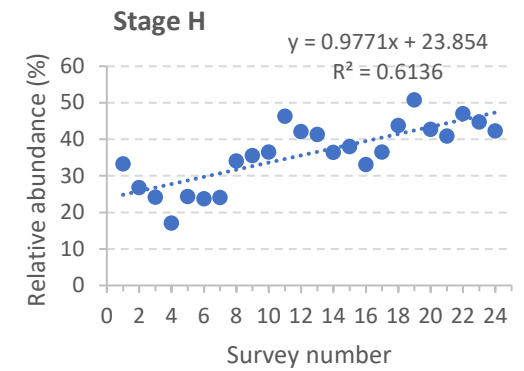
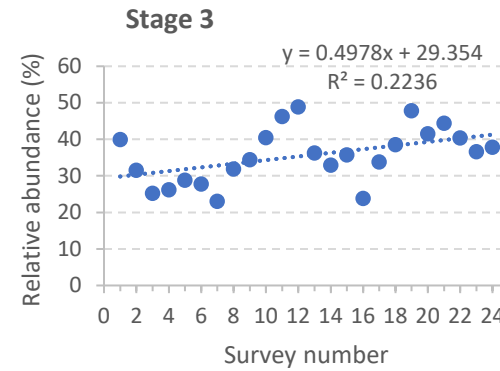
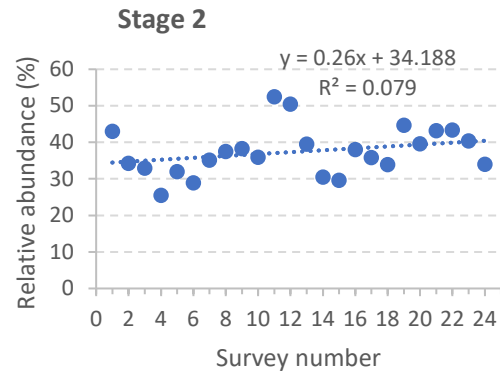
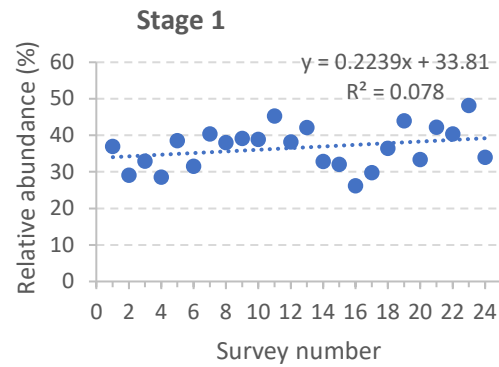
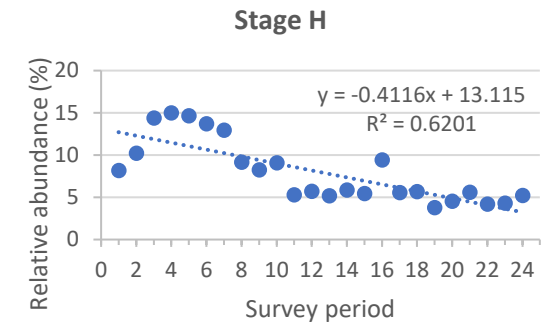
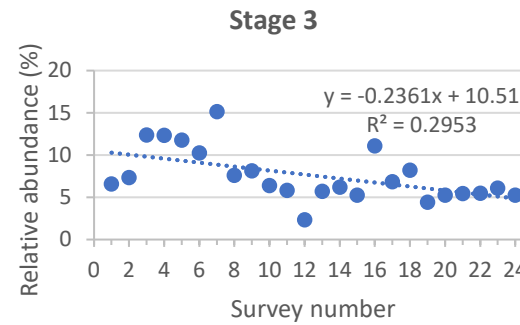
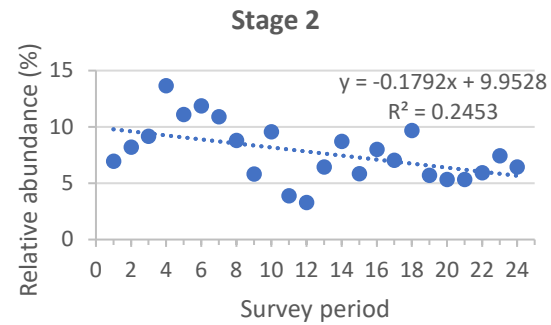
