

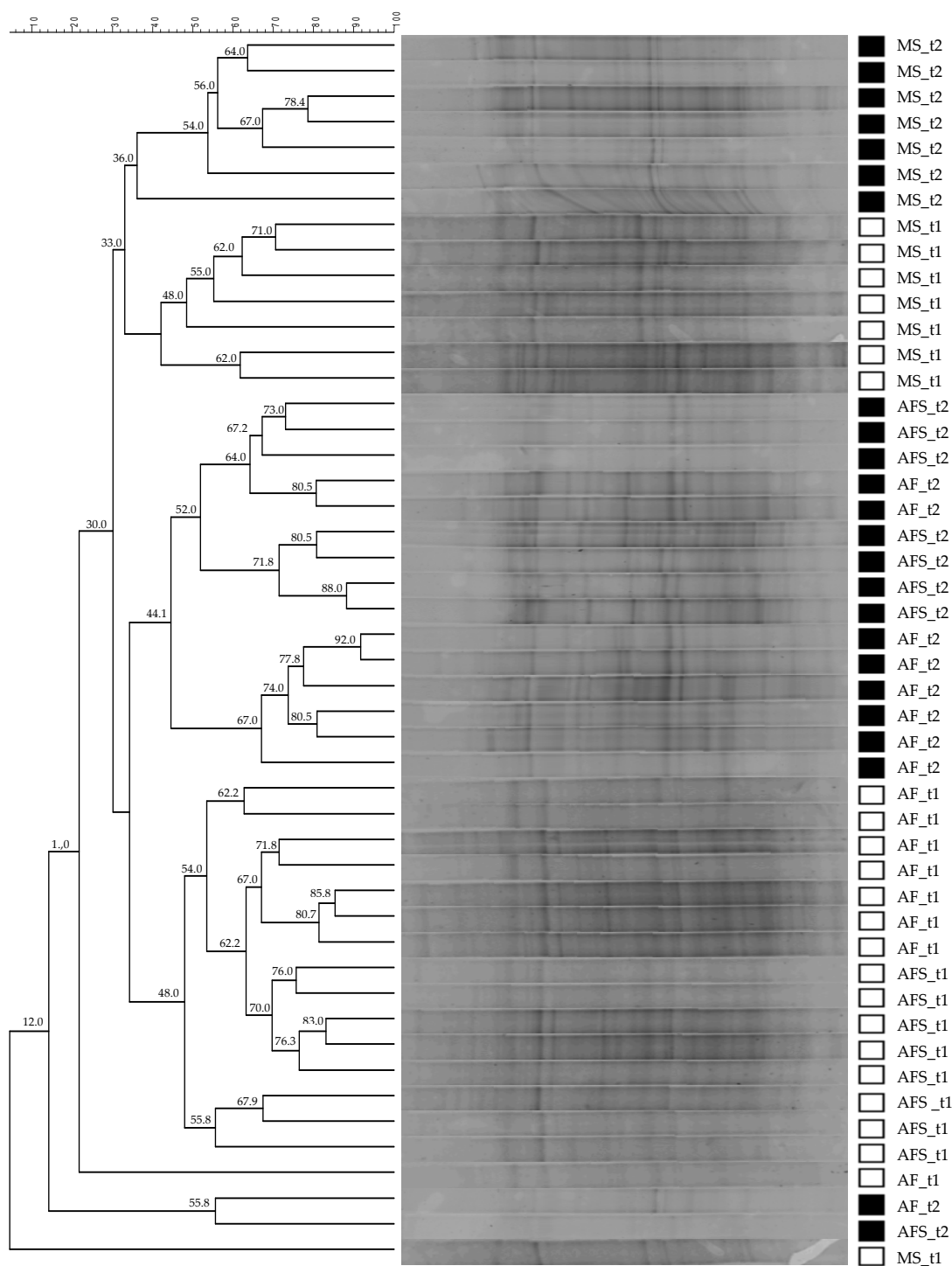
Supplementary Materials

Table S1. Quantitative test of antimicrobial substance (AMS) production by strain affiliated with the genus *Bacillus* sp.

