Isolation and characterization of halophilic soil fungi from the salt desert of Little Rann of Kutch, India

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Extremophiles are considered a cornucopian source of chemically diverse and often novel metabolites. Determination of their growth and distribution pattern and their chemical nature is therefore vital to fully gauge their existential uniqueness and potential as a fount of novel compounds. Present study deals with growth characterization and chemoprofiling of halophilic fungi inhabiting a hitherto unexplored terrain of Little Rann of Kutch, India. Thirty five morphologically discrete fungi, primarily belonging to phylum Ascomycota, were isolated from the soil, suggestive of the region's low microbial diversity. Calculation of fungal salt tolerance index identified one isolate as a halophile with the remaining being halotolerant. Morphological characteristics and 18S rDNA sequencing established the halophile's identity as Aspergillus versicolor. A. versicolor was further characterized for its salt tolerance potential and degree of halophily. The fungus grew optimally at 7.5% NaCl, thereby classifying it as a moderate halophile. Macro-morphology of the fungus corresponded well with its micro-morphology. At 0% and 10% NaCl, fungal specimen exhibited mycelial distortions, loss of cytoplasm and sparse conidiation; healthy growth features were observed at 7.5% NaCl. For chemoprofiling, A. versicolor was cultured on Czapek Dox broth and Malt Extract broth and the crude extract was analysed by liquid chromatography mass spectrometry (LC-MS). A comparative chemoprofile analysis determined Czapek Dox broth to be a better choice for profiling of this particular strain as it exhibited higher compound diversity. The rich chemical contour of A. versicolor suggests the fungus to be a potential source of novel bioactive molecules of pharmaceutical significance.

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20 <u>ABSTRACT</u>

Extremophiles are considered a cornucopian source of chemically diverse and often novel 21 22 metabolites. Determination of their growth and distribution pattern and their chemical nature is 23 therefore vital to fully gauge their existential uniqueness and potential as a fount of novel compounds. Present study deals with growth characterization and chemoprofiling of halophilic 24 25 fungi inhabiting a hitherto unexplored terrain of Little Rann of Kutch, India. Thirty five morphologically discrete fungi, primarily belonging to phylum Ascomycota, were isolated from 26 the soil, suggestive of the region's low microbial diversity. Calculation of fungal salt tolerance 27 index identified one isolate as a halophile with the remaining being halotolerant. Morphological 28 29 characteristics and 18S rDNA sequencing established the halophile's identity as Aspergillus versicolor. A. versicolor was further characterized for its salt tolerance potential and degree of 30 halophily. The fungus grew optimally at 7.5% NaCl, thereby classifying it as a moderate 31 halophile. Macro-morphology of the fungus corresponded well with its micro-morphology. At 32 33 0% and 10% NaCl, fungal specimen exhibited mycelial distortions, loss of cytoplasm and sparse conidiation; healthy growth features were observed at 7.5% NaCl. For chemoprofiling, A. 34 versicolor was cultured on Czapek Dox broth and Malt Extract broth and the crude extract was 35 36 analysed by liquid chromatography mass spectrometry (LC-MS). A comparative chemoprofile analysis determined Czapek Dox broth to be a better choice for profiling of this particular strain 37 as it exhibited higher compound diversity. The rich chemical contour of A. versicolor suggests 38 the fungus to be a potential source of novel bioactive molecules of pharmaceutical significance. 39

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43 **INTRODUCTION**

The kingdom fungi encompass an enormous diversity of microorganisms, approximately 1.5 44 45 million fungal species, which inhabit almost all known ecological niches (Hawksworth 2001). Survival in such diverse habitats has necessitated biochemical evolution and the development of 46 complex metabolic pathways that has resulted in production of a diverse array of primary and 47 48 secondary metabolites. Primary metabolites are produced by all living cells and are required for normal growth and functioning of cellular processes. Secondary metabolites are secreted only by 49 a few members of the species, often a defining characteristic of the organism synthesizing those 50 (Samson et al. 2014). Specifically, these are low molecular weight compounds, the secretions of 51 52 which are linked to the organism's morphological differentiation process, and are synthesized as families of related compounds (Zain 2013). Although secondary metabolites are not essential for 53 the organism's survival, yet their genes being maintained consistently suggests that these 54 compounds do provide critical benefits to the producer (Frisvad 2005). Some of their 55 56 documented roles are tolerance against abiotic and biotic stresses, metal transportation, as sex hormones, differentiation effectors, agents of symbiosis between microbes and plants, 57 nematodes, insects and higher animals (Wang et al. 1995; Demain and Fang 2000); many other 58 59 roles are yet to be discovered (Omura et al. 2001; Bentley 2002; Zain 2013). A fungus' chemoprofile is often a reflection of its genetic and biochemical makeup (Thrane et al. 60 61 2007). This property has consequently been employed in fungal chemotaxonomy, particularly for fungal genera such as the *Penicillium*, Aspergillus and Fusarium and their perfect states, since 62 these fungi produce consistent profile of secondary metabolites (Samson et al. 2014). A fungus' 63

64 chemoprofile also depends on the physicochemical nature of its habitat. For instance, fungi

65 growing under low water index (a_w) produce a class of compounds known as polyamines that act

as osmolytes (Laura and Jose 2014). Chemoprofile of fungi isolated from extreme ecological
niches such as salt marshes and solar salterns are subjects of much interest as such fungi are
expected to exhibit novel metabolic pathways and metabolites that are characteristic of that
particular species or strain.