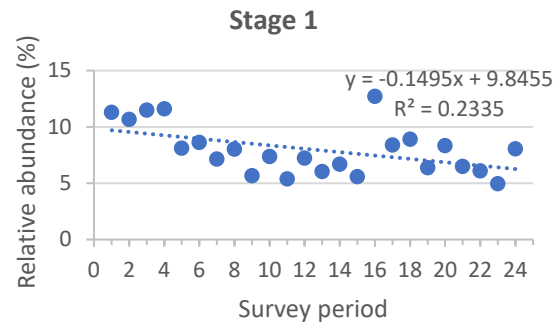


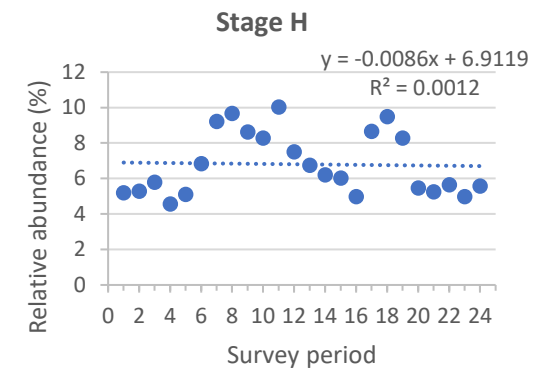
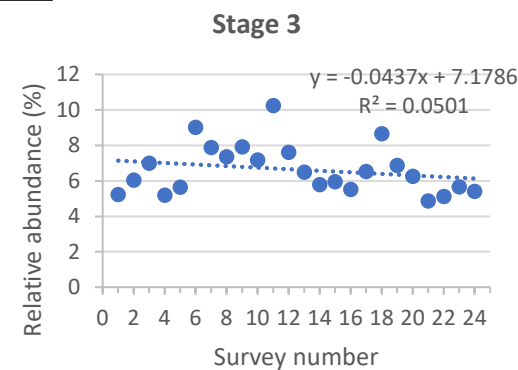
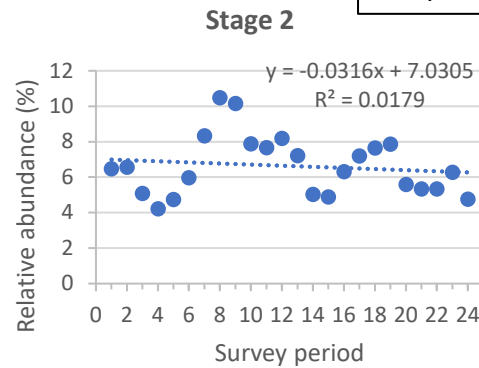
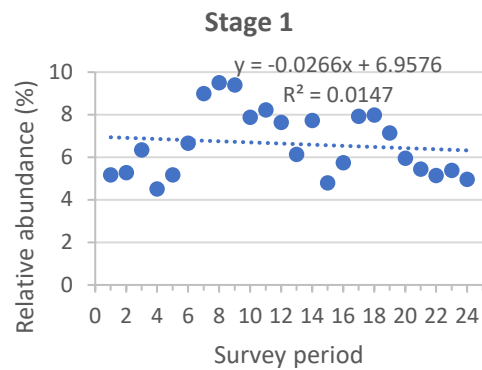
Streptomycetaceae



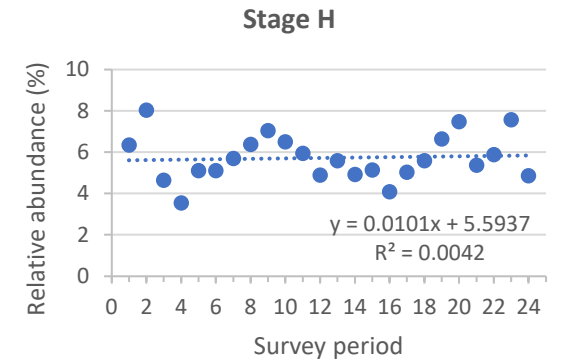
