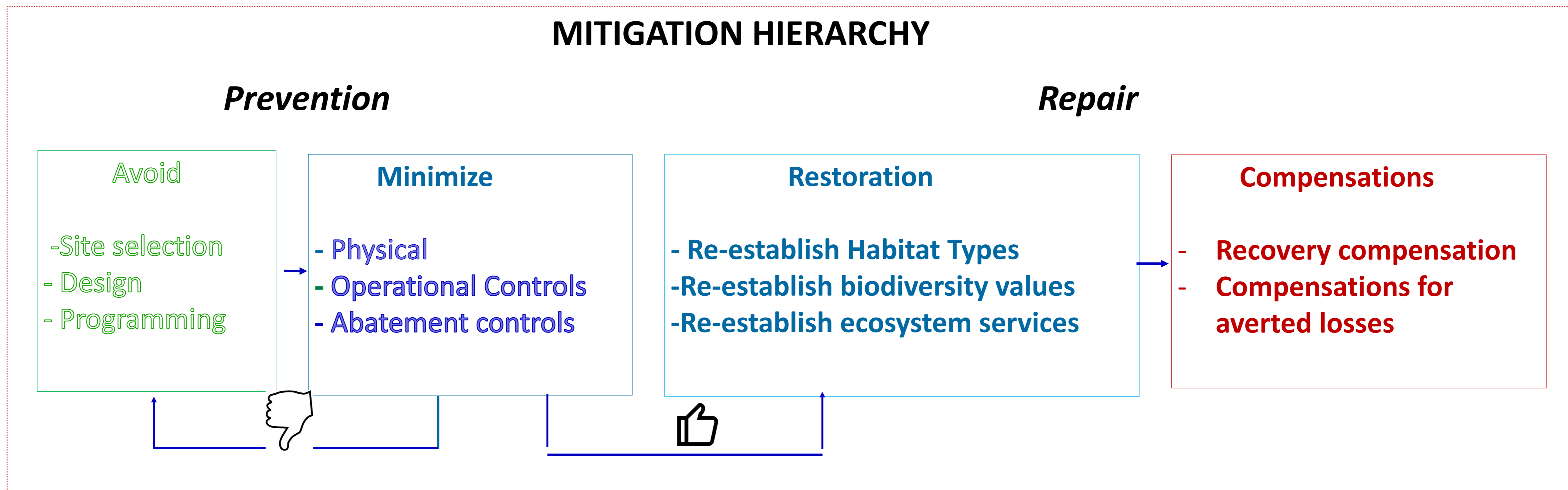


Mitigation of environmental damage by monitoring chemical-biological indices of disturbed soil

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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.