Hypersaline habitats are characterized by high salt concentrations, low water index (a_w), high 70 71 light intensity, low oxygen concentrations, neutral pH and believed to be inhabited mostly by algae, protozoa, Archaea and bacteria. Halophilic fungi, a term coined for those that require 72 some salinity for optimal growth, had previously been associated solely with foods treated with 73 salt or sugar for preservation. Only at the onset of 21st century did researchers discover 74 eukaryotes, particularly those belonging to kingdom Fungi, thriving in such extreme habitats 75 (Gunde and Cimmerman 2000). Since then, a number of fungal species and strains inhabiting 76 natural hypersaline environments have been described. Based on cardinal range, these can be 77 categorized as halotolerant, extremely halotolerant and halophilic (Kushner 1978). Studies on 78 79 fungal communities populating such extreme environments have been largely conducted in and around salterns along the Adriatic coast, the Mediterranean coast, the Red Sea coast, and the 80 81 Atlantic coast, Gulf of California, Great Salt Lake, Utah and the West Coast of Indian peninsula 82 (Gunde-Cimerman et al. 2005; Nazareth and Gonsalves 2014).

Rann of Kutch is a saline wasteland located between 22°55" to 24°35" North latitudes and
70°30" to 71°45" East longitudes, situated in the western state of Gujarat, India. The area is
characterized by scant and seasonal rainfall and extreme temperatures. Rapid erosion through
fluvial processes and capillary action has advanced the process of desertification by making the
area saline with surface salinity ranging from a minimum of 281.6 ppm to a maximum of 12,094
ppm (Gupta and Ansari 2012). Given the harsh environmental conditions, it would be interesting

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89 to study the halophilic mycobiota of the region for their growth and distribution patterns.

90 Chemoprofiling of such fungi would give an invaluable insight into its chemical nature and

91 possible mechanisms to counter abiotic stresses.

Present study was conducted to isolate and identify halophilic fungi inhabiting the soil of Little
Rann of Kutch and prepare a chemical portrait of the fungi using LC-MS technique. To the best
of authors' knowledge, this is first such attempt aimed at studying halophilic fungi inhabiting the
region.

96 MATERIALS AND METHODS

97 Soil sampling and analysis

98 Soil cores were extracted from 5 different sites within an area of 4 sq mi in the southern zone of Little Rann of Kutch (23°18' N, 71°27' E). A total of 25 soil samples, 5 samples from each site, 99 were collected in a zigzag pattern from a depth of 6 inches in March, 2014. Each soil sample 100 101 measuring 0.5 L was extracted using a post-hole auger and collected in properly labeled zip-lock bags. Samples were immediately transported to the Department of Agrochemicals at Indian 102 Agricultural Research Institute, New Delhi for further analysis. A composite sample was 103 prepared by mixing soil cores followed by preparation of 4 sub-samples. Each sub-sample was 104 analyzed for its sand, silt and clay content, pH, electrical conductivity (EC), organic carbon 105 content, total nitrogen and phosphorus content and soluble Na⁺, Ca²⁺, Mg²⁺ and K⁺. The 106 methodology adopted for each has been summarized in Table 1. Field moist soil samples were 107 used for all analytical tests. Soil pH and $EC_{1:1}$ was measured for a soil suspension containing 108 109 soil: water ratio of 1:1. Temperature was maintained at 25°C during the tests.

110 Isolation of fungi

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Fungal isolation was performed by serial dilution method. 10 g soil was dissolved in 100 mL 111 phosphate buffered saline and shaken in an orbital shaker at 150 rpm for 15 minutes. The 112 suspension was serially diluted to give concentrations of 10⁻¹, 10⁻³ and 10⁻⁵. From each dilution, 113 50 µL was pipetted out and dispensed onto Czapek Yeast Autolysate agar (CYA), Malt Extract 114 agar (MEA) and Potato Dextrose agar (PDA) plates. The experiment was performed in 115 triplicates. Rifampicin (100 µg mL⁻¹) was added to prevent any bacterial growth. The inoculated 116 plates were incubated reverse side up in dark at 25+1°C for 7 d. Subsequently, each 117 morphologically distinct fungal colony was sub-cultured on the above mentioned media for 118 obtaining pure isolates. The pure isolates were annotated as BBKF1- BBKF35 in ascending 119

120 order.

121 **Determination of halophily**

The isolated fungi were classified as halotolerant and halophilic on the basis of their salt olerance 122 levels, represented as salt tolerance index (T_i) . Each isolated fungus was cultured on plates 123 containing CYA and CYA amended with 2.5% - 10% NaCl. Colony diameters were measured on 124 6th day post inoculation. T_i was calculated as the ratio of colony diameters between CYA and 125 CYA+NaCl (Frisvad, 2005). T_i values were inversely proportional to halophily, i.e. lower the 126 index value higher the halophily. Fungi with index values lower than 1 were considered as 127 halophilic, while those above 1 as halotolerant. Based on the aforementioned study, only one 128 fungus was found to be halophilic, while the remaining isolates were found to be halotolerant. 129

130 Morphological and molecular identification

131 The halophilic fungus was further identified on the basis of colony morphology, microscopic

132 observations and rDNA sequencing.

133 Morphological identification

134 Czapek Yeast Autolysate agar, a medium recommended as standard for *Aspergillus*

characterization, was used for morphological identification (Samson et al. 2014). The medium was supplemented with 7.5% NaCl. Inoculated plates were incubated in dark at $25\pm1^{\circ}$ C for 8 d and observed for colony characteristics such as growth rate, extent of sporulation, mycelial color,

138 production of cleistothecia and rear side colony color.

139 Microscopic structures were observed using Scanning Electron Microscope (SEM). Briefly, a 1

140 cm² section of 8 d old fungal culture plate was used as specimen. Sample was immersed in 2.5%

141 glutaraldehyde and kept overnight at 4°C. The tissue was rinsed thrice with 0.1 M phosphate

buffer and subsequently immersed in 0.5% Osmium Tetroxide solution followed by washing in

143 0.1 M phosphate buffer. For dehydration, the tissue was transferred sequentially to 30%, 50%,

144 70%, 80%, 90%, 95%, and 100% alcohol. The sample was transferred into a 1:2 solution of

145 hexamethyldisilazane (HMDS): 100% ethanol (EtOH) and kept for 20 min. Fresh solution of 2:1

146 HMDS: EtOH was added and further transferred into 100% HMDS. Each step was repeated

147 twice for 20 min. After drying overnight, the sample was placed on a stub and sputter coated

148 with gold-palladium followed by mounting on a Carl Zeiss EVO18 Scanning Electron

149 Microscope. The specimen was observed under low vacuum mode for features such as shape of

150 conidial heads, seriation, morphology and ornamentation (Raper and Fennell 1965; Samson et al.