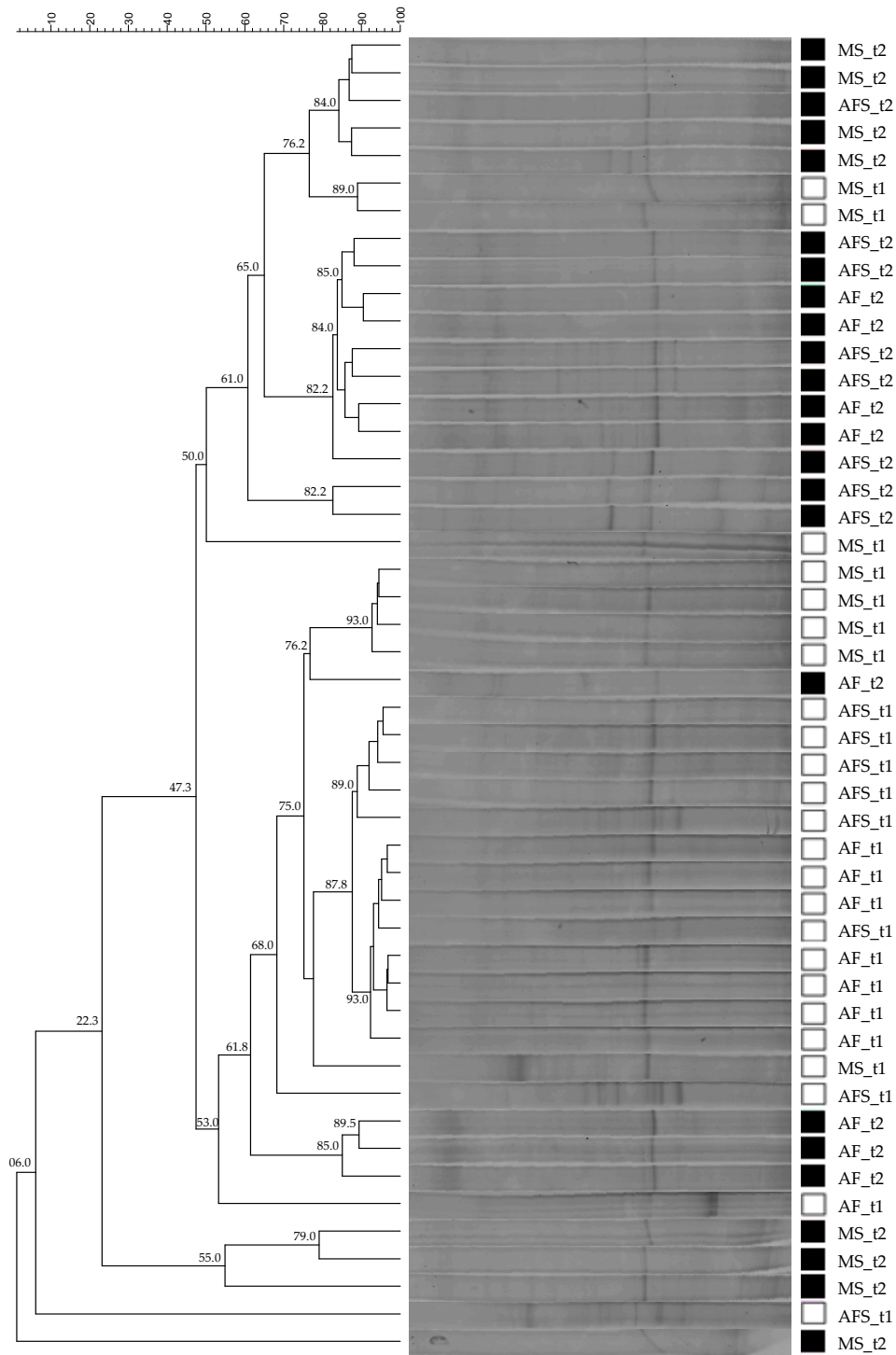
Bacterial strains	Inhibition (%)					
	<i>Colletotrichum</i>	<i>Curvularia</i>	<i>Fusarium</i>	<i>Pestalotiopsis</i>	<i>Pythium</i>	<i>Rhizoctonia</i>
CP1-28	59,15±3,00a	71,76±2,52a	75,71±2,00ab	47,15±1,15a	62,50±1,00ab	68,66±1,73ab
CP1-30	59,62±1,52a	76,85±1,15ab	84,29±9,54ab	56,91±1,15a	50,00±7,55a	65,17±1,15a
CP2-47	63,38±1,00a	77,78±2,65ab	85,24±9,07ab	58,54±1,00a	55,09±2,31ab	68,66±1,00ab
CP2-38	60,56±0,00a	75,00±4,36ab	66,19±3,06a	64,23±6,81a	60,65±2,31ab	72,14±2,52ab
CP2-13	62,91±1,52a	75,93±0,58ab	73,81±1,15ab	63,41±3,61a	61,57±7,23ab	69,65±3,79ab
CP3-40	100,00±0,00c	100,00±0,00c	100,00±0,00b	100,00±0,00b	69,44±0,00b	100,00±0,00c

Means ± SD with common letters in the same column do not show significant differences ($p < 0,05$) by Tukey's test.

