IJISET - International Journal of Innovative Science, Engineering & Technology, Vol. 1 Issue 10, December 2014.
www.ijiset.com
ISSN 2348 – 7968

Occurrence Of Arbuscular Mycorrhizae In Degraded Crop Fields Of Purna River Sub –basin

S.P. Khodke[1], P.W. Deotare[2] and R.C. Maggirwar[2]

[1] Dept. of Botany, VinayakVidnayanMahavidyalaya, Nandgaon (KH.),Dist.Amravati (M.S.) India

[2]Mycorrhizal Bio-technology Lab PG. Department of BotanyShriShivaji ScienceCollege, Amravati(M.S.)India

ABSTRACT

A survey has been conducted with the help of department of agriculture to know the salinity degraded crop fields and its mycorrhizal status of Purna river sub-basin of Amravati district. In all thirty-six different soil samples were collected and examined for AM fungal diversity. It has been found that the spore population ranged between 61 to 357 per 100 g of soil. The spore population was lower than salinity unaffected crop fields of neighboring areas. Though the spore density were less but explored maximum number of AMF species diversity from all the sampling units. In all sixty five species belonging to six different genera were recovered. The results showed that the degraded crop fields of Purna river sub-basin had rich AMF biodiversity and the dominanceof *Glomusfasciculatum*and*Glomusheterosporum* throughout the study region.

(*Keywords* :*AMF, biodiversity, Degraded soils*.)

1. INTRODUCTION

Purna river sub-basin soils of Vidharbha region include 4691 sq.km. affected area which have unique salinity and sodicity problem. Soil salinity is a state in which soil contains enough salts in the plant root zone to hinder plant growth. The major problems of Purna river sub-basin soils are poor hydraulic conductivity and poor drainage. Water moves up by capillary action to the soil surface bringing dissolved with it. These soils generally contain a high concentration of soluble salts such as calcium, sodium, magnesium, sulphates and chlorides. An excess of soluble salts in the soil leads to osmotic stress, which results in specific ion toxicity and ionic imbalances (Munns, 2002). AM fungi has been known to reduce the impact of environmental stresses such as drought (Sylvia and Williams, 1992) and salinity (Ruiz-Lozano et al., 1996). These fungal associations often results in a great yield of crop even under saline conditions (Poss*et al.*,1985).

Such soils can be managed by implementing mycorrhizal technology (Asghari, 2004) where arbuscularmycorrhizalfungi (AMF) could play a key role in sustainable conservation. These fungi are beneficial plant symbiontthat mutalistic relationship with roots of most crop plants.Mycorrhizal association benefits the plant by improving water and nutrient uptake, helps in development of roots, binds soil aggregates, control soil born pathogens and detoxify soil contaminated with toxic metals (Sheela and Sundaram , 2003).

The studies have been concentrated on the salinity affected region from the Amravati district to evaluate the status of AM fungal distribution and dominance.

2. MATERIALS AND METHODS

Talukas namelyAnjangoan, Achalpur, Chandurbazar, Daryapur and Bhatkuli belonging to Amravati district predominantly fall into alluvial tract. Out of which, the studies were concentrated mainly on Anjangoan, Bhatkuli, Chandur Bazar and Daryapurtalukas.(Figure No.1) Purna river sub-basin is an east – west elongated basin with latitude70^{0} 45’ to 21^{0}15’ and longitude 75 °15 to 77 °45’ with length about 100-150 KM. The area is characterized by mean maximum temperature being46 °C and minimum 8^{0}C.

A survey has been conducted with the help of Department of Agriculture (M.S) in the Amravati district and thirty- six different sites were identified as degraded crop fields of Purna river sub-basin. Soil samples were collected from the depth of 20cm in the month of May 2004 and preserved at 4° C. Soil physico-chemical analysis was done by standard methods (Jackson, 1967;Piper, 1964; Richards, 1954; Subbaih and Asija, 1956; Olsen *etal*., 1954). AMF spores were isolated by wet-sieving and decanting technique (Gerdemann and Nicolson, 1963) and mounted in polyvinyl alcohol lactoglycerol (PVLG). Taxonomic identification of isolated viable spores were carried out with the help of manual of Schenck and Perez (1990). Taxonomic keys of Morton and Benny (1990) and Mehrotra and Baijal (1994).