151 2014).

152 Molecular identification

Molecular identification based on 18S rDNA sequencing was done to confirm the identity of theisolate (White et al. 1990; Diaz et al. 2012).

Culture preparation and DNA extraction: Fungal biomass for DNA extraction was prepared by 155 inoculating 100 mL Czapek Dox broth with agar plug from a 10 d old culture. The broth was 156 incubated in an incubator cum shaker for 8 d at 25+1°C and 70 rpm. For obtaining genomic 157 DNA, fungal mycelium of the halophilic fungal isolate (BBKF4) was harvested, washed 158 thoroughly with distilled water and air dried. In a chilled mortar and pestle, 1 g biomass was 159 160 homogenized in 3.5 mL CTAB buffer and 100 μ L β -mercaptoethanol. The homogenate was collected in Eppendorf tubes, incubated in a water bath at 65°C for 45 min and allowed to cool to 161 room temperature. Equal volume of chloroform: isoamyl alcohol (24:1 v/v) was added and 162 mixed gently for 10 min. The suspension was centrifuged at 7000 rpm for 20 min at 25°C and the 163 supernatant was divided into three equal aliquots. 2/3rd volume of chilled isoamyl alcohol was 164 added to each and mixed gently. The suspension was centrifuged at 8000 rpm for 15 min at 4°C. 165 The pellet was collected and washed with 70% ethanol and air dried. It was then dissolved in 500 166 μ L TE buffer and stored at -20°C till further use. 167

168 Primers and PCR Amplification: Two universal fungal primers, (ITS 1, 5'-TCC GTA GGT GAA CCT GCG G-3'; ITS 4, 5'-TCC TCC GCT TAT TGA TAT G-3'), described by White et 169 al. (1990) were used for amplification of the ITS 1 and ITS 2 regions and the intervening 5.8S 170 171 gene. Primers were synthesized by Sigma Aldrich Chemicals Pvt. Ltd. Bangalore. The PCR reaction mixture consisted of the following (Diaz et al. 2012): 5x Proof buffer (10 µL), dNTP 172 mix (1 μ L), Forward primer (10 μ M, 2.5 μ L), Reverse primer (10 mM, 2.5 μ L), DNA template 173 50 ng, and DNA polymerase 0.5 µL. Final volume was made up to 50 µL with sterile water. 174 175 Template DNA was amplified using the protocol proposed by White et al. (1990). Initial denaturation 94°C, 60 s; denaturation 94°C, 30 s; annealing 55°C, 30 s; extension 72°C, 90 s. The 176 steps were repeated for 35 cycles followed by final extension at 72°C for 5 min. PCR amplicon 177

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178 quality was assessed. The PCR product was mixed with loading buffer and loaded onto 1%

agarose gel stained with ethidium bromide. 1 kb ladder was used for size reference.

180 *DNA Sequencing and analysis:* The PCR amplicon was sequenced by Gujarat State

- 181 Biotechnology Mission, India. The sequences were then used to perform individual nucleotide-
- nucleotide searches with the BLASTn algorithm.

183 <u>Determination of growth pattern of the halophilic fungi and the impact of salinity on</u> 184 <u>fungal morphology</u>

185 Growth pattern of halophilic fungus at different NaCl concentrations and incubation period was elucidated to determine optimum salinity level, the corresponding degree of halophily, and 186 growth rate. Fungus was grown in CYA plates supplemented with 0-10% NaCl and incubated at 187 25±1°C. Radius of the fungal colony growing at each salt concentration was measured 2, 4, 6 and 188 189 8 d post inoculation. A curve of growth against different time intervals was plotted. Radial growth rate (K_r) was calculated as $K_r = (R_l - R_0)/(t_l - t_0)$, where R_0 and R_l are colony radii at 190 time $t_0 = \text{day } 0$ and $t_1 = \text{day } 8$ (Reeslev and Kjoller 1995). 3 replicate plates were included for 191 each salt treatment. Based on growth characteristics at different salinities, the degree of halophily 192 193 was determined. The fungus was classified as being slightly halophilic (optimum growth at 1.2 -3% NaCl), moderately halophilic (optimum growth at 3 - 14.6%) or extremely halophilic 194 (optimum growth at 14.6% and above) (Kushner 1978). 195 Effect of salinity on morphological features of the halophilic fungus was assessed. The fungus 196 was grown on plates containing CYA without NaCl and CYA+7.5% NaCl. Colony 197 198 characteristics were studied and the specimen was observed under scanning electron microscope for fungal topography. 199

200 <u>Cultivation and extraction of fungal cultures</u>

Mycelia of *A. versicolor* cultivated on Malt Extract broth (MEB) and Czapek Dox broth (CDB) 201 202 was used for chemoprofiling and determining the influence of medium composition on the 203 fungus' metabolite profile. Agar plug from 10 d old plate culture of the isolate was inoculated in 100 mL each of CDB and MEB in 250 mL Erlenmeyer flasks. Each medium was supplemented 204 205 with 7.5% NaCl and the cultures were allowed to grow for 10 d in dark at room temperature. Fungal crude extracts were prepared by method proposed by VanderMolen et al. (2013) with 206 slight modifications. Post 10 d incubation, mycelial mats were harvested from each medium, 207 shredded and suspended in 100 mL 1:1 chloroform: methanol (CHCl₃:CH₃OH). Extraction was 208 done overnight in a rotary shaker at 100 rpm and later filtered using 0.45 micron vacuum filter. 209 To the filtrate, 90 mL chloroform and 100 mL distilled water was added and stirred for 1 h. The 210 mixture was then transferred to a separatory funnel. Bttom organic layer was collected and 211 evaporated to dryness in a rotavapor. To the dried organic extract, 100 mL 1:1 acetonitrile 212 213 CH₃CN: MeOH and 100 mL hexane was added and stirred for 1 h. The solution was subsequently transferred to a separatory funnel and the bottom organic layer was collected and 214 evaporated to dryness. The extract was stored at -20°C till further analysis. 215

