Innovative silvicultural treatments to enhance soil biodiversity in artificial black pine stands - SELPIBIOLIFE

Stefano Mocali

Florence, 29 September 2016

LIFE13 BIO/IT/000282

EU Biodiversity Strategy to 2020

Soil biodiversity is analysed considering its main components (flora, fungi, bacteria, mesofauna, nematods and microarthropods), according with the EU 2020 Biodiversity Strategy (2011/2307(INI)).

In particular:

<u>TARGET 3</u> - Increase the contribution of agriculture and forestry to maintaining and enhancing biodiversity:

1. **Action 11 - Encourage forest holders to protect and enhance forest biodiversity**
2. **Action 12 - Integrate biodiversity measures in forest management plans**

United Nations Decade on Biodiversity

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The main purpose of the project is to evaluate the effects of a selective thinning on soil biodiversity in young black pine stands.

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http://www.selpibio.eu/

Silvicultural management of black pine stands

The black pine is the most representative species for reforestation in Italy.
The reason is related to its rapid growth rate and adaptative skills, also in strongly degraded soils.

In the 60'-70's black pine was "temporarily" used to restore many areas with the intent to protect the territory

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The traditional thinning

The traditional thinning is "*selective from below*" and provide to leave the highest quality well-spaced trees.

However, it maintains essentially the same canopy

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The selective thinning

The innovative thinning is conceptually based on the identification of the dominant plants and the removing of the plants around. This approach provides the following results:

1. Enhance the pine succession and increase the economic value of the product
2. Enhance the pine dendrometric stability
3. Reduce the canopy cover and enhances the rate of light, water and temperature at the soil level

The global effect is an increasing of the functionality of the ecosystem and of the soil biodiversity

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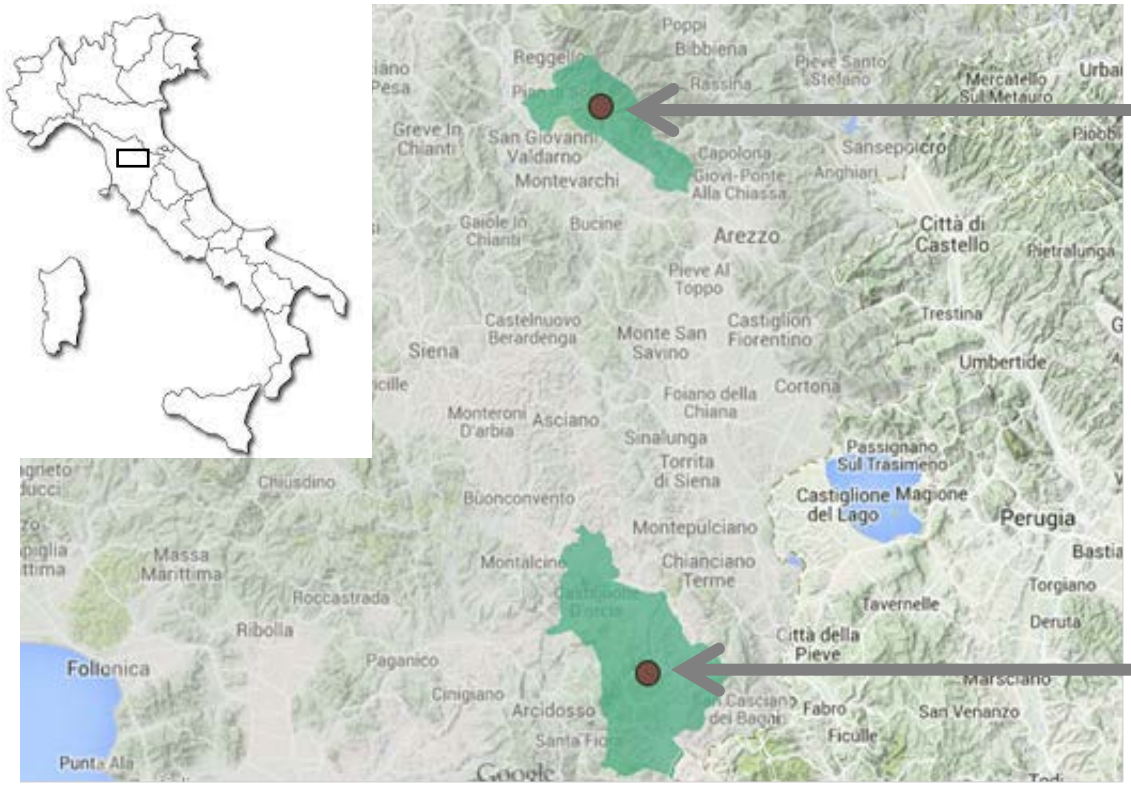
Before thinning

Traditional thinning

Selective thinning

Monitoring areas

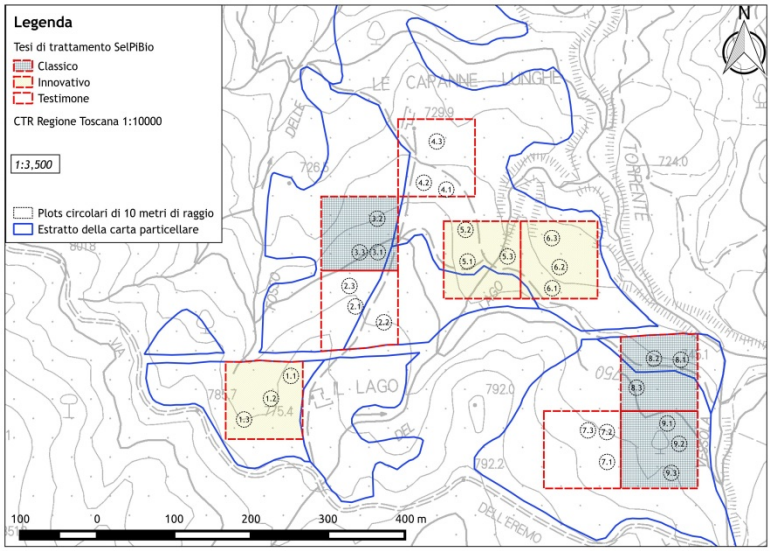


"Pratomagno-Valdarno"- «Pian della cucina» Comune di Loro Ciuffenna (AR) (PRATOMAGNO)