3.RESULTS AND DISCUSSION

All the soil samples which were analyzed showed the pH in the range of 7.50 to 9.02 and it’s electrical conductivity 0.13 to 1.27 dsm^{-1} (Table no.1) .The result revealed that the soil of degraded crop field are moderately to highly saline and sodic in nature . The clayey type of soil had moderately available nitrogen 129.3 to 376.22 kg/ha; low to moderate available phosphorus 10.80 to 64.8 kg/ha and high available potassium 215 to 860 kg/ha(Table no.1) .

AMF diversity with their respective species has depicted in table number 2. The spore population ranged from 61 to 357 spores per 100g of soil.The site number S_{32}harboured highest spore count with 357spores per100g, followed by soil number S_{25} with 257 spores per 100g,S_{24}-238 per 100g of soil and S_9 with 233 per 100 g of soil. The data indicates all the soil samples had low to moderate AMF spores number which may be due to toxic effect of soil salinity, which directly affect the growth and development of AM fungi. Such soils were directly affecting the crop productivity of the region.

In the present investigation six AMF genera with sixty five different species were defined *Glomus*were found to the to be the most dominant genus (Figure No.2)followed *by Acaulospora* , *Scutellospora* , *Sclerocystis* , *Gigaspora*and*Entrophospora*. The *Entrophospora*was recorded with only single species. The genus *Glomus*wereexplored with forty six different species. Out of all *Glomusfasciulatum*and *Glomusheterosporum* were found to be the most dominant which were isolated from maximum sites of saline belt. This indicated species survival and sustainability of dominant AMF even under salt stress conditions.

The dominancy of the genera and species can be sequenced as *Glomus*46>*Acaulospora* 11 >*Scutellosapora*6 >*GigasporaandSclerocystis* with species each. As far as AM fungal species distribution site number S_4 recorded the highest number of 21 AMF species which belonged to three different genera. The diversity and distribution pattern of AM fungi in the present investigation could be due to variation in the effect of edaphic factors on individual AM fungi. Earlier reports has shown that changes in edaphic factors played a key role in controlling sporulation of VAM fungi. Thus AMF is most widespread and found in diverse habitat like phosphorus poor wet-land by Cornwell *et.al.*, 2001 and in undisturbed vegetation of coastal grassland by Struken*et.al.*,2005.

As far as fungal species distribution, it gives a good representative picture of the major AMF species inhabiting the salt affected soil. Even though the soils are not suitable for high crop production due to salinity andsoditity the picture of AMF diversity was very good. The uniform distribution of mycorrhiza throughout the study sites confirms the occurrence of arbuscularmycorrhiza under salt stress condition.

4.Conclusions

The results suggest that AMF may be of considerable importance for the successes of saline soil stabilization programme. The AMF species which were found to be most dominant and widely distributed throughout the area may be beneficial for the crop production in the near future due to its high survival in salinity degraded soils.

