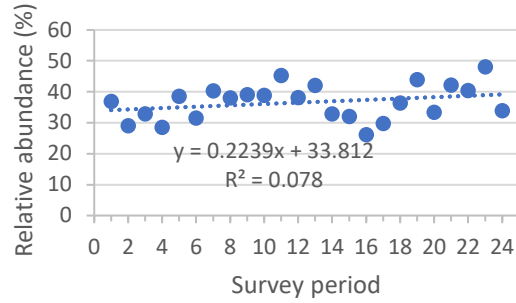
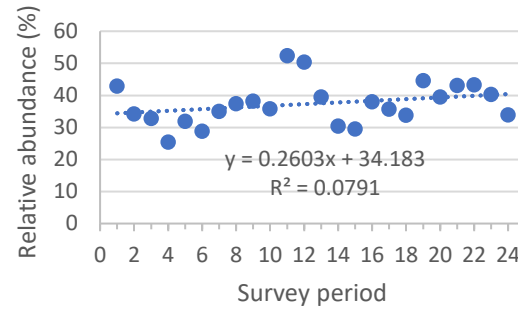


*Streptomycetaceae; Streptomyces*

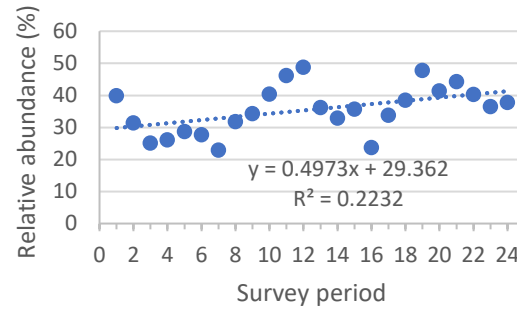
Stage 1



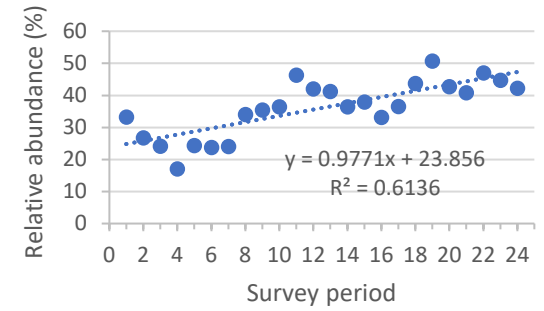
Stage 2



Stage 3

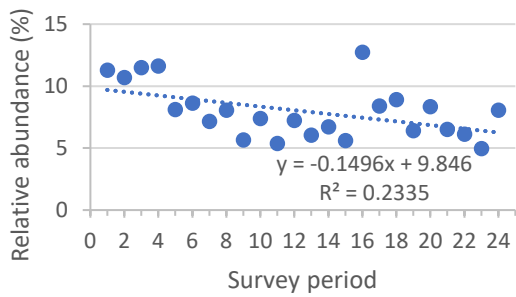


Stage H

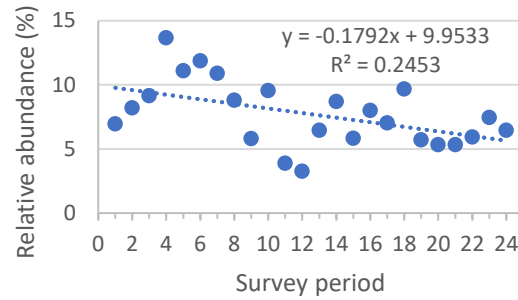


*Dongiaceae; Dongia*

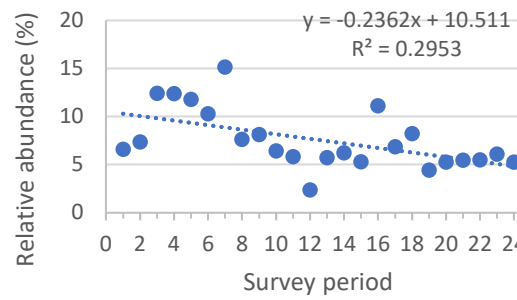
Stage 1



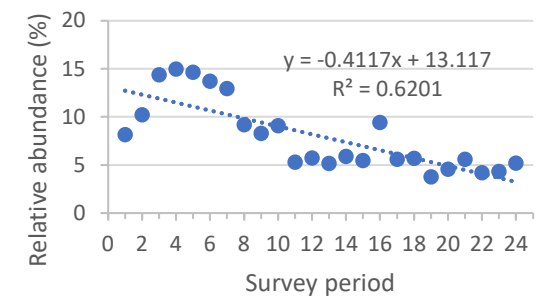
Stage 2



Stage 3

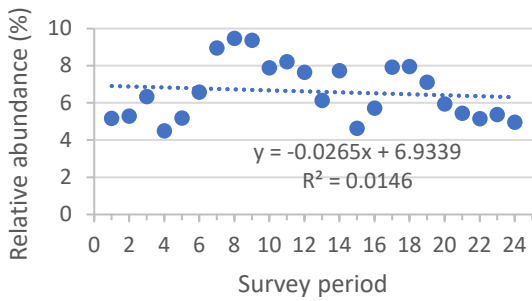