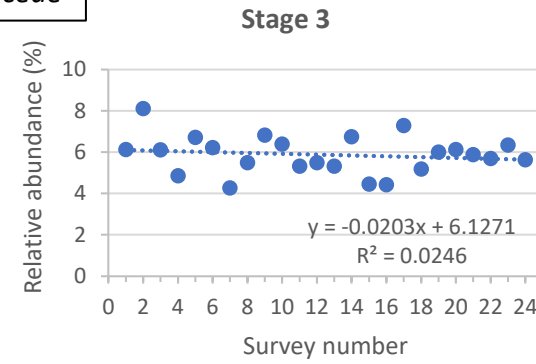
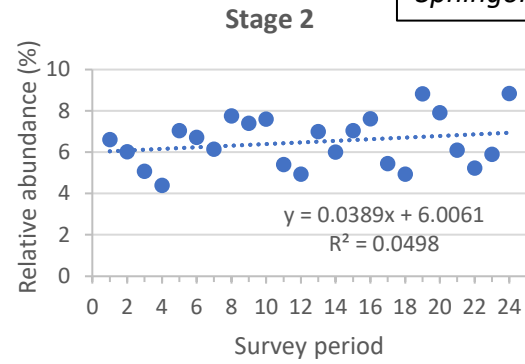
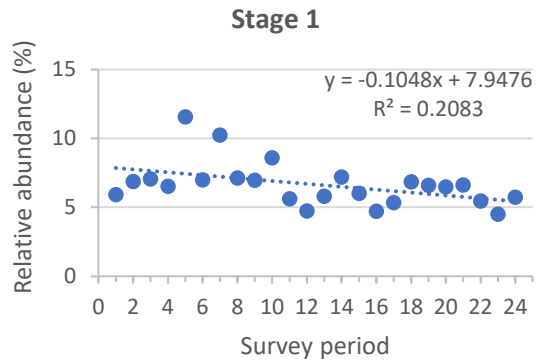
Dongiaceae



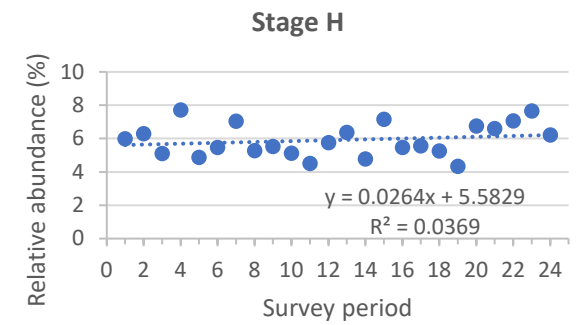
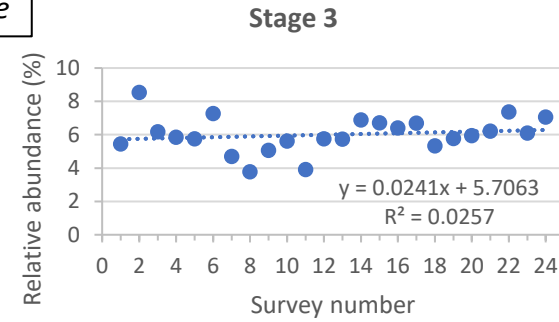
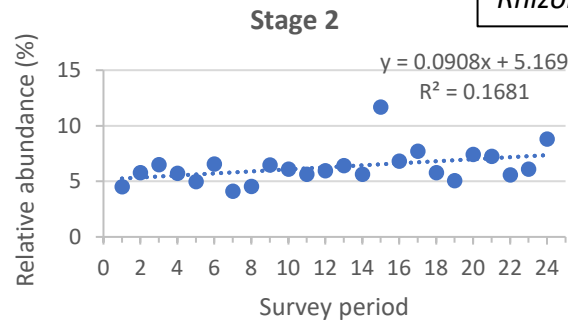