Analysis of fungal metabolite profiles by liquid chromatography-mass spectrometry (LC MS)

- 218 Extracts of *A. versicolor* cultured on each of the two medium were examined by LC-MS.
- 219 Analyses were performed using a Waters Acquity UPLC system utilizing a BEH C18 column
- 220 (Waters; 50 mm \times 2.1 mm i.d., 1.7 μ m). The mobile phase consisted of CH₃CN and 0.1% formic
- acid-H₂O, increasing linearly from 2% CH₃CN at the time of injection to 90% CH₃CN at 15 min.
- 222 The flow rate was 0.3 mL min⁻¹ and column temperature was 35°C. The UPLC system was

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- 223 coupled to a Thermo Scientific LTQ Orbitrap XL equipped with electrospray ionization (ESI)
- source. Crude extracts were dissolved in 100% MeOH at a concentration of 2.0 mg mL⁻¹; 6.0μ L
- were injected, and the peak areas of each metabolite measured. Metlin Database was used for the
- tentative identification of the fungal metabolites from the m/z values obtained.

227 <u>RESULTS</u>

228 Soil characteristics

Table 1 summarizes the physical and chemical characteristics of the soil. The soil had high EC
value indicating high salinity. The N, C and P contents were found to be low, suggesting low
nutrient content of the soil.

232 Isolation of fungi

- 233 86 soil fungi were isolated. Based on colony characteristics and digital microscopy, 35 distinct
- fungi were identified. These belonged to genus Fusarium (11), Penicillium (10), Aspergillus (8),
- 235 Curvularia (2), Rhizopus (2) and Dreschelera (2) (Fig. 1). The isolates were designated as
- 236 BBKF1 BBKF35 in ascending order.

237 Determination of halophily

- 238 Based on tolerance index values, halophily of 35 fungi were determined. BBKF 4 was
- established as a halophile. The remaining isolates were halotolerant as they did not require NaCl
- 240 for optimal growth. Isolate BBKF4 was selected for further identification and characterization
- 241 studies.

242 Morphological identification

Growth characteristics on different media, conidial pigmentation, mycelia and rear side colony
color were determined 8 d post inoculation. Thick mycelium with velvety texture and greyish
green conidia suggested that the isolate BBKF4 belonged to genus *Aspergillus* (Table 2, Fig. 2
A-B). Scanning electron microscopy studies suggested the isolate could be *Aspergillus versicolor*(Table 3, Fig. 2 C-D).

248 Molecular identification

ITS 1- 5.8S- ITS 2 region of the rDNA was sequenced for molecular identification. Based on
sequence homology and phylogenetic tree analysis, BBKF4 was identified as *Aspergillus versicolor*. The sequence has been submitted in NCBI GenBank (Accession no. KT164811) as *A. versicolor* KR87.

253 Growth pattern of halophilic fungi and impact of salinity on fungal morphology

A. versicolor KR87 was cultured on CYA having 2.5%, 5%, 7.5% and 10% salinity. Colony 254 radius was measured and a curve of growth against salinity at regular time intervals was plotted 255 to determine the optimal salinity and growth rate (Fig. 3). Based on colony radius on 8th d, it was 256 established that A. versicolor KR87 grew optimally at 7.5% NaCl concentration. The growth of 257 A. versicolor KR87 followed a linear trend. Radial growth rate was maximum at 7.5% salinity 258 (6.96±0.07 mm d⁻¹), closely followed by 5% salinity (6.42±0.2 mm d⁻¹). Growth rate was least at 259 0% (3.33±0.06 mm d⁻¹) and 10% (3.45±0.07 mm d⁻¹) salinity. The fungus could therefore be 260 considered as moderately halophilic (Kushner 1978). 261

262 To assess the impact of salinity on fungal morphology, *A. versicolor* KR87 was cultivated on

- 263 CYA and CYA+7.5% NaCl. Remarkable differences in colony and micromorphology were
- observed. At 7.5% NaCl concentration, mycelial mat was thick with vibrant greyish green

pigmentation and showed characteristic radial grooves with profuse conidiophores. At 0%
salinity, mycelia were thin and poorly developed. Microscopic observations revealed deformed
hyphae and poorly developed conidial heads. As equated to the fungal morphology at 7.5%
NaCl, fungal mycelia at 0% NaCl showed severe distortions indicating loss of cytoplasm (Fig.
4).

270 Liquid chromatography mass spectrometric analysis (LC-MS)

Crude extracts of A. versicolor KR87 grown on two different media were analyzed by LC-MS. 271 LC-MS chromatograms displayed significantly different profiles for each growth medium (Fig. 272 5). Growth on CDB yielded 23 different metabolites belonging to 13 different compound classes. 273 Majority of metabolites belonged to alkaloids (19%), amines (14%) and terpenes (9%) (Fig. 5A). 274 275 When grown on MEB, the fungus revealed a thinner metabolite profile with 15 compounds belonging to 9 different compound classes (Fig. 5B). The metabolites mostly belonged to 276 alkaloids, terpenes and flavonoid groups (20% each). Metabolites of certain compound classes 277 such as polyketides, alkaloids, terpenes, amines and amino acids occurred in both the metabolite 278 profiles (Fig. 6). Some of the important metabolites and their bioactivities have been summarized 279 in Table 4. 280

281 **DISCUSSION**

Little Rann of Kutch is a unique saline- inundated wasteland that is parched by high

temperatures in summers and flooded by tidal waters and seasonal rivers during monsoon.