Stage H

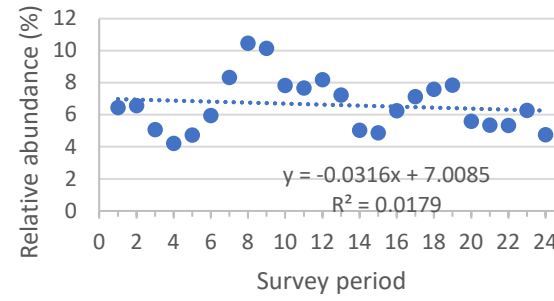


*Streptosporangiaceae; Nonomuraea*

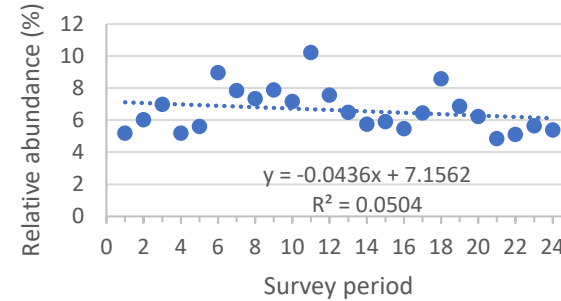
Stage 1



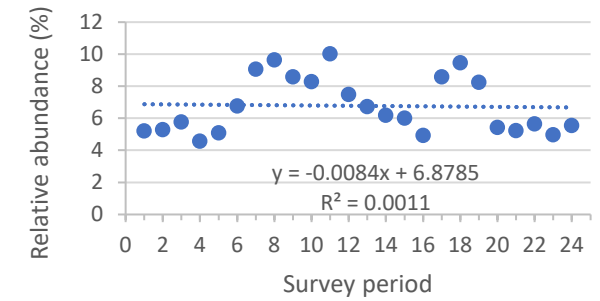
Stage 2



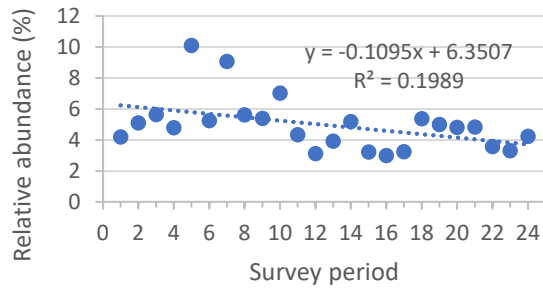
Stage 3



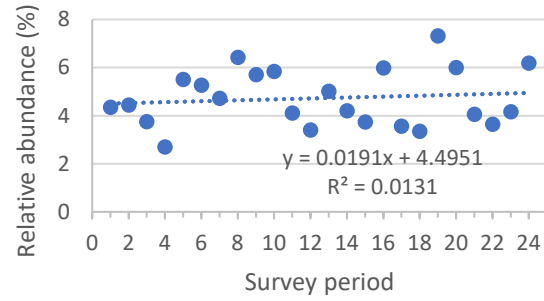
Stage H



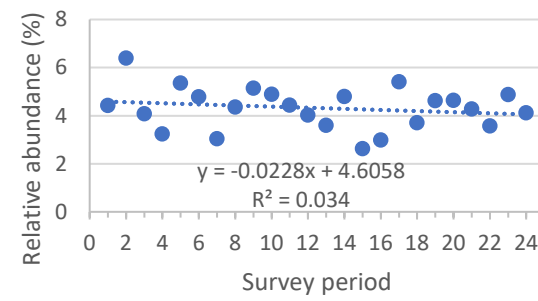
Stage 1



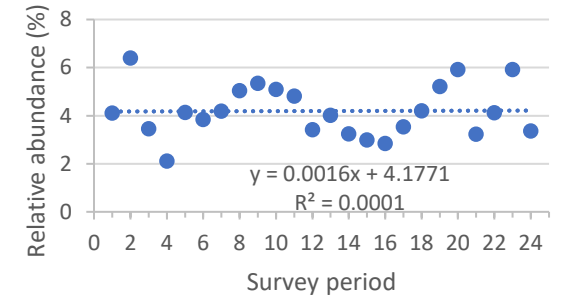
Stage 2

*Sphingomonadaceae; Rhizorhapis*

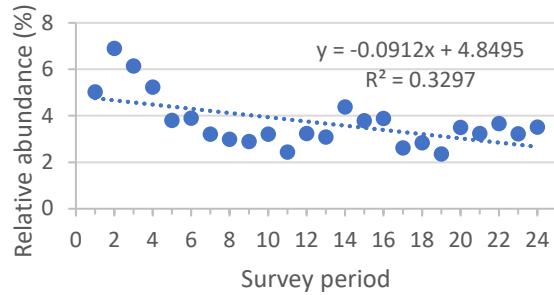