«Madonna delle Querce» - «Il Lago» Comune di Castiglione d'Orcia (SI) (AMIATA)

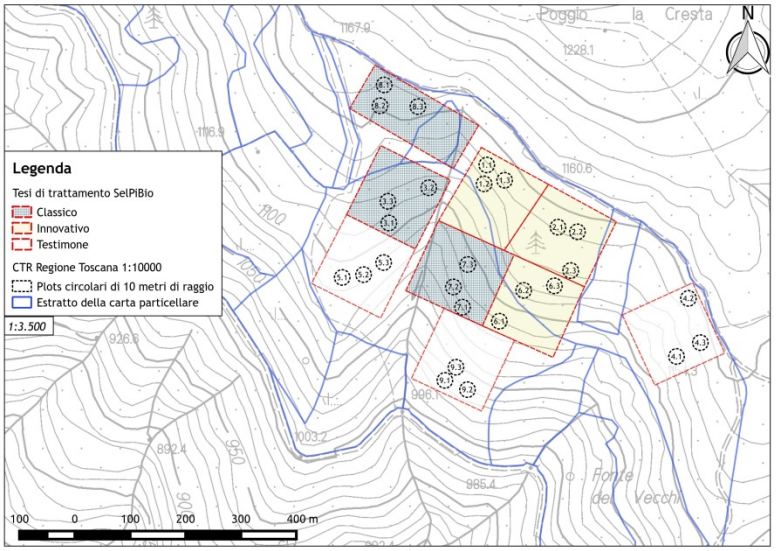
Brief description of the areas

Amiata



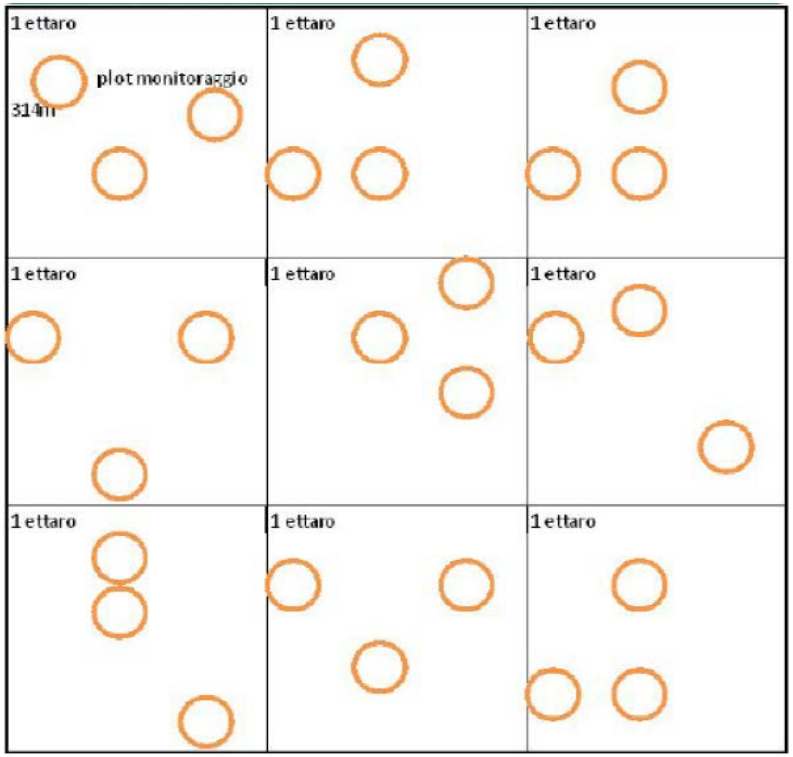
- Altitude: about 800 m a.s.l.
- Exposition: North-North-West
- Average slope: 3-6%.
- Vegetation: high
- pH : 6,9
- Total organic carbon (TOC): 1,73%

Pratomagno



- Altitude: about 1100 m a.s.l.
- Exposition: South- West
- Average slope: 20-25%
- Vegetation: low
- pH : 5,5
- *Total organic carbon* (TOC): 1,76%

Experimental scheme



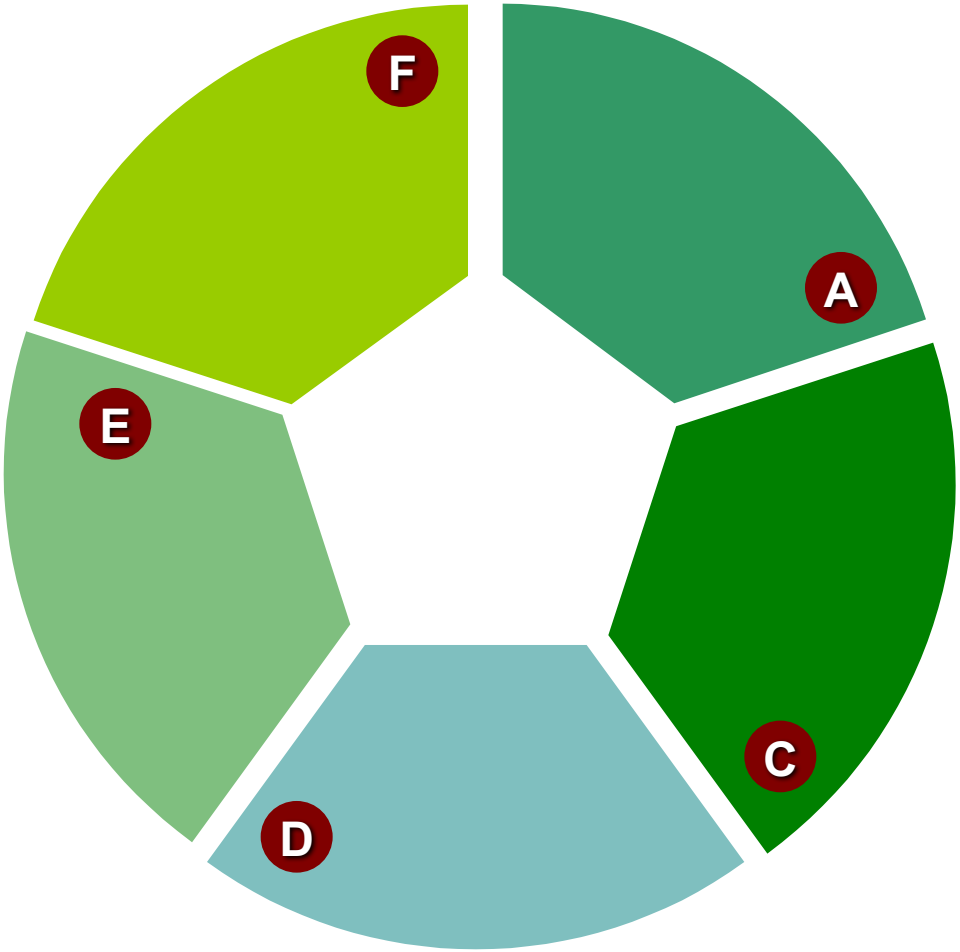
9 areas (1ha each) for each experimental site, with 3 replicates of each treatment:

- Control
- Traditional
- Selective

3 *plots* (20m diameter) for each area were selcted for sampling

A total of 27 *plots* for each site

Activities and tasks of the project



A Preparatory actions, elaboration of management plans and/or of action plans

C Concrete conservation actions

D Monitoring the impact of the project actions

E Public awareness and dissemination of results

F General management of the project and of the concrete conservation actions

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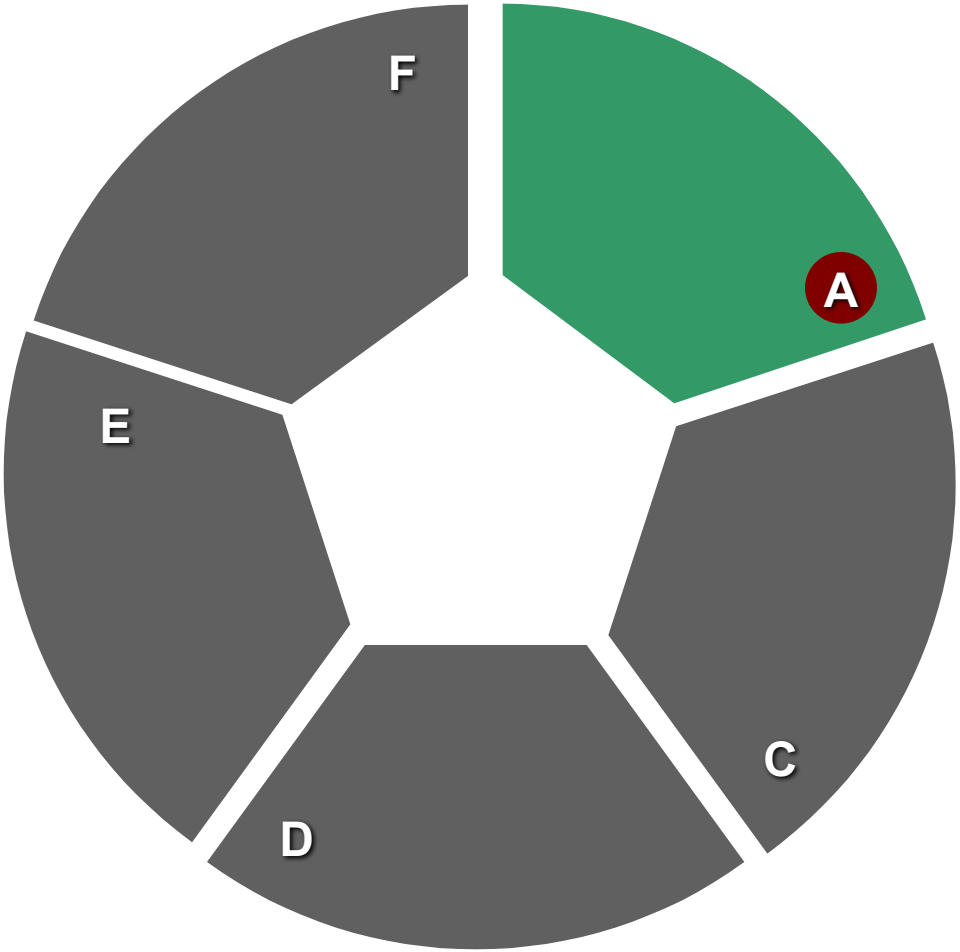
ACTION A: Preparatory actions, elaboration of management plans and/or of action plans



A1 Cognitive framework of the physical component of the landscapes and of the wood management

A2 Assessment of structural and dendrometric parametrs of the forest stands and the dead wood before treatment

A3 Assessment of the floristic diversity before treatments

A4 Assessment of the diversity of soil microbial communities and of the mesofauna before treatments

A5 Assessment of the mycologic diversity before treatments by means of macro-morphologic and molecular techniques

