

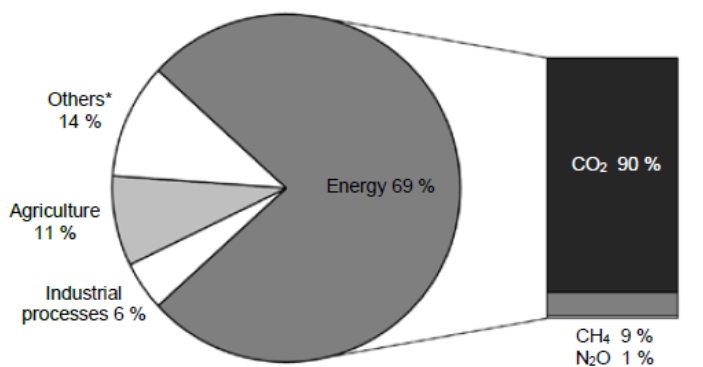
FE DE ERRATAS/ ERRATUM

Tesis Doctoral/ Doctoral Thesis

"SOIL BIOTA UNDER HIGH CO₂ EMISSIONS: FROM AN EXPERIMENTAL APPROACH TO NATURAL ENVIRONMENTS. Assessing environmental impacts of potential CO₂ leakages from a geological storage."

Las siguientes figuras presentaron errores de edición, se adjuntan las correctas/ Following figures had editing errors, revised figures are presented below:

Pag. 44. Figure 1.1 :



*Others include large-scale biomass burning, post-burn decay, peat decay, indirect N₂O emissions from non-agricultural emissions of NO_x and NH₃, waste and solvent use

Source: IEA estimates for CO₂ from fuel combustion and EGDAR 4.2 FT2010 estimates for all other sources.

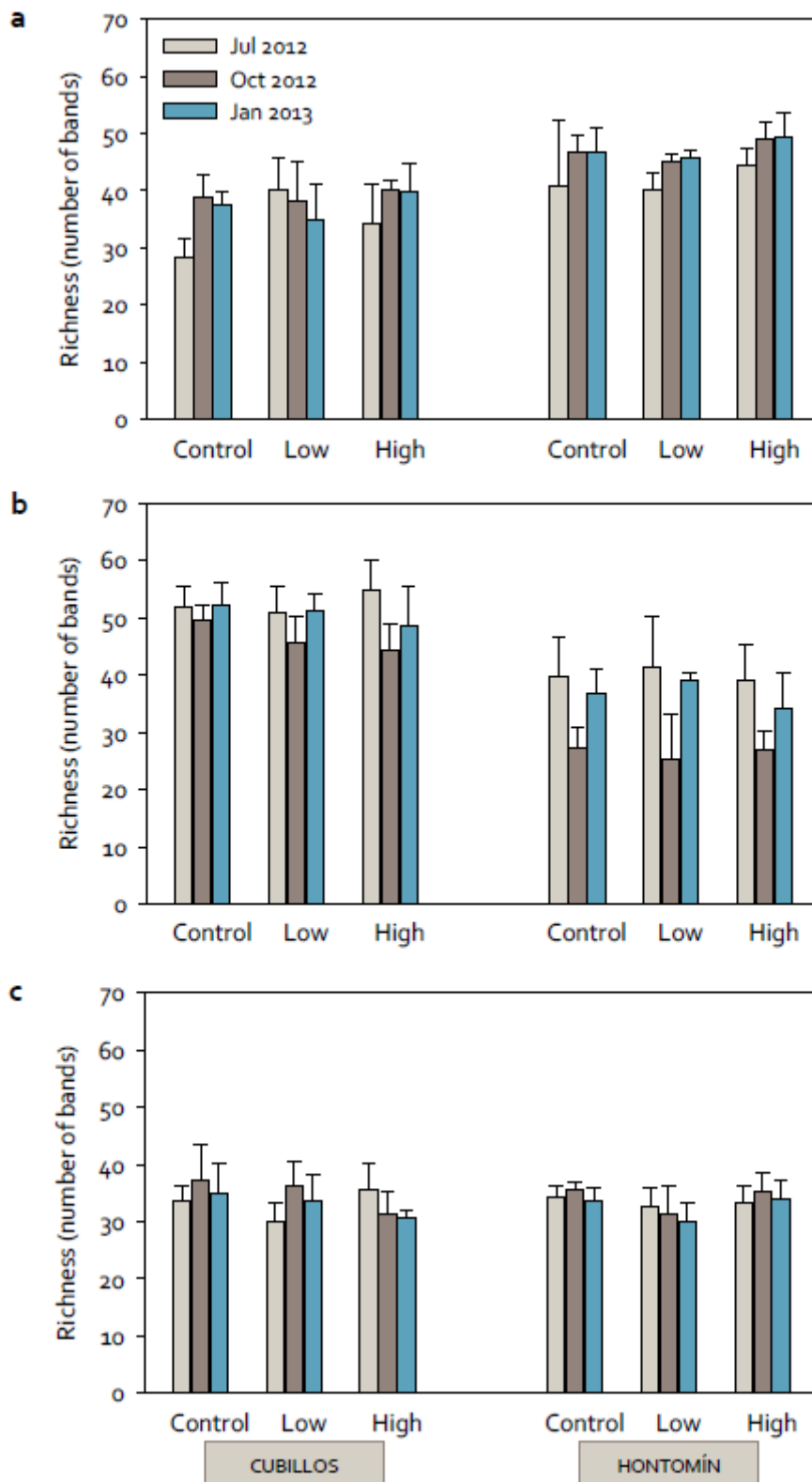
Pag. 56-58. Table 1.1 :