Stage 3



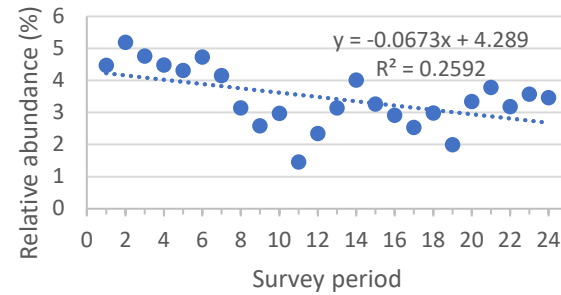
Stage H



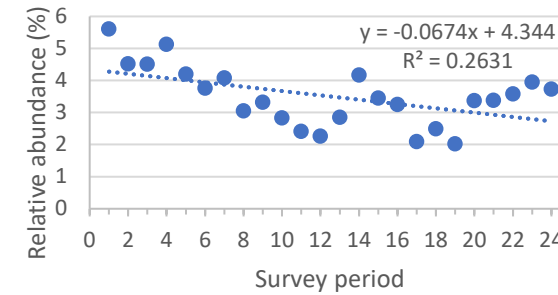
Stage 1



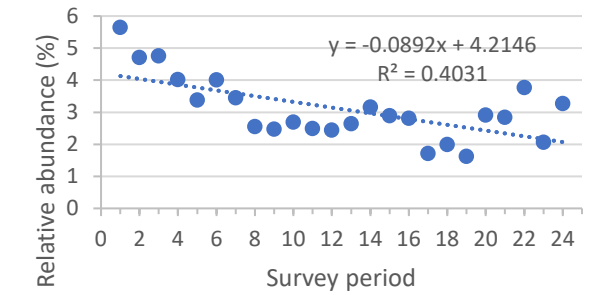
Stage 2

*Xanthobacteraceae; Ambiguous texa-51*

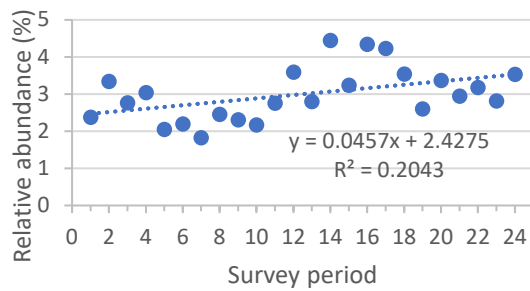
Stage 3



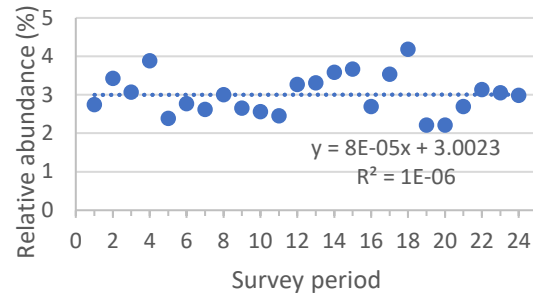
Stage H



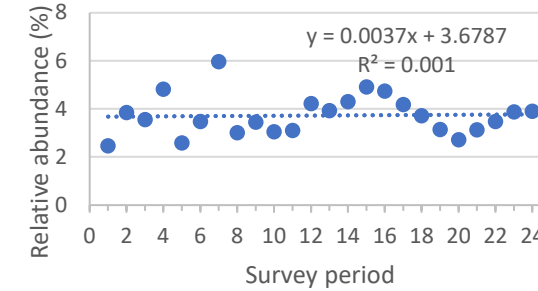
Stage 1



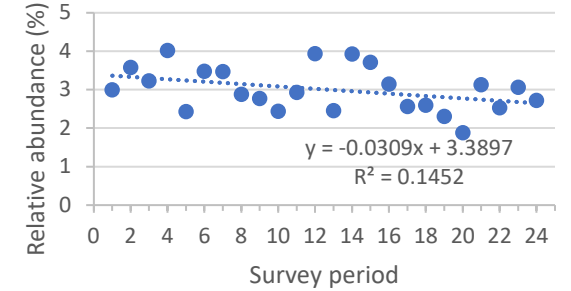
Stage 2

*Nocardiodaceae; Kribbella*

Stage 3

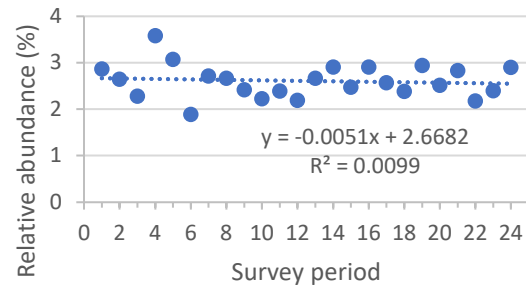