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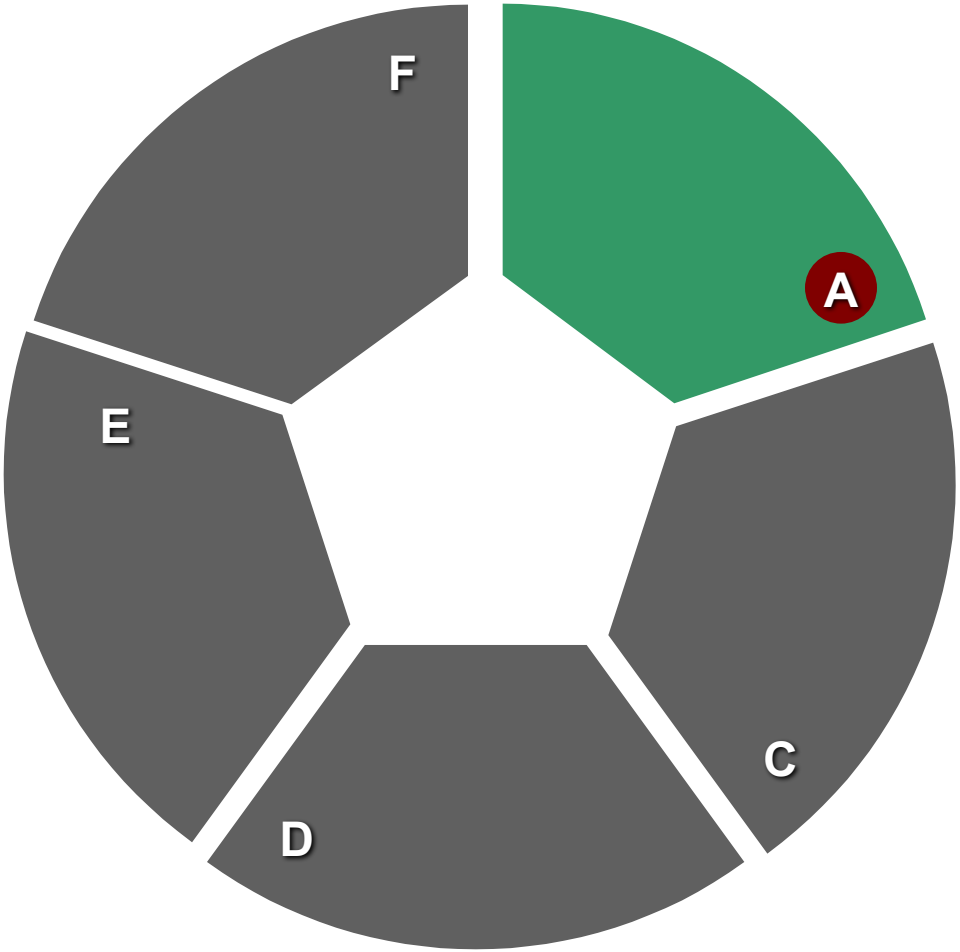
ACTION A: Preparatory actions, elaboration of management plans and/or of action plans



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“SOIL” BIODIVERSITY

A4

Assessment of the diversity of soil microbial communities and of the mesofauna before treatments

The assessment of soil biodiversity has been carried out across three different scales:

- Macrofauna (Coleoptera)
- Mesofauna
- Microorganisms

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A4

Assessment of the diversity of soil microbial communities and of the mesofauna before treatments

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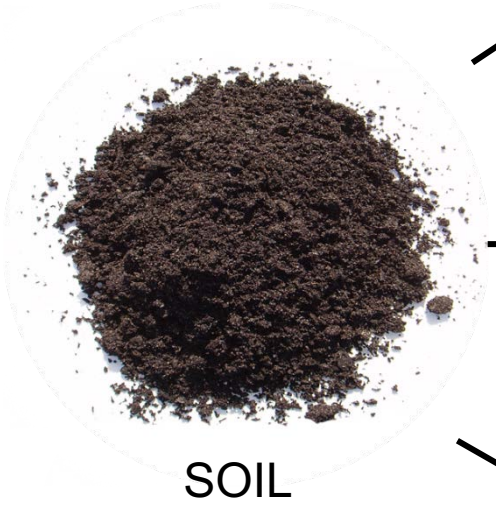
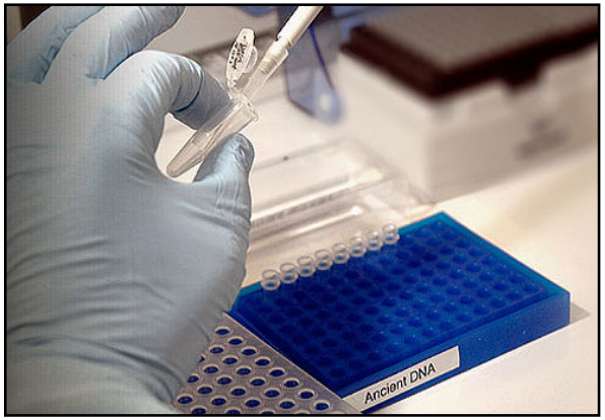
Microorganisms



SOIL

Analysis of the microbial community structure (454-pyrosequencing)

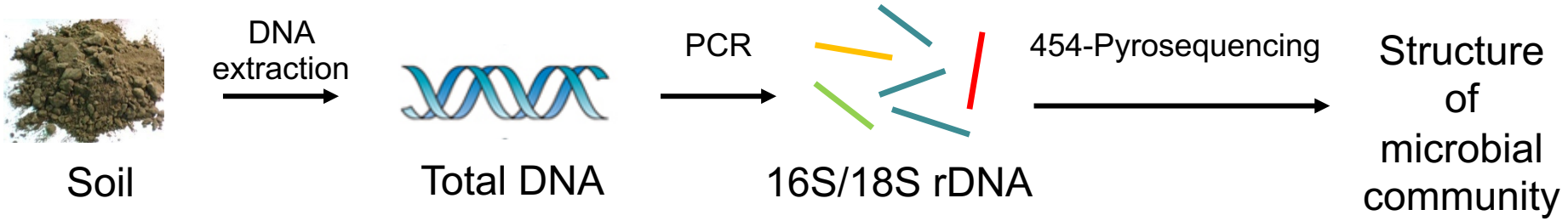


Soil microbial respiration (Alef, 1995)

Microbial C biomass (Vance et al., 1987)

Microorganisms

Analysis of the microbial community structure throughout 454-pyrosequencing



However, the 454-Pyrosequencing technology (Roche) was decided to be shut down from 2016. Thus, in order to make the results more comparable over time, we decide to use another NGS approach (Illumina Mi-seq). This inconvenient provided a delay of about 6 months in the analyses.