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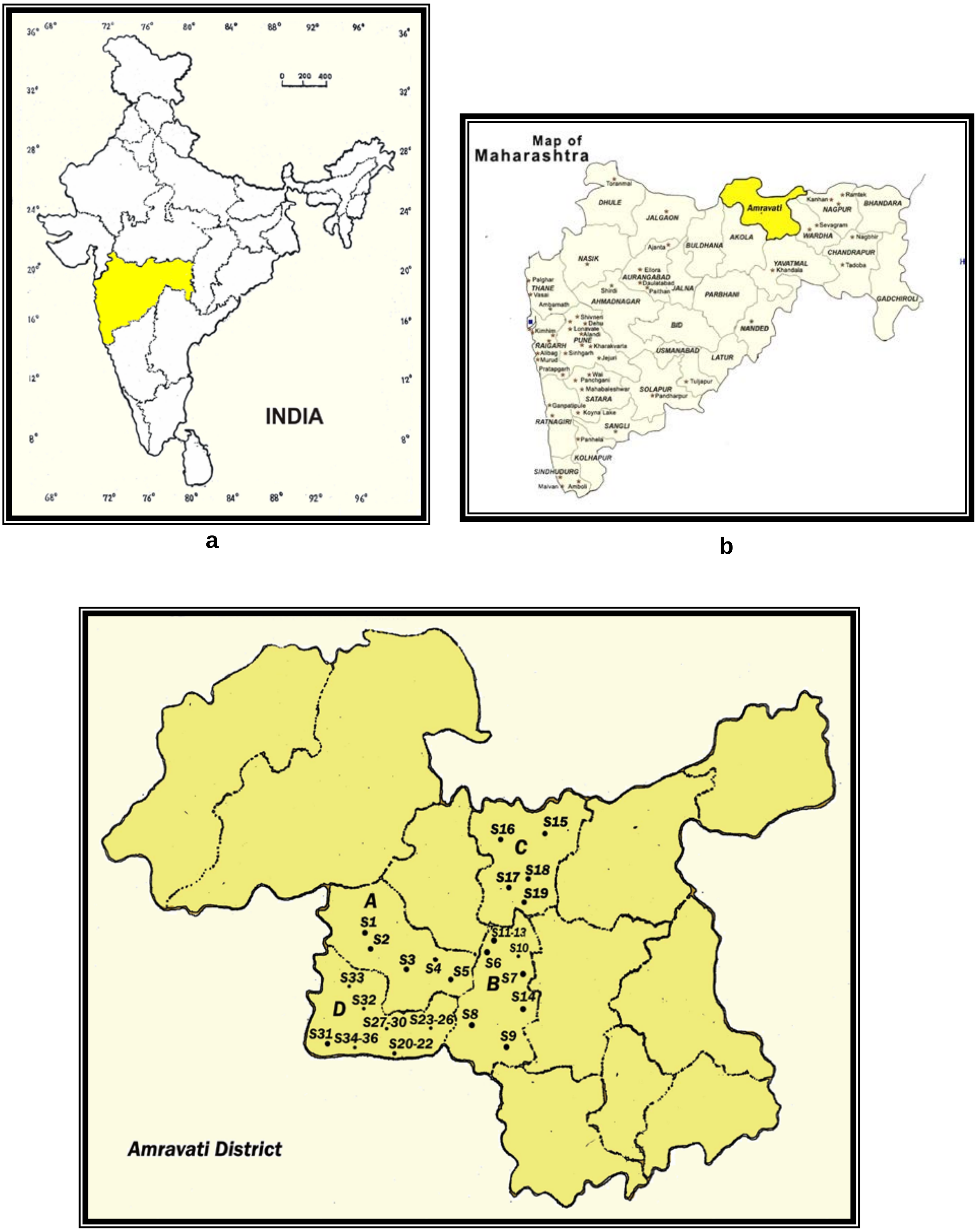


a

b

c

FIGURE NO.1 LOCATION MAP OF STUDY AREA

SiteCode	pH	Ece (dsm^{-1})	Available N kg/h	Available P kg/ha	Available K kg/ha	Organic carbon %
S_{1}	**9.03**	0.83	129.3	37.4	712	0.94
S_{2}	8.53	0.43	230.7	30.4	403	1.04
S_{3}	8.1	1.21	310.11	35.4	659	0.73
S_{4}	8.17	0.72	287.00	37.8	780	0.69
S_{5}	8.15	0.2	290.23	27.00	215	0.18
S_{6}	7.6	0.18	**376.32**	37.4	376	0.24
S_{7}	8.06	0.15	308.2	35.4	578	0.96
S_{8}	8.33	0.13	275.00	37.8	672	0.54
S_{9}	8.16	0.17	270.55	40.2	793	0.8
S_{10}	8.87	0.60	192.32	27.00	215	0.93
S_{11}	8.6	0.27	231.81	27.00	388	0.95
S_{12}	8.7	0.99	204.4	36.8	433	0.81
S_{13}	7.96	0.2	285.9	32.4	807	0.86
S_{14}	8.1	0.18	261.9	37.8	**847**	0.98
S_{15}	8.73	0.31	271.1	41.2	699	0.23
S_{16}	7.95	0.18	285.8	32.4	726	**1.07**
S_{17}	8.18	0.18	243.3	35.6	363	0.83
S_{18}	8.85	0.73	270.00	48.6	295	0.98
S_{19}	8.04	0.22	330.3	**64.8**	551	0.91
S_{20}	8.29	0.79	188.00	37.8	524	0.56
S_{21}	7.51	0.2	320.5	21.6	598	0.71
S_{22}	8.09	1.05	280.00	21.6	766	0.64
S_{23}	8.71	0.38	205.00	10.8	632	0.54
S_{24}	8.18	0.18	198.2	10.8	753	0.63
S_{25}	8.32	**1.27**	242.2	32.4	843	0.29
S_{26}	8.36	0.65	251.5	16.2	564	0.2
S_{27}	8.83	0.34	182.3	43.2	672	0.59
S_{28}	8.67	0.28	225.00	27.00	430	0.92
S_{29}	8.73	0.71	220.21	54.00	242	0.68
S_{30}	8.18	0.15	279.1	10.8	605	0.83
S_{31}	8.49	0.66	203.4	32.4	820	0.95
S_{32}	8.62	0.89	166.8	21.6	511	0.87
S_{33}	8.73	0.55	210.5	37.4	618	0.83
S_{34}	8.48	0.23	145.5	31.4	712	0.5
S_{35}	8.51	0.25	230.00	35.6	613	0.64
S_{36}	8.35	0.3	290.00	43.2	685	0.54

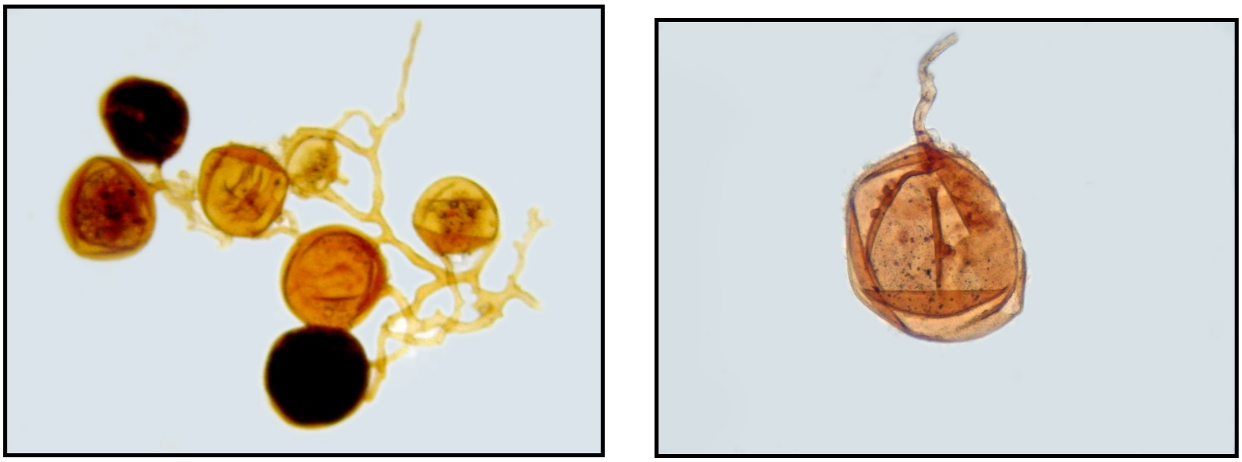
Table No. 1-Chemical Analysis of degraded soil samples

