

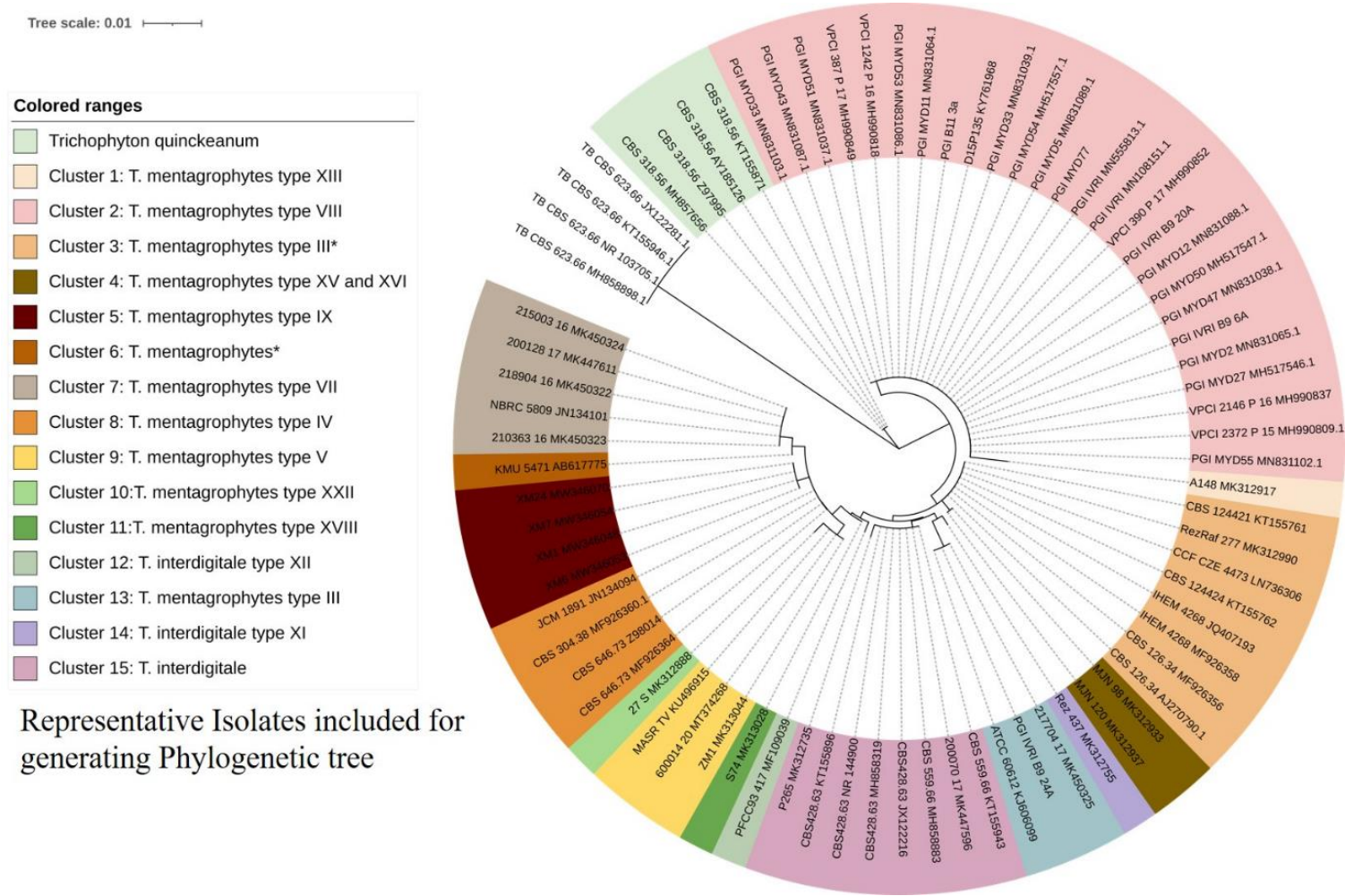
[illegible]