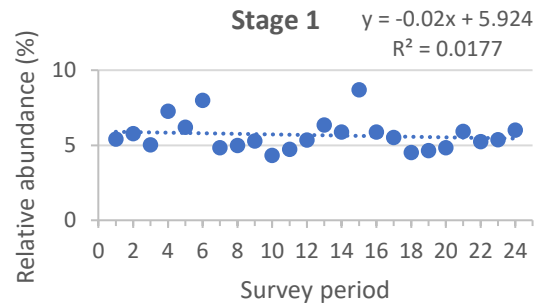
Streptosporangiaceae



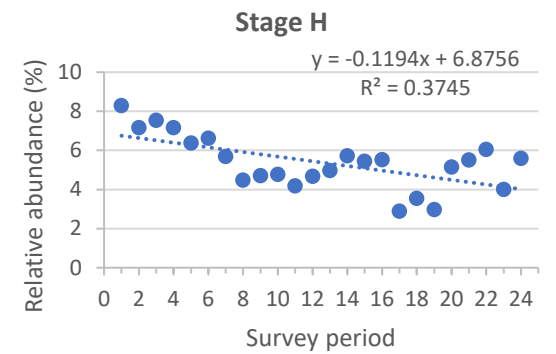
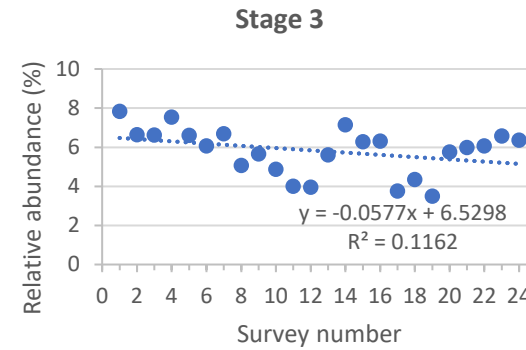
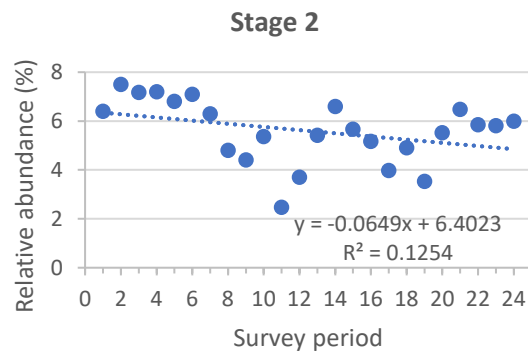
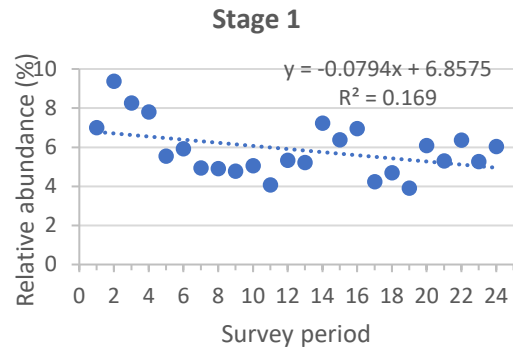
Sphingomonadaceae



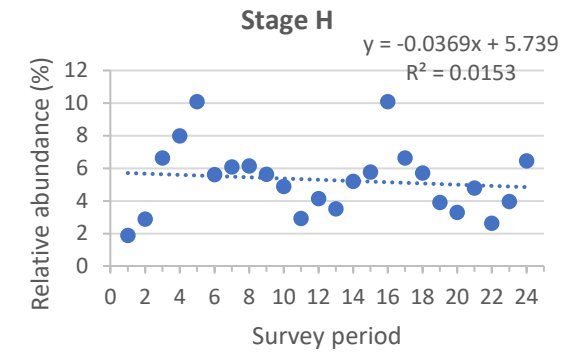
