

Centennial of the IUSS 2024 Florence, Italy 19th- 21th May, 2024

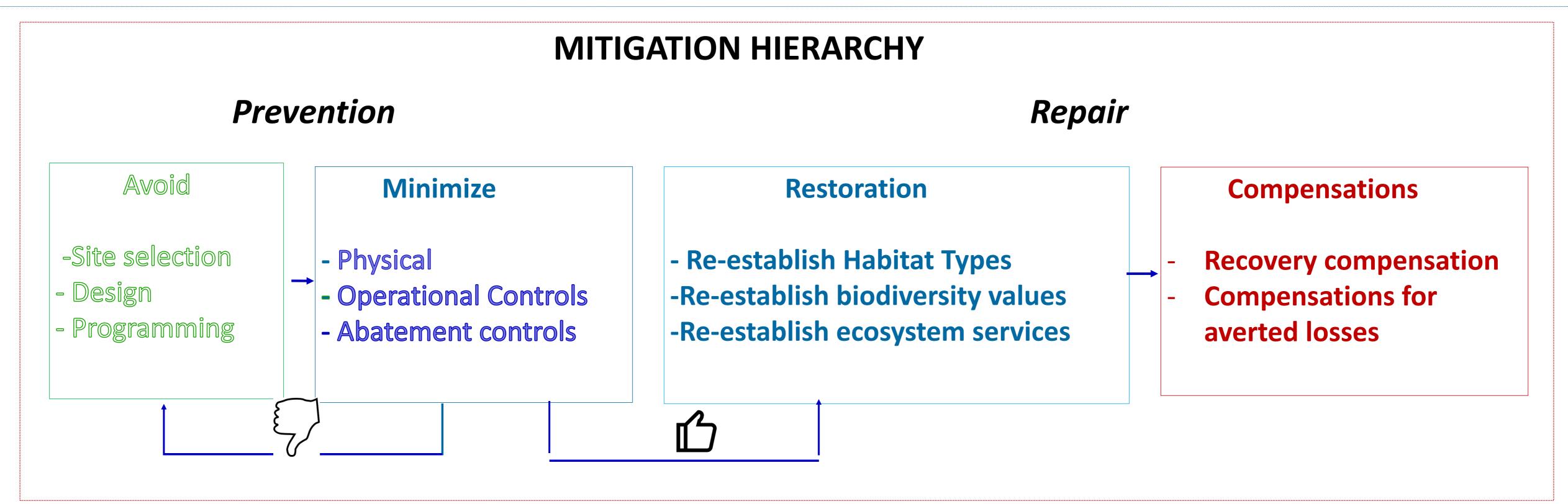
Mitigation of environmental damage by monitoring chemical-biological indices of disturbed soil





Laura Scrano, Lorenzo Montinaro and Sabino Aurelio Bufo University of Basilicata ITALY

The Soil Biodiversity platform has invited researchers, politicians, decision-makers, industries, and states to seriously consider soil biodiversity conservation, including all kinds of microorganisms: 'The maintenance of soil biodiversity is essential to both the environment and agricultural industries.' Moreover, since 2015, the 'Cross-Sector Biodiversity Initiative (CSBI)' has presented a platform for the development and sharing of 'good practices' to be implemented concerning the protection and restoration of 'biodiversity' in extractive activities. This platform is a collaborative tool to access the knowledge and collective experience of experts in the sector. It provides practical guidance, innovative approaches, and examples to support mitigation operationalizing. In addition, CSBI has developed some guides to limit, as far as possible, the negative impacts on the biodiversity of development projects and activate the processes of mitigating the damage and recovery of biodiversity.



