

Supplementary Figures

***Terfezia claverryi* MAT locus characterization uncovers evolutionary insights about sexual reproduction of Pezizomycetes and reveals mating type dynamics in mycorrhizal plants.**

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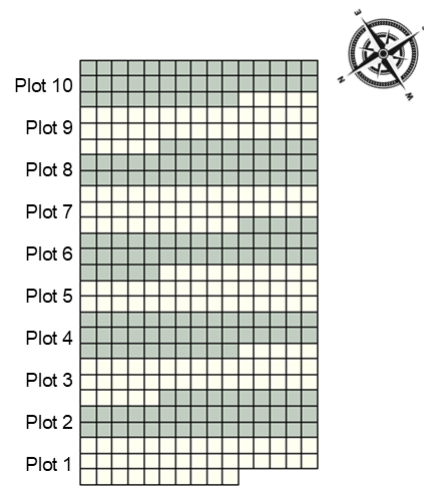


Figure S1. Graphical representation of the sampling field, showing ten different plots where root and soil samples were collected.

Terfezia clavaryi strain Ter1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence
Sequence ID: [MG845398.1](#) Length: 703 Number of Matches: 1

Range 1: 8 to 577 [GenBank](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
989 bits(535)	0.0	560/571(98%)	6/571(1%)	Plus/Plus
Query 7	GGGACTGCGGAGGACATTACTGAAAACT-TATCAAGttttttATACCCTTTGT---	62		
Sbjct 8	GGGACTGCGGA-GACATTACTGAAAACTATATCAAGTTTTTATACCCTTTGTTTAC	66		
Query 63	CTACCTATTGCTTCCACTGGACAGGTTTCACCTTGTTGGAACTCTGGCTTGTGTAA	122		
Sbjct 67	CTACCTATTGCTTCCACTGGACAGGTTTCACCTTGTTGGAACTCTGGCTTGTGTAA	126		
Query 123	AAGCACCTGCCAGAGAGTTGCTGGTGGGAAGAACATTACTAAAACTTGATTTTaaaa	182		
Sbjct 127	AAGCACCTGCCAGAGAGTTGCTGGTGGGAAGAACATTACTAAAACTTGATTTTAAAA	186		
Query 183	aaaTACAATGCTGAATAATTTCTTTAATGAAATAAACTTTCAACAACGGATCTCTAG	242		
Sbjct 187	AAATACAATGCTGAATAATTTCTTTAATGAAATAAACTTTCAACAACGGATCTCTAG	246		
Query 243	GCTCTTGATCGATGAAGAACGACAGTAAATGCGATAAGTAATGTGAATTGCAGAACTC	302		
Sbjct 247	GCTCTTGATCGATGAAGAACGACAGTAAATGCGATAAGTAATGTGAATTGCAGAACTC	306		
Query 303	GTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCATAGGGCATGCCTG	362		
Sbjct 307	GTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCATAGGGCATGCCTG	366		
Query 363	TCTGAGCGTCAGCTCCCCCTCACTCAAGTATCCTTTCATAAGAACTTGATTGCTTTGG	422		
Sbjct 367	TCTGAGCGTCAGCTCCCCCTCACTCAAGTATCCTTTCATAAGATACTTGATTGCTTTGG	426		
Query 423	AGAAGTAACGTGTATTAAGTTGCCCTCCAGAAATTTATAGGCAGTATTGTTGTACTTG	482		
Sbjct 427	AGAGGTAACGTGTATTAAGTTGCCCTCCAGAAATTTATAGGCAGTATTGTTGTACTTG	486		
Query 483	AACCAGACGTAATAATAATAAAATCGTTTGTGTAATGAATGATTGTACTTGCCCTCA	542		
Sbjct 487	AACCAGACGTAATAATAATAAAATCGTTTGTGTAATGAATGATTGTACTTGCCCTCA	546		
Query 543	CTCCACCCATTTTATTTTGGG-GACCTCAG	572		
Sbjct 547	CTCCACCCATTTTATTTTGGGTGACCTCAG	577		

