

The effect of thinning on the succession of deadwood inhabiting fungi and bacteria in a tropical forest of Taiwan

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Purpose: Coarse woody debris (CWD) namely deadwood, the major organic carbon pool in forest ecosystem provides plentiful nutrient sources and shelter for organisms, primarily fungi and saproxylic insects. However, some studies currently revealed that deadwood inhabiting bacteria have emerged as an important group taking part in the decomposition, but the interaction between fungi and bacteria still remains unknown.

Methods: The study was conducted at a 1-ha experimental site, established in five tree thinning degrees in Tajen Forest Station, located in tropical area of Taiwan. Fresh logs of *Cyclobalanopsis pachyloma* and *Machilus thunbergii* had been randomly laid on the ground for three years. Bacterial and fungal composition of the initial phase of the deadwood decomposition were disentangled by Illumina MiSeq and PacBio Sequel, respectively.

Results and conclusions: A total of 7,333,022 qualified bacterial and 243,615 qualified fungal sequences were obtained from 40 logs. A total of 18 phyla 45 classes 136 families 221 genera 242 species were detected with *Enterobacter sp.*, *Pseudomonas viridiflava* and *Pantoea agglomerans* dominated the bacterial assemblage while 8 phyla 40 classes 289 families 637 genera 976 species were detected with *Pestalotiopsis sp.*, *Pestalotiopsis maculans* and *Cryptococcus sp.* dominated the fungal assemblage. NMDS based on deadwood inhabiting bacterial and fungal composition at initial decayed phase indicates that both assemblages differed between the two deadwood species across the five thinning treatments. Moreover, both assemblages did not significantly interact at initial decomposition based on the procrustes analysis ($m= 0.96$, $r= 0.25$). In conclusion, both microbiome and mycobiome of initial decomposition were affected by deadwood species, not tree thinning degrees.