76	490	Tm type VIII	Ti	JN133999	Ti	KM678182	Ti	JF731044						
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79	VPCI 2004/P/16	Tm type VIII	Ti	MH990828										
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85	CBS 646.73_ATCC 28145_Type (Tm)	Tm type IV	Tv/Av	MF926364/Z98014			Tv	MF898389	Tv	MF893245				
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88	CCF<CZE>:4473	Tm type III*	Ti	LN736306										
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90	AF506034	Tm type III	Ab	AF506034										
91	JCM 1891	Tm type IV			Ti	KM678058	Av	JF731120	Av	AB075330				
92	CBS 232.76	Ti	Tm	KT155838			Tm	KT155518	Tm	KT155177				
93	CBS 110.65	Ti	Tm	MH858507			Tm	KT155378	Tm	MH870141 / KT155001				
94	CBS 559.66	Ti	Tm	MH858883/ KT155943			Tm	KT155588	Tm	MH870542 / KT155287				
95	CBS 113880	Ti	Tm	KT155711			Tm	KT155406	Tm	KT155030				
96	CBS 449.74	Ti	Tm	KT155904			Tm	KT155567.1	Tm	KT155249				
97	CBS 117723	Ti	Tm	KT155725			Tm	KT155418	Tm	KT155047				
98	CBS 119447	Ti	Tvio	KT155733			Tvio	KT155429	Tvio	KT155058				
99	CBS 124424	Tm type III*	Ti	KT155762			Ti	KT155454	Ti	KT155089				
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101	CBS 124401	Tm type III*	Tb	KT155753			Tb	KT155446	Tb	KT155080				
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103	CBS 120356	Tm type III*					Ti	KT155437	Ti	KT155068				
104	CBS 124426	Tm type III*	Ti	KT155764			Ti	KT155456	Ti	KT155091				
105	CBS 304.38 Type™	Tm type IV	Ti	MF926360					Ti	MF893229				
106	2642	Tm type III	Ti	FM986750										
107	MASR	Tm type V	Tver	KU496915										
108	Ahv-331	Tm type VIII	Ti	KT192500										
109	RV 27961	Tm type IV	Av	AF170453										
110	KMU 5471	Tm*	Av	AB617775										
111	XQ3_8	Tm type IX	Ti	KU315316										
112	NBRC 5974	Ti	Tm			KM678206	Tm	JF731087						
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114	CBS 126.34 Type (Tm)	Tm	Tm/Ti	MF926356/AJ270790										
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116	CBS 31 8.56	Tq	Tm/Ab	MH857656/KT155871/AY185126/Z97995	Tm	KM678083	Tm	KT155546/KU378223	Tm	MH869197/KT155215/KU205264	Tm	KM387110		

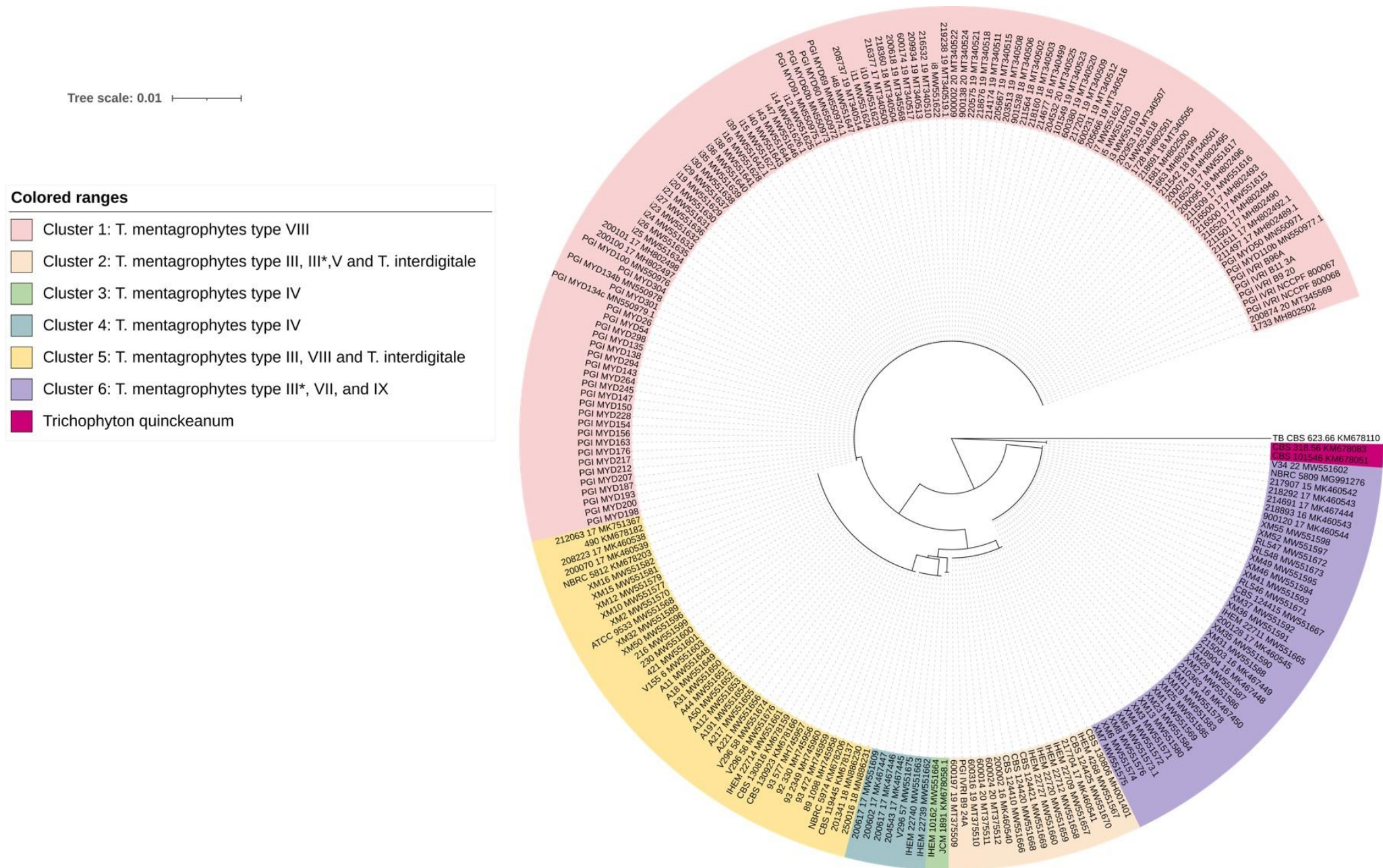
Tm- *Trichophyton mentagrophytes*, Ti- *Trichophyton interdigitale*, Tindo- *Trichophyton indotineae*, Av- *Arthroderma vanbreuseghemii*, Tv- *Trichophyton vanbreuseghemii*, Tb- *Trichophyton benhamiae*, Tver- *Trichophyton verrucosum*, Tvio- *Trichophyton violaceum*, Ab-*Arthroderma benhamiae*

