

Supplementary Material

Global-scale structure of the eelgrass microbiome

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Supplementary Figure

Figure S1

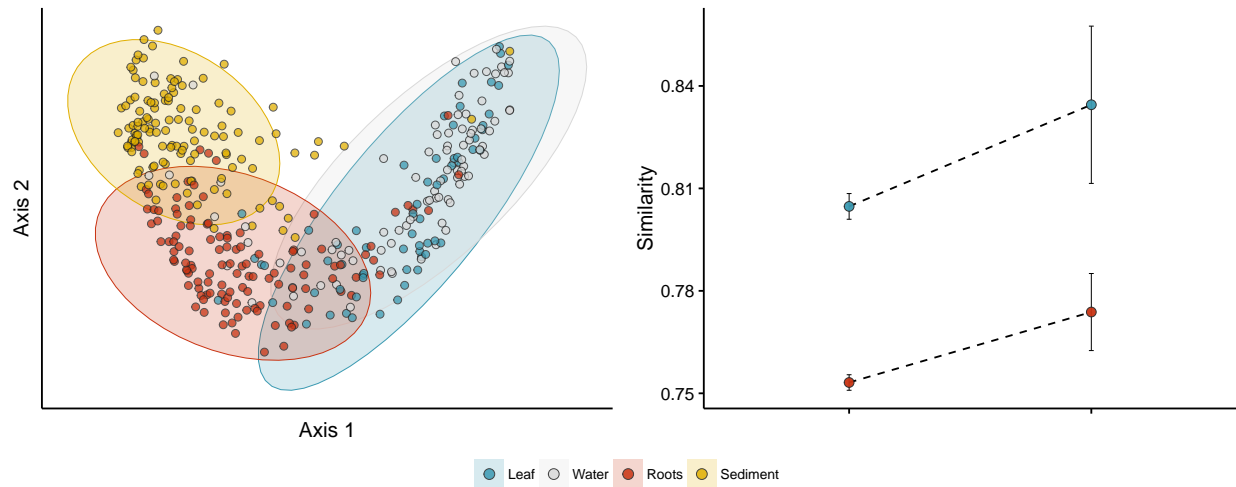


Fig. S1. Results of β -diversity analysis of unweighted UniFrac distances (Lozupone and Knight, 2005) are qualitatively similar to those of Canberra distances (compare with Fig. 1 in *main text*). (Left panel) Ordination plots show results of a 2-dimensional PCoA. Colors are the same as in Fig. 1 in the *main text*. Ellipses represent group-specific 95% confidence intervals assuming a multivariate t-distribution. (Right panel) Comparisons of host-environment phylogenetic similarities within- versus between seagrass beds. Points represent mean similarities between leaves and water (blue points), and roots and sediment (red points) \pm SEM. Patterns in phylogenetic diversity within- versus between seagrass beds followed the same qualitative patterns as compositional diversities, but were statistically non-significant ($P = 0.18$ for leaves; $P = 0.19$ for roots). This suggests that eelgrass leaf and root microbiomes were only marginally more phylogenetically related to their adjacent environments compared to all others.

References

Lozupone, C. and Knight, R. (2005). Unifrac: a new phylogenetic method for comparing microbial communities. *Applied and environmental microbiology*, 71(12):8228–8235.