The effects of primer pairs, PCR conditions, and peptide nucleic acid clamps on plant root fungal diversity assessment

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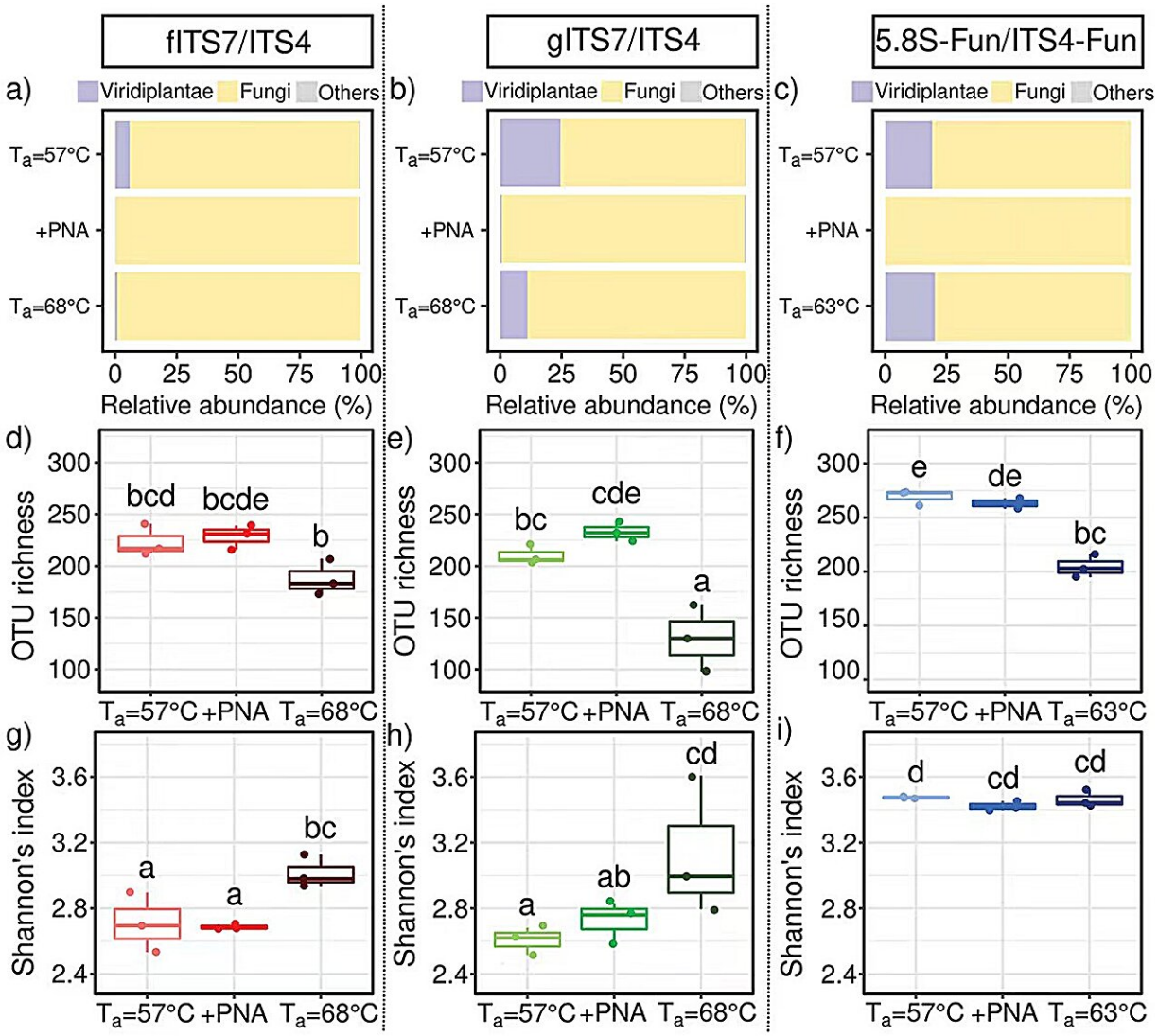

Abundance, richness, and diversity of fungi in *Urtica dioica* roots for the three

primer pairs tested fITS7/ITS4, gITS7/ITS4, and 5.8S-Fun/ITS4-fun (Ta = 57 °C), the addition of PNA clamps (+PNA) and the increase of Ta (Ta = 68 °C or 63 °C). (a–c) Relative abundance of reads of Viridiplantae, fungi, and other phyla (i.e. Amoebozoa, Choanoflagellozoa, Heterolobosa, Ichthyosporia, Metazoa, Protista, Rhizaria, rhodoplantae, Stramenopila, and NA); (d–f) Richness and (g–i) Shannon's index. Boxes with the same letters did not differ significantly from each other using a Tukey-adjusted comparison and Kruskal-Wallis analysis followed by a post-hoc test using Fisher's least significant difference, respectively, *P*