

Supporting Information

***Quercus ilex* phyllosphere microbiome environmental-driven structure and composition shifts in a Mediterranean context**

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Fig. S1 Modularity classes of phyllosphere microbiome of *Q. ilex*; x-axis shows the number of modularity class, y-axis show the number of OTUs falling into each modularity class



Table S1 Correlations and topological properties of microbiome networks from phyllosphere of *Q. ilex*.

Network properties	
Number of nodes ^a	146
Number of edges ^b	3,164
Modularity ^c	0.44
Number of communities ^d	4
Network diameter ^e	5
Average path length ^f	2.34
Average degree ^g	21.62
Av. clustering coefficient ^h	0.614
Positive edges ⁱ	2,532
Negative edges ^l	632

^aMicrobial taxon (at ASV level) with at least one significant ($P < 0.05$) and strong (Spearman's correlation coefficient > 0.8 or < -0.8) correlation;

^bNumber of connections/correlations obtained by Spearman analysis;

^cThe capability of the nodes to form highly connected communities, that is, a structure with high density of between nodes connections (inferred by Gephi);

^dA community is defined as a group of nodes densely connected internally (Gephi);

^eThe longest distance between nodes in the network, measured in number of edges (Gephi);

^fAverage network distance between all pair of nodes or the average length off all edges in the network (Gephi);

^gThe average number of connections per node in the network, that is, the node connectivity (Gephi);

^hHow nodes are embedded in their neighborhood and the degree to which they tend to cluster together (Gephi).

ⁱSpearman positive correlation (> 0.5 with $P < 0.05$);

^lSpearman negative correlation (< -0.5 with $P < 0.05$).

Table S2 Functional metagenomic data (Kegg pathway code: ec00624); number of reads per samples are shown [Table S2 is an excel file submitted separately]