

From the field to the table: grape microbiome as a signature of field origin for wine traceability

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INTRODUCTION

Geographical origin is a critical aspect for food traceability, safety and sustainability. This is important in products such as wine, in which the geographical traceability is fundamental for its distinctive autochthonous peculiarities. The environment in which vineyards are grown is defined as the so-called wine *terroir*. In the case of grapevine (*Vitis vinifera* L.), the plant microbiota can act as a signature of grape origin and contributes to characterize wine *terroir*. Identifying the 'local' microbiota of wine is crucial for wine traceability.

AIM

The aim of this study is to describe the microbial communities of soil and grapes collected in different localities in the North of Italy for the production of Chardonnay wine cultivar and to identify a signature of field origin for wine traceability using high-throughput DNA sequencing.

MATERIAL AND METHODS

SAMPLING

Soil and grapes were collected from three different areas in Northern Italy: North of Garda Lake (NG), South of Garda Lake (SG) and South of Iseo Lake (SI).

DNA ISOLATION

DNA was isolated using the Power Soil kit (QIAGEN). Microbial pellet from grape was isolated after washing and concentration using physiological water.

LIBRARY PREPARATION

Illumina library was prepared following the standard workflow (for soil and grape).

Nanopore MinION library was prepared using SQK-RAB204 protocol (for soil) and a MinION MinION Mk1B.