Evaporation of water in summers results in a monotonous flat saline surface composed of halite

and gypsum crystals. These geomorphic features render the soil of Little Rann of Kutch high in

salinity and low in nutrient content. Present study was conducted in the southern zone of Little

Rann of Kutch. In any soil sampling and analytical study due consideration should be given to 287 the methodology adopted. Sampling methodology, sample area and design, instruments used, 288 soil depth, soil volume collected and soil moisture content at the time of sampling are a few 289 factors significantly influencing the measured parameters. Soil collected from the study region 290 was analyzed for its chemical properties. Field moist soil samples were used as they are 291 292 considered the most valid in terms of the existing soil-biological environment and the variability between in vivo and in vitro soil data is negligible (Jackson 1973). At a pH of 6.63±0.3, the soil 293 was practically neutral. $EC_{1:1}$ value of the soil (8.61±0.28) classifies it as being highly saline. 294 Low N, P and organic C contents indicated the soil's poor nutrient status. Various methods are 295 available for soil chemical analysis. These methods vary among each other in terms of ease of 296 performance, sensitivity, specificity and rapidness. For example, the Walkely-Black method 297 adopted in this study is better suited for determining organic C content as it rules out extraneous 298 sources of organic carbon such as graphite and charcoal, thereby ruling out any false 299 300 measurement. Kjeldahl method, though laborious, still remains the most sensitive method of N determination. Chlorostannous-reduced molybdophosphoric blue color method is the most 301 sensitive method of P estimation and therefore most suitable for infertile soil samples. Flame 302 303 emission spectrophotometric method is advantageous over conventional gravimetric and titrimetric methods in terms of accuracy, simplicity and rapidity (Jackson 1973). 304

Identification based on colony morphology and microscopic studies revealed that the majority of
isolates belonged to genus *Fusarium, Penicillium* and *Aspergillus*. Microbial diversity of the
region was found to be low, in accordance with the studies conducted in other hypersaline
habitats around the world. (Borut 1960; Ranzoni 1968; Salama et al. 1971; Khodair et al. 1991;
Gunde-Cimmerman et al. 2000; Grishkan et al. 2003; Evans et al. 2013). Tolerance index of

fungi revealed the isolates as being predominantly halotolerant, with only Aspergillus versicolor 310 KR87 being a halophile. Further growth characterization based on radial growth rate (K_r) 311 confirmed A. versicolor KR87 as a moderate halophile. Impact of salinity on fungal morphology 312 was evaluated. Distorted hyphae, poorly developed mycelium and low density of conidial heads 313 were the characteristics of A. versicolor cultivated on a salt free medium, suggesting the fungus 314 315 to be an obligate halophile. Certain metabolites such as polyamines play a pivotal role in fungal growth, development and differentiation processes (Laura et al. 2012; Laura and Jose 2014). In 316 obligate halophiles, the pathway for polyamine metabolism is activated only in the presence of 317 osmotic stress, which in this case, is triggered by high salinity. Lack of osmotic stress in a salt 318 free medium might therefore lead to non-activation of polyamine metabolism pathway, 319 ultimately resulting in poor fungal growth. Species of Aspergillus have usually been found to be 320 halotolerant to varying degrees, irrespective of their source. Aspergilli are one of the most 321 common fungal species and have been reported regularly from regions of extreme salinity 322 (Buchalo et al. 1999; Molitoris et al. 2000; Kis-Papo et al. 2003), non-saline soils and house dust 323 samples collected from around the world (Visagie et al., 2014). The outcomes of the present 324 study support important observations made in earlier reports; prevalence of fungi in saline 325 326 habitats that are halotolerant rather than halophilic (Hujslova et al. 2010; Nayak et al. 2012); halotolerant and halophilic traits are intrinsic characters of a particular species, rather than an 327 adaptation in response to salt stress (Frisvad 2005); hypersaline environments do not harbor a 328 329 characteristic fungal community of specialized taxa. It can hence be said that the fungi inhabiting hypersaline soils of Little Rann of Kutch have limited diversity, are mostly halotolerant and 330 331 exhibit cosmopolitan nature.

Frisvad (2005) proposed that extrolites are produced by a species irrespective of its habitat. 332 Further, metabolites are often produced in highest diversity and amounts at up to 5% NaCl 333 concentration, beyond which there is a steady decline in metabolite profile. The metabolite 334 profile of A. versicolor KR87 displayed chemically diverse compounds. A comparative analysis 335 of the metabolites secreted by A. versicolor cultivated in CDB and MEB gave significantly 336 337 different profiles. Fungus grown in CDB medium showed a greater chemical diversity with metabolites belonging to over 13 compound groups as compared to that of MEB which exhibited 338 9 compound groups. Polyketides, alkaloids, terpenes, amines and amino acids were the 339 compound families shared by either growth medium. An organism's metabolome is greatly 340 dependent on culture conditions such as nutrient source, light, temperature, pH etc. (Calvo et al. 341 2002; Yin and Keller 2011). Further detailed studies need to be carried out to formulate a 342 medium that is ideal for secondary metabolite production. However, the findings of the current 343 study suggest that CDB is the medium of choice for studying the fungi's metabolome. Earlier 344 345 works also report CDB as an excellent media for metabolite production (Jennessen et al. 2005). Ever since the discovery of Penicillin G 1, a secondary metabolite of *Penicillium notatum*, 346 filamentous fungi have been voraciously researched and exploited for their pharmaceutical 347 348 potential. Systematic drug discovery programs by pharmaceutical companies have led to discovery of compounds that have antibiotic, immunosuppresant, antineoplastic and lipid 349 lowering activity, to name a few (Zain et al. 2013). Many of the metabolites secreted by A. 350 versicolor KR87 have potential applications as antimicrobials, anti-cancer agents and lipid 351 352 lowering drugs. For example, quinazoline acetic acid is an important component of pharmacologically active compounds with anticonvulsant, antibacterial and anti-diabetic 353 activities (Pandeya et al. 1999). Tegafur, a chemotherapeutic fluorouracil prodrug inhibits DNA 354

