

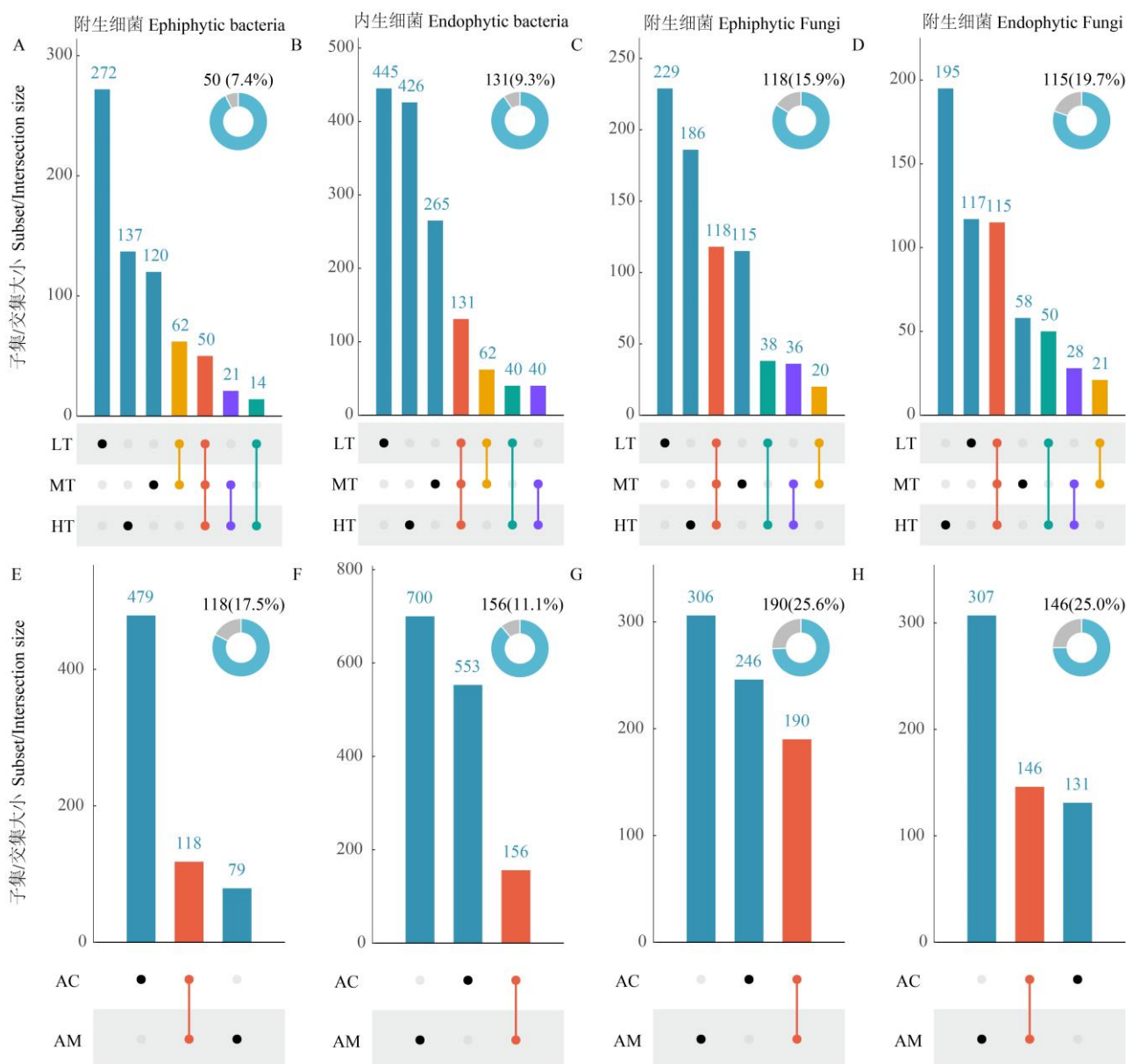
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DOI: 10.17521/cjpe.2025.0421

RAO CK, TANG L (2026). Characteristics and drivers of mangrove phyllosphere microbial communities across different tidal elevations. *Chinese Journal of Plant Ecology*, 50, 987-1002. DOI: 10.17521/cjpe.2025.0421
http://www.plant-ecology.com/CN/10.17521/cjpe.2025.0421

附录I 扩增子序列变异体(ASV)在不同潮位和植物宿主间的分布

Supplement I Distribution of amplicon sequence variants (ASV) among different tidal levels and plant hosts



A–D分别表示附生细菌、内生细菌、附生真菌和内生真菌在三种潮位(LT, 低潮位; MT, 中潮位; HT, 高潮位)间的共有与特有ASV。**E–H**分别表示两种植物(AC, 蜡烛果; AM, 海榄雌)间对应四类群落的共有与特有ASV。柱状图为各集合或交集的ASV数量, 下方点阵表示该交集涵盖的分组, 右上角环状饼图表示三种潮位或两种宿主共有ASV的数量及其占总ASV的比例。

A–D, The shared and unique ASV across the three tidal regimes (LT, low tidal elevation; MT, middle tidal elevation; HT, high tidal elevation) for epiphytic bacteria, endophytic bacteria, epiphytic fungi, and endophytic fungi, respectively. **E–H**, The shared and unique ASV between the two host species (AC, *Aegiceras corniculatum*; AM, *Avicennia marina*) for the corresponding four microbial categories. The bar charts quantify the ASV counts for each set or intersection, with the dot matrices indicating the constituent sets involved in the intersections. The upper-right circular pie charts indicate the total number and proportion of ASV shared among the three tidal elevations or the two host species.