Following Roche's Decision to Shut Down 454, Customers Make Plans to Move to Other Platforms

Oct 22, 2013 | Julia Karow

Premium

Following Roche's disclosure last week that it will shut down 454 Life Sciences and stop supporting 454 sequencing instruments by 2016, customers are making plans to move their sequencing over to other platforms, if they have not done so already.

While Illumina, Life Tech's Ion Torrent, and Pacific Biosciences are eager to step in to fill the void, some customers say aspects of 454's technology cannot be replaced by other platforms at this point. Also, those customers who have started to use 454 for routine clinical applications need to revalidate their assays on a new platform.

Roche said last week that it will close down 454, which is based in Branford, Conn., and lay off about 100 employees over the next three years (*GWDN 10/15/2013*). By mid-2016, it will stop supporting the 454 sequencing platforms, the GS FLX+ and the GS Junior.

Roche's decision to pull the plug on 454 came to light less than a month after the company announced a deal with Pacific Biosciences, worth up to $75 million, to develop a sequencing system and assays for clinical diagnostics using PacBio's single-molecule real-time sequencing technology (*IS 10/1/2013*).

Breaking News

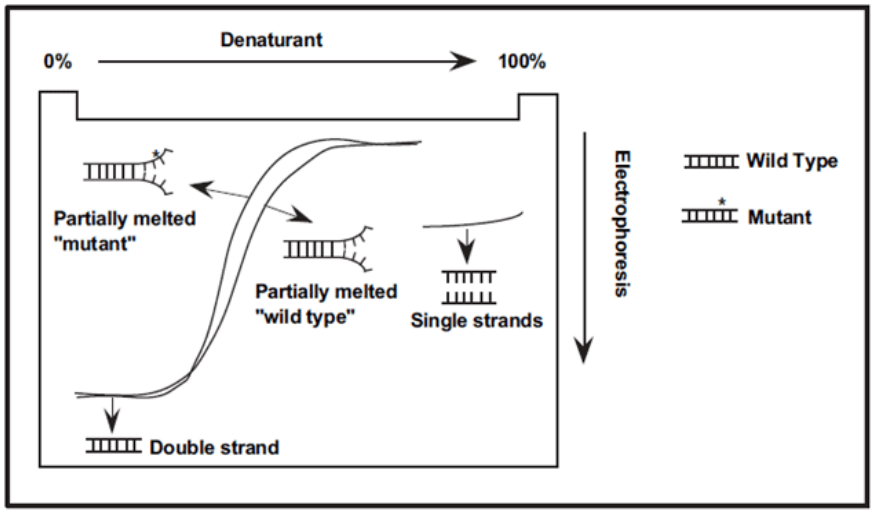
- RainDance Reorganizes, Focusing on New Products for Single-Cell Analysis, Linked Reads for Phasing
- In Brief This Week: Qiagen; CareDx; Dovetail Genomics; and More
- At AGBT, Illumina Provides Additional Details on Project Firefly
- People in the News: Warren Kocmond, Marc Haugen, and more
- UCSF-led Team IDs Blood Expression Signature in Individuals With Acute Lyme Disease
- Researchers From Protagen, Targos, Elsewhere ID Protein Biomarkers for Prostate Inflammation

Microorganisms

Analysis of bacterial community structure by means of DGGE

Molecular analysis:

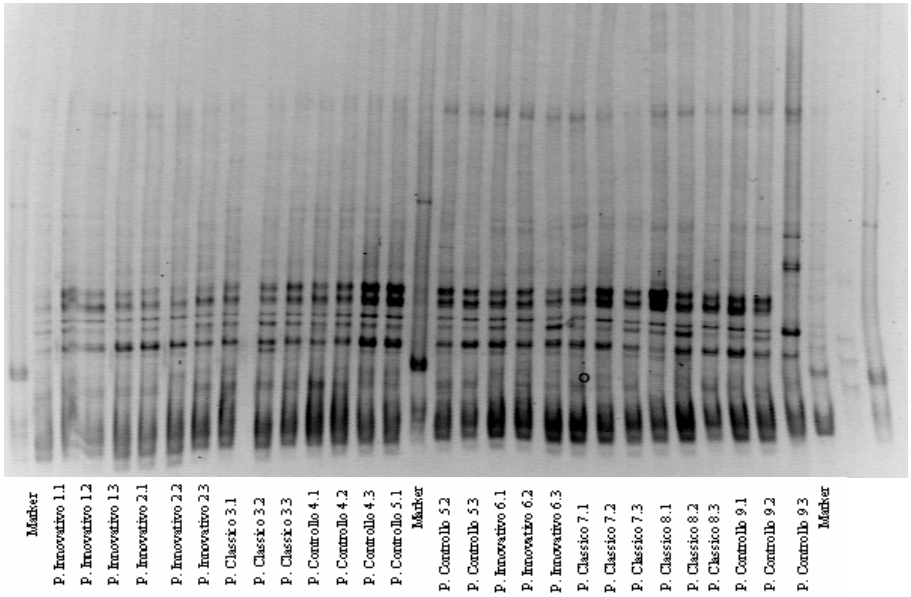
- Total DNA extraction from soil
- *Polymerase Chain Reaction* (PCR) of 16S rRNA genes
- DGGE (*Denaturing Gradient Gel Electrophoresis)*

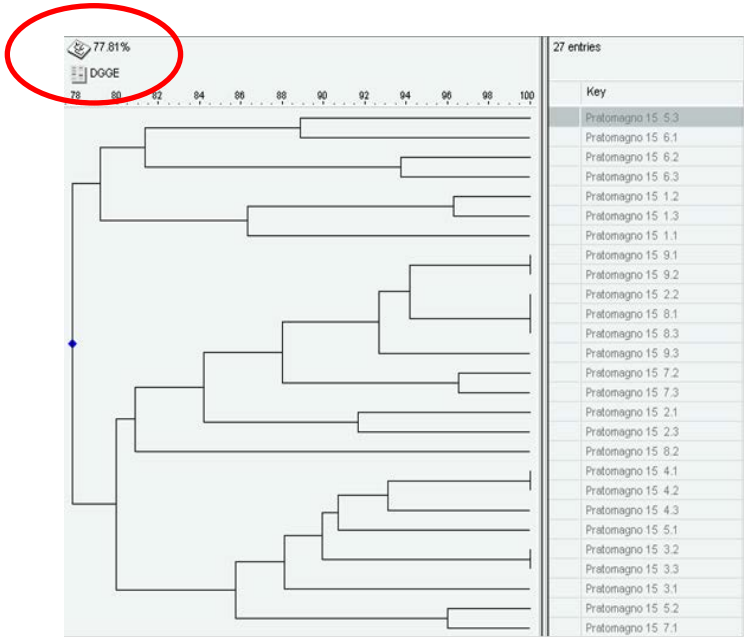


Microorganisms

Analysis of bacterial community structure by means of DGGE

Pratomagno



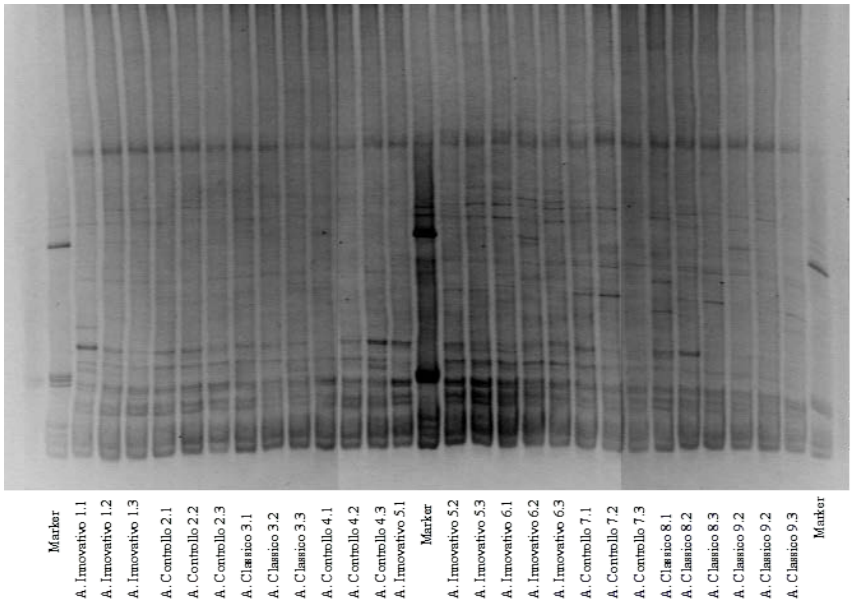


The similarity value of the Pratomagno area was relatively high (77%) compared to Amiata, indicating a quite homogeneous distribution of bacterial communities. Despite samples from plots 1 and 6 clustered separately compared to the other areas, such differences appeared to be poorly relevant.

