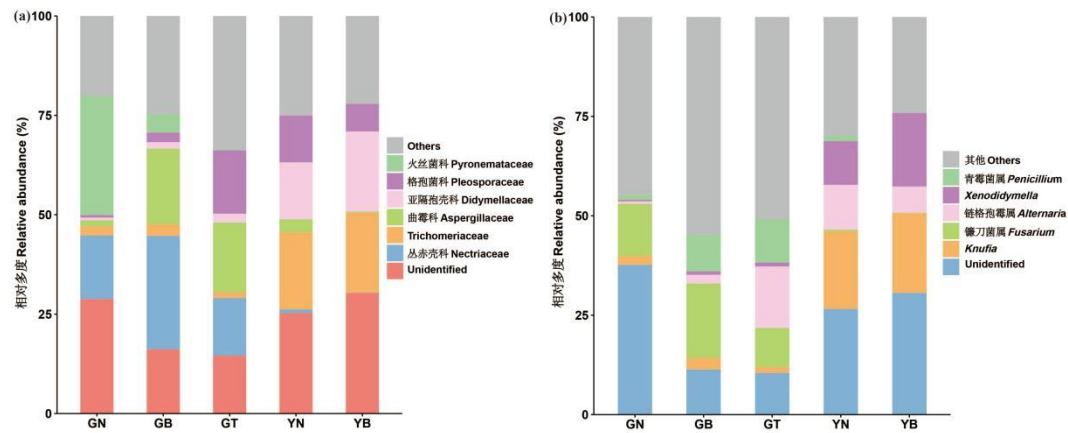


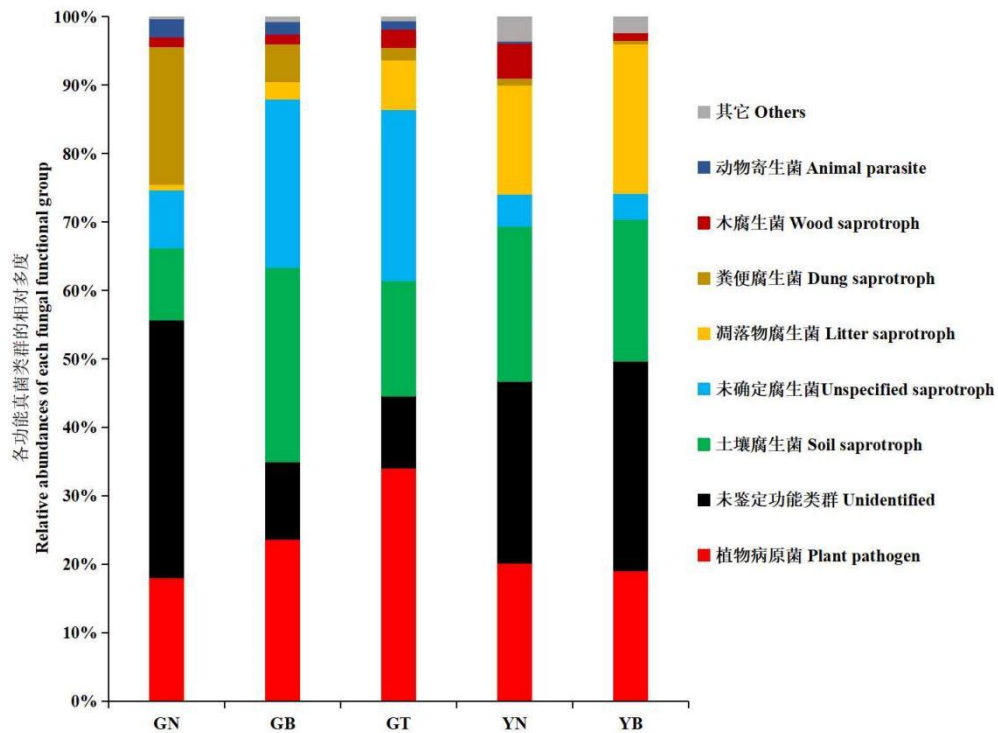
附录 1 四合木不同部位腐生菌和病原菌的 alpha 多样性分析。(a-d)腐生真菌的丰富度指数, Shannon 指数, 辛普森指数和 Chao1 指数; (e-h)病原真菌的丰富度指数, Shannon 指数, 辛普森指数和 Chao1 指数。GN: 根内; GB: 根表; GT: 根际土壤; YN: 叶内; YB: 叶表。

Appendix 1 Analysis on alpha diversity of saprotrophic and pathogenic fungi in different parts of *Tetraena mongolica*. (a-d) Richness, Shannon, Simpson and Chao1 indices of saprotrophic fungi in different plant compartments; (e-h) Richness, Shannon, Simpson and Chao1 indices of pathogenic fungi in different plant compartments. GN: Root endophytic fungi; GB: Root epiphytic fungi; GT: Rhizosphere soil; YN: Phyllosphere endophytic fungi; YB: Phyllosphere epiphytic fungi.