Figure S2. Most significant alignment for the Tc1705 strain amplified with ITS1F-ITS4 primers, obtained from BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

Terfezia claverryi isolate J027 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence
Sequence ID: [MK910033.1](#) Length: 657 Number of Matches: 1

Range 1: 15 to 621 [GenBank](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1079 bits(584)	0.0	601/608(99%)	5/608(0%)	Plus/Plus
Query 1	ACAAGGTTTCCGTAGGTGAACCTGCGG-AGGATCATTACTGAAAACTATATCAAGtttt	59		
Sbjct 15	ACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGAAAACTATATCAAGTTTT	74		
Query 60	tttATACCTATTGTTTACCTACCTATTGCTTCCACTGGACAGGTTTACCTTGTGTGG	119		
Sbjct 75	TTTATACCTATTGTTTACCTACCTATTGCTTCCACTGGACAGGTTTACCTTGTGTGG	134		
Query 120	AACCCCTGGCTCGTGTGAAAAGCACCTACCAGAGAGTTGCCGGTGGTAAGAACTATTT	179		
Sbjct 135	AACCCCTGGCTCGTGTGAAAAGCACCTACCAGAGAGTTGCCGGTGGTAAGAACTATTT	194		
Query 180	ACCAAACTTGATTTTTT---aaaaaaaTACAATGCTCGAATAATTTCCCTTAATGAAA	236		
Sbjct 195	ACCAAACTTGATTTTTTAAAAAAAAAACAATGCTCGAATAATTTCCCTTAATGAAA	254		
Query 237	TAAAACTTCAACAACGGATCTCTAGGCTCTTGCAATCGATGAAGAACGCAGTGAAATGCG	296		
Sbjct 255	TAAAACTTCAACAACGGATCTCTAGGCTCTTGCAATCGATGAAGAACGCAGTGAAATGCG	314		
Query 297	ATAAGTAATGTGAATTGCAGAATCTCGTGAATCATTGAATCTTTGAACGCACATTGCGCC	356		
Sbjct 315	ATAAGTAATGTGAATTGCAGAATCTCGTGAATCATTGAATCTTTGAACGCACATTGCGCC	374		
Query 357	CTTTGGTATTCATAGGGCATGCCTGTCTGAGCGTCAGCTCCCCCTCACTCAAGTATTCT	416		
Sbjct 375	CTTTGGTATTCATAGGGCATGCCTGTCTGAGCGTCAGCTCCCCCTCACTCAAGTATTCT	434		
Query 417	TTAATAAGATACTTGGATTGCTTTGGAGATGTAACGTGTATTAAAGTTGCCCTCCAGAAA	476		
Sbjct 435	TTAATAAGATACTTGGATTGCTTTGGAGATGTAACGTGTATTAAAGTTGCCCTCCAGAAA	494		
Query 477	TTCATAGGCAGTATGGTTTGACTTGAACCTAGACGTAATAATAATAAAATCGTTTGT	536		
Sbjct 495	TTCATAGGCAGTATGGTTTGCTTGAACCTAGACGTAATAATAATAAAATCGTTTGT	553		
Query 537	GGGTATGATTGATTGTAATGCTTGCCTCAACTCCACCCATTTTATTTTGGGTGACCTCAGAT	596		
Sbjct 554	GGGTATGATTGATTGTAATGCTTGCCTCAACTCCACCCATTTTATTTTGGGTGACCTCAGAT	613		
Query 597	CAGGTAGG 604			
Sbjct 614	CAGGTAGG 621			

Figure S3. Most significant alignment for the TcLlano strain amplified with ITS1F-ITS4 primers, obtained from BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