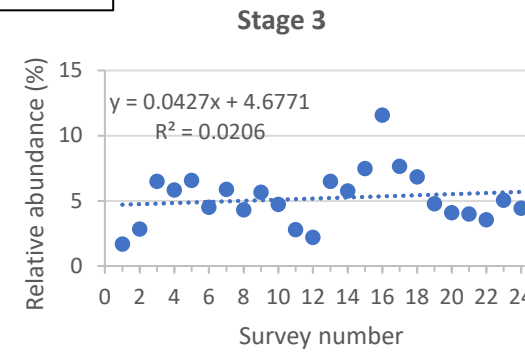
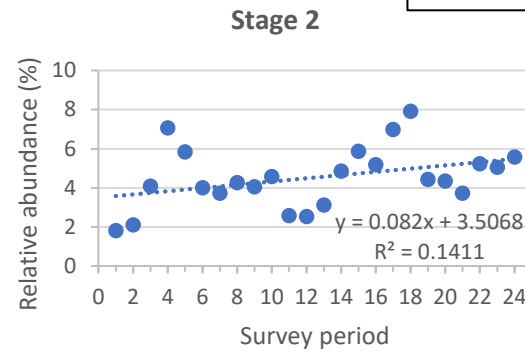
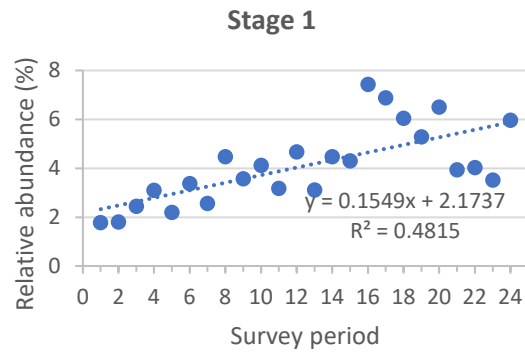
Rhizobiaceae



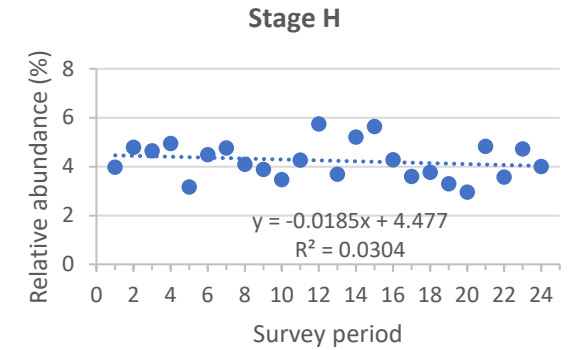
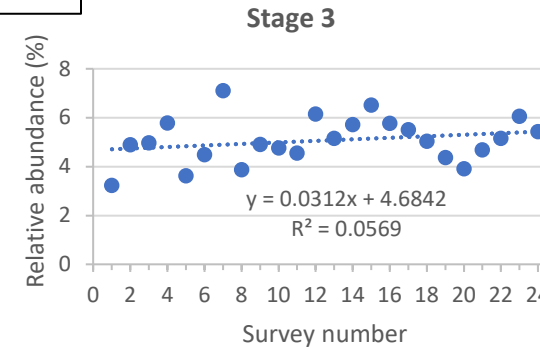
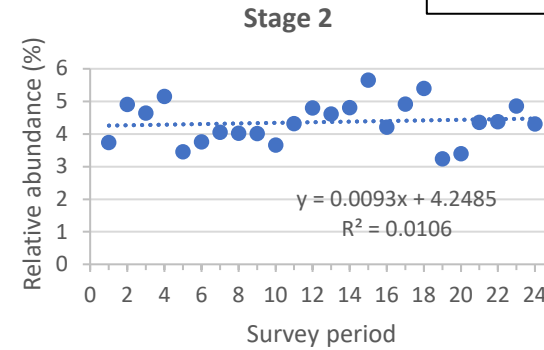