Stage H

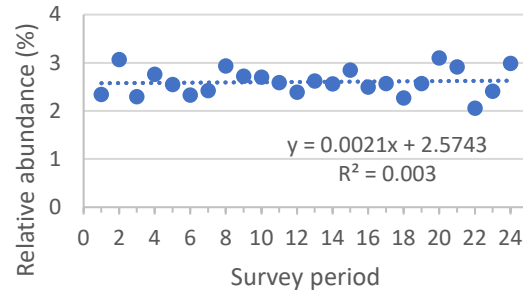


*Rhizobiaceae; Ensifer*

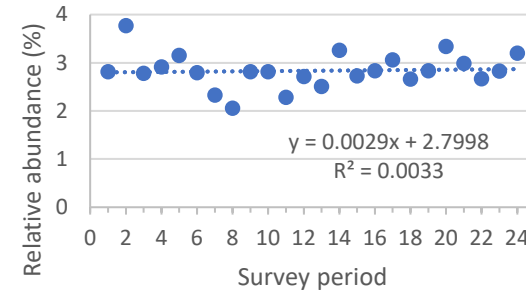
Stage 1



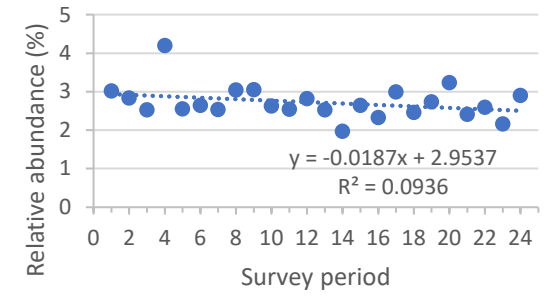
Stage 2



Stage 3

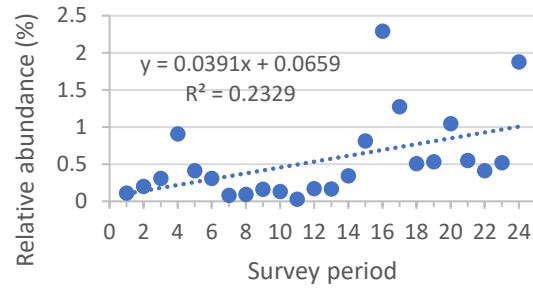


Stage H

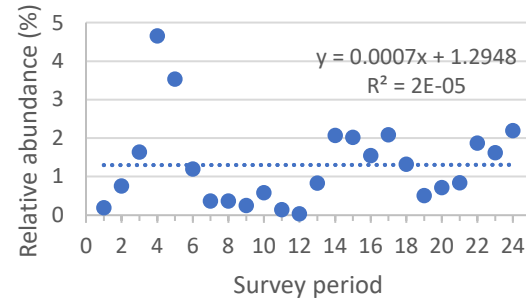


*Pseudonocardiaceae; Labedaea*

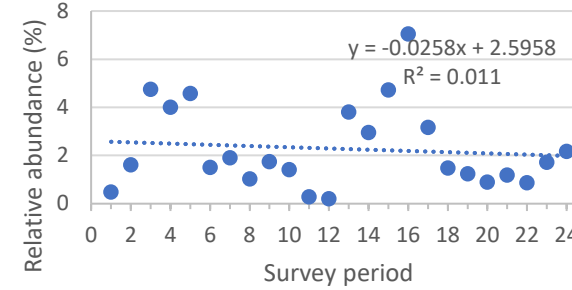
Stage 1



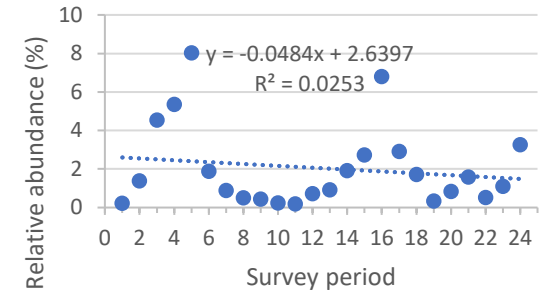
Stage 2



Stage 3

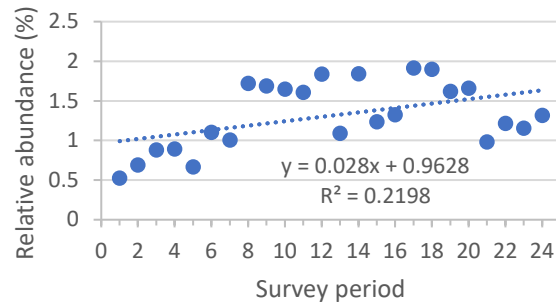