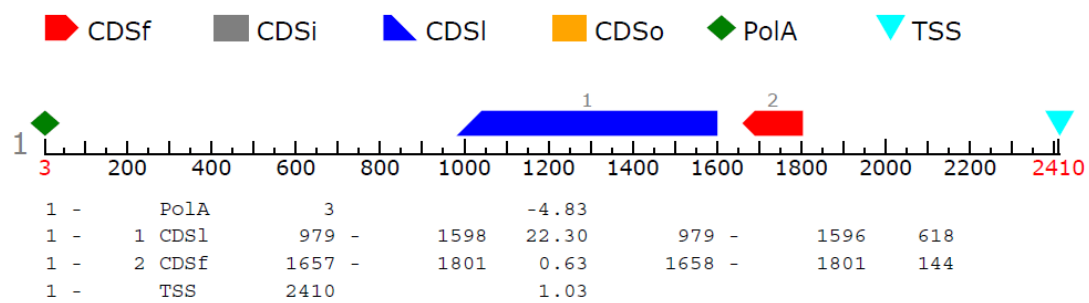


Figure S4. Prediction of TcMAT1-1 idiormorph based on the Tc1705 amplicon sequence obtained using primers 453-455.

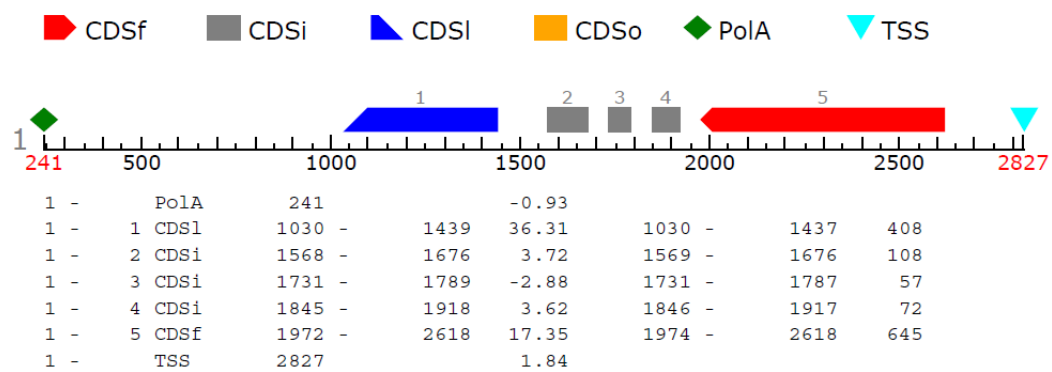


Figure S5. Prediction of TcMAT1-2 idiormorph based on the TcLlano amplicon sequence obtained using primers 453-455.

