

Tracking the associations of tree-pathogenic fungi and Scolytinae beetles across the United Kingdom

Angelina Ceballos-Escalera

Bark and ambrosia beetles (Coleoptera: Scolytinae) associate with fungi to colonise trees. Some tree-killing diseases are caused by pathogenic fungi vectorised by these beetles, with serious ecological and economic consequences. To major outbreaks, it is crucial to fully understand beetle-fungi associations, by identifying the factors mediating in beetle-fungi interactions. With this aim, the fungal communities coexisting inside bark and ambrosia beetles were investigated. Beetles were trapped in healthy forests to analyse their inner fungal communities through Metabarcoding. This technique identifies entire fungal communities from individual beetle specimens through their DNA barcodes, which are short standardised sequences of DNA that work as unique species identification markers. Firstly, the fungal communities found in beetles captured in three major British forest types (pine, spruce and oak) were analysed. More specifically, the fungal richness, composition and abundance of 160 specimens from seven beetle species were compared to try to clarify the effect of beetle species and forest type on these fungal communities. Secondly, a biodiversity survey of fungi retrieved from 12 different beetle species trapped across the UK was conducted to correlate fungal communities with geographic variables. Results show some beetle species playing a major role to influence fungal community composition and abundance. Forest type –especially spruce- may also determine fungal diversity. Preliminary results indicate also an effect on these communities of abiotic factors such as latitude or longitude. A major outcome of this project is a tested methodology to monitor beetle-fungal communities using DNA from trapped beetles for early detection of pathogenic fungi.