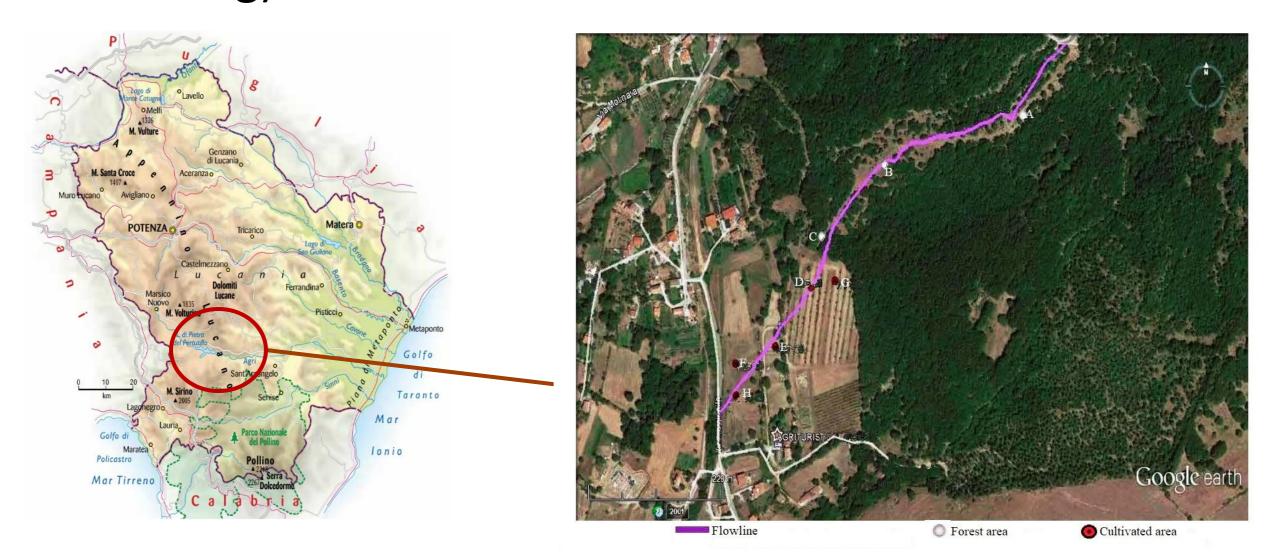
Graphic representation of the iterative process aimed primarily at avoiding and minimizing impacts expected on biodiversity and ecosystem services, and then manage the residual impacts through the restoration phases and ecological compensation (from Mitigation Hierarchy, www.csbi.org.uk)

In the last years there has been a change in biodiversity in the world as ecosystems try to adapt to climatic and anthropic changes. All biological indicators (floristic-vegetation, bacterial and fungal) show us the resilience of the soil and its entire community of macro and microscopic living beings

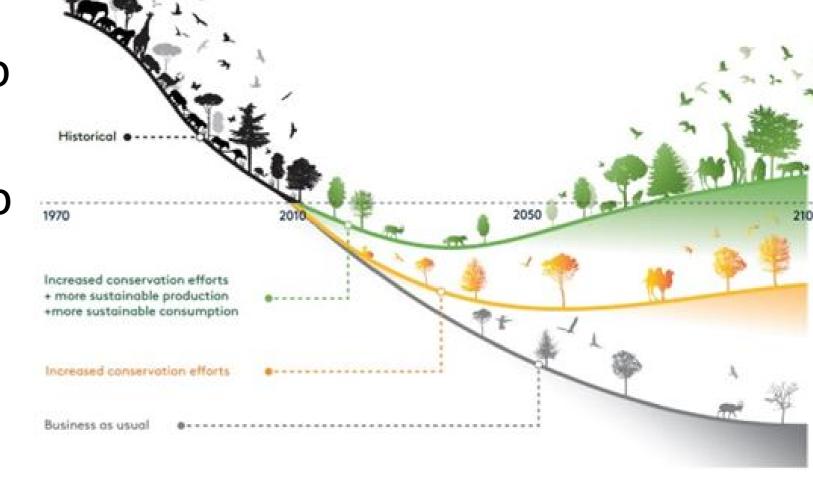
Our Research

Study Area. Basilicata region near an excavation 4 m wide, 4 m deep and approximately 1500 m long created for flowline transporting crude oil to the desulphurization plants. The area is located between arable land and tree crops.

Period of study: from June 2013 (pre-work monitoring) to July 2016 (postwork monitoring)



The chemical-biological indices after one year highlighted a change in the biological fertility of the soil. In particular, a differential abundance was observed for Methylobacteriaceae, which use methanol and other one-carbon compounds as energy sources. Differences where also found for Geobacteraceae, which oxidize monoaromatic hydrocarbons, such as toluene and benzene (Table 1). In three years of monitoring, the presence and rapid growth of particular bacterial groups in the studied area highlighted the general and natural bioremediation process that the soil and its entire community implement to restore optimal conditions. In **conclusion** to restore soil quality, it is necessary to encourage long-standing practices of land management aimed at increasing levels of soil biomass diversity. It is possible to evaluate the biological quality of soil by attributing a score calculated from biological parameters linked to the microbial biodiversity present in the soil.