SEQUENCING



Grape and soil

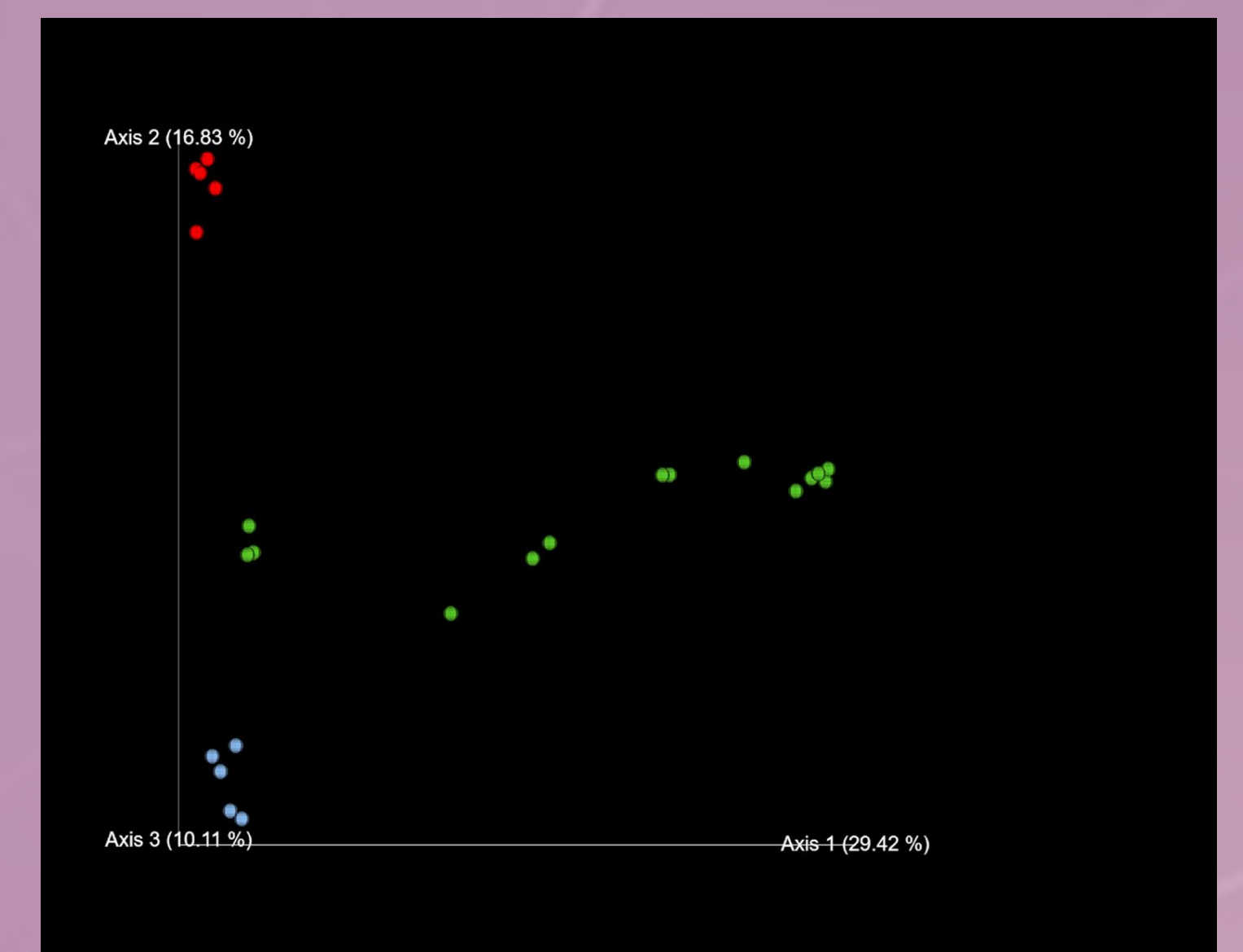
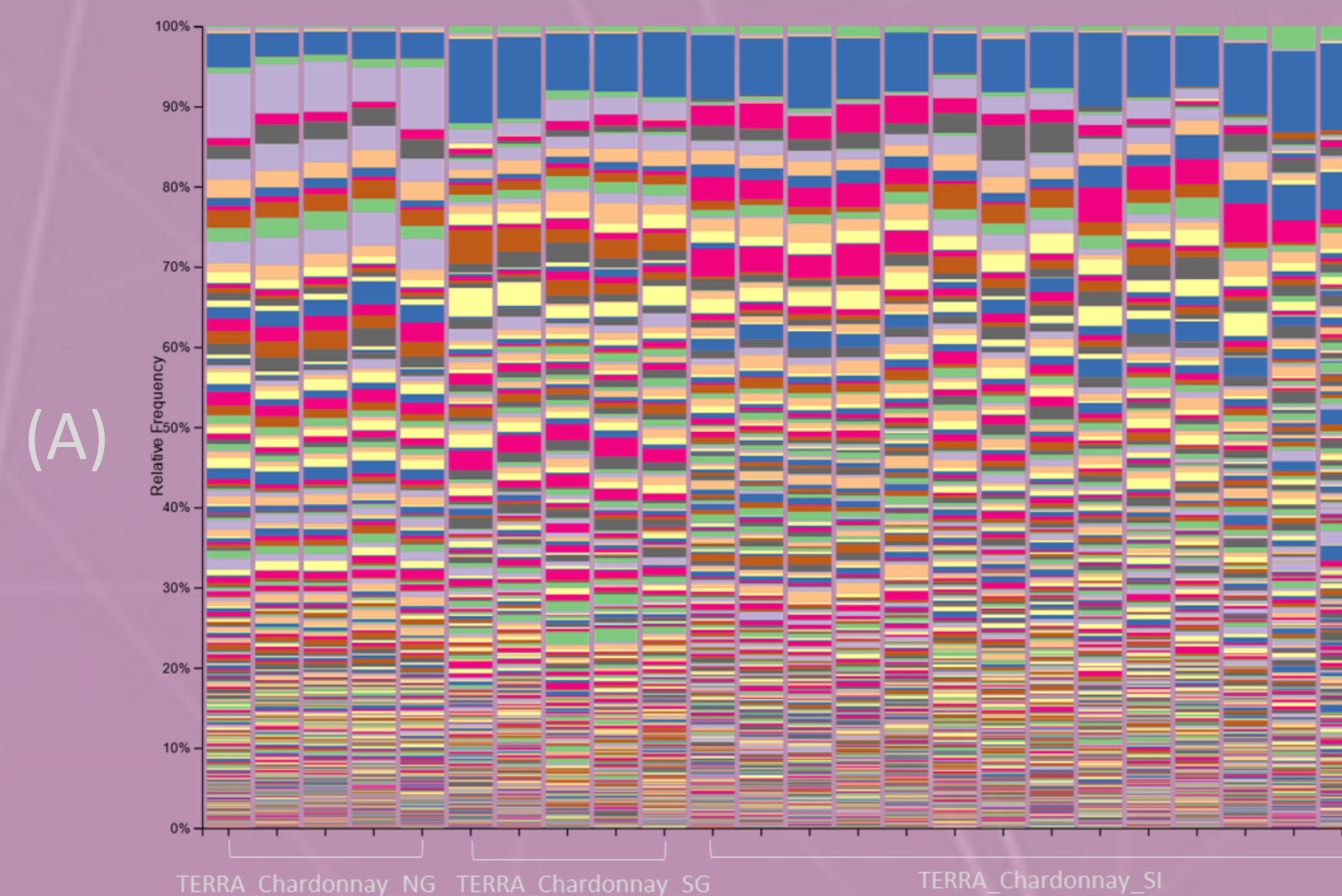