Microorganisms

Analysis of bacterial community structure by means of DGGE

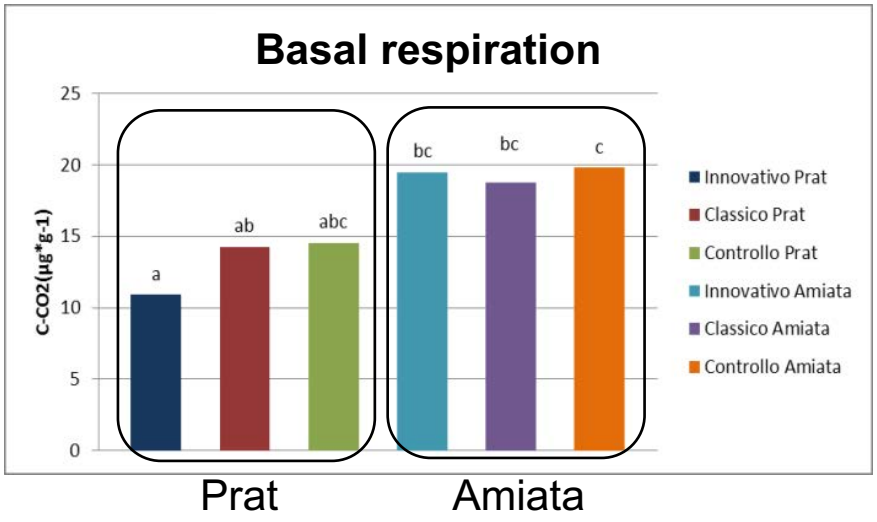
Amiata

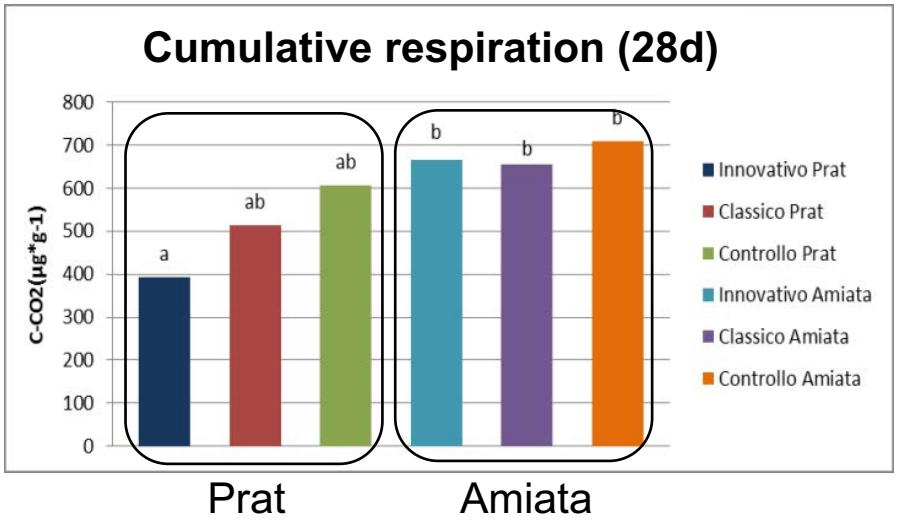


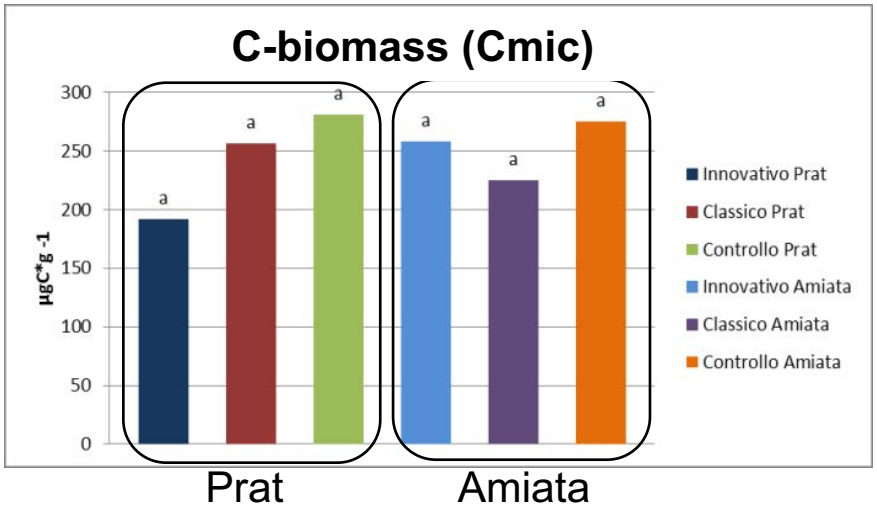
The similarity value of the Amiata area was relatively low (45%), indicating a more eterogeneous distribution of bacterial communities compared to Pratomagno. Samples from plots 8 and 9 clustered separately as compared to the other areas, suggesting a notable soil variability.

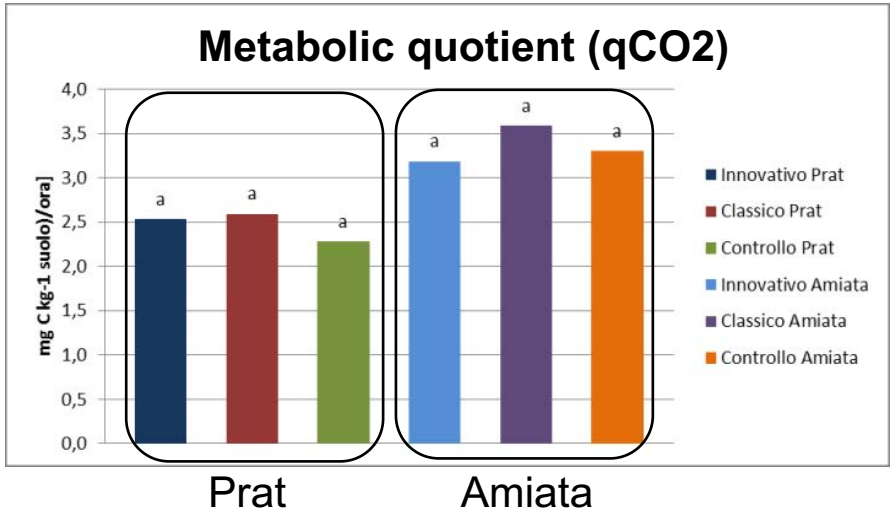
Microorganisms

Soil respiration and microbial C-biomass









Microorganisms

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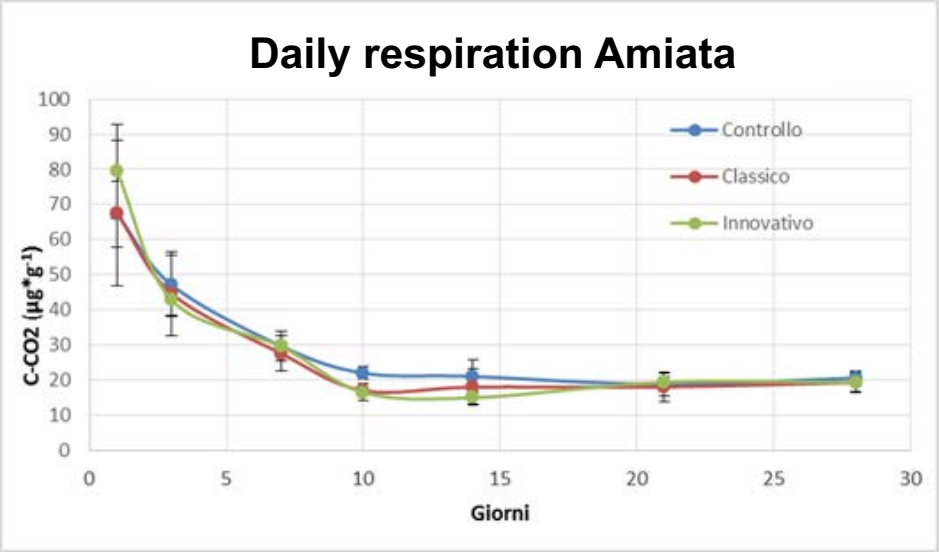
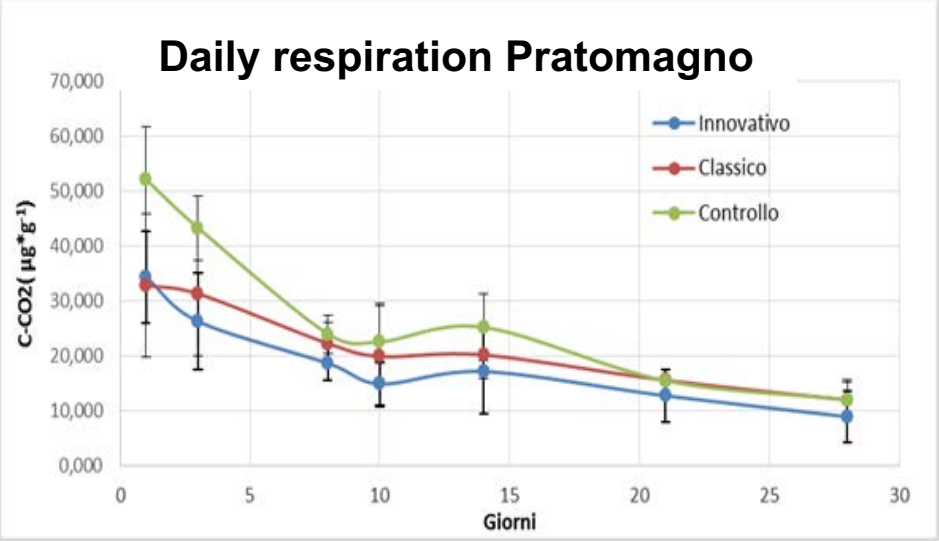


