

Supplementary Figure S2. Latex clearing protein (lcp) amino acid sequence alignment of the 18 clear zone forming strains to determine the 13-residue long highly conserved region.

Dactylosporangium sp. AC04546	KTRLVHA AVRHLLEQSPYWA AVAD-EEIPISQRDMMVTW HSLPTTVMQKLT
Micromonospora sp. AC00493	KTRLVHA AVRHLLEQSPYW PQVAD-EEIPISQRDMMVTW HSLPTTVMQKLV
Micromonospora sp. AC03293	-----MMVTW HNLPTTVMQKLT
Micromonospora sp. AC00064	KTRLIHA AVRHLLEKSPYW QQSAD-EEIPISQADMMVTW HSLPTTVMKTLQ
Micromonospora sp. AC00503	KTRLTHA AVRHLLEQSA PWRGVTD-HPIPI SNGDILITFHSLGTYV H RKLL
Micromonospora sp. AC03275	KTRLTHA AVRHLLEQSA PWRGVTD-HPIPI SNGDILITFHSLGTYV H RKLL
Micromonospora sp. AC03913	KTRLTHA AVRHLLEQSA PWRGVTD-HPIPI SNGDILITFHSLGTYV H RKLL
Microtetraspora sp. AC03312	KTRLTHA AVRHLLEQSA PWRGVTD-HPIPI SNGDILITFHSLGTYV H RKLL
Microtetraspora sp. AC03326	KTRLTHA AVRHLLEQSA PWRGVTD-HPIPI SNGDILITFHSLGTYV H RKLL
Microtetraspora sp. AC03309	KTRLVHA AVRHLLEKSPYW QKSAD-EEIPISQADMMVTW HSLPTTVMKTLQ
Microtetraspora sp. AC03313	KTRLVHA AVRHLLEKSPYW QKSAD-EEIPISQADMMVTW HSLPTTVMKTLQ
Microtetraspora sp. AC03316	KTRLVHA AVRHLLEKSPYW QKSAD-EEIPISQADMMVTW HSLPTTVMKTLQ
Microtetraspora sp. C03318	KTRLVHA AVRHLLEKSPYW QKSAD-EEIPISQADMMVTW HSLPTTVMKTLQ
Microtetraspora sp. AC03330	KTRLVHA AVRHLLEKSPYW QKSAD-EEIPISQADMMVTW HSLPTTVMKTLQ
Nonomuraea sp. AC03182	KTRLVHA AVRHLLEQSPYW PQVAD-EEIPISQRDMMVTW HSLPTTVMQKLV
Nonomuraea sp. AC03289	KTRLVHA AVRHLLEQSPYW SQVAD-EEIPISQRDMMVTW HSLPTTVMQKLV
Streptomyces sp. AC04842	RGDLLRPVLR TDVEIERAVRRDVLGATLR LTPRALALAV EDGVVTLTGRL E
Streptomyces sp. AC00383	KTRMVHA AVRHLLEQSPGW KQVSGGQTVPISQADILVTW HSLATYAMRKLR