Figures-

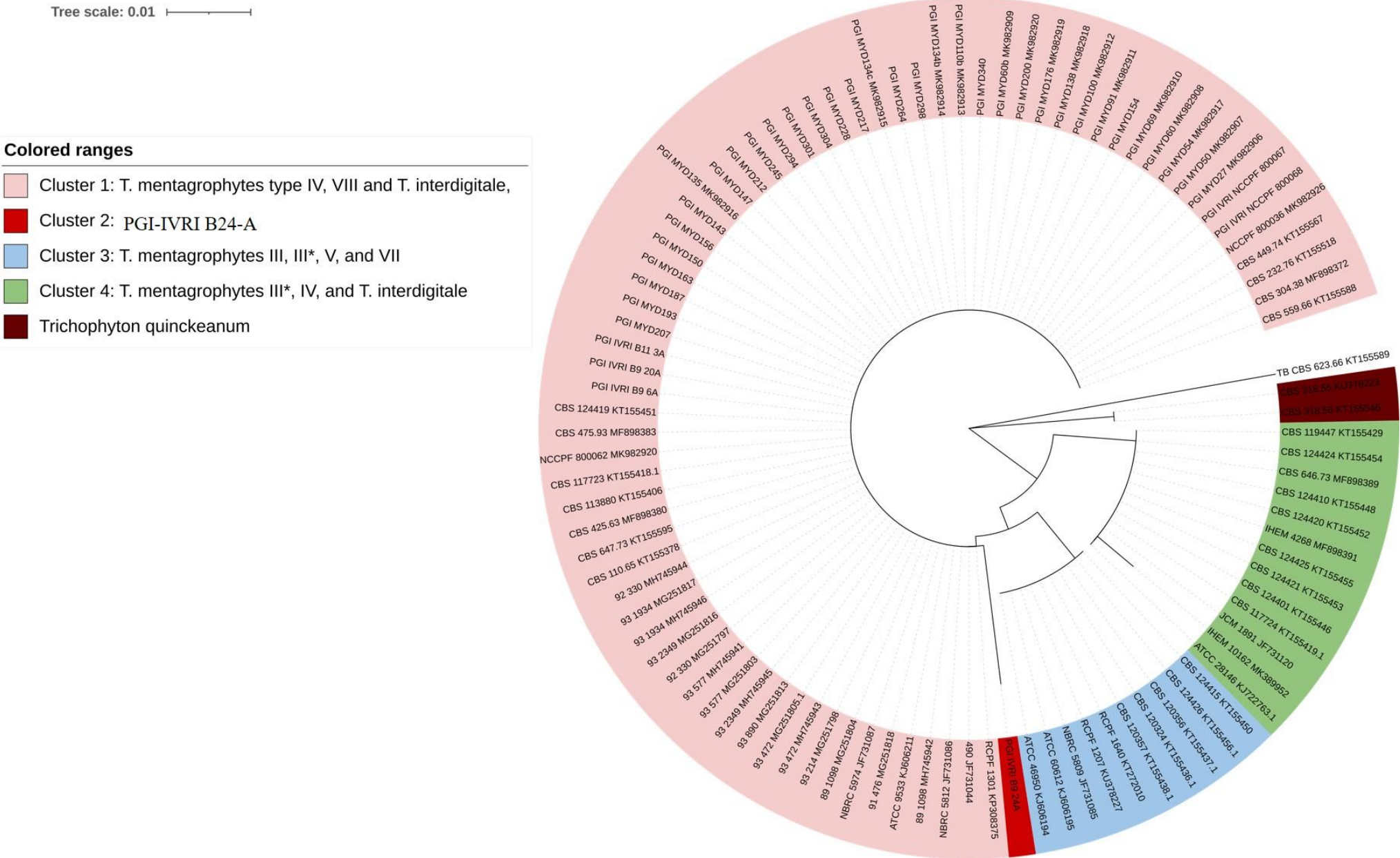


Representative Isolates included for generating Phylogenetic tree

Supplementary Figure S1: Phylogenetic tree based on ITS sequences Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates). The evolutionary distances were computed using the Kimura 2-parameter method. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA X.



Supplementary Figure S2: Phylogenetic tree based on TEF sequences Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates). The evolutionary distances were computed using the Kimura 2-parameter method. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA X.

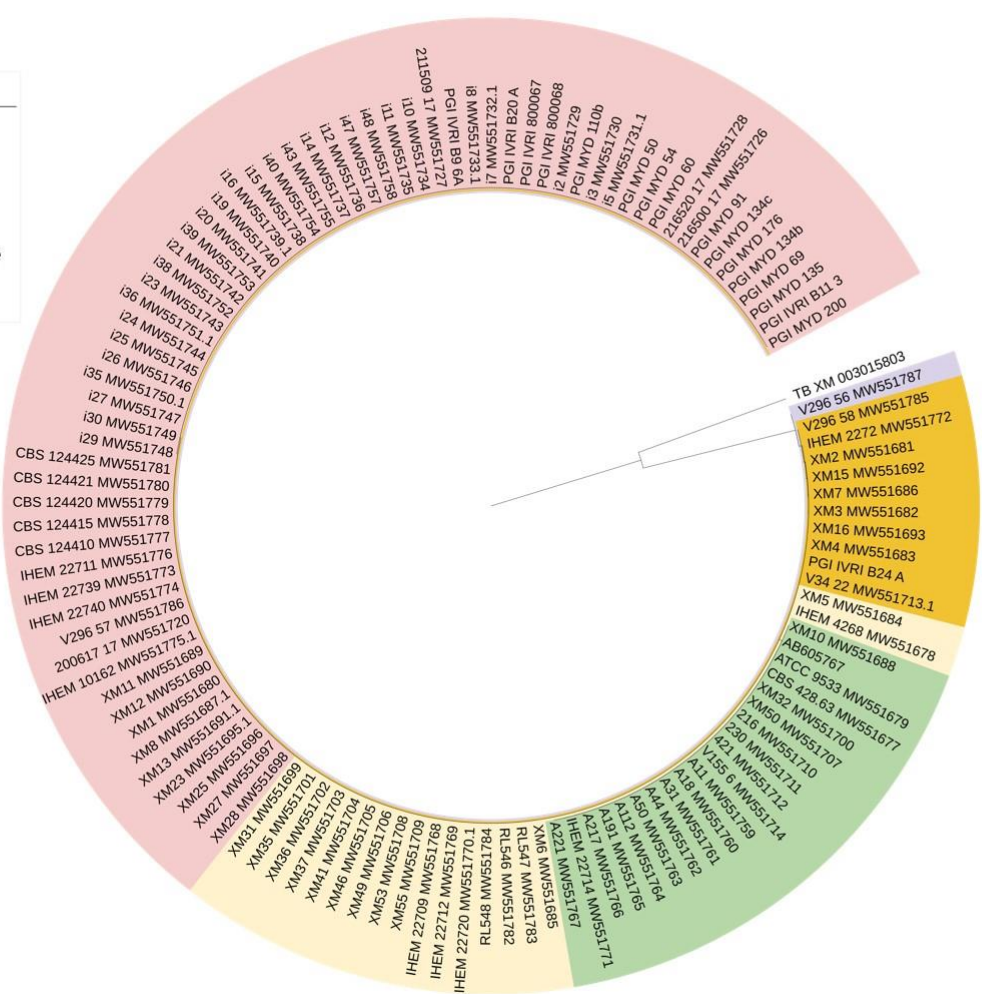


Supplementary Figure S3: Phylogenetic tree based on BT sequences Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates). The evolutionary distances were computed using the Kimura 2-parameter method. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA X.

Tree scale: 1

Colored ranges

- Cluster 1: T. mentagrophytes type VIII
- Cluster 2: T. mentagrophytes type III, III*, IV, IX
- Cluster 3: T. interdigitale
- Cluster 4: T. mentagrophytes type III, III*, IX and T. interdigitale
- Cluster 5: T. interdigitale



Supplementary Figure S6: Phylogenetic tree based on HMG sequences Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates). The evolutionary distances were computed using the Kimura 2-parameter method. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA X