

Spore community structure and composition of arbuscular mycorrhizal fungi in a Mexican tropical rain forest: effect of land use and disturbance level



Sánchez-Gallen, I.*; J. Álvarez-Sánchez*, L. Varela, D. Trejo, I. Barois, E. Amora-Lazcano, P. Guadarrama, L. Lara and R. Zulueta

Universidad Nacional Autónoma de México, Hongos y Derivados, S.A., Universidad Veracruzana, Instituto de Ecología, A.C., Instituto Politécnico Nacional
 irene.sgallen@ciencias.unam.mx; * javier.alvarez@ciencias.unam.mx

INTRODUCTION

Humid tropical ecosystems undergo severe habitat alteration due to land use changes from tropical rain forests to cattle ranch and agricultural lands. Microenvironmental conditions, such as air and soil temperature, soil compactness, organic matter, and pH, are altered. Several studies have researched land use changes impacts on aboveground community component and as, an immediate consequence, plant diversity losses occur; nevertheless belowground communities behavior is not well understood.

Belowground communities are composed by a great number of bacteria, soil fauna and fungi. Arbuscular mycorrhizal (AM) fungi are soil organisms that form a mutualistic association with most plants. AM fungi capture nutrients from soil and transfer them through their hyphae to their host plants, more efficiently than plant roots, in exchange they receive carbohydrates and a habitat where to live. Besides nutrient allocation, AM fungi are important because they improve plant tolerance to root pathogens and water stress. AM fungi give also advantages in terms of plant growth and competition. At the community and ecosystem level they play key roles in plant structure, diversity, and productivity. Furthermore, mycorrhizal hyphae contribute to soil aggregation and conservation. As a direct consequence of all these features, AM fungi are promising natural resources for promoting strategies of sustainable development.

Changes in land use often lead to low plant diversity, and as a result AM fungi diversity can decrease, be maintained or increase. But also, microenvironmental changes such as water stress affect AMF diversity and abundance when land use change occurs.

OBJECTIVE

The aim of this study was to analyze the patterns of spore abundance, species richness and diversity in relation to land use and habitat changes in a Mexican tropical rain forest, as well as their composition changes.

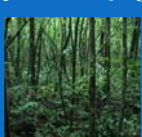
Study site

Los Tuxtlas region is the northern geographic edge of the moist Neotropical forest in North America and is characterized by its notable plant and animal diversity.



We considered, at least for this region, that forest cover is inversely related to ecosystem disturbance level, agricultural use intensity, and social poverty. According to these considerations we selected three field sites (habitats) at the southern part of Los Tuxtlas Biosphere Reserve, Adolfo López Mateos (High) (75 percent of tropical rain forest cover), San Fernando (Medium) (50 percent of mountain cloud forest cover) and Venustiano Carranza (Low) (25 percent of tropical rain forest cover).

Inside each habitat, we collected soil from four land uses (primary forest, agroforestry, pasture and maize crop). At first, a total of 96 soil samples were taken in December 2003 and January 2004, during the rainy and cold season, we took eight replicates per land use and habitat. We separated spores from 50 g of dry soil.



Primary forest



Agroforestry



Pasture for cattle ranching

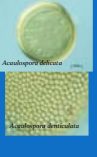


Maize crop

RESULTS

We found a total of 42 947 spores distributed in 59 morphologically distinctive AM fungi morphospecies

Habitat	Land use	Low				Medium				High				
		A	F	M	T	A	F	M	T	A	F	M	T	
Glomerulales														
Glomeraceae														
	<i>Glomus albidum</i> C. Walker & L.H. Rhodes	7	6	3	13	5	0	0	0	0	4	0	34	72
	<i>Glomus ambisporum</i> G.S. Sm. & N.C. Schenck	0	5	182	5	186	601	2224	4188	17	28	2	31	7438
	<i>Glomus constrictum</i> Trappe	0	0	0	12	10	4	0	0	3	0	0	0	29
	<i>Glomus fasciculatum</i> (Thaxt.) Gerd. & Trappe emend. C. Walker & Koske	2	274	506	0	94	17	503	22	12	64	6	1530	
	<i>Glomus geosporum</i> (T.H. Nicolson & Gerd.) C. Walker	11	2	23	17	300	8	21	332	7	0	2	150	873
	<i>Glomus macrocarpum</i> Tul. & C. Tul.	724	2909	3697	2136	1836	740	3820	2967	990	524	250	2029	22641
	<i>Glomus pusillum</i> Koske, Fritze, G. Walker & Delpé	49	4	440	68	10	0	5	0	3	0	7	0	385
	<i>Glomus rubiforme</i> (Gerd. & Trappe) R.T. Alsheldt & N.C. Schenck	1	0	0	0	0	0	2	0	0	0	0	0	5
	<i>Glomus viscosum</i> T.H. Nicolson	2	0	0	0	0	0	0	0	0	0	0	0	2
	<i>Glomus</i> sp. 1	0	4	8	3	18	41	21	8	0	0	6	0	108
	<i>Glomus</i> sp. 2	3	13	56	143	61	10	127	75	3	14	0	7	511
	<i>Glomus</i> sp. 3	4	6	0	0	0	0	0	3	0	0	0	0	13
	<i>Glomus</i> sp. 4	0	0	0	0	14	0	1650	0	0	0	0	0	1664
	<i>Glomus</i> sp. 5	2	0	0	0	5	0	88	15	0	0	0	0	110
	<i>Glomus</i> sp. 6	3	0	0	0	0	0	14	0	0	0	0	0	17
	<i>Glomus</i> sp. 7	9	9	155	56	17	13	106	70	41	2	3	0	482
	<i>Glomus</i> sp. 8	0	0	0	14	6	0	0	5	8	0	0	2	35
	<i>Glomus</i> sp. 9	0	24	4	33	0	2	18	0	0	0	0	0	80
	<i>Glomus</i> sp. 10	0	11	25	29	2	0	12	0	40	0	0	2	120
	<i>Glomus</i> sp. 11	0	0	0	0	152	0	3	0	0	0	0	0	155
	<i>Glomus</i> sp. 12	0	0	1881	0	0	0	45	5	0	0	0	0	1936
	<i>Glomus</i> sp. 13	0	0	0	0	29	0	34	0	0	0	0	0	63
	<i>Glomus</i> sp. 14	0	0	0	0	0	0	3	0	0	0	0	0	3
	<i>Glomus</i> sp. 15	14	0	0	8	206	0	0	12	0	5	3	248	
	<i>Glomus</i> sp. 16	42	0	0	0	0	0	0	0	0	0	0	0	42
Diversisporales														
Gigasporaceae														
	<i>Gigaspora ramuliporophora</i> Spain, Sieverd. & N.C. Schenck	18	10	9	2	161	6	33	137	21	11	0	20	427
Scutelloporaceae														
	<i>Scutellospora pellucida</i> (T.H. Nicolson & N.C. Schenck) C. Walker & F.E. Sanders	0	0	0	3	0	0	0	0	0	0	0	0	6
	<i>Scutellospora senana</i> C. Walker & Beeder	0	7	0	0	15	0	0	0	7	1	0	0	30
	<i>Scutellospora</i> sp. 1	0	0	0	2	0	0	0	0	2	0	0	0	3
	<i>Scutellospora</i> sp. 2	0	1	3	2	0	3	1	3	25	0	2	2	42
Acutisporaceae														
	<i>Acutispora delicata</i> C. Walker, C.M. Pfeiff. & Bloss	28	41	49	250	89	20	91	135	20	33	66	115	938
	<i>Acutispora denticulata</i> Sieverd. & S. Toro	0	0	0	0	1	0	0	5	0	0	0	0	6
	<i>Acutispora excavata</i> Hagleby & C. Walker	0	2	0	0	0	7	0	0	82	0	0	0	2
	<i>Acutispora foveolata</i> Trappe & Jans	0	25	28	24	6	17	51	31	15	0	6	2	205
	<i>Acutispora melita</i> Spain & N.C. Schenck	2	24	12	5	27	48	17	24	6	0	6	5	175
	<i>Acutispora morroviae</i> Spain & N.C. Schenck	9	8	6	15	2	35	10	3	18	2	0	0	109
	<i>Acutispora rhemii</i> Sieverd. & S. Toro	7	0	11	0	19	0	0	10	2	0	0	10	59
	<i>Acutispora scutellulata</i> Trappe	70	4	51	7	206	30	24	66	79	25	45	10	617
	<i>Acutispora spinosa</i> C. Walker & Trappe	11	2	24	12	221	12	67	23	16	21	15	14	437
	<i>Acutispora undulata</i> Sieverd.	2	0	0	0	138	4	50	22	4	2	0	0	222
	<i>Acutispora</i> sp. 1	0	1	0	0	0	6	0	2	0	0	4	2	14
	<i>Acutispora</i> sp. 2	9	0	0	0	0	0	9	0	0	0	0	0	18
	<i>Acutispora</i> sp. 3	2	0	3	0	23	2	0	12	0	0	0	3	45
	<i>Acutispora</i> sp. 4	0	0	0	0	0	0	9	0	2	3	0	0	13
	<i>Acutispora</i> sp. 5	0	0	0	2	1	9	0	3	9	0	0	2	40
	<i>Acutispora</i> sp. 6	0	0	3	0	0	11	31	20	3	3	5	7	87
	<i>Acutispora</i> sp. 7	0	0	0	0	0	0	11	2	0	0	0	0	13
	<i>Acutispora</i> sp. 8	5	0	1	7	0	0	59	65	2	6	0	0	145
	<i>Acutispora</i> sp. 9	15	2	0	0	0	0	0	0	2	0	0	0	18
	<i>Rhizoglyphus tenuissimus</i> Oehl & Sieverd.	0	0	0	0	0	0	17	137	9	2	0	0	3
Entrophosporaceae														
	<i>Entrophospora infrequens</i> (R. Hall) R.N. Ames & R.W. Schield	0	0	0	0	91	4	12	31	3	0	0	0	140
	<i>Entrophospora</i> sp. 1	4	0	0	3	11	2	1	0	8	0	0	3	33
Pactisporaceae														
	<i>Pactispora chimonobambuae</i> C. Walker, Vestberg & Schuessler	0	0	0	9	1	9	0	3	0	0	0	0	22
	<i>Pactispora franciscana</i> Oehl & Sieverd.	0	0	0	0	0	0	0	4	3	0	0	0	7
	<i>Pactispora</i> sp. 1	0	3	3	0	0	8	0	0	3	0	0	0	16
Paraglomeraceae														
	<i>Paraglomerula</i> sp. 1	0	0	1	0	3	0	0	3	0	0	0	0	7
Ambisporales														
Ambisporaceae														
	<i>Ambispora appendiculata</i> C. Walker	0	0	0	0	0	0	0	25	0	7	0	0	32



