



How to collaborate with the QBOL project

How to act: step by step (example)

You are interested in working on the fungus *Atropellis pinicola* and *Atropellis piniphila*.

- Step 1: You review the fungal target list of specimens on the QBOL website (www.qbol.org) and contact the QBOL coordinator of the taxon involved. You make suggestions for species to be included in the study and you indicate which specimens of the species and closely related species you have available in your own collection.
- Step 2: Indicate if specimens need to be included in QBOL culture collections. If permits are needed, the QBOL coordinator of the taxon involved will initiate the process of obtaining the appropriate permit.
- Step 3: Select the genes for barcoding. The QBOL coordinator of the taxon involved may give you advice which genes are most appropriate.
- Step 4: Use generic PCR primers (if available) to amplify the barcoding region and determine the sequence of that region. Sequences and trace files need to be included into the QBOL database.
- Step 5: DNA samples can be sent to QBOL DNA bank. Contact the central QBOL coordinator for which specimen DNA samples are needed and for correct shipment.
- Step 6: Check the QBOL databases design for the different taxa if you want to include other characters for the specimen into the QBOL database.