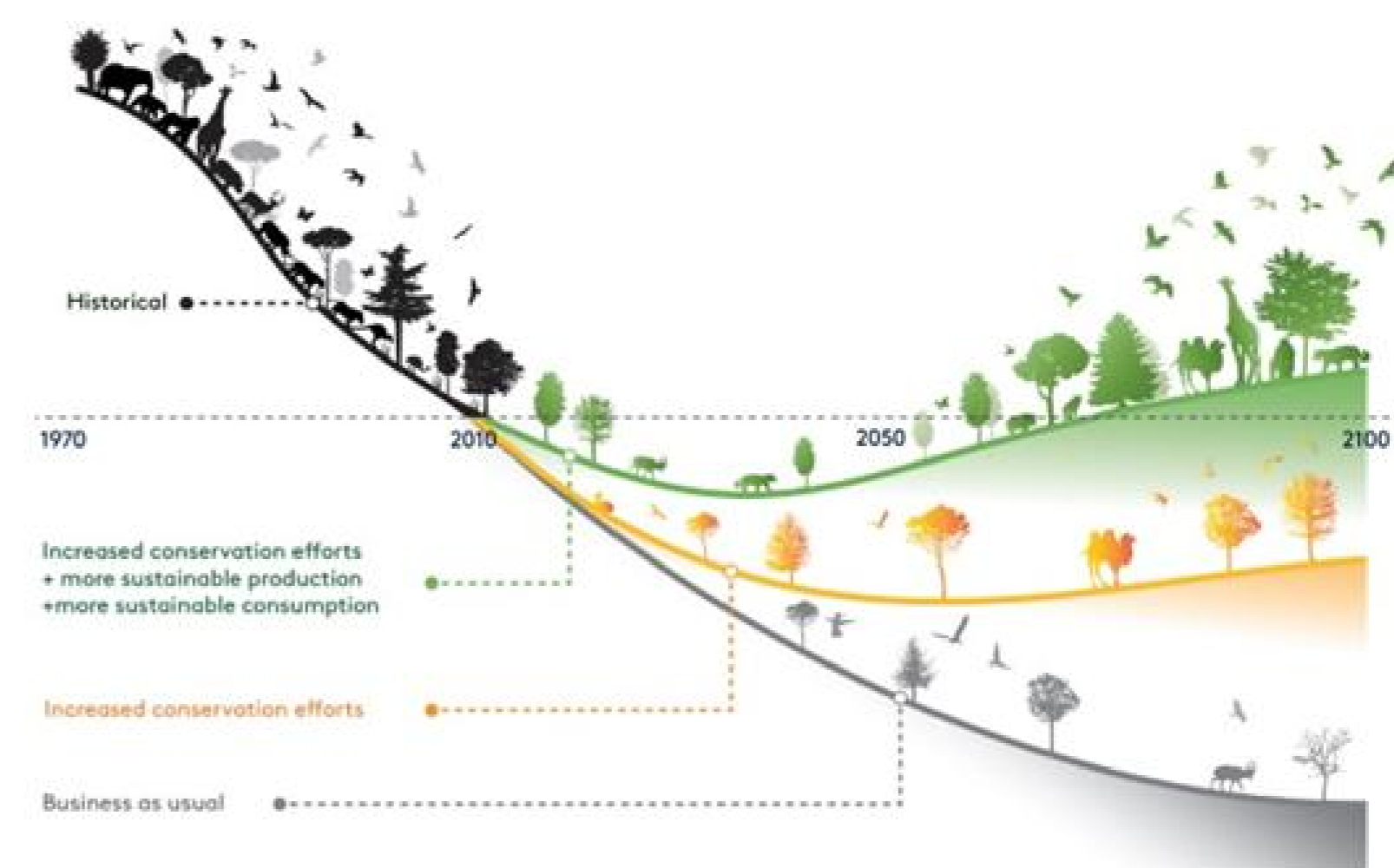
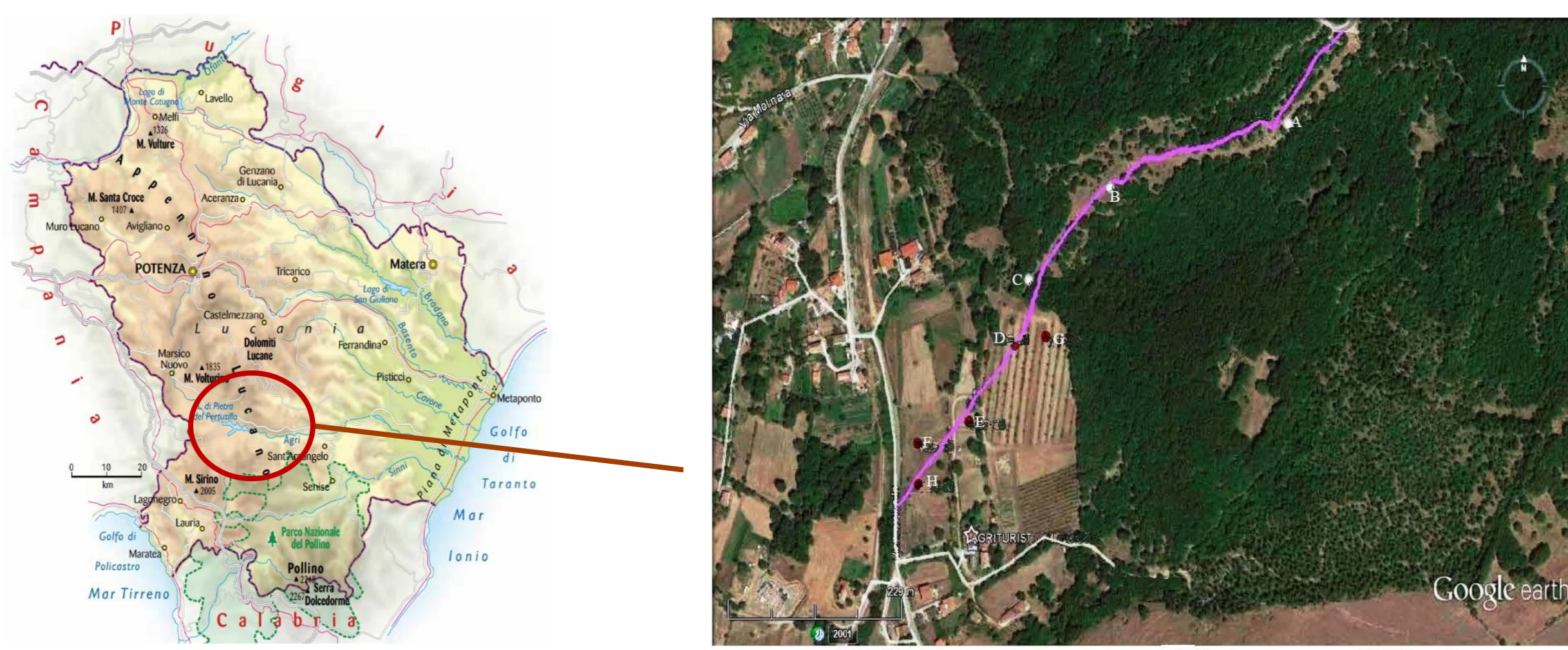
Graphic representation of the iterative process aimed primarily at avoiding and minimizing impacts expected on biodiversity and ecosystem services, and then manage the residual impacts through the restoration phases and ecological compensation (from Mitigation Hierarchy, www.csbi.org.uk)