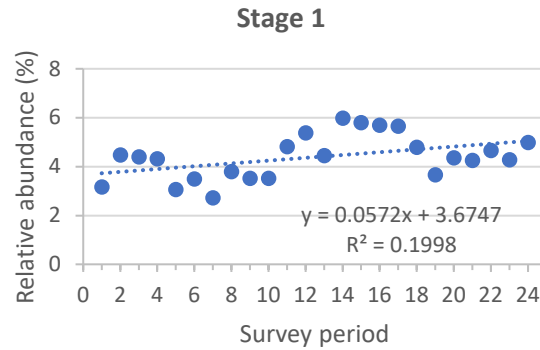
Xanthobacteraceae



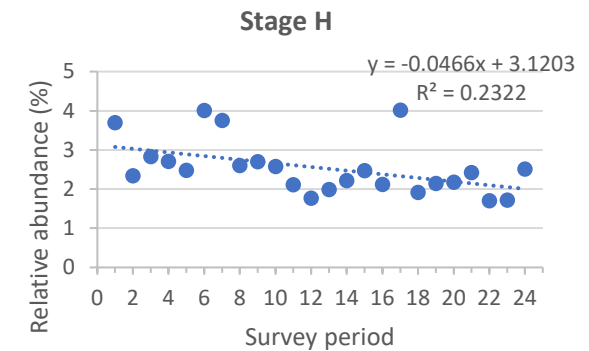
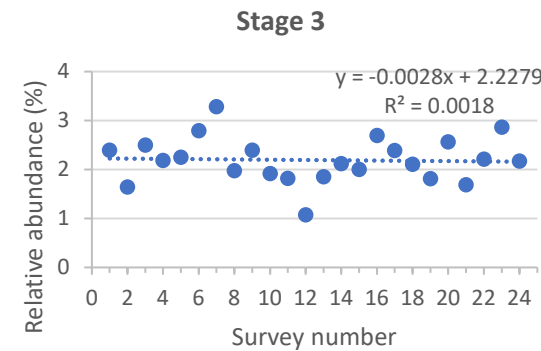
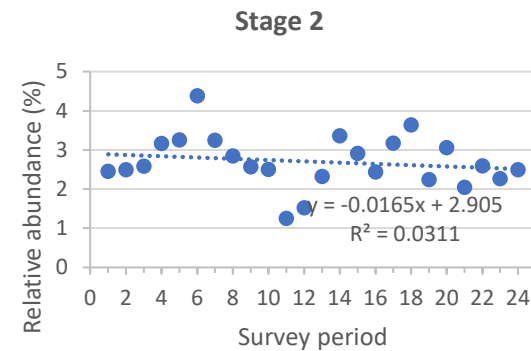
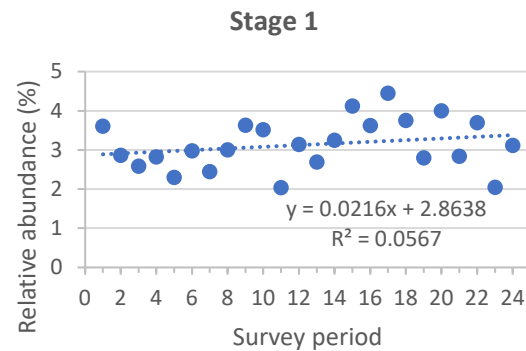
Pseudonocardiaceae



Nocardoidaceae



Micromonosporaceae