Source: International Institute for Applied Systems Analysis (IIASA), 2020 (Credit: Adam Islaam)

Table 1. Taxa identified at taxonomic level of family in soil samples of forest area collected in the 3 years following the installation of the oil pipeline (2014, 2015, 2016). Taxa are reported as more (over-represented) or less (under-represented) abundant compared to the reference year (2013), and their abundance has been described as the decimal loga rithm of the fold change (log FC, i.e., the number of times that the abundance is significantly changed compared to the reference)

2014				2015				2016				
OTUs Under-represented	LogFC	OTUs Over-represented	LogFC	OTUs Under-represented	LogFC	OTUs Over-represented	LogFC	OTUs Under-represented	LogFC	OTUs Over-represented	LogFC	
Psychromonadaceae	-6.06327276	Hymenobacteraceae	7.888895127	Brevibacteriaceae	- 3.16186973	Cyclobacteriaceae	4.66440479	Psychromonadaceae	- 6.48599001	Microcoleaceae	6.45362388	
Neisseriaceae	-5.62965830	Gloeobacteraceae	7.888878258	Bacillaceae	-1.28151207	Cellvibrionaceae	4.55881690	Leuconostocaceae	-5.24088706	Pinaceae	4.10986600	
Propionibacteriaceae	-5.46734860	Alicyclobacillaceae	6.370363515			Glycomycetaceae	3.55458094	Hydrogenophilaceae	-3.40865156	Williamsiaceae	4.06749720	
Leptotrichiaceae	-5.36114366	Sphingobacteriaceae	6.314451742			Williamsiaceae	3.23929522	Tissierellaceae	-3.37275403	Marinifilaceae	3.90363172	
Sphagnaceae	-5.32059292	Oxalobacteraceae	6.150946723			Hyphomonadaceae	2.36438174	Erysipelotrichaceae	-3.00831050	Cellvibrionaceae	3.60524439	
Pasteurellaceae	-5.04593850	Erwiniaceae	5.652816453			Nocardiaceae	1.86393770	Propionibacteriaceae	-2.78856420	Hyphomonadaceae	3.06740116	
Ktedonobacteraceae	-4.92775787	Cellvibrionaceae	5.593468041			Cytophagaceae	1.82351153	Clostridiales Family XIII. Incertae Sedis	-2.46836969	Cryomorphaceae	2.89053543	
Prevotellaceae	-4.91290704	Cyclobacteriaceae	5.427717144					Alicyclobacillaceae	-2.30524104	Isosphaeraceae	2.69205937	
Akkermansiaceae	-4.87990999	Hafniaceae	4.930928318					Peptococcaceae	-1.89791808	Flammeovirgaceae	2.63898185	
Dietziaceae	-4.61547249	Flavobacteriaceae	4.924584859					Syntrophomona- daceae	-1.82125746	Nocardiaceae	2.47110072	
Peptoniphilaceae	-4.45037741	Pseudomonadaceae	4.783010581					Ruminococcaceae	-1.77561340	Mycobacteriaceae	2.41353519	
Staphylococcaceae	-4.20204296	Rhabdochlamydiaceae	4.680061978					Sporomusaceae	-1.60058263	Streptomycetaceae	2.32343025	
Catenulisporaceae	-4.07816386	Holosporaceae	4.509087642					Clostridiaceae	-1.53632553	Cytophagaceae	2.31584838	
Ferritrophicaceae	-3.91210126	Thermonemataceae	4.432242017					Thermodesulfobacte- riaceae	-1.50303662	Bdellovibrion- aceae	2.04844576	
Bacteroidaceae	-3.83778397	Peptostreptococcaceae	4.423008784					Thermoleophilaceae	-1.14555465	Rhizobiaceae	1.94187171	
Veillonellaceae	-3.83001210	Francisellaceae	4.216568515					Thermoanaerobacte- raceae	-0.99888133	Nannocystaceae	1.84166128	
Selenomonadaceae	-3.78102334	Micrococcaceae	4.049633374							Rhodanobacte- raceae	1.70150532	
Actinospicaceae	-3.75944153	Marinifilaceae	4.04475163							Sphingobacte- riaceae	1.66053291	
Lactobacillaceae	-3.73908507	Bernardetiaceae	3.869712263							Nocardioidaceae	1.16464077	
Corynebacteriaceae	-3.63505712	Flatidae	3.84154994							Acetobacteraceae	0.75039264	
Frankiaceae	-3.61926727	Rhizobiaceae	3.84072105									
Fusobacteriaceae	-3.61836305	Clostridiaceae	3.595571114									
Aerococcaceae	-3.60792038	Haliscomenobacte- raceae	3.474238951									
Nakamurellaceae	-3.40746280	Oscillatoriaceae	3.472564336									

