

Figure S1. Rarefaction curves of OTUs observed using 16S rRNA amplicon sequencing across all samples tested

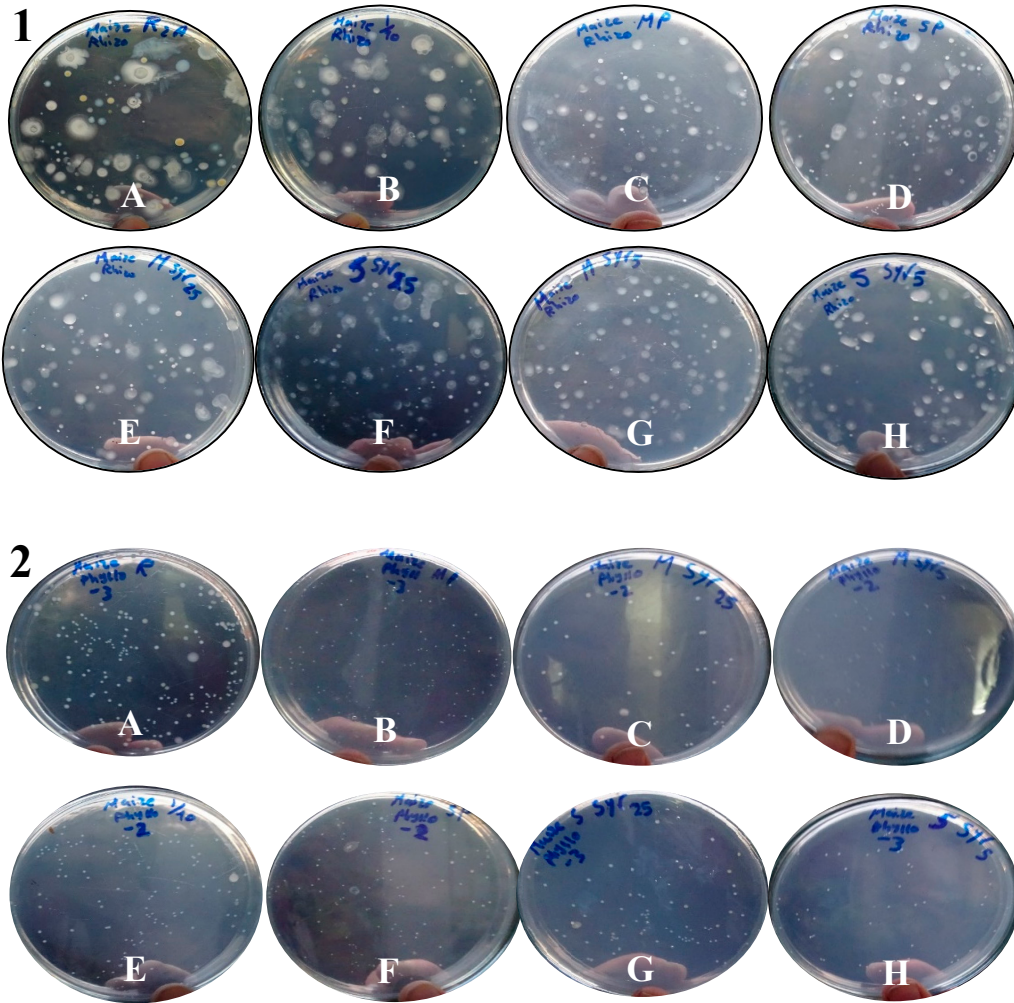


Figure S2. 1, CFUs of maize endo-rhizosphere (dilution 10^{-4}); 2, CFUs of maize endo-phyllosphere (dilution 10^{-2} and 10^{-3}) developed on tested agar plates: A) R2A; B) 1/10 R2A; C) maize powder teabag; D) sunflower powder teabag; E) maize broth (25 ml L^{-1}); F) sunflower broth (25 ml L^{-1}); G) maize broth (5 ml L^{-1}); H) sunflower broth (5 ml L^{-1}).

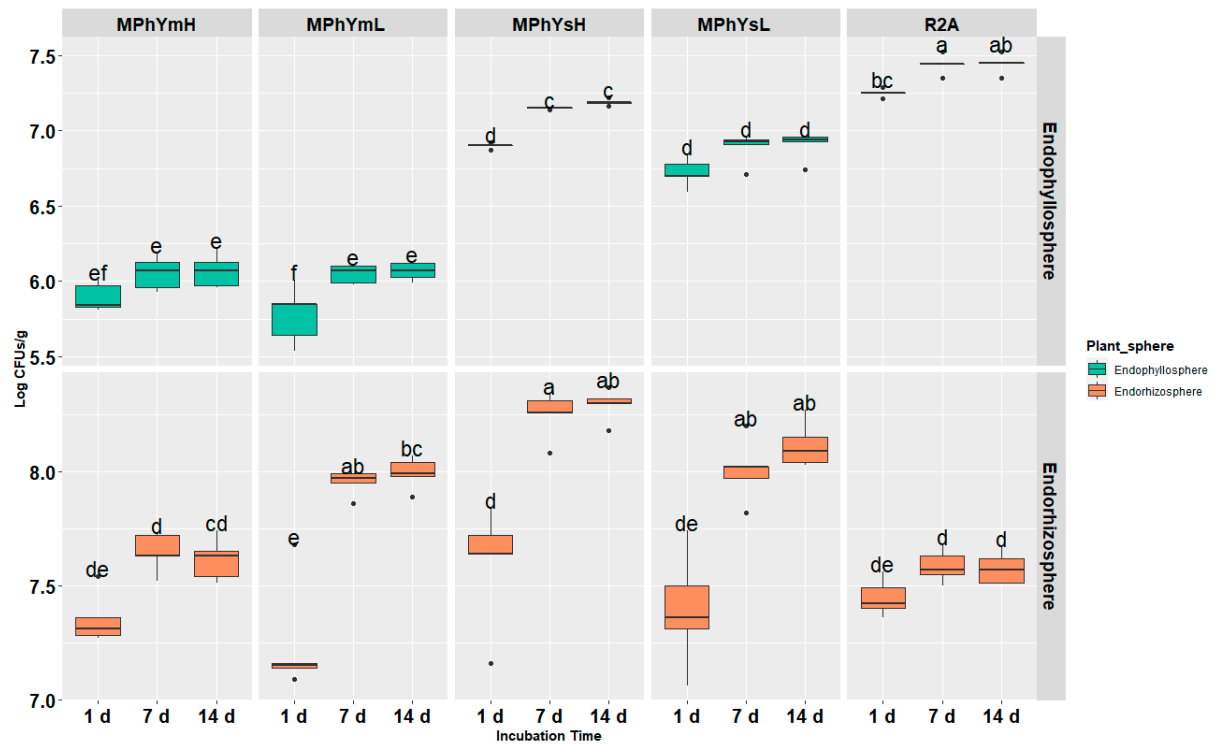


Figure S3. Log colony forming units (CFUs) counts A for cultivable endophytic bacteria recovered from the maize endo-rhizosphere (orange boxplots) and endo-phyllosphere (green boxplots) during incubation time (1, 7 and 14 days), cultivated on homologous (MPhYmH, maize broth 25ml L⁻¹; MPhYmL, maize broth 5ml L⁻¹) and heterologous (MPhYsH, sunflower broth 25ml L⁻¹; MPhYsL, sunflower broth 5ml L⁻¹) plant-based culture media as well as chemically-synthetic culture media (R2A) Statistical significant differences are indicated by different letters (*P* value ≤ 0.05 , *n*= 5)

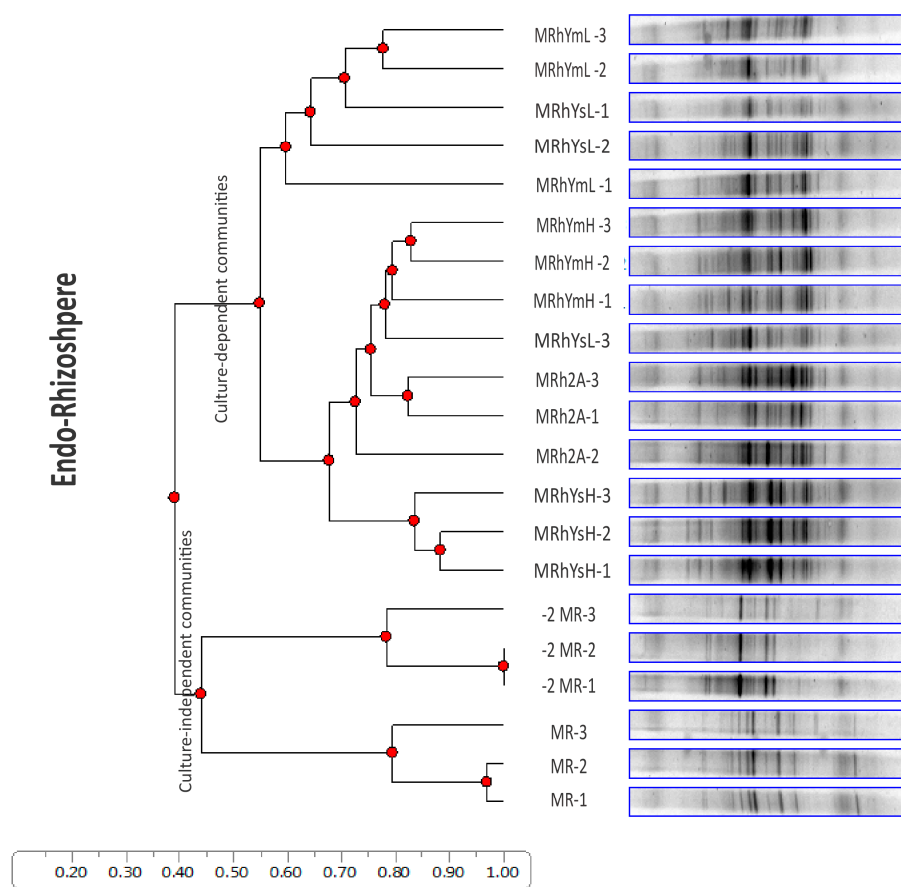


Figure S4. UPGMA clustering of Euclidean distances of DGGE fingerprints of culture-dependent and culture-independent maize endo-rhizosphere bacterial communities. Each culture medium and endo-rhizosphere mother culture is represented by three replicates (plates 1–3).

ML, culture-independent mother leaf; -2ML, 1/10 dilution of culture-independent mother leaf; MPhYmH MPhYmH, culture-dependent on homologous maize broth 25mL-1; MPhYmL, culture-dependent on homologous maize broth 5mL-1 ; MPhYsH culture-dependent on heterologous sunflower broth 25mL-1; MPhYsL, culture-dependent on heterologous sunflower broth 5mL-1; MPh2A, culture-dependent of R2A culture medium.