Table No. 2

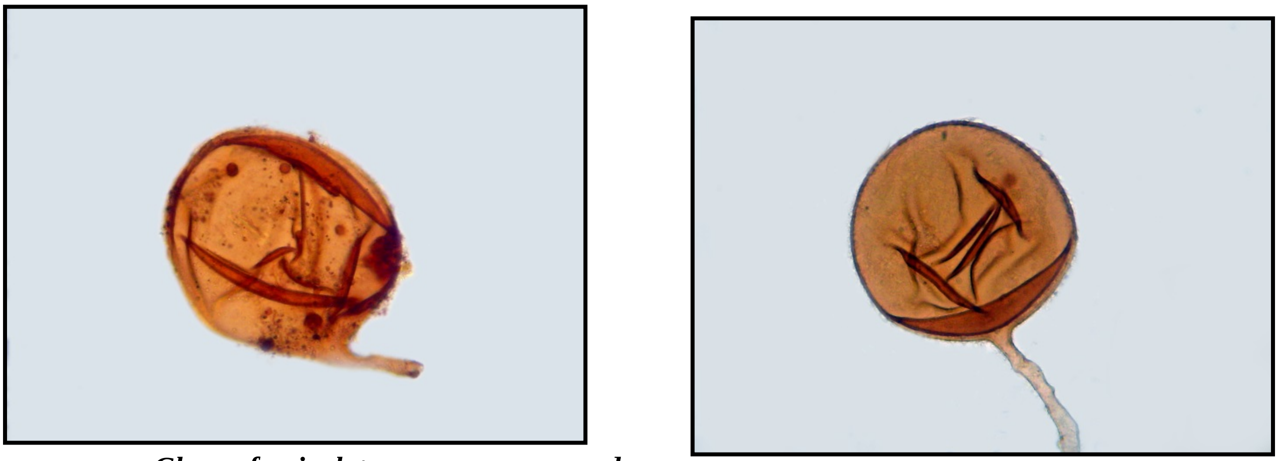
AMF Spore Density and Occurrence as per respective sites

Sr. No.	SITE	SPORE DENSITY/ 100gm	**AM FUNGAL SPECIES CODE**	**TOTAL AM FUNGI ISOLATED**
1	S1	183	LABD, LABS. LCRD, LFSC, LGSP, LGBF, LHTS, LLPT, LMLS, LMSS, ALVS, AMLL, LFMS, LFST	14
2	S2	140	LCST, LFSC, LFST, LGSP, LLPT, LMCL, LMSS	7
3	S3	180	LABD, LAGR, LDST, LFSC, LLPT, LRTC, LTRT	7
4	S4	186	LABD, LAGR, LETC, LFSC, LGSP, LGBF, LHTS, LLPT, LMCL, LMLS, LMST, LRTC, LPVN, LPSH, ANCS, CCLS, GRMS	17
5	S5	155	LABD, LABS, LDST, LDMI, LETC, LFSC, LFST, LGSP, LPST, LPSH	10
6	S6	82	LABD, LABS, LETC, LFSC, LGSP, LHTS, LINR, LLPT, LMCL, LMLS, LPST, EIFQ, ABRT	13
7	S7	114	LABD, LAGR, LCLR, LFSC, LFMS. LGSP, LMCL, LHOI, LRTC	9
8	S8	165	LDMR, LETC, LFSC, LGSP, LHTS, LLPT	6
9	S9	233	LABD, LAGR, LCLR, LDMR, LETC, LFSC, LFSC, LGBF, LHTS, LMSS, LMNS, LPSH	12
10	S10	118	LABD, LABS, LAGR, LDMR, LFSC, LINR, LLPT, LMCL, LMSS, LVSF	10
11	S11	202	LABD, LABS, LAGR, LBTR, LCLD, LCRD, LFSC, LFGS, LFMS, LFST, LGSP, LHOI, LHTS, LMCL, LMLS, LRTS	16
12	S12	134	LAGR, LFSC, LGSP, LHTS, LRTC, ANCS	6
13	S13	189	LABD, LAGR, LCST, LDMR, LFTC, LFSC, LFST, LGSP, LGBF, LHTS, LMCL, LPST, LRTC, EIFQ	14
14	S14	238	LABD, LAGR, LCLR, LCVL, LDST, LETC, LFSC, LLPT, LMSS, LMNH, SPCC	11
15	S15	156	LABD, LABS, LCLR, LFSC, LFST, LGSP, LGBF, LHTS, LHOI, LLPT, LMCL, LMSS, LPSH, LTRT	14
16	S16	116	LABD, LAGR, LCLR, LETC, LFSC, LFMS, LFST, LGSP, LHTS, LINR, LMCL, LPST, LPVN	13
17	S17	187	LABD, LAGR, LFSC, LGSP, LGBF, LMAG, LTRT, ALVS	8
18	S18	152	LABD, LCLR, LDMR, LETC, LFSC, LFST, LLPT, LMLS, LMSS, LMNH, LOCT, LRTC, LTNB, ADLC	14
19	S19	204	LABD, LABS, LAST, LCRD, LDST, LDMR,LETS, LFSC,LFMS, LFST, LGSP, LHTS, LLPT, LMLS, LMNH, LMCC,LPSH, ABRT, AELG	19
20	S20	61	LABD, LABS, LFST, LHTS, LMLS, LPST, LRTC	7

