterial activity too (Shrikant et al., 2012 and Varalakshmi et al., 2010). The fermented beverages developed by natural yeast may be beneficial for diabetic and obese people as these two diseases states are interlinked. Such fermented beverages may have very low sugar and slight alcohol content.

The main objective of this study is to evaluate indigenous yeast strains as a wine starter culture based on their glucose tolerance, ethanol tolerance and alcohol production ability.

# MATERIALS AND METHODS

#### Materials

Sugar dics, Sabouraud Chloramphenicol agar, yeast extract-peptone-dextrose (YPD) agar medium, dextrose, Sodium chloride, yeast extract, potassium chloride, monopotassium phosphate, manganese sulphate, magnesium sulphate, glycerol, ferric chloride, calcium chloride, sodium hydroxide and Phenol, chloroform, ethyl alcohol, bromocresol green were procured from Himedia laboratories, India and Merck Millipore, India respectively. 2,2-diphenyl-1-picrylhydrazyl (DPPH) was procured from Sigma Chemicals.

#### Isolation of yeast

Tropical fruits Jamun and Kokum were provided as a kind gift by Dr. Hedgewar Smruti Seva Prakalpa, Sawantwadi, Maharashtra. Microbial samples were taken from rind of fruits and rotten fruits. Isolates were grown on Sabouraud Chloramphenicol agar for selective cultivation of yeast at 30° C for 48 hrs. Yeast like colonies were further streaked onto fresh Sabouraud Chloramphenicol agar. For further differentiation among isolates with same colony characters were grown in Wallerstein Laboratory Nutrient (WLN) agar. Morphologically distinguished colonies were selected & gram nature was observed under microscope at 100X magnification. Pure culture was maintained on yeast extract-peptone-dextrose (YPD) agar medium. Glycerol stocks of the isolates were prepared and stored at -20° C for future use. Cultures were revived by inoculating them in YPD broth at 30° C, 200 rpm for 72 hrs.

#### Screening for ethanol tolerance

Ethanol tolerance of the isolates was evaluated by growing the isolates separately in sterilized YPD broth containing varying concentration of ethanol from 6 - 15% v/v. The isolates were then incubated at  $30^{\circ}$  C for 72 hrs at 200 rpm in an orbital incubator shaker (Orbitek). Growth of the isolates was monitored up to 72 hrs using spectrophotometer and taking the optical density at 660 nm after every 6 hrs using UV-visible spectrophotometer (Shimadzu 1800). The experiment was performed in triplicates.

# Screening for Sugar tolerance of ethanol tolerant isolates

Ethanol tolerant yeast cultures were then evaluated for its sugar tolerance. The isolates were inoculated in Yeast extract-peptone broth containing varying concentration of dextrose (10%, 15%, 20% & 25%) and incubated at 30° C for 72 hrs at 200 rpm. Growth was monitored by recording the turbidity of the flasks at 660 nm using UV-visible spectrophotometer (Shimadzu 1800). The experiment was performed in triplicates

# Identification & molecular characterization of ethanol-sugar tolerant isolates

Standard routine tests were followed for the morphological and biochemical characterization of the isolates (Bernette *et al.*, 2000; Kurtzman & Fell, 1998). Basal media mentioned by Bernette *et al.*, (2000) was used for carbon and nitrogen assimilation/fermentation tests. Isolates were observed for fermentation (gas production in durhams tubes) and assimilation (growth). Genetic characterization was performed in accordance with the methods reported by White *et al.*, 1990. Active, vegetative biomass of the isolates was harvested by centrifugation at 10000 rpm, 10° C for 15 min. Phenol-chloroform method was

used for genomic DNA isolation. ITS region was amplified by PCR using ITS primers-ITS 1 (5'-TCCGTAGGTGAACCTGCGG-3'), ITS 2 (5'-GCTGCGTTCTTCATCGATGC-3'), ITS 4 (5'-TCCTCCGCTTATTGATATGC-3') (White *et al.*, **1990**). PCR product was further sequenced in ABI 3730 XL sequencing machine. The sequences were analyzed with "Type strains" from NCBI nucleotide database.