Soil

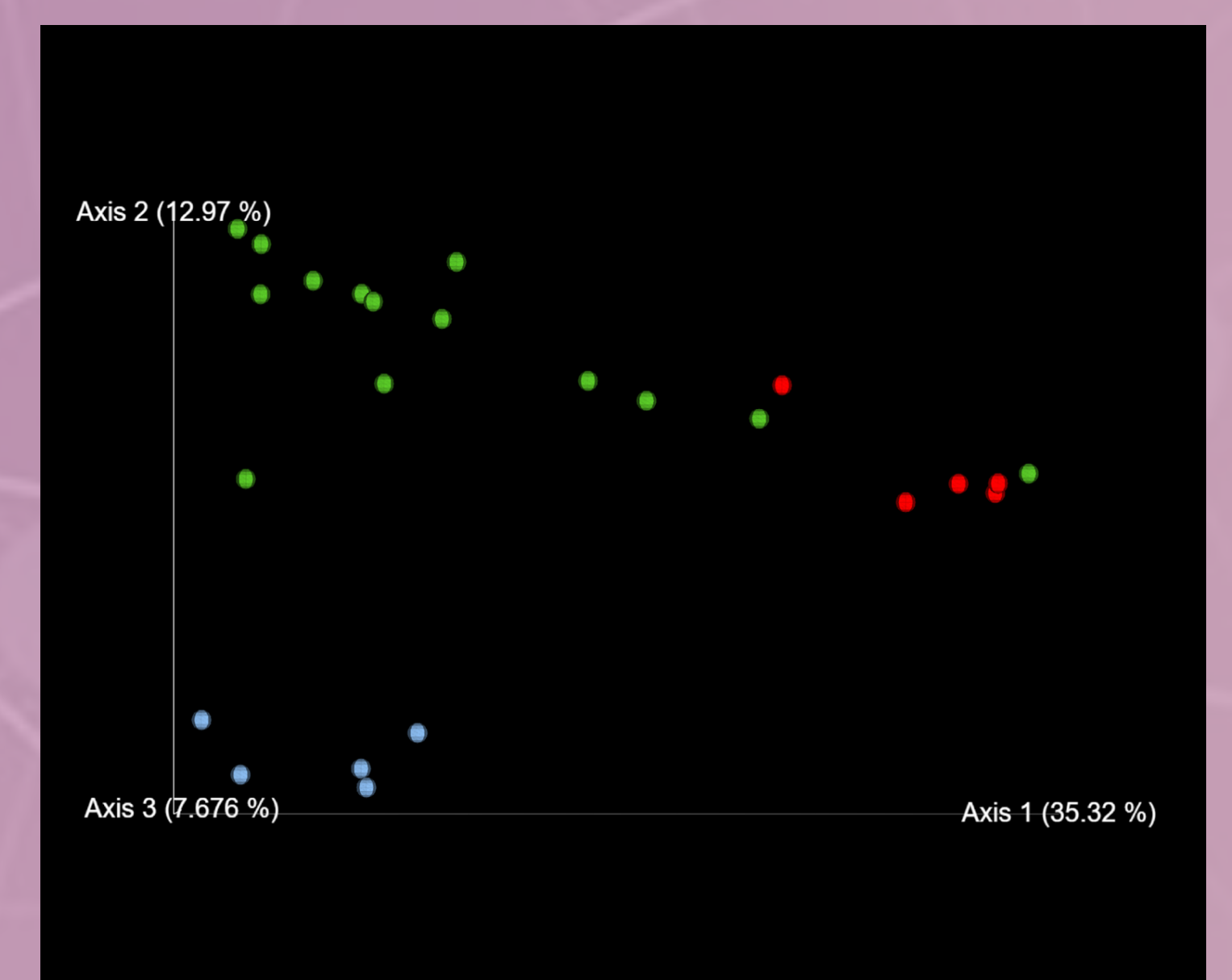
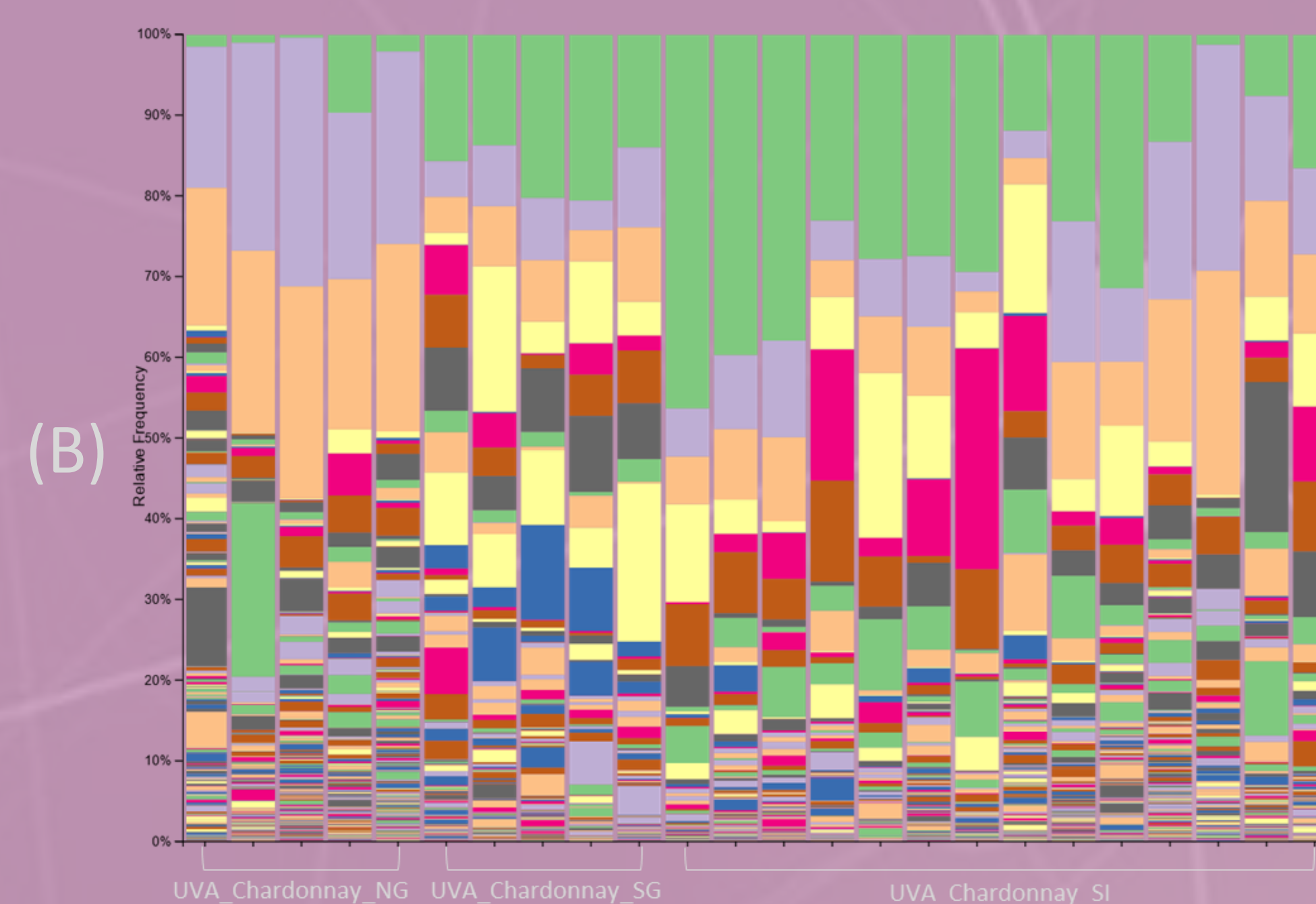
RESULTS

ILLUMINA RESULTS

The region V3-V4 of 16S rDNA was sequenced by Illumina methodology for both soil and grape samples. Below are showed the taxa bar plot and a Bray-Curtis PCoA of soil (A) and grape (B) samples.