21	S21	155	LCST, LGSP, LHTS, LLPT, LMLS, LPST, LPSH, AELG,CARG	9
22	S22	139	LABD, LAGR, LCLR, LGMR, LFSC, LGSP, LINR, LLPT, LMLS, LPST, GRMS	11
23	S23	143	LABD, LCRD, LDST, LDMR, LETC, LFSC, LFMS, LGSP, LMCL, LMLS, LTNU	11
24	S24	75	LABD, LAGR, LFSC, LFMS, LFCS, LHTS, LLPT, LPSH, LMNS, LRTC, AFVT, SPCC, STWN	13
25	S25	257	LAGR, LAST, LCST, LCVL, LETC, LFSC, LGSP, LHTS, LINR, LLPT, LMCL, LMLS, LMGC, LMSS, LMNS, LRTC, ADLC, CARN.	18
26	S26	102	LABD, LFSC, LMCL	3
27	S27	170	LBTR, LCLD, LCLR, LDMR, LFSC, LFMS, LGSP, LINR, LLPT, LMLS, LPSH	11
28	S28	108	LCLR, LFSC, LGSP, LMSS	4
29	S29	127	LABD, LABS, LAGR, LBTR, LCLD, LCRD, LCLR, LCVL, LDPH, LFSC, LHOI, LINR, LLPT, LMCC, LMCL, LMST, LINR, LGRT, ADLC, SCCG, CRTC, GABD	21
30	S30	137	LABD, LABS, LAGR, LBTR, LDST, LETC, LFSC, LFLS, LGSP, LGBF, LHLN, LHOI, LINR, LLPT, LMCL, LMLS, LMLS, LMNS, LTRT	19
31	S31	224	LABD, LAGR, LBTR, LCLD, LFSC, LFST, LGSP, CFLG, LMTC, LRTC	10
32	S32	357	LABD, LABS, LAGR, LBTR, LCST, LDMR, LDPH, LETC, LFSC, LFST, LFMS, LGSP, LLPT, LMSS, AFVT	15
33	S33	141	LABD, LABS, LAGR, LCLR, LFSC, LFST, LGBF, LHTS, LLPT, LMLS, LMNS, LMSS, LPSH, LTRT	14
34	S34	129	LABD, LABS, LAGR, LAST, LCLL, LCLD, LDMR, LDPH, LETC, LFSC, LGSP, LHTS, LLPT, LMCL, LMLS, LMTC, LPSH, LRTC, ADLC, ARHM, CCLS	21
35	S35	196	LABD, LAGR, LCST, LDST, LETC, LFSC, LGSP, LMCL, LMCC, LPSH, LPST	11
36	S36	140	LABD, LAGR, LAST, LETC, LFSC, LFST, LGSP, LLPT, LMCL, LPST, AMLL	11