#### Phylogenetic analysis

The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei, 1987). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. The tree was drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were then computed using the Kimura 2-parameter method (Kimura, 1980) and were in the units of the number of base substitutions per site. The rate variation among sites was modelled with a gamma distribution (shape parameter = 1). All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA5 (Tamura, 2007).

# Microvinification

Jamun fruit was used for microvinification studies with selected yeast isolates including standard yeast, *S. cerevisiae* NCIM 3215. 75 ppm potassium metabisulphate was added to the must before fermentation. The must was inoculated yeast isolates FJ 10, KF 01 and NCIM 3215 separately in duplicate. Fermentation was carried out at  $28 \pm 1^{\circ}$  C for 5 days in specially designed fermentation assembly. Fermentation process was observed on the basis of total soluble solids (°brix). Fermentation must were centrifuged at 5000 rpm, 4° C and filtered through 1µm filter using vacuum. Wine was kept at 4° C till analysis. Titratable acidity of the wine and must was estimated as per AOAC, 2000 protocol. Residual sugars were estimated by Dinitrosalicylic Acid reagent method (Miller Gail Lorenz., 1959). Total Anthocyanin's were estimated by pH differentiation method as described by Lee *et.al.*,(2005). Per cent free radical scavenging activity of wine was estimated by using the 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay (Abe *et.al.*,1998).

#### Gas Chromatography

Alcohols were analysed by direct injection of 0.5  $\mu$ l of sample into Agilent 7820A gas chromatograph with flame ionization detector (230° C) and a Porapack Q column (6 ft., mesh size 80/100, 1/8 in. OD, 2 mm ID). The carrier gases were nitrogen and hydrogen at a flow rate of 25 ml/min and 50 ml/min respectively. The split ratio was 1:10 with air flow 300 ml/min. The standard with different concentration and sample were injected with isopropyl alcohol as an internal standard. Analysis was done in triplicates.

# **RESULTS AND DISCUSSION**

#### **Isolation of Yeast**

Tropical fruits *viz*, Kokum and Jamun are abundant in the anthocyanin content which makes them suitable substrate for isolation of yeast for colored fermented beverages production. Fruit rind and pulp of decayed Jamun and Kokum was used as a source for yeast isolation. Microbial suspension was prepared in sterilized saline and inoculated onto selective medium, Sabourad Chloramphenicol agar. Controls were run parallely along with the test experiments to eliminate the errors. The medium being selective to yeast, helped to distinguish the desired organism from bacterial contaminants. The yeast colonies were then sub-cultured, purified and maintained on YPD agar medium. Twenty eight distinct yeast colonies were isolated from the rind and pulp of fresh and decayed Kokum and Jamun fruits. The isolates so obtained were preserved as glycerol stock and maintained at -20°C.

# **Ethanol and Sugar Tolerance**

In fermented beverages production, such as wine, yeast cell consumes sugar and produces ethyl alcohol. In the initial fermentative phase yeast cells experience high sugar concentration (20-24 % W/V) while during production phase sugar concentration is reduced and ethanol starts accumulating (8-14 % v/v). Yeast which can withstand to these stressors is considered as a suitable strain for wine production. Hence all the twenty eight isolates were subjected first to access their ethanol tolerance followed by their sugar tolerance of only the ethanol tolerant isolates.

A 5% v/v of each of the isolates (in its logarithmic phase) was inoculated into YPD broth containing 6-15% v/v ethanol concentration. The flasks/tubes were incubated at 30° C at 200 rpm and OD was monitored upto 48 hrs. Most of the commercial ethanol production has ethanol concentration varying from 6-15% in the reactors and hence the similar range was used in our study to evaluate the ethanol tolerance among the twenty eight yeast isolates. Similar study of ethanol

tolerance was evaluated of yeast isolated from grapes (Ali *et al.*, 2014; Lee *et al.*, 2011), Cashew apple juice (Osho A., 2005), apple and strawberry (Lee *et al.*, 2011).

Except for the three isolates *viz*, FJ 10, JR 01 and KF 01, all the other isolates showed almost 75% reduction in growth after 48 hrs at the minimum ethanol concentration of 6% v/v (Table 3). FJ 01, FJ 06, FJ 09, KF 02 showed a marginal growth (20%) at 6% v/v ethanol concentration. Maximum growth was observed of 98%, 96% and 64% by the three isolates KF 01, FJ 10 and JR 01 respectively. Ethanol tolerance of the three most tolerant isolates at varying ethanol concentration is as shown in Figure 1 along with *Saccharomyces cerevesiae* (NCIM 3215) as a reference strain. FJ 10 and KF 01 showed significant ethanol tolerance up to 12% while a drastic decrease in the biomass is observed thereafter.

Ethanol tolerant yeasts also display the phenomenon of sugar tolerance (Gray, 1944). Sugar tolerance of the ethanol tolerant three isolates was evaluated by measuring the biomass (in terms of its optical density) of the isolates grown at varying sugar concentration. The study was performed by varying the sugar concentration up to 25% w/v as the maximum concentration. The maxima were as selected as the commercial wine production from must generally contains initial sugar concentration of 24% w/v (Salunkhe and Kadam, 1995). All the three isolates displayed similar pattern for sugar tolerance. Yeast with high sugar tolerance are capable to overcome the substrate inhibition leading into maximum growth and hence the product (Osho A., 2005).



Figure 2 Sugar tolerances of isolates FJ 10, KF 01, JR 01, NCIM 3215



Figure 1 Ethanol tolerance of isolates JR 01, FJ 10, KF 01 and reference strain *Saccharomyces cerevisiae* NCIM 3215

# **Characterization of isolates**

Three ethanol and sugar tolerant yeast isolates JR 01, FJ 10 and KF 01 were then characterized on the basis of its morphological, biochemical and molecular traits. Table 4 enumerated below gives an overview of the morphological traits of all the three isolates.

FJ 10 and KF 01 displayed almost similar morphological traits except for their differences in appearance and bromocresol green uptake on Wallerstein Laboratory Nutrient (WLN) agar. JR 01 and KF 01 uptake the bromocresol green dye thereby changing the initial green colour of the medium to colourless. Thus both these isolates are capable of assimilating the dye without its metabolization. However, FJ 10 is unable to take up the dye and the medium colour is retained even after incubation of the isolate for six days. Bromocresol green dye is used in the selective isolation and identification of yeasts based on the color and morphological features of colony (**Dennis** *et al.*, 2004, **Ronald**, **M. A.**, 1946). **Dennis** *et al.*, (2004) reported that yeast colonies take variety of shades of green on WLN media but not all strains have this ability. Our results are in agreement with **Dennis et al.** (2004).

 Table 3 Percent reduction in growth of isolate and standard with respect to different alcohol concentration.

Isolata	OD without	Percent	reduction								
Isolate	alcohol 72 hrs	6 %	7 %	8 %	9 %	10 %	11 %	12 %	13 %	14 %	15 %
FJ 10	2.217±0.064	9.74	20.11	41.94	58.97	70.86	86.89	87.57	89.24	88.58	88.22
KF 01	2.24±0.091	17.76	22.94	29.44	35.22	39.64	45.06	50.75	58.01	84.35	87.70
JR 01	2.198±0.101	35.10	38.64	38.62	46.90	46.74	49.90	62.69	63.10	90.15	90.71
NCIM 3215	2.074±0.042	13.74	30.47	36.47	40.04	44.45	48.52	51.71	57.40	74.63	89.58

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ID Fruit Form Elevation Margin Surface Color Appearance Size Bromocresol green uptake	Gram nature
FJ 10 Jamun Circular Umbonate Entire Smooth Creamy white Dull Medium No	Positive
JR 01 Jamun Circular Convex Filiform Smooth Hairy border White Dull Small Yes	Positive
KF 01         Kokum Circular Umbonate         Entire         Smooth         Creamy white Slightly shiny medium         Yes	positive

Biochemical characterization includes ability of three isolates towards assimilation and fermentation of different carbon and nitrogen sources (Bernette *et al.*, 2000; Kurtzman& Fell, 1998). Total of twenty two different sugars and three nitrogen sources were selected for the said study. Four sugars viz, glucose, sucrose, galactose and maltose were both assimilated and fermented by all the three isolates indicating them as the prolific carbon sources.