Location	Fluxes	Concentrations (depth)	Studied group	Methodology used	Main effects observed	References
Cheb Basin, Czech Republic	> 28,000 l h ⁻¹	> 99.83% (60 cm)	Microbiota	Pyrosequencing, acetogenic/methanogenic potential	Lowered diversity, acidotolerant, and methanogens and acetogens favoured and anaerobic	Beulig et al., 2015
Florina, Greece	40-10,000 g m ⁻² d ⁻¹	20-100% (average of 10, 20, 40 and 60 cm)	Collembola	Berlese-Tullgren funnels	Decreased richness, species, abundances increased when CO ₂ low fluxes	Russell et al., 2011
Hakanoa Springs, New Zealand		8-90% (20 cm)	Microbiota	qPCR, MPR	Trends to decrease in bacterial and archaeal numbers (65 cm deep), increased methanogenesis	Ziogou et al., 2013
Laacher See, Germany	177-550 g m ⁻² d ⁻¹	0.04-0.39% (atmospheric, 20 cm in height)	Nematoda	Whitehead tray method	Decrease in abundance and diversity	Yeates et al., 1999
		4-30% (15 cm)	Microbiota	qPCR, DGGE, MPR, MOR, SRR, CPR	Increased AOA (Thaumarchaeota) and SRR; decreased methanogenic archaea and methane oxidation	Frerichs et al., 2013
		20-90% (60 cm)	Microbiota	qPCR, MPR, MOR, SRR, CPR	Lower bacterial numbers, Archaea increased. Reduction in methane oxidation, favoured methanogenesis	Krüger et al., 2009; 2011