and RNA synthesis and is used in cancer treatment (Ishikawa 2008). Likewise, Procarbazine, a 355 benzene derivative, is an antineoplastic drug used for treatment of Hodgkin's lymphoma and 356 certain brain cancers (Ogawa et al. 2003). Brefeldin A is a lactone antibiotic that inhibits protein 357 transport from endoplasmic reticulum to Golgi apparatus indirectly by preventing formation of 358 COPI-mediated transport vesicles (Klausner et al. 1992). 14-Hydroxy-6-O-methylerythromycin 359 360 A, a polyketide, is known to have twice the antimicrobial efficacy of erythromycin (Fernandes et al. 1988). Dehydrofalcarinone, a carbonyl compound, is used as a fungicide, pesticide and 361 phytoalexin. As mentioned earlier, polyamines play an important role in fungal growth and 362 differentiation. They are also recognized as stress metabolites, aiding the organism's survival 363 under abiotic stresses such as osmotic shock. N- carbamoyl putrescine is an important 364 intermediate in polyamine biosynthetic pathway (Laura et al. 2012). Presence of this metabolite 365 in A. versicolor KR87 metabolome sheds light on the probable mechanisms adopted by the fungi 366 to survive and thrive in hypersaline conditions. 367

368 It is also imperative to acknowledge the role of halophiles in industrial and biotechnological arenas. Halophilic fungi have been used since ages for production of fermentation based foods 369 such as soy sauce and fish sauce. Their modern day applications range from biorhodopsin 370 371 production for optical computing to synthesizing biosurfactants and exopolysaccharides for oil recovery and compatible solutes as stress protectants (Margesin and Schinner 2001). Halophilic 372 and halotolerant fungi can act as valuable sources of transgenes for imparting tolerance to 373 industrially important microbes such as Saccharomyces cerevisiae, which are subjected to 374 various abiotic stresses. Their genes can also be used for imparting halotolerance to plants, 375 enabling them to grow in soils with high salinity and low water index (Munns 2002; Ashraf and 376 Akram 2009). 377

Given the uniqueness of this extreme ecological niche, the saline wasteland of Rann of Kutch merits a more exhaustive and systematic study of the soil mycobiota. Such studies are bound to throw up certain atypical microorganisms that are imperative not just from academic perspective but are also of industrial significance.

382 CONCLUSION

Based on tolerance index and growth pattern at different salinities, *A. versicolor* KR87 was
identified as a moderate halophile. Czapek Dox broth was found to be a preferred growth
medium for chemoprofiling. The fungus exhibited diverse metabolites of pharmacological
importance, indicating that it may be a promising source of novel drug lead compounds. Further
research is being done to quantify the pharmacologically important compounds.

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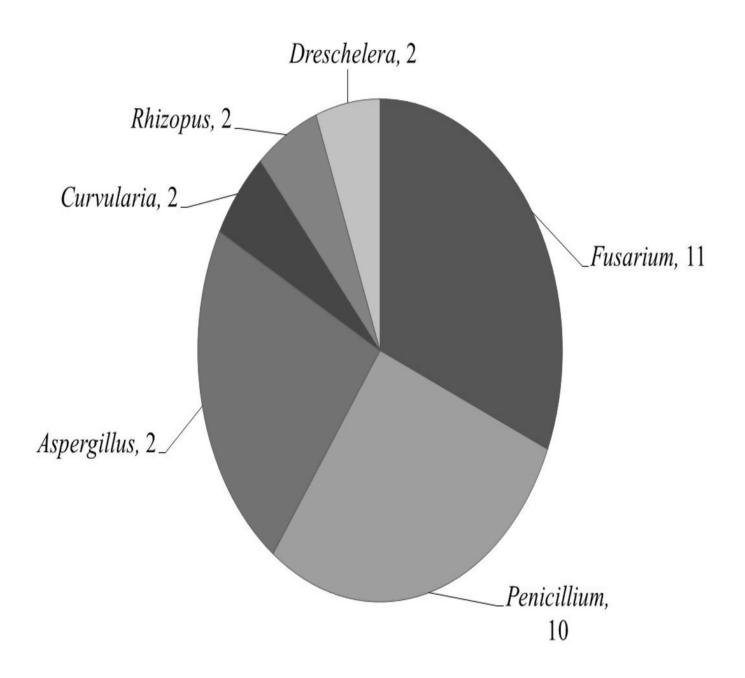
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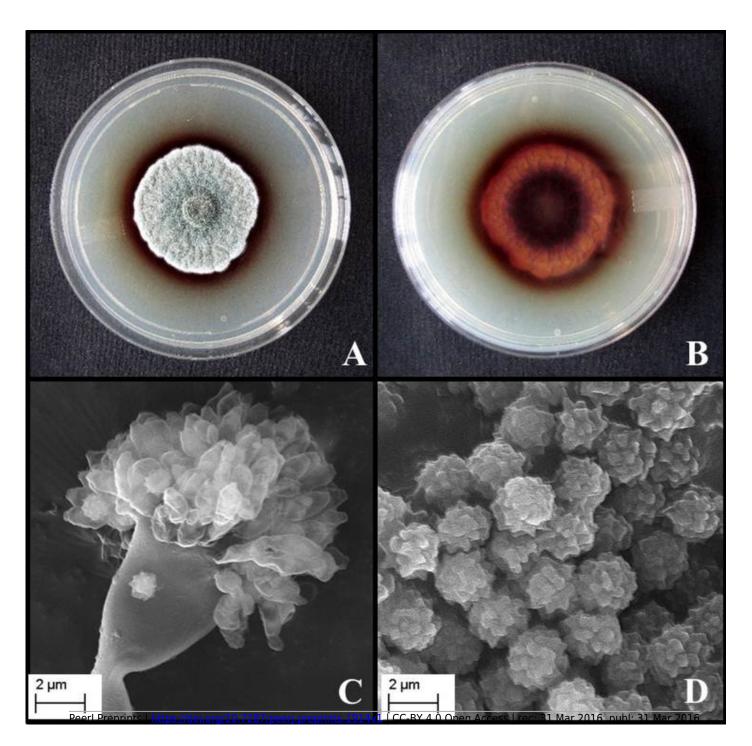
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Species richness of the study area.