Thus it can be concluded out of fifteen sources five sources can acts as good energy as well as metabolic precursors. Molecular identification involved amplification of ITS region of the three isolates using the fungal ITS primers (White *et al.* **1990**). The derived sequences were aligned by BLAST and sequence homology was used to identify the isolate. Based on the sequence identity FJ 10, KF 01 and JR 01 was identified as *Saccharomyces sp.*(98-99 %), *Saccharomyces sp.*(97-99 %) and *Candida tropicalis* (98-100 %) respectively. The phylogenetic tree representing each isolates separately and all together is showed in Figure 3,4,5,6. Phylogenetic analysis details are showed in Table 6.

The optimal tree with the sum of branch length = 0.04030169, 0.04556388, 0.49273311 is shown for FJ 10, KF 01and JR 01 respectively. The percentage of replicate trees with clustered texa is shown next to the branches (**Felsenstein J. 1985**). There were a total of 677, 531 and 407 positions in the final dataset of FJ 10, KF 01 and JR 01. The topology of the phylogenetic tree showed that FJ 10 and KF 01 shared a common branch point whereas along with JR -01 they share common origin.

# Table 5 Biochemical properties of isolates

Source	FJ	10	KF	01	JR 01		
Source	Fermentation	assimilation	Fermentation	assimilation	Fermentation	assimilation	
Arabinose	-	-	-	-	-	-	
Cellobiose	-	-	-	-	-	-	
Dextrose	+	+	+	+	-	+	
Galactose	-	+	-	+	-	+	
Inositol	-	-	-	-	-	-	
Inulin	-	-	-	-	-	-	
Lactose	-	-	-	-	-	-	
Maltose	+	+	+	+	-	+	
Mannitol	-	-	-	-	-	-	
Rhamnose	-	-	-	-	-	-	
Raffinose	-	-	-	+	-	-	
Sorbitol	-	-	-	-	-	-	
Sucrose	+	+	+	+	+	+	
Trehalose	-	-	+	+	+	+	
Xylose	-	-	-	-	-	-	
Nitrate	NA	-	NA	-	NA	-	
Nitrite	NA	-	NA	-	NA	-	
DAP	NA	+	NA	+	NA	+	

**Legend:** +,- and NA means positive results, negative results and not applicable respectively. DAP: Diammonium Phosphate







0.002

Figure 4 Evolutionary relationship of KF 01isolate with its closest related species.



Figure 5 Evolutionary relationship of JR 01 isolate with its closest related species.

Table 6 Phylogenetic analysis details of I	Table 6 Phylogenetic analysis details of FJ 10, KF 01, JR 01.							
Parameters	FJ 10	KF 01	JR 01					
Total number of sites for the analysis	702	678	498					
Percent similarity with type strain	98-99 %	97-99 %	98-100 %					
Conserved sites	665	515	315					
Variable site	28	25	171					
Parsimony informative sites	20	17	72					
Analysis	Phylogeny Reconstruction	Phylogeny Reconstruction	Phylogeny Reconstruction					
Statistical Method	Neighbor-joining	Neighbor-joining	Neighbor-joining					
Test of Phylogeny	Bootstrap	Bootstrap	Bootstrap					
No. of Bootstrap Replications	1000	1000	1000					
Substitution Model	Kimura 2-parameter model	Kimura 2-parameter model	Kimura 2-parameter model					
Substitutions to Include	Transitions + Transversions	Transitions + Transversions	Transitions + Transversions					
Rates among Sites	Gamma Distributed (G)	Gamma Distributed (G)	Gamma Distributed (G)					
	Same (Homogeneous)	Same (Homogeneous)	Same (Homogeneous)					
Pattern among Lineages	Same (Homogeneous)	Sume (Homogeneous)						
Gaps/Missing Data Treatment	Complete deletion	Complete deletion	Complete deletion					