Forest area											
2014		2015				2016					
OTUs Under-represented	LogFC	OTUs Over-represented	LogFC	OTUs Under-represented	LogFC	OTUs Over-represented	LogFC	OTUs Under-represented	LogFC	OTUs Over-represente	LogFC d
Porphyromonadaceae	-3.22918041	Clostridiales Family XII. Incertae Sedis	3.400473793								
Pseudonocardiaceae	-3.18042590	Oligoflexaceae	3.302744387								
Roseiflexaceae	-3.00834859	Deinococcaceae	3.300654812								
Thermaceae	-2.89337022	Halothiobacillaceae	3.228044845								
Methylobacteriaceae	-2.80724413	Bacteriovoracaceae	3.045339681								
Anaerolineaceae	-2.66960077	Bdellovibrionaceae	2.924723969								
Tissierellaceae	-2.62661255	Cytophagaceae	2.923583399								
Hydrogenophilaceae	-2.46663879	Lewinellaceae	2.910131074								
Micromonosporaceae	-2.43512398	Crocinitomicaceae	2.891005883								
Isosphaeraceae	-2.39201177	Enterobacteriaceae	2.861893096								
Atopobiaceae	-2.28180376	Caulobacteraceae	2.826834131								
Jiangellaceae	-2.17383769	Chitinophagaceae	2.670955823								
Anaeromyxobacteraceae	-2.16691247	Coleofasciculaceae	2.66427167								
Verrucomicrobia Subdi- vision 3	-2.15842037	Beutenbergiaceae	2.611973333								
Syntrophomonadaceae	-2.15170610	Sporolactobacillaceae	2.580366721								
Thermomonosporaceae	-2.15036281	Bacillaceae	2.550785896								
Alteromonadaceae	-2.07875561	Amoebophilaceae	2.537815722								
Actinomycetaceae	-2.07430734	Xanthomonadaceae	2.503417977								
Euzebyaceae	-2.05095497	Sutterellaceae	2.40189153								
Streptosporangiaceae	-1.94537245	Hyphomonadaceae	2.400816655								
Geobacteraceae	-1.93234036	Pectobacteriaceae	2.328801718								
Solibacteraceae	-1.92872557	Comamonadaceae	2.25932381								
Bradyrhizobiaceae	-1.92604737	Planococcaceae	2.177317534								
Thermoanaerobacterales Family III. Incertas Sedis	-1.75416278	Acholeplasmataceae	2.146014836								
Demequinaceae	-1.73685700	Flammeovirgaceae	2.094420124								
Nocardiopsaceae	-1.73315518	Mycoplasmataceae	2.092104113								
		•									
Forest area											
2014				2015				2016			
OTUs Under-represented	LogFC	OTUs Over-represented	LogFC	OTUs Under-represented	LogFC	OTUs Over-represented	LogFC	OTUs Under-represented	LogFC	OTUs Over-represented	LogFC
Microthrixaceae	-1.55348794	Morganellaceae	2.066591591							-	
Thermodesulfobacte- riaceae	-1.50559896	Shewanellaceae	2.049714384								
Sphaerobacteraceae	-1.50133850	Gallionellaceae	2.041974323								
Cellulomonadaceae	-1.29261153	Nocardioidaceae	1.931478609								
Thermoanaerobacte-	-1.25679848	Sphingomonadaceae	1.919595269								