## **RESEARCH ARTICLE**

# Screening of antimicrobial Actinomycetes from saline belt of Vidarbha Region

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#### ABSTRACT Manuscript details: Received: 22 August, 2014 Total 147 Actinomycetes were isolated from saline belt of Purna river Revised : 19 November, 2014 basin which appears in Akola, Amravati and Buldhana district of Vidarbha Revised received: 24 November, 2014 region. 147 actinomycetes isolates were recovered during primary Accepted: 28 November, 2014 screening and out of that 87 isolates (59.18 %) showed an antibacterial Published : 30 December, 2014 activity against two test bacteria such as Staphylococcus aureus and Escherichia coli by agar overlay method and 19 isolates were recorded antibacterial against both these test bacteria. These 19 isolates were **Editor: Dr. Arvind Chavhan** subjected to secondary screening and found antimicrobial against Staphylococcus aureus (MTCC 7443), Bacillus subtilis (MTCC 441), Escherichia coli (MTCC 443), Pseudomonas aeruginosa (MTCC 424), Aspergillus niger (MTCC 281) and Candida albicans (MTCC 3017) by agar well diffusion method. Nearly 78.94% isolates were active against Citation this article as: Staphylococcus aureus followed by 68.42% against Bacillus subtilis, Deshmukh AA and Vidhale NN (2014) Screening of antimicrobial Actinomy-52.63% against Escherichia coli, 47.36% against Candida albicans, 42.10% cetes from saline belt of vidarbha against Pseudomonas aeruginosa and 26.31% against Aspergillus niger. region, Int. J. of Life Sciences, 2(4): 355-Similarly actinomycetes isolate N8 showed activity against all the test 358. microorganisms.

Keywords: Actinomycetes, Saline belt, Vidarbha region, Antimicrobial.

#### **INTRODUCTION**

**Copyright:** © 2014 | Author(s), This is an open access article under the terms of the Creative Commons Attribution-Non-Commercial - No Derivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is noncommercial and no modifications or adaptations are made. The emergence as well as spread of multidrug resistance in microorganism is proving to be a great threat for global public health (Rajan *et al.*, 2010). The spread of resistant strains are linked to antibiotic use as well as to the migration of people, who disperse resistant strains among people in remote communities where the use of antibiotics is very limited (Allen *et al.*, 2010). Also, improper use of antibiotic was playing a vital role for drug resistance in pathogenic microbes.

To face such kind of situations there is an interest to improve or discover novel class of antibiotics, which provide different mechanisms of action worldwide (Parungao *et al.*, 2007). For microorganisms and their antimicrobial products soil work as a natural reservoir (Dancer, 2004). Some organisms such as bacteria, fungi, plants, actinomycetes

and so forth are responsible for creating secondary metabolites (Berdy, 2005). The actinomycetes are important in the field of pharmaceutical industries as well as in agriculture. Antibiotics are the best known products of actinomycete. For their virtual success against pathogenic microorganisms antibiotics can be truly referred as the 'wonder drugs' (Demain, 1999). This remarkable group of compounds forms a heterogeneous assemblage of biologically active molecules with different modes of action and structures and they are effectively used in the treatments for bacterial infections. Actinomycetes were predominating in black saline soils than other type like alluvial, lateric and coastal saline (Konde, 1978). Actinomycetes have more ability to bear not only at high salt concentration but also at high pH than bacteria and fungi. In uncultivated saline soil high population of actinomycetes was observed whatever may be the degree of salinity of soil (Zaharan et al., 1992). In salt affected soil, the population of actinomycetes is higher at pH 7.5 to 8.0 than other pH range (Supanekar and Patil, 1995). Hence the present study was undertaken to isolate actinomycetes from saline belt of Vidarbha region and assess their antimicrobial potential.

# MATERIALS AND METHODS

**Collection of soil samples:** 54 soil samples were collected from 18 villages from three district of Vidarbha region, Amravati, Akola and Buldhana at different depth (10-15 cms) in sterile polythene bags with the help sterile spatula and were transported to laboratory for further processing.

**Isolation of Actinomycetes from saline soil:** The collected soil samples were air dried for 24-48 hours, crushed and sieved. Then soil samples were pretreated with 1% CaCO<sub>3</sub> (w/v) under humid condition to increase the number of actinomycetes propagules in the samples (Tsao *et al.*, 1993).

Actinomycetes were isolated by serial dilution and spread plate method from collected saline soil samples on selective agar medium such as Actinomycetes isolation agar (M490, Hi-media Lab. Pvt. Ltd Mumbai, India) supplemented with 5 gm glycerol/l and antifungal antibiotic Nystatin 50  $\mu$ g/ml to avoid fungal contamination (Gurung *et al.*, 2009). The isolates showed dry, tough and leathery colonies on the isolation media were selected and purified by streak plate method on Actinomycetes isolation agar.

# Screening of antibiotic producing actinomycetes:

The screening method consists of two steps, Primary screening and secondary screening. Total actinomycete isolates were first primarily screened with *Staphylococcus aureus* and *Escherichia coli* by using agar overlay technique (Singh *et al.*, 2006).

