

Mylo *et al.*, 2021 - Plants

Name of primer	Sequence (5'-3')
p5 (forward, 18S, plant-specific)	CCTTATCAYTTAGAGGAAGGAG
u4 (reverse, 26S, universal)	RGTTTCTTTTCCTCCGCTTA

[illegible]

**Figure 1.2: Chromatogram of sequenced PCR-product, image created with Chromas 2.6.6 (Technelysium).**

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O_tomentosa_JF787069.1  GAAGGATCATTCGAAACCTGCCAGCAGAAAGACCCCGGAACATGTTTCCCATGAACACGGGGAGGGGGCCCTCT 80
O_megacantha_EU930377.1 GAAGGATCATTCGAAACCTGCCAGCAGAAAGACCCCGGAACATGTTTCCCATGAACACGGGGAGGGGGCCCTCT 80
O_schumannii_JF787004.1 -----TCGAAACCTGCCAGCAGAAAGACCCCGGAACATGTTTCCCATGAACACGGGGAGGGGGCCCTCT 80
MM3_p5  GAAGGATCATTCGAAACCTGCCAGCAGAAAGACCCCGGAACATGTTTCCCATGAACACGGGGAGGGGGCCCTCT 80
.....50.....60.....70.....80.....90.....100.....110.....120...

*****
O_tomentosa_JF787069.1  GCGCCCTCCCTGGCGCAACAAACAAACCCGGGGCGAACCGCGCCAAAGAACAGAACTAAAGGGCTCCCGCCCGGGCC 160
O_megacantha_EU930377.1 GCGCCCTCCCTGGCGCAACAAACAAACCCGGGGCGAACCGCGCCAAAGAACAGAACTAAAGGGCTCCCGCCCGGGCC 160
O_schumannii_JF787004.1 GCGCCCTCCCTGGCGCAACAAACAAACCCGGGGCGAACCGCGCCAAAGAACAGAACTAAAGGGCTCCCGCCCGGGCC 160
MM3_p5  GCGCCCTCCCTGGCGCAACAAACAAACCCGGGGCGAACCGCGCCAAAGAACAGAACTAAAGGGCTCCCGCCCGGGCC 160
.....130.....140.....150.....160.....170.....180.....190.....200...

*****
O_tomentosa_JF787069.1  GGTCCGCGGGCGGGGGGGGGGACCTGTCCCTACTTAAAACTAACGACTCTCGGCAACGGATATCTCGGCTCTCGCA 240
O_megacantha_EU930377.1 GGTCCGCGGGCGGGGGGGGGGACCTGTCCCTACTTAAAACTAACGACTCTCGGCAACGGATATCTCGGCTCTCGCA 240
O_schumannii_JF787004.1 GGTCCGCGGGCGGGGGGGGGGACCTGTCCCTACTTAAAACTAACGACTCTCGGCAACGGATATCTCGGCTCTCGCA 240
MM3_p5  GGTCCGCGGGCGGGGGGGGGGACCTGTCCCTACTTAAAACTAACGACTCTCGGCAACGGATATCTCGGCTCTCGCA 240
.....210.....220.....230.....240.....250.....260.....270.....280...

*****
O_tomentosa_JF787069.1  TCGATGAAGAAAGCTAGCGAAATCGGAACTTGGTGTGAATTCAGAAATCCCGTGAACCATCGAGTCTTTGAAGCCAAAGTT 320
O_megacantha_EU930377.1 TCGATGAAGAAAGCTAGCGAAATCGGAACTTGGTGTGAATTCAGAAATCCCGTGAACCATCGAGTCTTTGAAGCCAAAGTT 320
O_schumannii_JF787004.1 TCGATGAAGAAAGCTAGCGAAATCGGAACTTGGTGTGAATTCAGAAATCCCGTGAACCATCGAGTCTTTGAAGCCAAAGTT 320
MM3_p5  TCGATGAAGAAAGCTAGCGAAATCGGAACTTGGTGTGAATTCAGAAATCCCGTGAACCATCGAGTCTTTGAAGCCAAAGTT 320
.....290.....300.....310.....320.....330.....340.....350.....360...