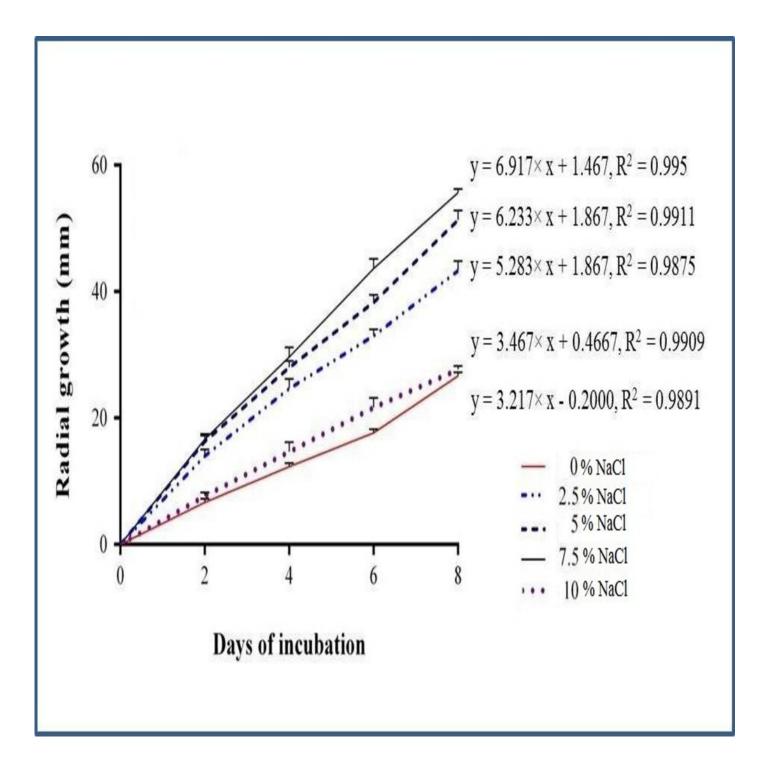


Morphological features of the halophilic isolate BBKF4.

(A) and (B) represent the front and reverse side colony morphology. Scanning electron micrograph of the conidial head (C) and conidia (D). The fungus was cultivated on CYA for 6 days at $25\pm1^{\circ}$ C.



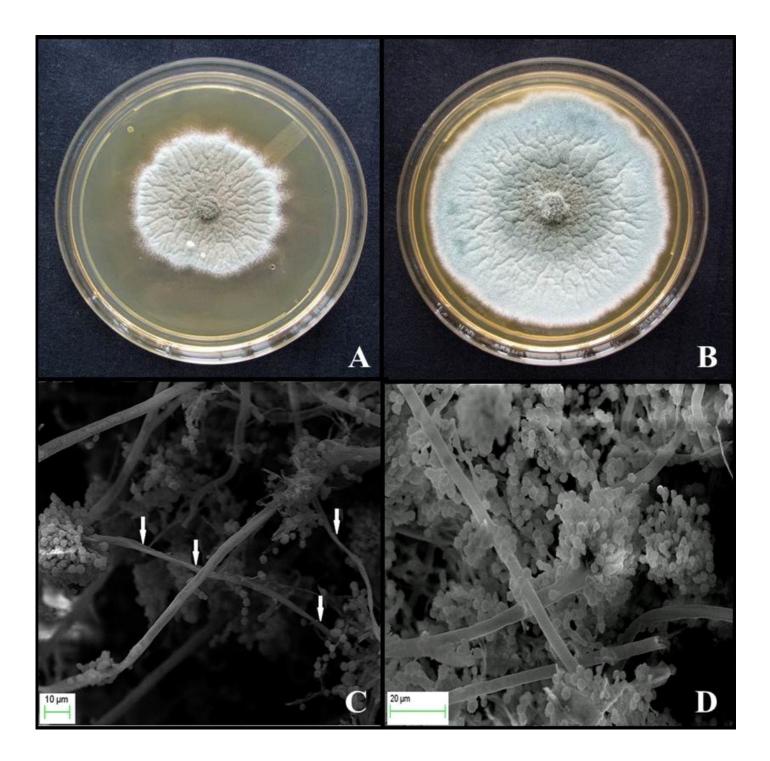
Radial growth of *A. versicolor* KR87 at different incubation periods and salt concentrations.



Impact of salinity on morphology of *A. versicolor* KR87.

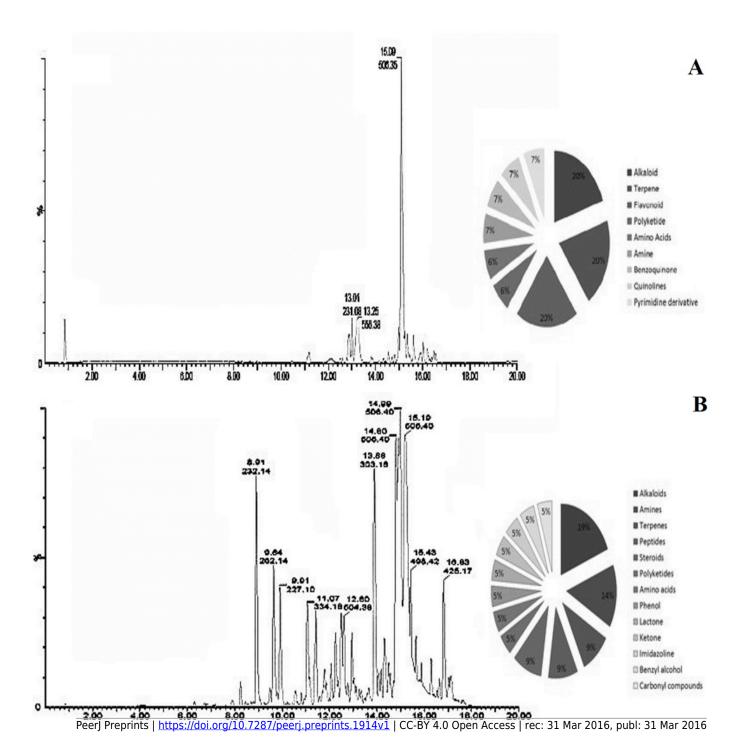
Figures (A) and (B) represent the colony morphology of the fungus at 7.5% and 10% NaCl respectively. Figures (C) and (D) represent the micrographs of the fungus at 7.5% and 10% NaCl concentration respectively. The arrows in figure (D) indicate distortion in mycelia and loss of cytoplasm at 10% salinity. Conidiation is also scanty at 10% NaCl.