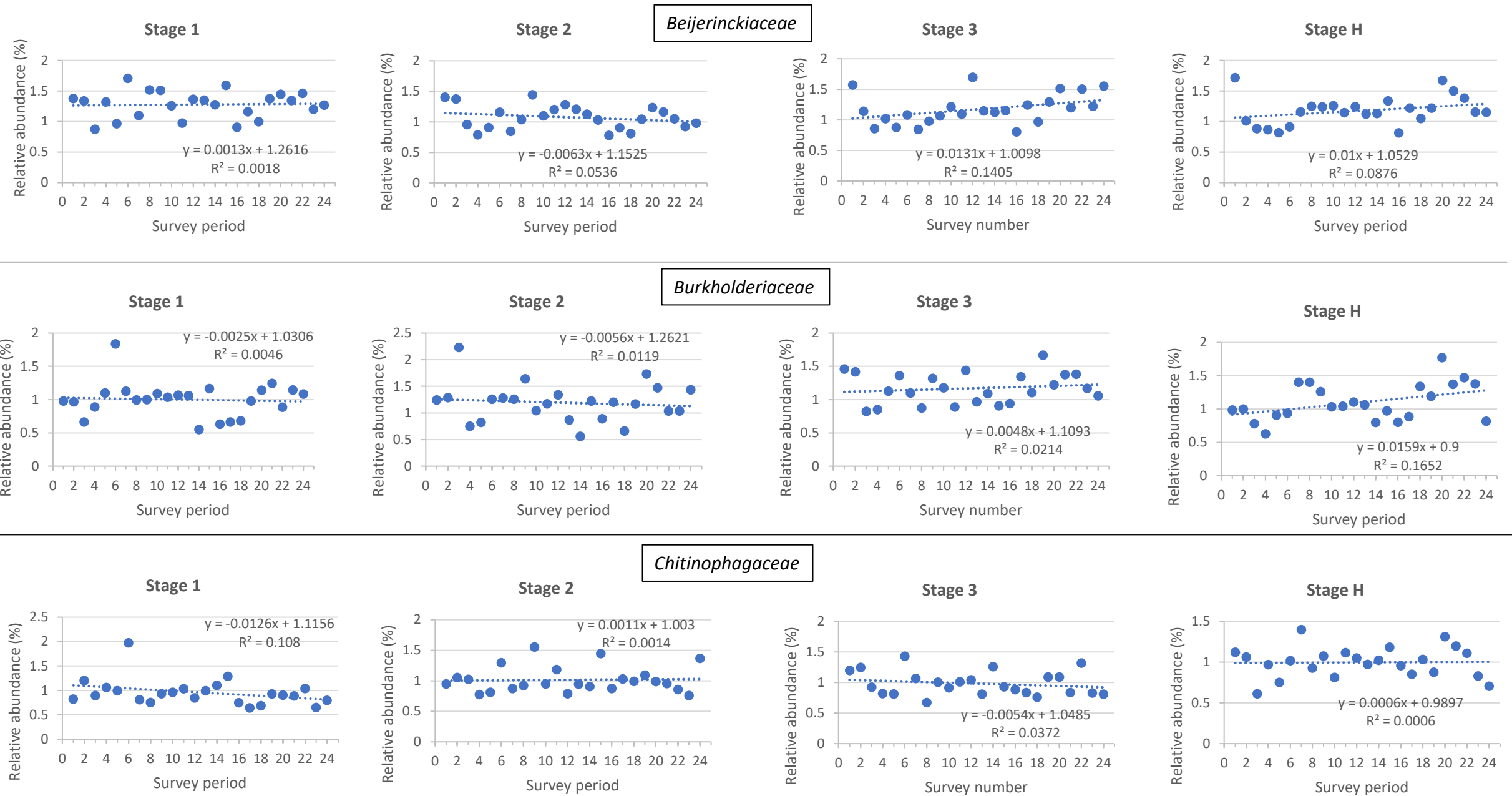


Figure S1. The changes in the relative abundance of twelve bacterial families with $\geq \sim 1\%$ relative abundance over 24 consecutive monthly survey periods. The linear regression equation and R square value were indicated in the figure.