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 (post-work monitoring)



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

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 log₁₀ 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	LogFC	OTUs	LogFC	OTUs	LogFC	OTUs	LogFC	OTUs	
Under-represented		Over-represented		Under-represented		Over-represented		Under-represented	
Proteobacteria	-4.0627276	Hydrothermabacteriaceae	7.88895127	Bacteroidetes	-3.1619073	Cyberobacteriaceae	4.6644929	Planctomycetaceae	-6.8279901
Nitrospirae	-5.6295830	Gliobacteriaceae	7.88895128	Bacillales	-1.28151207	Cyberobacteriaceae	4.55881660	Leucosporangiaceae	-5.24088706
Proteobacteria	-5.4673460	Alphaproteobacteria	6.37080515	Glycomycetaceae	3.2929252	Hydrothermabacteriaceae	-3.40861516	Williamsiaceae	4.06749720
Lepidobacteriaceae	-5.36114366	Sphingobacteriaceae	6.314451742	Williamsiaceae	3.2929252	Tinctoribacteriaceae	-3.37274403	Mariifaciaceae	3.90651172
Sphingaceae	-5.3209292	Ordiobacteriaceae	6.150948723	Hydrothermabacteriaceae	2.6438174	Fryxellaceae	-3.00810100	Cyberobacteriaceae	3.60824419
Planctomycetaceae	-5.0493980	Erviniaceae	5.62828453	Nocardiaceae	1.8659370	Proteobacteriaceae	-2.7858420	Hydrothermabacteriaceae	3.06780116
Kinobacteriaceae	-4.9277597	Cyberobacteriaceae	5.50340801	Cytophagaceae	1.82191155	Chloroflexi Family XIII_Incertae sedis	-2.8683699	Cytophagaceae	2.98955543
Planctomycetaceae	-4.9128074	Cyberobacteriaceae	5.42771744	Alphaproteobacteria	-2.30524104	Leptothraceae	2.6920997	Planctomycetaceae	2.63808185
Alkalinimicrobiales	-4.8799099	Hydrothermabacteriaceae	4.939820318	Planctomycetaceae	-1.89794108	Flammarovirgaaceae	2.63808185	Planctomycetaceae	2.47110072
Dinorthisaceae	-4.61547249	Flammarovirgaaceae	4.924584859	Syntrophomonadaceae	-1.82120746	Nocardiaceae	2.47110072	Nocardiaceae	2.47110072
Planctomycetaceae	-4.45037741	Planctomycetaceae	4.783000581	Ruminococcaceae	-1.7581340	Myxobacteriaceae	2.41355519	Myxobacteriaceae	2.41355519
Stylobacteriaceae	-4.2024206	Rhizobiales	4.680061978	Sporobolaceae	-1.6095261	Streptomyces	2.3234825	Streptomyces	2.3234825
Comamonadaceae	-4.07816366	Holoproteaceae	4.509067642	Clavidiaceae	-1.53632553	Cytophagaceae	2.31584838	Cytophagaceae	2.31584838
Ferriplasmaceae	-3.91210126	Thermotomaceae	4.43242017	Thermotomaceae	-1.50303662	Bacteroidetes	2.04844576	Bacteroidetes	2.04844576
Bacteroidetes	-3.82778397	Pyrenitiphilaceae	4.423008784	Rhizobiales	-1.14554665	Rhizobiales	1.9418171	Rhizobiales	1.9418171
Verrucomicrobiales	-3.83001210	Planctomycetaceae	4.216564515	Thermotomaceae	-0.99888133	Nannocystaceae	1.84164128	Nannocystaceae	1.84164128
Sclerothricales	-3.78102334	Micromonadaceae	4.049633374	Rhizobiales	-0.99888133	Rhizobiales	1.70150532	Rhizobiales	1.70150532
Actinobacteriales	-3.75944153	Mariifaciaceae	4.04475163	Actinobacteriales	-3.7908507	Brevardiacetaceae	3.869712263	Actinobacteriales	3.869712263
Cyberobacteriaceae	-3.48700712	Planctomycetaceae	3.841374994	Planctomycetaceae	-3.48700712	Planctomycetaceae	3.841374994	Planctomycetaceae	3.841374994
Planctomycetaceae	-3.46810277	Rhizobiales	3.841374994	Rhizobiales	-3.46810277	Rhizobiales	3.841374994	Rhizobiales	3.841374994
Planctomycetaceae	-3.46343635	Planctomycetaceae	3.841374994	Planctomycetaceae	-3.46343635	Planctomycetaceae	3.841374994	Planctomycetaceae	3.841374994
Actinobacteriales	-3.40720208	Halicomonadaceae	3.474238951	Nannocystaceae	-3.40720208	Nannocystaceae	3.474238951	Nannocystaceae	3.474238951
Nannocystaceae	-3.40746200	Oxidobacteriaceae	3.472264336	Nannocystaceae	-3.40746200	Nannocystaceae	3.472264336	Nannocystaceae	3.472264336

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 were 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.