*****
O_tomentosa_JF787069.1  GCGCCCGAAGCCTTCGGCCGAGGGGACGCTGTCCCTGGGCGTCAAGCATCGGCTCTCCCCCGCGCCCGGGGGGAAGG 400
O_megacantha_EU930377.1 GCGCCCGAAGCCTTCGGCCGAGGGGACGCTGTCCCTGGGCGTCAAGCATCGGCTCTCCCCCGCGCCCGGGGGGAAGG 400
O_schumannii_JF787004.1 GCGCCCGAAGCCTTCGGCCGAGGGGACGCTGTCCCTGGGCGTCAAGCATCGGCTCTCCCCCGCGCCCGGGGGGAAGG 400
MM3_p5  GCGCCCGAAGCCTTCGGCCGAGGGGACGCTGTCCCTGGGCGTCAAGCATCGGCTCTCCCCCGCGCCCGGGGGGAAGG 400
.....370.....380.....390.....400.....410.....420.....430.....440...

*****
O_tomentosa_JF787069.1  ATGATGGCCTCCCGTACCTAAACGGGCGGGCGTGGCTTAAACGGGAGCCCGGGGACGAGCTGACGGCGATTGGT 480
O_megacantha_EU930377.1 ATGATGGCCTCCCGTACCTAAACGGGCGGGCGTGGCTTAAACGGGAGCCCGGGGACGAGCTGACGGCGATTGGT 480
O_schumannii_JF787004.1 ATGATGGCCTCCCGTACCTAAACGGGCGGGCGTGGCTTAAACGGGAGCCCGGGGACGAGCTGACGGCGATTGGT 480
MM3_p5  ATGATGGCCTCCCGTACCTAAACGGGCGGGCGTGGCTTAAACGGGAGCCCGGGGACGAGCTGACGGCGATTGGT 480
.....450.....460.....470.....480.....490.....500.....510.....520...

*****
O_tomentosa_JF787069.1  GGTGGACGAGGCTTAGAGGCCCTGTGTCATCGGCTCGGCAAGCAGCCGCTCGGGGAAGGGCTCGTTGGACCTTAAG 560
O_megacantha_EU930377.1 GGTGGACGAGGCTTAGAGGCCCTGTGTCATCGGCTCGGCAAGCAGCCGCTCGGGGAAGGGCTCGTTGGACCTTAAG 560
O_schumannii_JF787004.1 GGTGGACGAGGCTTAGAGGCCCTGTGTCATCGGCTCGGCAAGCAGCCGCTCGGGGAAGGGCTCGTTGGACCTTAAG 560
MM3_p5  GGTGGACGAGGCTTAGAGGCCCTGTGTCATCGGCTCGGCAAGCAGCCGCTCGGGGAAGGGCTCGTTGGACCTTAAG 560
.....530.....540.....550.....560.....570.....580.....590.....600...

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O_tomentosa_JF787069.1  GTGTGCTGAAAAGCACAAACCGTTGCGACCCCAAGGTACGGCGGGGCTACCCGCTGAGTTTAAGCATATCAATAA----- 640
O_megacantha_EU930377.1 GTGTGCTGAAAAGCACAAACCGTTGCGACCCCAAGGTACGGCGGGGCTACCCGCTGAGTTTAAGCATATCAATAAGCGGA 640
O_schumannii_JF787004.1 GTGTGCTGAAAAGCACAAACCGTTGCGACCCCAAGGTACGGCGGGGCTACCCGCTGAGTTTAAGCATATCAATAAGCGGA 640
MM3_p5  GTGTGCTGAAAAGCACAAACCGTTGCGACCCCAAGGTACGGCGGGGCTACCCGCTGAGTTTAAGCATATCAATAAGCGGA 640
.....610.....620.....630.....640.....650.....660.....670.....680...

O_tomentosa_JF787069.1 ----- 655
O_megacantha_EU930377.1 GGAA----- 655
O_schumannii_JF787004.1 ----- 655
MM3_p5  GAAAAAAAAACWAA----- 655
.....690.....

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Figure 1.3: Alignment of the sample's ITS-region (MM3\_p5) to those of closely related species. Database accession numbers are given after each species name. Picture created with ClustalX ([www.clustal.org](http://www.clustal.org)).