Isolates showing antibacterial activity against both bacteria were subjected to secondary screening. The spore suspension of actinomycetes isolates were prepared by scraping 7 day old slant culture of actinomycetes isolates in 5 ml sterile distilled water and this spore suspension was added into a 250 ml Erlenmeyer flask containing 50 ml of glucose soybean medium and incubated at 30°C on a rotary shaker at 220 rpm for 7 days. Then the cultures were collected and centrifuged at 4000 rpm for 20 minute and filtered through whatman's No. 1 filter paper and filtrate was used to test antimicrobial activity. Antimicrobial activity was assayed by using modified agar well diffusion method against Staphylococcus aureus (MTCC 7443), Bacillus subtilis (MTCC 441), Escherichia coli (MTCC 443), Pseudomonas aeruginosa (MTCC 424), Aspergillus niger (MTCC 281) and Candida albicans (MTCC 3017. Results were recorded in terms of zone of inhibition (mm) produced by actinomycete isolates against these microorganisms and the experiment was performed in triplicates for each microorganism tested.

# **RESULTS AND DISCUSSION**

In primary screening, out of 147 actinomycete isolates 87 isolates (59.18%) showed an activity against 2 test bacteria such as *Staphylococcus aureus* and *Escherichia coli* by agar overlay technique. Out of which 45 (51.72%) isolates active against *S. aureus* while 23 (26.43%) isolates active against *E. coli* and 19 (21.83%) were active against both (Fig. 1).

From results it is obvious that the activities against Gram positive bacteria were more frequent than against Gram negative bacteria. This frequency of activities against Gram positive bacteria is similar to previous results reported by Basilio *et al.*, (2003); Oskay *et al.*, (2004).

In secondary screening, only 19 highly active primary isolates were selected for determining their antimicrogram against 6 test microorganisms i.e. *Staphylococcus aureus* (MTCC 7443), *Bacillus subtilis* (MTCC 441), *Escherichia coli* (MTCC 443), *Pseudomonas aeruginosa* (MTCC 424), *Aspergillus niger* (MTCC 281) and *Candida albicans* (MTCC 3017) by agar well diffusion method. The results of secondary screening of actinomycete isolates are depicted in Table 1.

Nearly 78.94% isolates were active against *Staphylococcus aureus* followed by 68.42% against *Bacillus subtilis*, 52.63% against *Escherichia coli*,

47.36% against *Candida albicans*, 42.10% against *Pseudomonas aeruginosa* and 26.31% isolates against *Aspergillus niger* (Fig 2). D6, D8 and S9 showed activity against only Gram positive bacteria and C1 showed activity against only Gram negative bacteria. Similarly, actinomycetes isolate N8 showed activity against all the test microorganisms. To support above findings following observations can be quoted.

Table	1: Secondary	screening of	actinomycete	isolates by	agar well	diffusion	method.
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	Isolate code	Mean Zone of inhibition (mm)								
Sr. No		Test Microorganisms								
		S. aureus	B. subtilis	E. coli	P. aeruginosa	A. niger	C. albicans			
1	H5	-	20	23	19	-	15			
2	H6	-	-	21	-	-	21			
3	HT2	21	23	-	-	-	17			
4	KR4	19	15	24	21	-	-			
5	N2	14	16	-	-	14	-			
6	N3	19	21	24	23	-	-			
7	N4	16	19	-	-	-	19			
8	N5	19	21	-	-	-	17			
9	N8	30	29	27	26	14	15			
10	D1	20	-	26	19	18	14			
11	D6	19	20	-	-	-	-			
12	D8	21	22	-	-	-	-			
13	Y3	20	15	21	-	-	-			
14	C1	-	-	26	20	-	-			
15	С3	-	-	21	19	20	-			
16	C4	16	19	-	-	-	20			
17	С6	25	24	20	26	-	13			
18	S6	22	-	-	-	14	-			
19	S9	26	-	-	-	-	-			







Oskay et al., (2004) isolated actinomycetes from dry alkaline conditions of farming soils. Chougule and Deshmukh AM (2006) also isolated actinomycetes from saline belt of Sangli district. Gurung *et al.*, (2009) studied antibacterial potential of seventy-nine actinomycetes from soil of Kalapatthar (5545 m), Mount Everest region and recorded 27 isolates (34.18%) antibacterial against at least one testbacteria among two Gram positive and nine Gram negative bacteria in primary screening bv perpendicular streak method and also 13 isolates (48.15 %) showed antibacterial activity in secondary screening. Hozzein et al., (2011) studied the antimicrobial activities of desert actinomycetes as potential producers of active metabolites. Out of the 75 actinomycetes strains isolated from the Egyptian desert habitats, 32 (42.67 %) showed activity against the used test organisms.

#### CONCLUSION

From the present study it can be concluded that Saline belt of Vidarbha region shows great diversity regarding antimicrobial actinomycetes which provide platform for researchers to discover newer efficient antibiotic, helpful in combating many human and plant diseases

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