Latera Caldera, Italy	Up to 2,000-3,000 g m ⁻² d ⁻¹	Up to 93 % (20 cm)	Microbiota	qPCR, DGGE, MPR, MOR, SRR, CPR	Decreased Bacteria, Archaea and Eukarya numbers, enhanced methanogens and SRB	Oppermann et al., 2010
	10-2,000 g m ⁻² d ⁻¹	10-100 % (20 cm)	Microbiota	ATP biomass, bacterial counts, qPCR, MPR, MOR, SRR	Lowered microbial biomass, bacterial and archaeal abundances, increased SRR	Beaubien et al., 2008
Mammoth Mountain, USA	25 to >6,000 g m ⁻² d ⁻¹	< 1 to > 90 %	Microbiota	PLFA, ARISA, qPCR	Lowered microbial biomass, fungi highly affected, low abundance of bacteria and fungi gene copies	McFarland et al., 2013
Muszyna, Poland		> 25 %	Microbiota	Bacterial culture	<i>Clostridium kluyveri</i> , Thiobacillus and nitrification as possible bioindicators	Tarkowski, 2008; 2009
Sima de Calatrava, Spain	0.57 g m ⁻² d ⁻¹ , 547 kg m ⁻² d ⁻¹		Microbiota	Pyrosequencing	Relative abundance of Chloroflexi increased, Acidobacteria, Verrucomicrobia and Gemmatimonadetes decreased	Sáenz de Miera et al., 2014
	14.7-1,163 g m ⁻² d ⁻¹		Protozoa	Protozoan culture and counting	Shift to Colpodea dominated community, lowered diversity, decreased rapacious ciliates	Gabilondo and Bécáres, 2014
Stavešinci, Slovenia		0.2 %-13.8-85.5 % (15 cm)	Microbiota	T-RFLP, clone libraries	Changes to anaerobic; increased Methanomicrobia, lowered Thermoplasmata, Chloroflexi, Firmicutes	Šibanc et al., 2014
	228 - 400 μmol m ⁻² seg ⁻¹		AM fungi	T-RFLP, pyrosequencing, clone libraries	Dominance of specific taxa in hypoxic soil, community turnover (beta diversity)	Mačėk et al., 2011

Location	Fluxes	Concentrations (depth)	Studied group/exposure time	Methodology used	Main effects observed	References
ASGARD, Nottingham (UK)*	60 l h ⁻¹	14-5±4 % (30 cm)	Microbiota/10 weeks	Microbial biomass and activity (Biolog GN2 and respiration)	No significant changes in microbial biomass or carbon utilisation; trend towards reduced microbial respiration	Pierce and Sjögersten, 2009
	180 l h ⁻¹	Up to 75-87 % (20 cm)	Microbiota/19 weeks	Total bacterial numbers, activity (ATP)	Bacterial numbers decreased, ATP below detection limits at 87 %-CO ₂ plot	West et al., 2009
	180 l h ⁻¹	Up to 50 %	Microbiota/1 year and 4 months	Total bacterial numbers, qPCR, activity (ATP), CPR, MPR, MOR	Increased methanogenesis and decreased methane oxidation, decreasing bacterial and archaeal DNA copy numbers; seasonal-dependent variations	Smith et al., 2013
PISCO ₂ , León (Spain)*	20/40 l h ⁻¹		Protozoa	Protozoan culture and counting	Changes in ciliate community composition, decrease in Equitability and Margalef index, and increased Colpodid/Polyhymenophorean ratio	Gabilondo et al., 2015
	20/40 l h ⁻¹		Microbiota	Pyrosequencing	Partial shifts in bacterial community composition, but no consistent effects on the richness and diversity, in one soil type	Sáenz de Miera et al., under revision
ZERT, Montana (USA)*	700-6,500 g m ⁻² d ⁻¹	Up to 13-14 % (30 cm)	Microbiota/1 + 2-5 weeks	Pyrosequencing, qPCR (specific functional groups mediating N and C transformat.)	Seasonal-dependent variations; altered abundance (DNA) and activity (mRNA) of; decrease in bacterial richness, shifts in bacterial community composition	Morales and Holben, 2013; 2014
Gininderra, Australia*	144/218 kg d ⁻¹	80 % (100 cm)	Microbiota/2+2+2-5 months	Geochip	Favoured anaerobic and acid/metal tolerant species, increased Nitrospira and Firmicutes	Feitz et al., 2014

Pag. 77 Fig. 3.5:



Pag. 90. Figure 4.3a:

