Table S1. *Micromonospora* strains used in this study

Bacterial strain	**Origin (country)**
Micromonospora alfalfae 50	South Africa
Micromonospora alfalfae 53	South Africa
Micromonospora alfalfae 55	South Africa
Micromonospora inaquosa 30	South Africa
Micromonospora inaquosa 33	South Africa
Micromonospora inaquosa 152	South Africa
Micromonospora inaquosa 230	South Africa
Micromonospora inaquosa N2	South Africa
Micromonospora purpureochromogenes N5	South Africa
Micromonospora tulbaghiae 48	South Africa
Micromonospora tulbaghiae N4	South Africa
Micromonospora violae 29	South Africa
Micromonospora violae 43	South Africa
Micromonospora violae 45	South Africa
Micromonospora violae 66	South Africa
Micromonospora violae 126	South Africa
Micromonospora violae 249	South Africa
Micromonospora lupini 5052	Poland
Micromonospora purpureochromogenes 5056	Poland

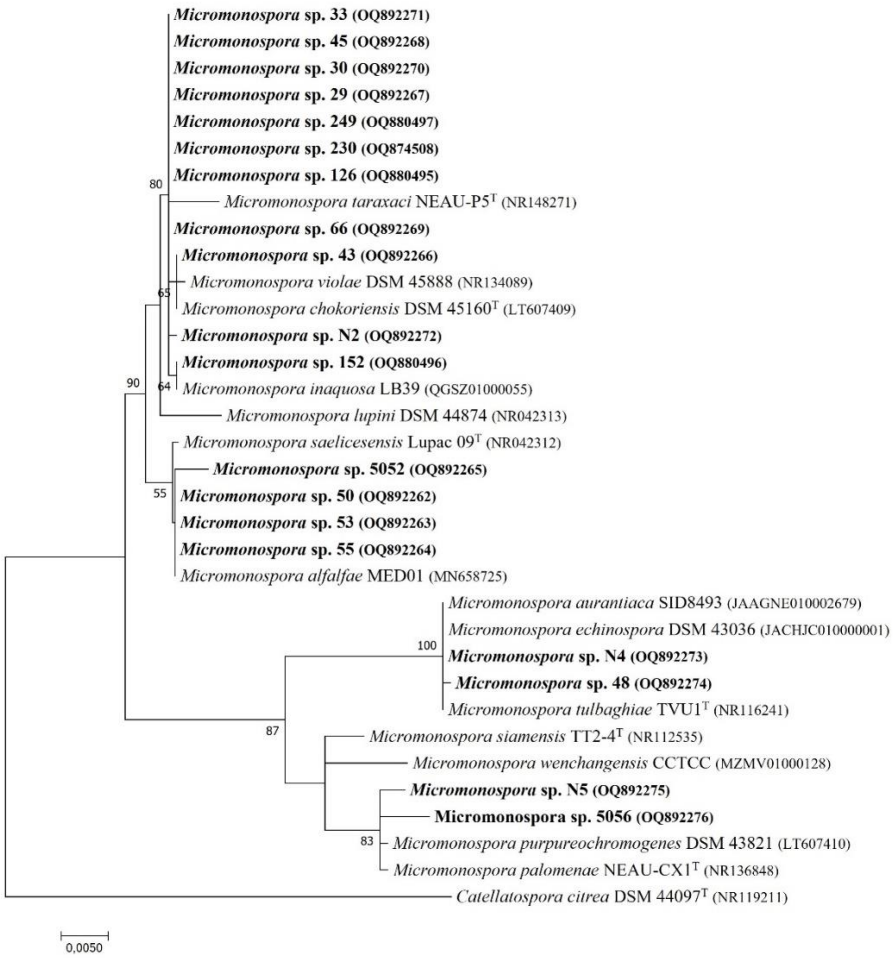

Figure S1. The maximum-likelihood phylogenetic tree of 16S rRNA gene fragments of the nineteen endophytic isolates and fourteen most closely related taxa was constructed using the Tamura-Nei model [49]. Discrete Gamma (+G) distribution was used to model evolutionary rate differences among sites and the rate variation model allowed some sites to be evolutionarily invariant (+I). Bootstrap values [%] higher than 50 are shown next to the branches. The scale bar represents 0.005 substitutions per nucleotide position.

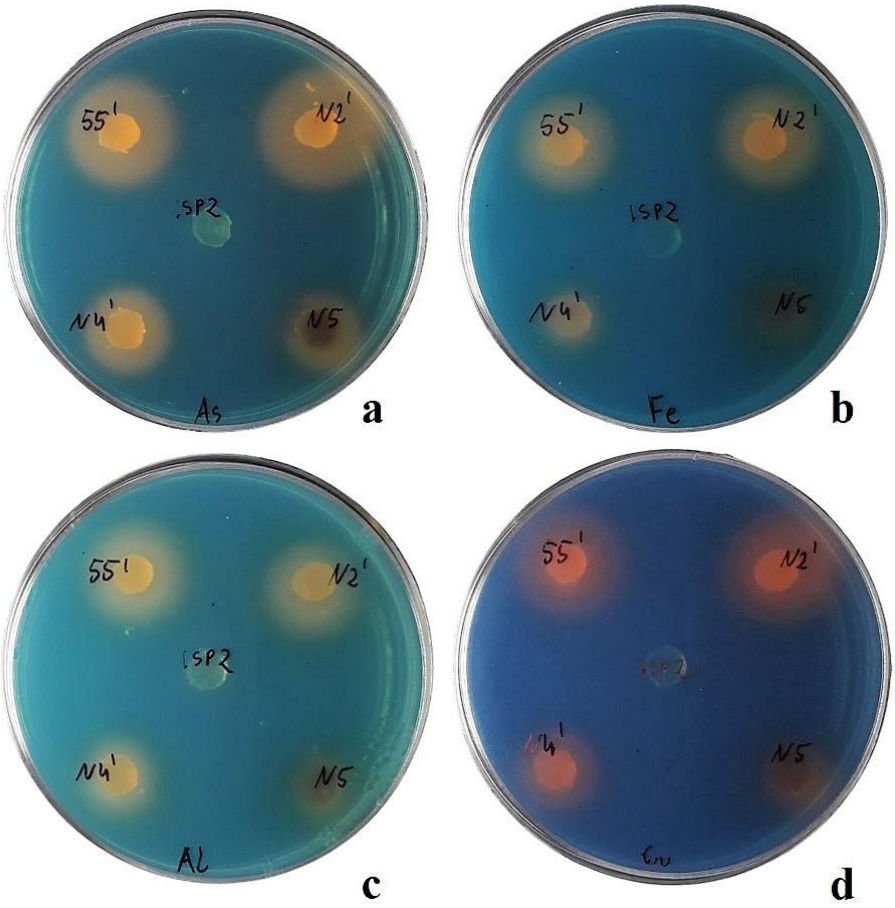

Figure S2. Production of metallophores - sterile ISP2 agar plugs placed in the centre were used as a negative control (no halo).