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LC-UV-MS chromatogram of crude extract of *A. versicolor* KR87 grown in MEB (A) and CDB (B).

Adjacent to each chromatogram is a pie-chart of the metabolite profile of *A. versicolor* KR87. Metabolite diversity is represented as % abundance of metabolites of each compound class.



Compound classes exhibited by *A. versicolor* KR87 grown in CDB (A) and MEB (B) and the compound classes found in either metabolite profile (C).

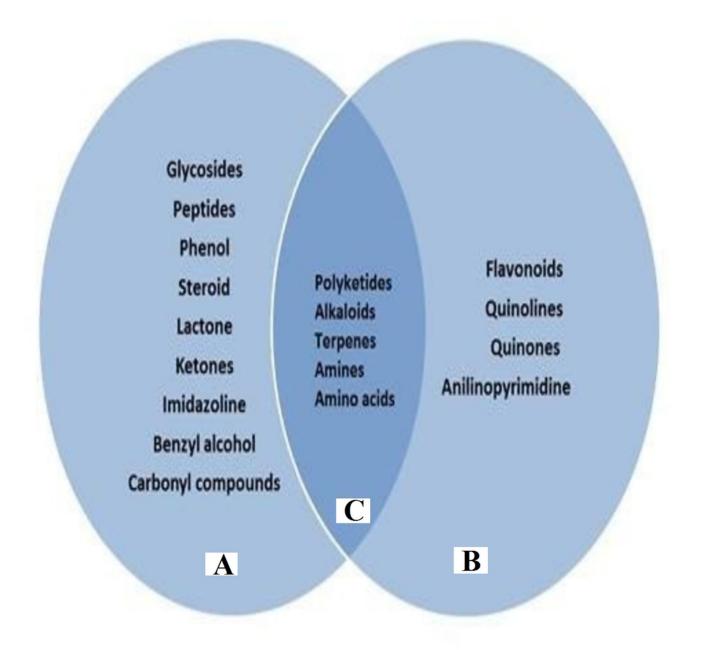


Table 1(on next page)

Physical and chemical properties of the soil samples collected from Little Rann of Kutch.

Property	Measured value	Methodology	Reference
Sand (g/Kg)	210	Hydrometer method	Tan (1996)
Silt (g/Kg)	650		"
Clay (g/Kg)	86	دد	
рН	6.63±0.3	Glass electrode	Smith and Doran (1996)
Electrical conductivity (EC _{1:1}) (dSm ⁻¹)	8.61±0.28	EC Probe	Jackson (1973)
Organic C content (%)	0.23	Walkley-Black method	Walkley (1947) Jackson (1973)
Total N content (%)	0.1	Modified Kjeldahl method	Bremner (1960) Jackson (1973)
Total P content (%)	0.2	Chlorostannous– reduced molybdophosphoric blue color method, in sulfuric acid system	Jackson (1973)
Elemental analyses (%)			
Na ⁺	0.39	Flame emission	Jackson
Ca ²⁺	0.4	spectrophotometer	(1973)
Mg^{2+}	0.35		دد
K ⁺	0.41		

Table 2(on next page)

Macroscopic characteristics of BBKF 4 grown on CYA for 8 days at $25\pm1^{\circ}$ C.

Color	Texture	Colony diameter (mm)	Colors on CYA		
			Conidia	Mycelia	Reverse
Greyish green	Suede-like with radial grooves	50±4	Greyish green	White	Red/ reddish brown

1

Table 3(on next page)

Microscopic features of BBKF4 as observed under scanning electron microscope.

Stipes		Vesicles			Conidia			
Length	Texture	Color	Diameter	Shape	Seriation	Diameter	Shape	Texture
300- 400 μm	Smooth	Pale brown	10-12 μm	Pyriform	Biseriate	2-3 μm	Globose	Finely roughened

Table 4(on next page)

Biological activity of some metabolites secreted by A. versicolor KR87.

Metabolites	Potential applications	References	
Carnosols, Isouvaretin	Anti-cancer agents	Hufford and Lasswell Jr. 1976	
Flindersine	Antibacterial, antifungal	Duraipandiyan V et al. 2009	
Nordihydroguaiaretic Acid	Antioxidant, anti-carcinogenic	Arteaga et al. 2009	
Ginsenoside Rg5	Agent for the treatment of Alzheimer's disease	Chu et al. 2014	
Boesenbergin A	Anti-inflammatory, cytotoxic and antioxidant activities	Isaa et al. 2013	
Quinazoline acetic acid	Anticonvulsant, antibacterial, antidiabetic	Pandeya et al. 1999	
Tegafur	Anticancer agent	Ishikawa, T 2008	
Nepodin	Anti-diabetic	Ha et al. 2014	
Simvastatin	Lipid lowering activity	Todd et al. 1990	
Procarbazine	Anticancer activity, treatment of Hodgkin's lymphoma	Ogawa et al. 2003	

1