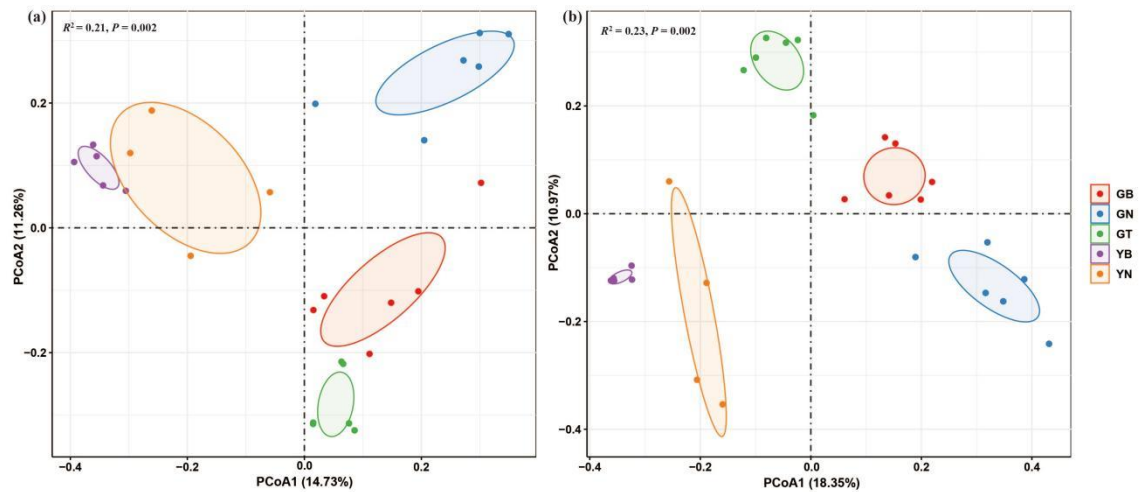
附录 2 四合木真菌群落科和属水平上优势类群(高于总序列数 5%)的相对多度。(a)科水平;(b)属水平。GN: 根内; GB: 根表; GT: 根际土壤; YN: 叶内; YB: 叶表。

Appendix 2 Relative abundance of dominant fungal taxonomy associated with *Tetraena mongolica* at the family and genus levels (more than 5% of total reads). (a) Family level; (b) Genus level. GN: Root endophytic fungi; GB: Root epiphytic fungi; GT: Rhizosphere soil; YN: Phyllosphere endophytic fungi; YB: Phyllosphere epiphytic fungi.



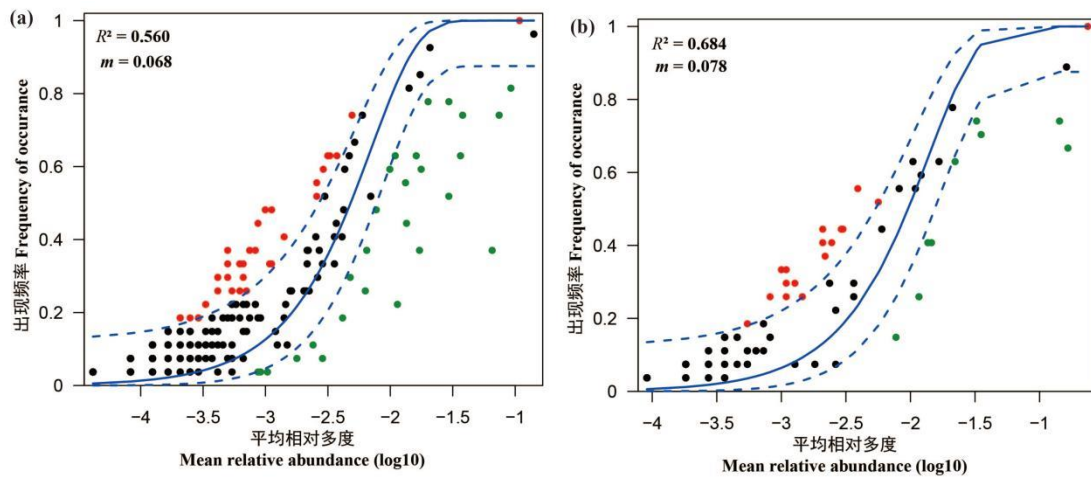
附录 3 主要真菌功能类群在植物各部位的相对多度。GN: 根内; GB: 根表; GT: 根际土壤; YN: 叶内; YB: 叶表。

Appendix 3 Relative abundances of dominant fungal functional groups in each plant compartment. GN: Root endophytic fungi; GB: Root epiphytic fungi; GT: Rhizosphere soil; YN: Phyllosphere endophytic fungi; YB: Phyllosphere epiphytic fungi.



