**PHYLOGENETIC ANALYSIS**

**ITS gene**

>LesA [organism=Lessonia spicata] [country=Chile: Castillo channel, Torpedo Island, Katalalixar National Reserve] internal transcribed spacer 1, partial sequence

ACCCCCCCGCTCTACAAATTGTCTGTGACGT-CGCCGTGGAAACTCCCTCGGAGGCGAGCGA-GCGATCGTCTAA---ACCCCGAGAAAGTGAAGCCGTTATGCGAAGTTGGGCGAGGGGCGCCTCGCCGAGGGTTTTTCTTTTCCCTTTCCCCTTCTTGTCTC-TTTTCTTCCCTTTTCGGGGATTTACGGGACGGGACGGGAAGGGTGAAGGAAGCTCTCGAACCAAAGCGCACCCCACTTTTCAACCCCATTAAACTCTGAATCTGAACTC-AAAGGGGGGCAGCGCTGTGCCGCGGCTCCCCCAACCTTTAACGTTGTAAAACTTTCAGCGACGGATGTCTTGGCTCCCACAACGATGAAGAACGCAGCGAAATGCGATACGTCTTGCGACTTGCAGAATCCAGTGAATCATCAAAACTTTGAACGCACCTTGCGCTTCCGGGTTACTCCTGGGAGCATGCTTGTCGGAGTGTCTGTTGACACCACTCGCCCCCCGCCCCCTCTCCTCCCTCGGGAGAGAGGGGTCGCGTGGGCGGACTCTGAGTGTTCCGGAGCATCCCACGCTCCGAGTGCACCAAATCTCGTGAACGAAGCCTCTCGCG-CCCTGCCGCACAAGAGTTGTTGACGGCGTTCGCTTCGGCGGCGACTCTCGACTCACGAAACGTGCGCGCAGAGCCGCGGGCTTCTTCCGGCGCTCCAGAGAAGAACTGGAATCCGTACCACTTT

>LesB [organism=Lessonia spicata] [country=Chile: Castillo channel, Torpedo Island, Katalalixar National Reserve] internal transcribed spacer 1, partial sequence

ACCCCCCCGCTCTACAAATTGTCTGTGACGT-CGCCGTGGAAACTCCCTCGGAGGCGAGCGA-GCGATCGTCTAA---ACCCCGAGAAAGTGAAGCCGTTATGCGAAGTTGGGCGAGGGGCGCCTCGCCGAGGGTTTTTCTTTTCCCTTTCCCCTTCTTGTCTC-TTTTCTTCCCTTTTCGGGGATTTACGGGACGGGACGGGAAGGGTGAAGGAAGCTCTCGAACCAAAGCGCACCCCACTTTTCAACCCCATTAAACTCTGAATCTGAACTC-AAAGGGGGGCAGCGCTGTGCCGCGGCTCCCCCAACCTTTAACGTTGTAAAACTTTCAGCGACGGATGTCTTGGCTCCCACAACGATGAAGAACGCAGCGAAATGCGATACGTCTTGCGACTTGCAGAATCCAGTGAATCATCAAAACTTTGAACGCACCTTGCGCTTCCGGGTTACTCCTGGGAGCATGCTTGTCGGAGTGTCTGTTGACACCACTCGCCCCCCGCCCCCTCTCCTCCCTCGGGAGAGAGGGGTCGCGTGGGCGGACTCTGAGTGTTCCGGAGCATCCCACGCTCCGAGTGCACCAAATCTCGTGAACGAAGCCTCTCGCG-CCCTGCCGCACAAGAGTTGTTGACGGCGTTCGCTTCGGCGGCGACTCTCGACTCACGAAACGTGCGCGCAGAGCCGCGGGCTTCTTCCGGCGCTCCAGAGAAGAACTGGAATCCGTACCACTTT

>LesC [organism=Lessonia spicata] [country=Chile: Castillo channel, Torpedo Island, Katalalixar National Reserve] internal transcribed spacer 1, partial sequence

ACCCCCCCGCTCTACAAATTGTCTGTGACGT-CGCCGTGGAAACTCCCTCGGAGGCGAGCGA-GCGATCGTCTAA---ACCCCGAGAAAGTGAAGCCGTTATGCGAAGTTGGGCGAGGGGCGCCTCGCCGAGGGTTTTTCTTTTCCCTTTCCCCTTCTTGTCTC-TTTTCTTCCCTTTTCGGGGATTTACGGGACGGGACGGGAAGGGTGAAGGAAGCTCTCGAACCAAAGCGCACCCCACTTTTCAACCCCATTAAACTCTGAATCTGAACTC-AAAGGGGGGCAGCGCTGTGCCGCGGCTCCCCCAACCTTTAACGTTGTAAAACTTTCAGCGACGGATGTCTTGGCTCCCACAACGATGAAGAACGCAGCGAAATGCGATACGTCTTGCGACTTGCAGAATCCAGTGAATCATCAAAACTTTGAACGCACCTTGCGCTTCCGGGTTACTCCTGGGAGCATGCTTGTCGGAGTGTCTGTTGACACCACTCGCCCCCCGCCCCCTCTCCTCCCTCGGGAGAGAGGGGTCGCGTGGGCGGACTCTGAGTGTTCCGGAGCATCCCACGCTCCGAGTGCACCAAATCTCGTGAACGAAGCCTCTCGCG-CCCTGCCGCACAAGAGTTGTTGACGGCGTTCGCTTCGGCGGCGACTCTCGACTCACGAAACGTGCGCGCAGAGCCGCGGGCTTCTTCCGGCGCTCCAGAGAAGAACTGGAATCCGTACCACTTT