Mean estimated species richness, spores density, Shannon-Wiener diversity and evenness (\pm E.E.) for the three studied habitats and the four sampled land uses. Species richness data are standardized to the lowest number of spores found (4250 for habitat, and 2600 for land use).

Factor	n	Mean estimated species richness (\pm E.E.)	Mean number of spores (\pm E.E.)	Mean Shannon-Wiener diversity index (\pm E.E.)	Mean evenness value (\pm E.E.)
Habitat	High	28	51.55 \pm 2.45	151.46 \pm 38.45	1.12 \pm 0.097 ab
	Medium	23	54.83 \pm 1.59	610.87 \pm 172.72	1.43 \pm 0.099 b
	Low	29	44.82 \pm 1.73	470.65 \pm 90.46	0.97 \pm 0.098 a
Land use	Agroforestry	18	42.06 \pm 2.13	612.83 \pm 139.06	1.14 \pm 0.114
	Maize	15	73.91 \pm 3.97	175 \pm 37.58	1.44 \pm 0.105
	Pasture	27	42.92 \pm 1.88	496.87 \pm 148.81	1.10 \pm 0.100
	Forest	20	56.30 \pm 2.99	242.79 \pm 66.41	1.04 \pm 0.142

Levels of forest cover: High=75%, Medium=50%, Low=25%

DISCUSSION

Land use change did not explain the differences in species richness, number of spores, and diversity, whereas habitat factor explained changes in diversity and evenness. However, it is important to mention that maize crop showed the highest species richness, diversity and evenness. Environmental interhabitat variations were larger than those when land use change occurred, this is probably related to low impact agriculture, which is a common practice in the zone, and tends to maintain soil original characteristics. Also, resistance of the AMF community can be very high because they are able to continue even when disturbance clearly modified its environment.

ACKNOWLEDGEMENTS

We would like to thank Wendy Sangabriel and Diego Morales for spore separation. Also we thank Martin de los Santos and Dr. José Antonio García for field sample collection.