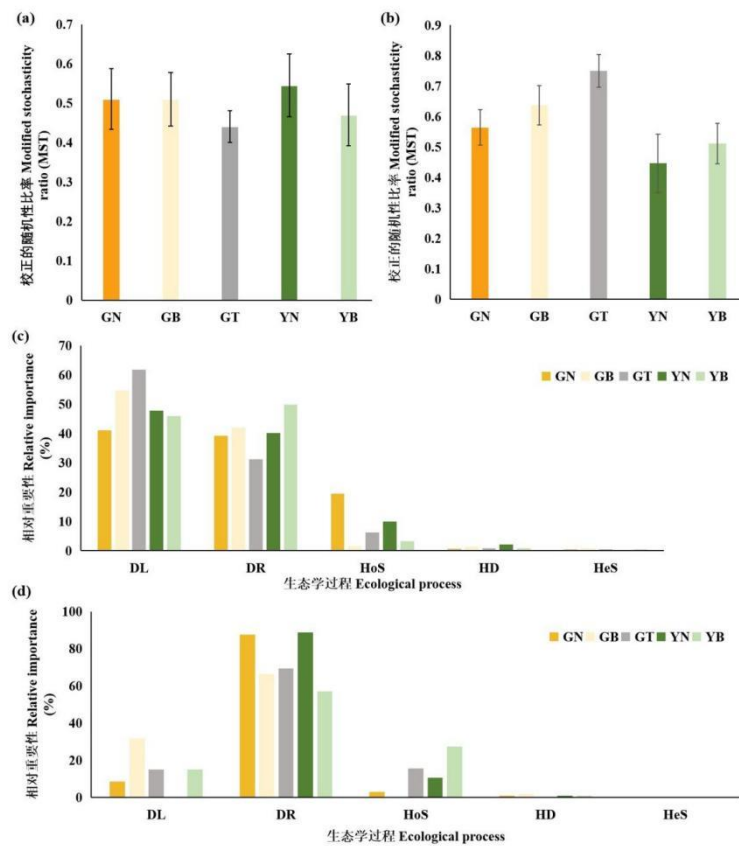
附录 4 基于 Bray-Curtis 距离矩阵的四合木植物各部位腐生真菌和病原真菌的群落主坐标排序分析。(a) 腐生真菌; (b)病原真菌。GN: 根内; GB: 根表; GT: 根际土壤; YN: 叶内; YB: 叶表。

Appendix 4 Principle coordinate analysis (PCoA) of saprotrophic and pathogenetic fungal communities in *Tetraena mongolica* based on Bray-Curtis distance. (a) Saprotrophic fungi; (b) Pathogenetic fungi; GN: Root endophytic fungi; GB: Root epiphytic fungi; GT: Rhizosphere soil; YN: Phyllosphere endophytic fungi; YB: Phyllosphere epiphytic fungi.



附录 5 腐生真菌和病原真菌的群落中性群落模型(NCM)分析。(a)腐生真菌; (b)病原真菌

Appendix 5 Neutral Community Model (NCM) analyses for saprotrophic and pathogenetic fungal communities. (a) Saprotrophic fungi; (b) Pathogenetic fungi.



附录 6 四合木各部位腐生真菌和病原真菌的群落构建机制。(a) 植物不同部位腐生真菌群的校正的标准化随机率(MST)分析; (b) 植物不同部位病原真菌群的校正的标准化随机率(MST)分析; (c) 各生态过程对腐生真菌群落构建的重要性; (d) 各生态过程对病原真菌群落构建的重要性。GN: 根内; GB: 根表; GT: 根际土壤; YN: 叶内; YB: 叶表; DL: 扩散限制; DR: 生态漂变; Hos: 同质化选择; HD: 均质化扩散; HeS: 异质化选择。

Appendix 6 Ecological assembly mechanisms of saprotrophic and pathogenetic fungal communities in different compartments of *Tetraena mongolica*. (a) Modified stochasticity ration (MST) analyses for saprotrophic fungal communities. (a) Modified stochasticity ration (MST) analyses for pathogenetic fungal communities. (c) The relative importance of ecological processes in driving saprotrophic fungal community assembly. (d) The relative importance of ecological processes in driving pathogenetic fungal community assembly. GB: Root epiphytic fungi; GT: Rhizosphere soil; YN: Phyllosphere endophytic fungi; YB: Phyllosphere epiphytic fungi. DL: Dispersal limitation; DR: Drift; Hos: Homogeneous selection; HD: Homogenizing dispersal; HeS: Heterogeneous selection.