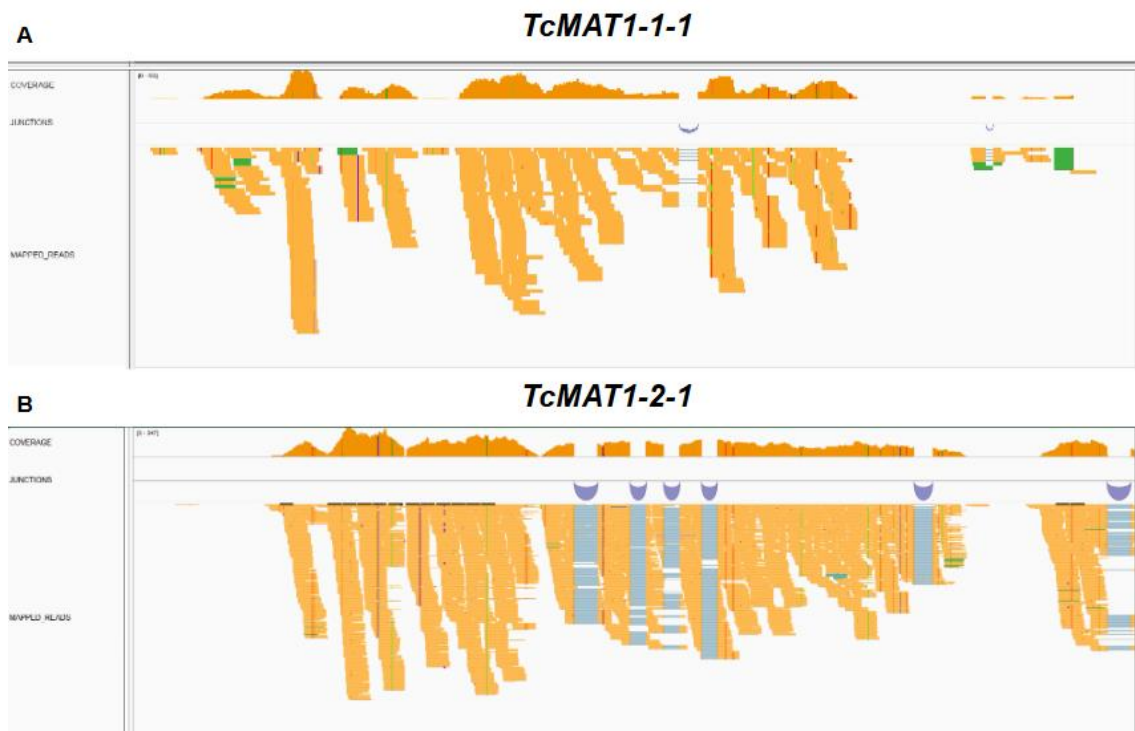


Figure S6. Visualization of RNA-seq reads from well-watered and drought-stressed *H. almeriense* $\times$ *T. claveryi* mycorrhizal roots (SRA ID: SRP272077; Marqués-Gálvez et al. 2021) mapped against the *TcMAT1-1-1* and *TcMAT1-2-1* amplicon sequences.

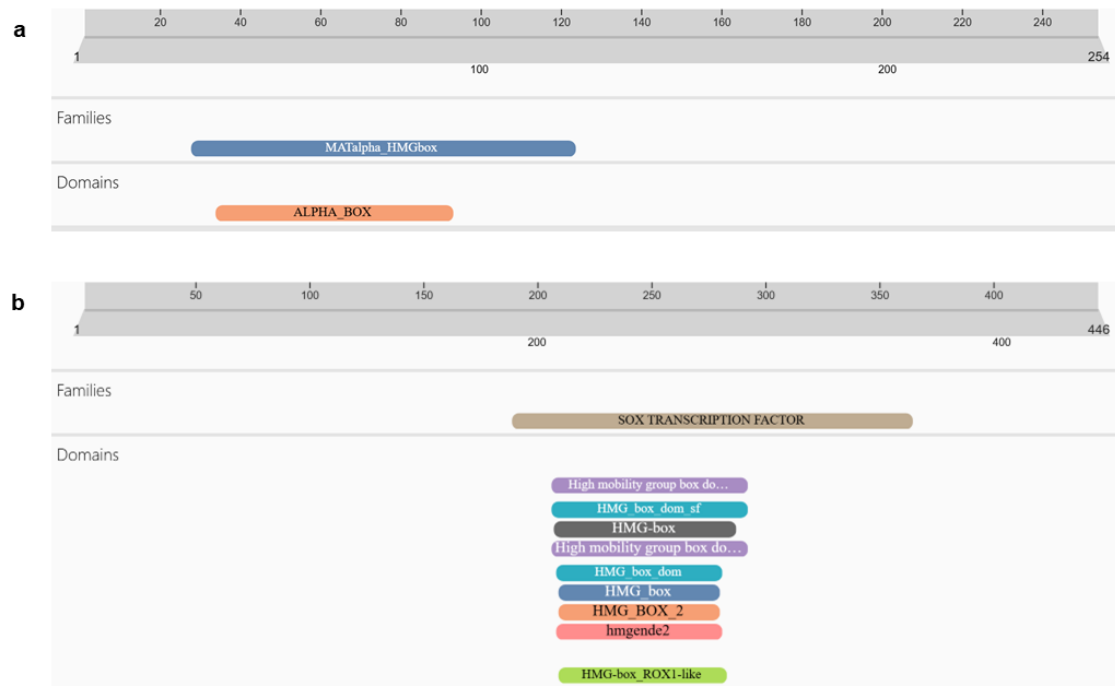


Figure S7. Protein domain analysis of the TcMAT1-1-1 (a) and TcMAT1-2-1 (b) protein sequences predicted by InterPro.