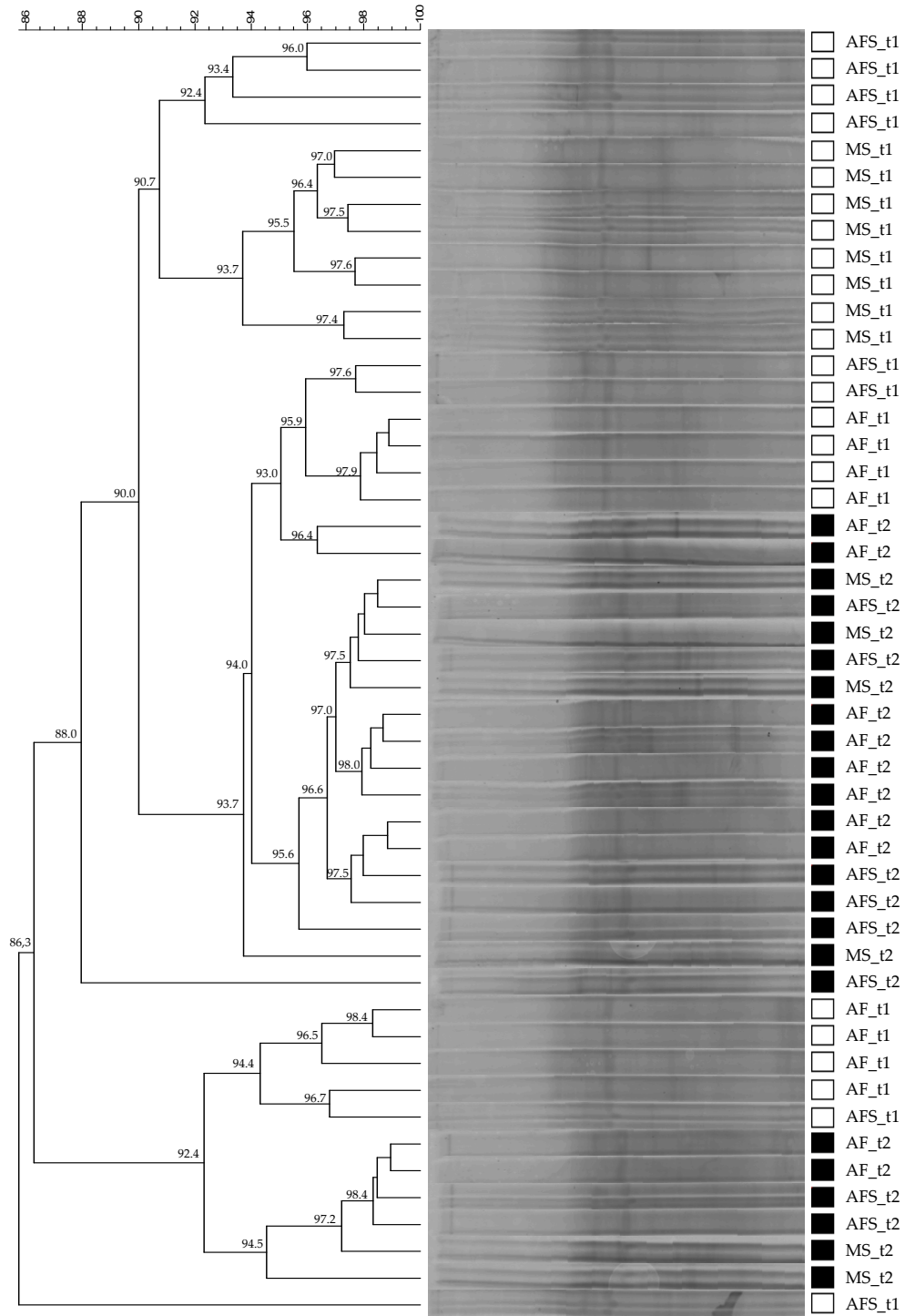
A



B



C



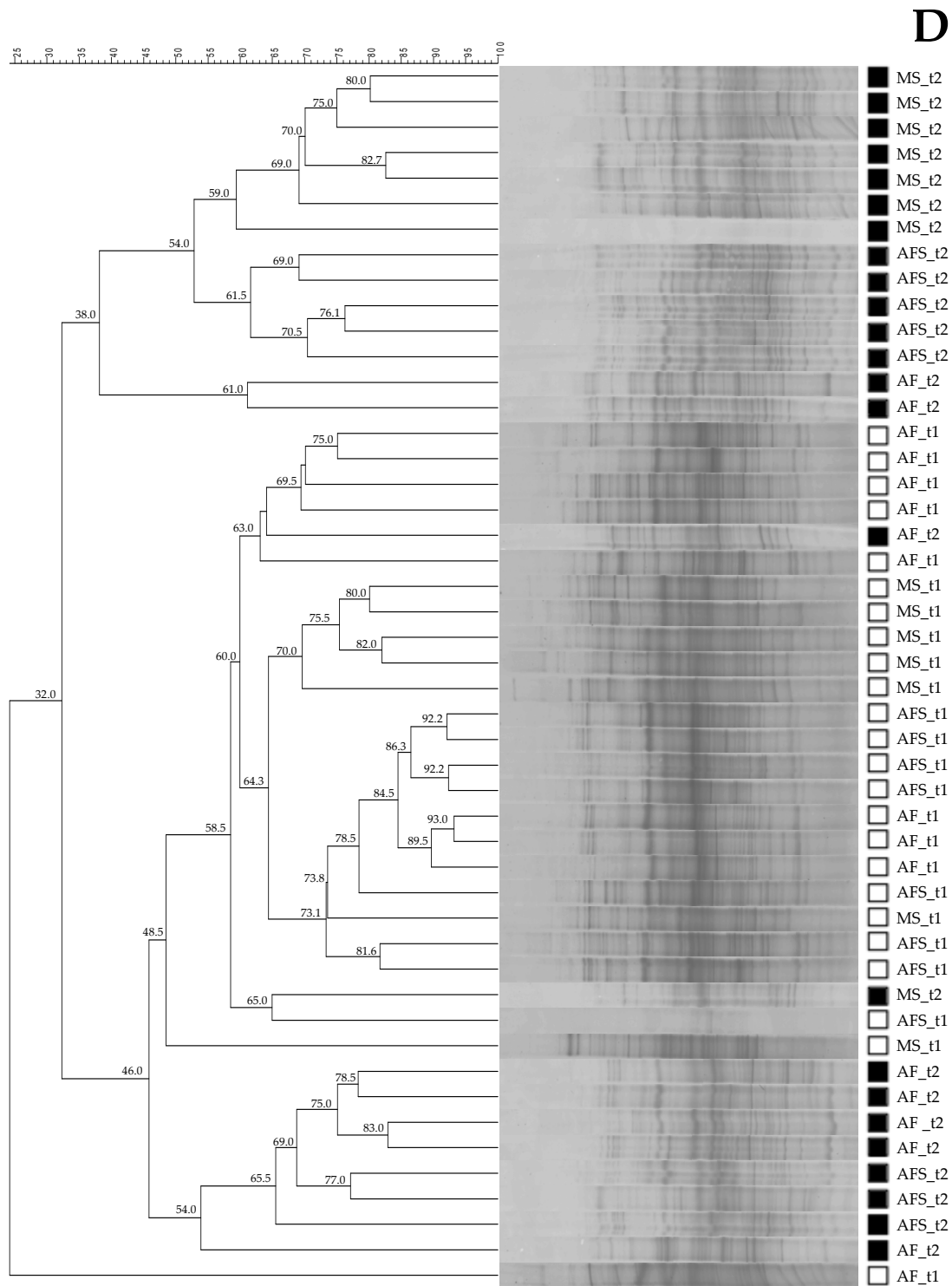


Figure S1. UPGMA cluster analysis of the DGGE fingerprint of bacterial communities (A), phosphate-solubilizing bacteria (B), diazotrophic (C), and fungi (D) in AFS, MS e AF systems during dry (t1) and rainy (t2) seasons.