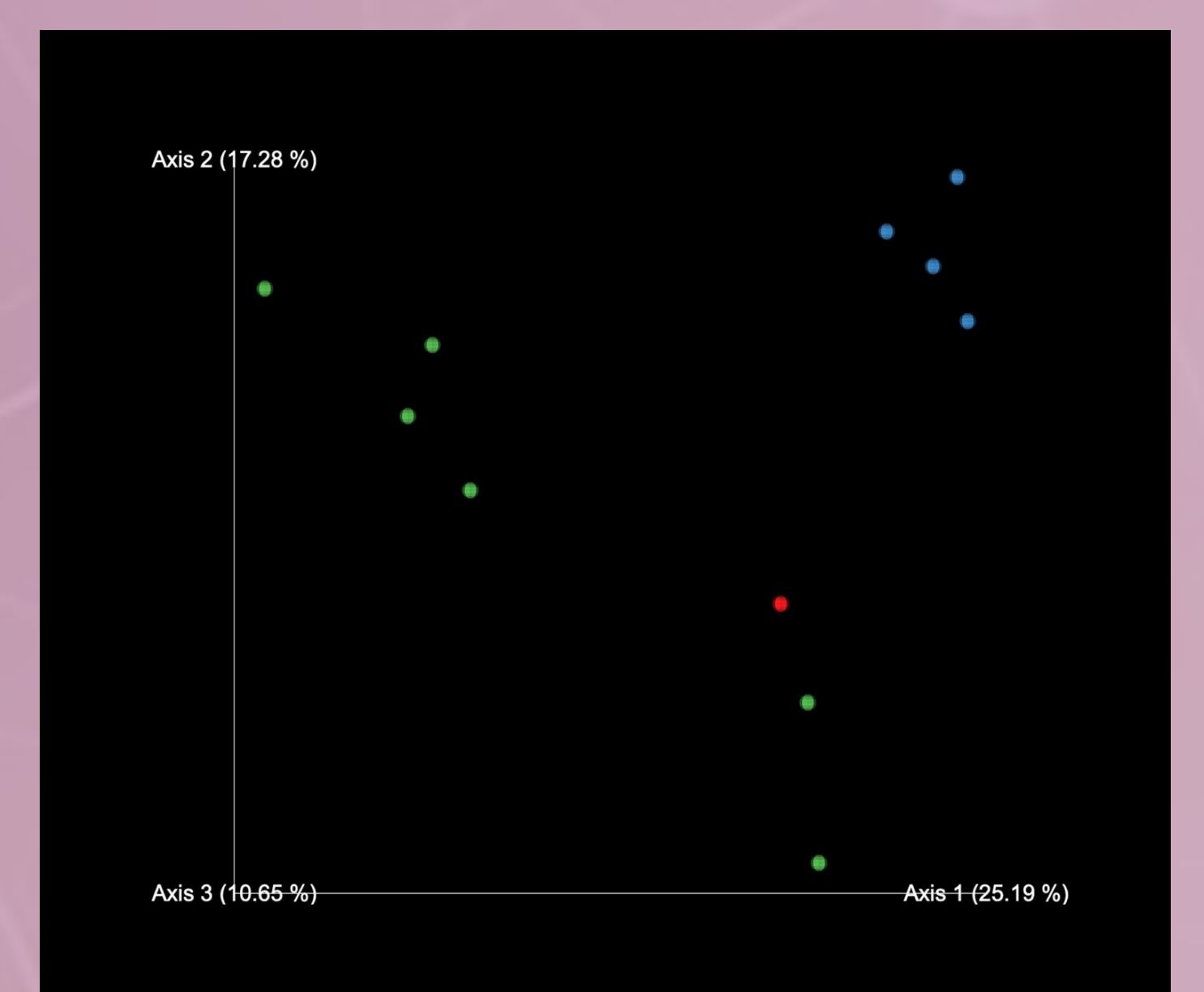
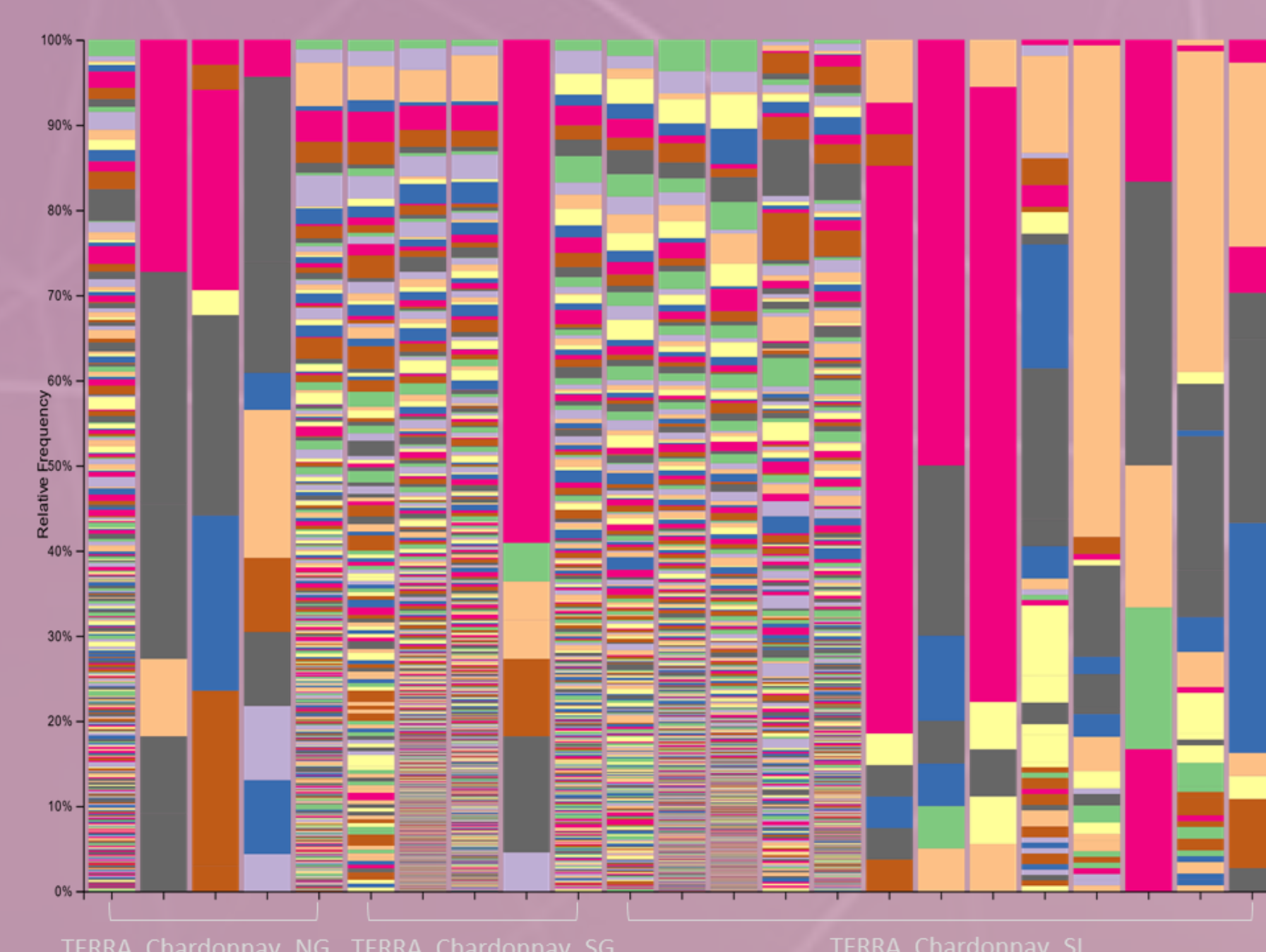
Bray-Curtis PCoA for soil samples. In red samples from NG, in blue samples from SI and in green samples from SG



Bray-Curtis PCoA for grape samples. In red samples from NG, in blue samples from SI and in green samples from SG

NANOPORE MINION RESULTS

Grape samples were analysed also with Nanopore full-length 16S rDNA sequencing. Below are showed the taxa barplot and a Bray-Curtis PCoA. For biodiversity exploration only samples with > 300 reads are shown.



Bray-Curtis PCoA for soil samples. In red samples from NG, in blue samples from SI and in green samples from SG.

CONCLUSION

Our preliminary results suggest that all geographical areas (NG, SG and SI) are related to a peculiar microbial community, leading us to explore a core microbiota and geographical signature characterizing the Chardonnay wine *terroir*. Moreover, we observed differences in the vineyard locations considering the microbial biodiversity. Both Illumina and Nanopore MinION technology are useful methodology for wine traceability.