1. Authors should describe indicators such as grape yields in each region.

   Unfortunately, we did not retrieve the grape yield data along the study. Indeed, our main goal was to evaluate the variability of the microbiota associated with grapes through the study of samples of two different varieties, an international grapevine and a local one, taken in four different areas of the world. To further investigate the local variance, for each country an average of 4 sampling sites for each variety were analyzed. So our purpose was to apply an "international-vs local" approach to explore the variability of distant geographic places contemporarily and takes care of by decreasing differences in the experimental approach that would sometime limit the possibility of comparisons between such data sets.
2. I suggest that authors do not use descriptions from the first global-scale study.

   We agree. This issue has been solved in question 10 of reviewer 1 where we have replied: *"… we have changed the statement "global scale study" along the text with:*
   Abstract: "This study puts in evidence new insight of grape microbial community in two continents and the importance of both location and cultivar for the definition of the grape microbiome."
   Discussion: Lines 385-390"…although the present work analyzed the mycobiota in two continents, this finding provides evidence that the grape variety could act as a factor affecting the composition of fungal communities also at global scale. Further metagenomics investigations should include retrieving of grape from other regions located on different continents in comparison to those here analyzed to confirm our previous hypothesis"

3. the relationship between environmental factors (e.g. soil physical and chemical properties, temperature, humidity, light, etc.) and microbial communities is not explored in detail in the manuscript. I would therefore suggest that the authors describe them at least in the discussion.

   We thank you reviewer 3 for the suggestion at points 3 and 4. Actually, the present study did not include the evaluation between environmental factors and microbial communities; however, at lines 398-425 we have discussed the significant OTUs (identified as potential drivers of differentiation at a local level) with the following text: "*It must be considered that in this work an effort was made so that the local effects were as homogeneous as possible between fields in the collection of the samples from common and local cultivars. This result may be due to different causes, most likely human practic-es related to the management of the vineyard and the different agricultural techniques that may be influencing the observed grouping. Similarities in the fungal communities among different wineries in the same regions has been recently reported [18]; however, thought our output confirms this evidence, further studies are required to establish potential factors driving the fungal community profiles on vineyard blocks (or fields) with different microclimatic, viticultural, and topographical conditions, beyond the aim of the present work. In particular, at the local level, the genera significantly different among fields were Botrytis in South Africa, Rhizopus in Spain and Neoscytalidium in Italy. In this case, the climatic conditions could have determined the success in the development of some pathogenic fungi, but further analyzes are necessary to verify a possible correlation between the climatic parameters and pathogenic fungi locally found considering both the vintage under study and the three interested wine-producing areas. Botrytis is a genus of ana-morphic fungi in the family Sclerotiniaceae including B. cinerea, an airborne filamentous fungus that causes grey mold disease [29]. This necrotrophic phytopathogenic fungus is ubiquitous and climate conditions including mean temperature, humidity, and precipitation are considered the main variables influencing the botrytization process [30,31]. Rhizopus was found to be the main*

components of the wine grape mycobiota in Tokaj grape berries of Slovak regions and part of the fungal community in Slovakian wine grapes from small Carpathians wine region [32-34]. Some species of this genus provoke the Rhizopus rot, common on soft fruits, more abundant in warm, humid climates than in cool climate viticulture. Finally, the genus Neoscytalidium, belonging to the Botryosphaeriaceae family, in-cludes species associated with Botryosphaeria dieback on grapevines. Also, for this taxa, geographical distribution of some Botryosphaeriaceae species has been shown to be asso-ciated with climate [35]."

4. I suggest that some environmental similarities between geographical areas are discussed, which may also partially explain the similarity of microbial communities across geographical areas.

We agree with Reviewer 3 that a correlation between environmental factors and fungal communities is very interesting. Unfortunately, we did not have climate data to discuss well, and with rigor, this point. However, to follow the reviewer suggestion, at lines 398-425 we introduce some more details.