Stage H

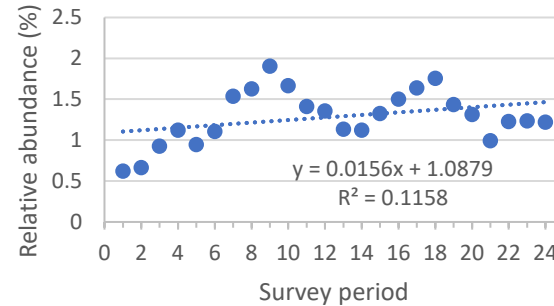


*Pseudonocardiaceae; Pseudonocardia*

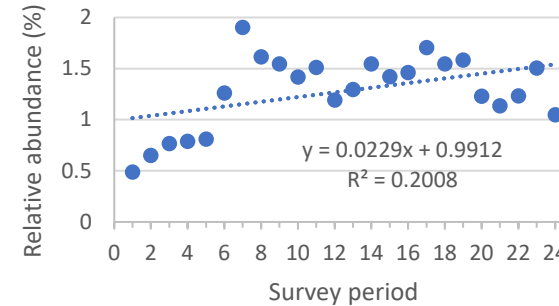
Stage 1



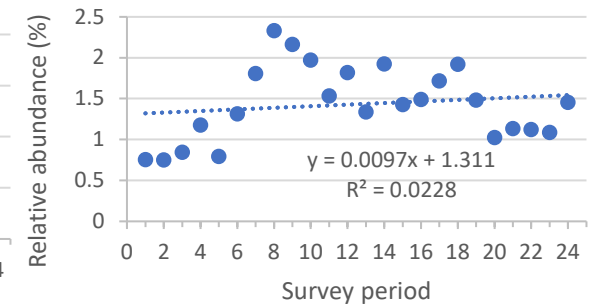
Stage 2

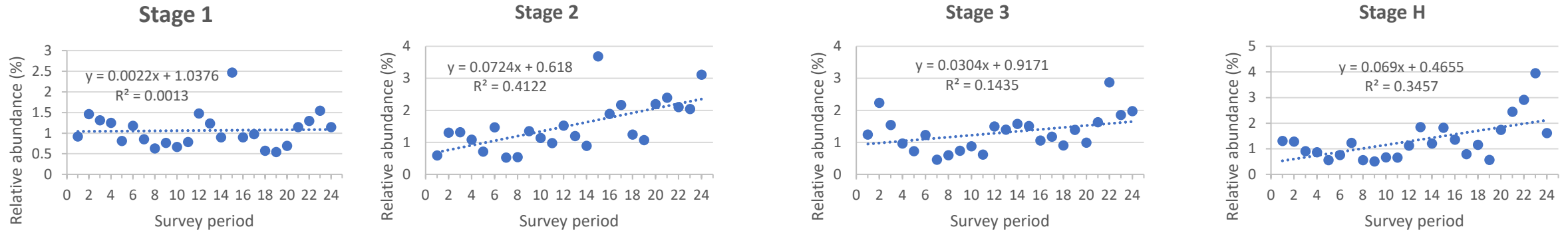


Stage 3



Stage H





**Figure S2.** The changes in the relative abundance of top ten most abundant bacterial genera over 24 consecutive monthly survey periods. The linear regression equation and R square value were indicated in the figure.