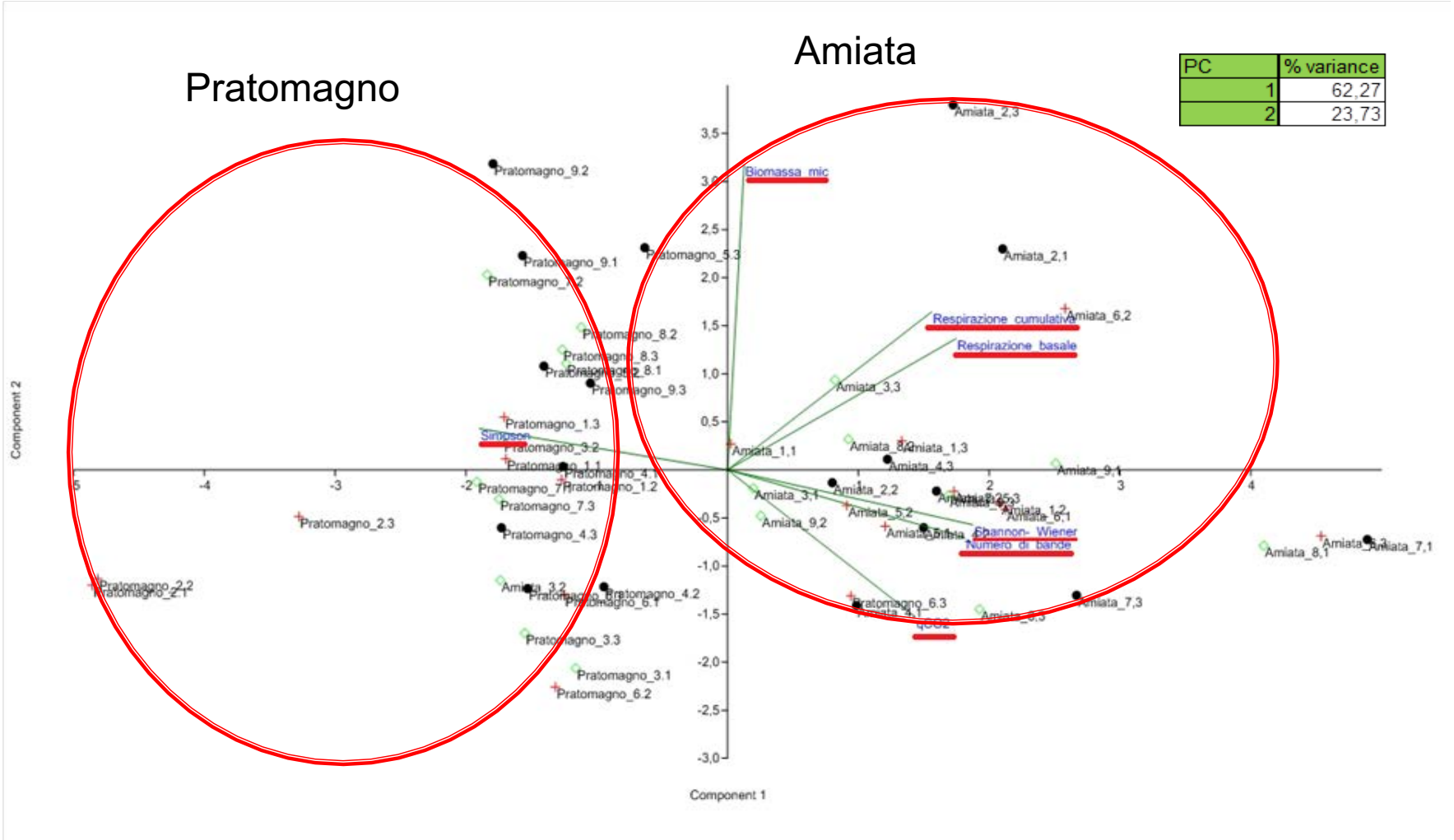
Microbial activity revealed by soil respiration, biomass and metabolic quotient, highlighted higher values in Amiata areas compared to Pratomagno which, in contrast, appeared to be more metabolically efficient.



Nevertheless, the mineralisation rate of the soil organic C exhibited an higher variability in Pratomagno plots, likely due to their spatial distribution along the relevant slope.

Microorganisms

Principal Component Analysis



Overall, the preliminary results analyzed by PCA showed two distinct monitoring areas, characterized by different native biodiversity.

PARTNERS

1. CREA – SEL (Dr.Paolo Cantiani – Coordinator): silvicultural management, Project Management
2. CREA – ABP (Dr. Stefano Mocali, Drs. Isabella De Meo, Drs. Elisa Bianchetto, Drs. Silvia Landi,): silvicultural management, Microbial diversity,Floral diversity, Nematodes and arthropods
3. University of Siena (Drs. Elena Salerni): Fungal diversity
4. Compagnia delle Foreste (Dr. Paolo Mori, Drs. Silvia Bruschini): Dissemination
5. UCP (Stefano Samaden): silvicultural management
6. UCAVO (Piergiuseppe Montini) : silvicultural management

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THANK YOU