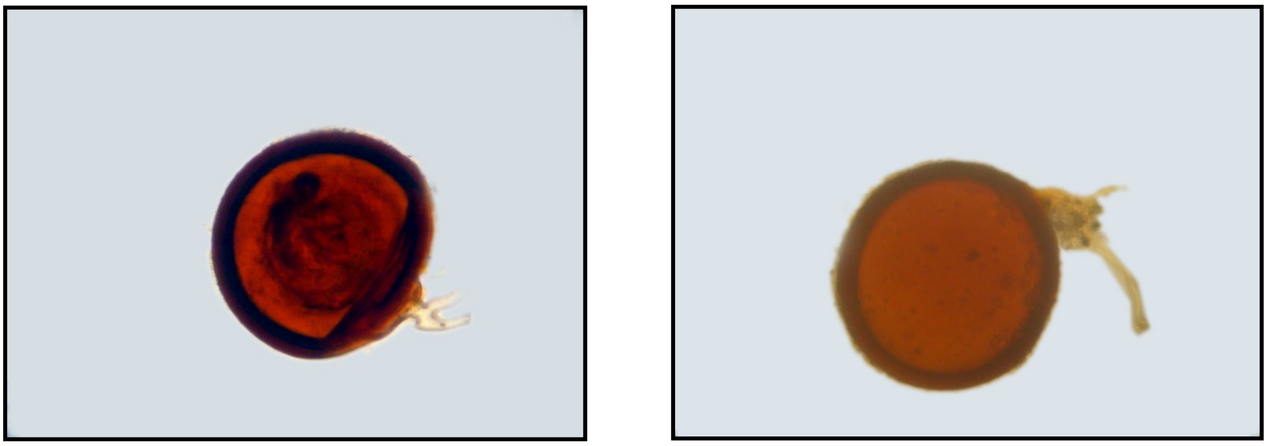


a .Sporocorp of Glomusfasciculatum *b. Glomusfasciculatum*



c. Glomusfasciculatum *d.*

Glomusfasciculatum



e.Glomusheterosporum *f.Glomusheterosporum*

Figure no.2- DominantAMFspecies

FIRST AUTHOR-

1. Name (in Block Letters) : SUCHITA PRAVIN KHODKE

2. Department : BOTANY

4. Current Designation : ASSISTANT PROFESSOR

6. Address for correspondence (with Pin code)- KHODKE PLOT GADGE NAGAR, AMRAVATI-444603

EXAM.	NAME OF THE UNIVERSITY/BOARD	YEAR OF PASSING	DIVISION
B.SC.	Sant Gadge baba Amravati university ,Amravati	1992	II
M.SC. (Botany)	Sant Gadge baba Amravati university ,Amravati	1994	I
Ph.D	Sant Gadge baba Amravati university ,Amravati	2009	-

Number of paper published- 12

Area of Research- MYCORRHIZAL BIOTECHNOLOGY

Second Author

Name:- Dr.Prakash W.Deotare

Department:- Botany

Current Designation:- Professor and Head

(M.Sc.Ph.D.P.C.C.R.)

Number of papers published-15

Area of Research:- Mycorrhizal Biotechnology

Third Author

Name:- Dr.Rekha C.Maggirwar

Department:- Botany

Current Designation:- Assistant Professor(Stage II)

Academic Qualification

Sr.No.	Exam Passed	University	Subjects	Year of passing	Percentage
1.	B.Sc.	Pune	Phy,Chem&Bio.	1987	66%
2.	M.Sc.	Amaravati	Botany	1990	64%
3.	M.Phil	Amaravati	Botany	1994	68%
4.	B.Ed.	Amaravati	Bio&Chem	1994	68%
5.	SET	Pune	Life Science	2003	Pass
6.	Ph.D.	Amaravati	Botany	2005	-Awarded-

Number of papers published-19

Area of Research:- Mycorrhizal Biotechnology