Saccharomycetes.sp. HZ140 (GU213441) Saccharomyces sp.(KF-01) Saccharomyces sp.(FJ-10) Saccharomyces bayanus CHFY0321 (EU719073) Saccharomycessp. VIN13 (AY942705) Saccharomycessp. Actiflore RB2 (AY942704) Saccharomycetes cerevisiae (GQ376091) Saccharomycetes cerevisiae Sc11 (KC515365) accharomycetes cerevisiae ATCC (KC881067) Saccharomycetes cerevisiae (KC881067) Saccharomycetes cerevisiae (NR\_111007) Saccharomycetes sp. 98c (KC834825) Wickerhamomyces (JF781478) accharomycetes cerevisiae CBS1171 (NR\_111007) Saccharomycetes paradoxus (AY046148) Saccharomycetesparadoxus (AY046148) Saccharomycetesparadoxus CBS432 (AJ229059) Saccharomycetes paradoxus (AJ229059) Saccharomycetes sp. (GU213443) Saccharomyces pastorianus (AY046151 Saccharomyces pastorianus (AY046151) accharomycetes bayanus (Z95945) Saccharomycetes bayanus (Z95945) Saccharomycetes bayanus CBS380 (AJ229058) Saccharomycetes bayanus (AJ229058) accharomycetes sp. (AY 942697) Saccharomyces.kudriavzevii ATCC MYA 4449 (NR\_111355) Saccharomyces kudriavzevii (NR. 111355) Saccharomyces mikatae (NR 111354) Saccharomyces mikatae ATCC MYA-4448 (NR 111354) Candida sojae CBS 7871 (JQ647916) Candida neerlandica (EF658662) Candida labidurida run ATCC MY (A4368 NR) Candida tetrigidarum (NR \_11411) Candida albicans (HQ876043) - Candida viswanathii (KJ651204) Candida tropicalis L6 (KF806464) Candida tropical is CBS94 (NR 111250) Candida tropical is (KF728802) Candida sp. (JX406283) Candida tropicalis (EF151451) Candida tropical is ZA001 (FJ697166) Candida tropicalis(JR-01) Candida tropical is ATCC (KJ651200) Candida tropicalis (AF287910) Tryptococcus neoformans (KJ175193)

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**Figure 6** Phylogenetic tree representing FJ 10, KF 01 and JR 01 isolates together and their closest related species. The tree was constructed by the neighbor joining method with the Kimura two parameter distance method. Bootstrap values are indicative for 100 replicates.

# Microvinification

All the twenty eight isolates were subjected to tolerance study. The aim of this strategy was to obtain only capable strains and to save time and resources needed for study. Microvinification results proved it. Both isolates shows promising results. All the wine analysis parameters like ethanol, residual sugar,titratable acidity, pH, total anthocyanin's and per cent radical scavenging activity are satisfactory as compared to standard *Saccharomyces cerevisiae* NCIM 3215 starter culture. Isolate FJ 10 shows better results than standard strain used in this study (Table 7). Although *Candida tropicalis* is used for alcoholic fermentation from lignocellulosic wastes and (Sonali and Banwari 2007, Harinder et al., 2010, Latifa et al., 2007), there are no reports on its use as wine starter culture. Recently *Candida tropicalis* is considered as emerging pathogenic yeast (Kothavade et al., 2010). Therefore isolate *Candida tropicalis* JR 01 is rejected from further studies.

0.01

Table7 Microvinification results by yeast isolates and standard yeast

Strain	Ethanol (% v/v)	Residual sugar (g/l)	Titratable acidity (g/l)	рН	Total Anthocyanin (mg/l)	% radical scavenging Activity
FJ 10	10.30±0.15	3.13±0.2	6.75±0.13	3.47	420.24±0.27	81.90±0.12
KF 01	9.81±0.20	3.94±0.17	6.70±0.21	3.45	419.37±0.14	81.14±0.19
NCIM 3215	10.15±0.12	3.24±0.11	6.80±0.26	3.49	418.13±0.19	80.56±0.09

# CONCLUSION

Indigenous yeast flora isolated from *Syzygium cumini* and *Garcinia indica* belong to two genera *Saccharomyces sp.* (2) and *Candida sp.* (1) which is confirmed by ITS gene sequencing studies. Sequence alignment and phylogenetic study revealed close relatives of isolates in a cluster. Alcohol and sugar tolerance study of isolates gives promising results and it is also proved by microvinification

study. Finally we conclude that *Saccharomyces sp.* (FJ 10 and KF 01) are suitable as wine starter cultures, especially for red wine. Further research is needed to find out the exact species.

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